



UNIVERSIDAD DE GRANADA

DOCTORAL THESIS

Doctoral Programme in Information and Communication Technologies

Intelligent Monitoring of Diabetes Mellitus by means of Mobile and Wearable Devices

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September 29, 2024

Editor: Universidad de Granada. Tesis Doctorales
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ISBN: 978-84-1195-693-2
URI: <https://hdl.handle.net/10481/102532>

Acknowledgments

With all the technical complexity, time, and effort that completing this doctoral thesis has required, I can say with certainty that writing this section has been one of the most challenging. The mere thought of someone who has contributed directly or indirectly to carrying out this titanic project fills me with fear and sadness. But I will not let these feelings paralyze me. I will make a profound effort to present my deepest gratitude as fairly as possible to each person who has helped me carry this project forward.

I thank God for giving me the confidence to keep going, for knowing that He guides my path and that despite everything, He is good, just, and faithful. Without His support, not only this thesis but nothing in my life would have been possible.

I thank Claudia and Oresti, who, more than my supervisors, have become my friends. Thank you for placing your trust in me for this project, for all your unconditional sacrifice, for giving me your valuable time beyond what the rules require, and for showing me how to gradually carve out a path in the Spanish academic environment.

I also thank the entire team of clinical and interdisciplinary experts who have been part of this research. The results would not have been the same without your support and contributions. Forming a multidisciplinary team has helped ensure that the results are not purely technical but applicable in the real world. To Mariola, Manolo, Pablo, Miguel, and Jonatan, thank you for always being available to me, your quick responses, and your commitment to improving the quality of life of patients with type 1 diabetes mellitus.

I would also like to share the credit for this work and thank the students who have contributed through their undergraduate or master's projects.

I am deeply grateful to my entire family. Thank you always for your support, trust, and words of encouragement. For those sayings, "Don't worry; in the end, you always pull through." It's a fact that I wouldn't be where I am today without you all. Thank you to my little girl, Siana, because despite being so young, you always understand that your dad had to spend time away from you to move forward with these projects and provide you with a better life and future. Thank you to Ana Jailén for her constant support since this project was in its conceptual stage and for taking on the household responsibilities in my absence. Thank you to my mother, Zermaida, for always being interested in all my projects, for praying incessantly for me before God, and for encouraging me in each of the "final stretches." Will this be the last one, my dear old lady? Probably not, but I always think of you in each of them. Thank you to my father, Ciro, who, although no longer with me at this stage, his teachings and life advice often resonate in my mind and help me make decisions. Thank you to my siblings, Mayelín and Edel, for always looking out for and caring for me throughout my life. Thanks to my cousins, especially Diley, Daiyana, and Osbel, for welcoming me into their homes so warmly many times and always being willing to carry out essential tasks to help move this project forward.

Thank you to María Daniela for supporting me in the final stage of this project and for your words and advice that brightened my soul. Thank you for being there.

Thank you to the staff at the Hospital Universitario San Cecilio in Granada, especially the Clinical Unit of Endocrinology and Nutrition, for opening your doors to me so I could better understand the daily life of patients with type 1 diabetes, the struggles they face, as well as the effort the healthcare staff puts in to improve the quality of life for those who suffer from this disease.

Thanks to the staff at CIDODE of the University of Granada for managing my research stays, especially to Domingo Barrera, for his unconditional support at all times, for clarifying so many doubts, and for all his guidance and advice.

It may sound like a cliché, but I am immensely grateful to each of the teachers and professors who have contributed to my education throughout all this time, providing academic knowledge and lifetime lessons that have shaped the person I am today.

Thanks to my landlords, Ana, Paco, and Javier, for trusting in me and my word even when you didn't know me. The world needs more people like you.

Lastly, and no less important, thanks to all my brothers and sisters in faith and friends, both in Cuba and Spain, who have played a part in this work, sometimes without even realizing it. I am deeply grateful to you all.

Ciro

Agradecimientos

Con toda la complejidad técnica, tiempo y esfuerzo que ha conllevado realizar esta tesis de doctorado puedo decir con seguridad que elaborar esta sección ha sido una de las más complejas. El mero hecho de pensar que alguien que ha aportado de manera directa o indirecta a llevar a cabo este titánico proyecto me llena de temor y tristeza. Pero no dejaré que estos sentimientos me paralicen y hago un esfuerzo profundo por presentar lo más justo posible mi más profundo agradecimiento por cada uno de los seres que me ha ayudado a llevar adelante este proyecto.

Agradezco a Dios, por darme la confianza de seguir adelante, por saber que Él guía mi camino y que a pesar de todo Él es bueno, justo y fiel. Sin su sustento, no solo esta tesis, sino que no hubiese podido lograr nada en la vida.

Agradezco a Claudia y Oresti, más que mis directores se han convertido en mis amigos. Gracias por poner vuestra confianza en mí para este proyecto, gracias por todo vuestro sacrificio incondicional, gracias por brindarme su preciado tiempo más allá de lo que establecen las normas y gracias por mostrarme como abrirme camino poco a poco en el ambiente académico español.

Agradezco también a todo el equipo de expertos clínicos y de otras disciplinas que han formado parte de esta investigación, sin vuestro apoyo y aporte los resultados no serían los mismos. La conformación de un equipo multidisciplinar ha ayudado a que los resultados no sean puramente técnicos, sino que se revistan de aplicabilidad en el mundo real. A Mariola, Manolo, Pablo, Miguel y Jonatan gracias por siempre estar disponibles para mí, por sus prontas respuestas siempre y vuestra disposición para mejorar el estilo de vida de los pacientes con diabetes mellitus tipo 1.

También me gustaría compartir el crédito de este trabajo y agradecer a estudiantes que han contribuido a través de sus trabajos de fin de grado o de máster.

Agradezco profundamente a toda mi familia. Gracias siempre por vuestro apoyo, por su confianza y palabras de aliento siempre, por esos “no te preocupes, si al final tu siempre lo sacas todo adelante”. Es un hecho que sin ustedes no podría haber llegado a donde estoy hoy. Gracias a mi niña Siana, porque a pesar de ser tan pequeña siempre comprendes que tu papá ha tenido que estar tiempo lejos de ti para lograr llevar adelante estos proyectos y poder brindarte una vida y un futuro mejor. Gracias a Ana Jailén por su apoyo siempre desde que este proyecto estaba en etapa de concepción, y por asumir las responsabilidades de un hogar en mis ausencias. Gracias a mi madre Zermaida por siempre estar interesada en todos mis proyectos, por orar incesantemente por mí ante Dios y por alentarme en cada una de las “rectas finales” ¿será la última esta mi vieja? Seguramente no, pero siempre te recuerdo cuando estoy en cada una de ellas. Gracias a mi padre Ciro, que, aunque ya no estuvo conmigo en esta etapa, muchas veces sus enseñanzas y consejos de vida resuenan en mi mente y me ayudan a tomar decisiones. Gracias a mis hermanos Mayelín y Edel, por siempre estar pendientes de mí y cuidarme a lo largo de mi vida. Gracias a mis primos, en especial a Diley, Daiyana y Osbel por acogerme

tantas veces en sus hogares de una manera tan cálida y siempre estar dispuestos a realizar gestiones imprescindibles para llevar a cabo este proyecto.

Gracias a María Daniela, por apoyarme en la etapa final de este proyecto, por sus palabras y consejos que me alegran el alma, gracias por ser y estar.

Gracias al personal del Hospital Universitario San Cecilio de Granada, en especial al de la Unidad Clínica de Endocrinología y Nutrición, por abrirme sus puertas para que pudiese comprender mucho mejor cómo es el día a día de los pacientes diabéticos tipo 1, las luchas que enfrentan, así como el esfuerzo que lleva a cabo el personal sanitario para mejorar la calidad de vida de los que padecen esta enfermedad.

Gracias al personal del CIDODE de la Universidad de Granada por la gestión de mis estancias de investigación, en especial a Domingo Barrera, por su apoyo incondicional a toda hora, por tantas dudas aclaradas, por toda su guía y consejos.

Puede sonar como un cliché, pero agradezco mucho a cada uno de los maestros y profesores que han aportado a mi formación a lo largo de todo este tiempo, no solo aportando conocimientos académicos, sino lecciones de vida que han contribuido a ser la persona que soy hoy.

Gracias a mis caseros Ana, Paco y Javier. Por confiar en mí y mi palabra aún cuando no me conocían, el mundo necesita de su ejemplo.

Por último, y no menos importante, gracias a todos mis hermanos de fe y amigos, tanto en tierras cubanas como españolas, que han aportado parte en este trabajo, a veces incluso sin darse cuenta de ello. A todos les estoy muy agradecidos.

Ciro

Abstract

Introduction

Type 1 diabetes is primarily characterized by a severe issue in insulin secretion. Patients with this condition must rely on external sources of insulin to regulate their blood glucose levels, a task complicated by the high variability in glucose patterns across different individuals. These variations are influenced by lifestyle, metabolism, and sex, among others. Consequently, it is common for patients with type 1 diabetes to use continuous glucose monitoring devices to better manage their condition, as they provide real-time information about blood glucose levels. However, having an application that predicts future glucose levels would be valuable, helping patients take preventative measures to avoid complications arising from out-of-range glucose levels. Predicting these levels is inherently complex. On the one hand, general prediction models, which use continuous glucose data from multiple patients for training and evaluation, fail to fully capture the individual differences in glucose patterns. On the other hand, developing personalized prediction models for each patient is impractical, as it requires a large amount of continuous glucose data, meaning new patients would have to wait for an extended period before receiving accurate predictions. Additionally, there are very few open-access datasets with a sufficient number of patients and long-term continuous glucose measurements to support robust experimentation.

In this context, the goal of this thesis is to investigate intelligent techniques to support the management of type 1 diabetes mellitus in real-world settings by leveraging continuous glucose measurement data collected from mobile and wearable devices. To achieve this main goal, the following specific objectives are set: create an extensive, long-term, open-access longitudinal dataset consisting of blood glucose level measurements collected through continuous glucose monitoring sensors to develop new intelligent models; comprehend the capacity of existing evaluation methods for estimating the performance of blood glucose level prediction models in real-world settings, identify patient groups with common characteristics based on patients' longitudinal blood glucose level measurements; and evaluate the performance of group-based blood glucose level prediction models in real-world settings. For this evaluation, three types of prediction models will be developed and compared: general, group-based, and personalized prediction models, using both clinical and non-clinical evaluation metrics. This will determine the feasibility of the proposed approach for its use in blood glucose prediction in realistic settings.

To address this problem, a dataset with a sufficient number of continuous glucose measurements and an adequate number of patients is first collected, ensuring a solid foundation for the proposed experimentation. Next, general blood glucose prediction models are developed, where training and evaluation are performed using continuous glucose data from all patients in the dataset. This allowed for the identification of the most appropriate evaluation strategies for these types of prediction models. Once these strategies are understood, patient groups are cre-

ated using various unsupervised learning algorithms. Given the various configurations tested, group sizes, dataset versions, and algorithms, the clustering results are extensive. The most promising results are selected using an internal clustering evaluation metric, supplemented by a procedure developed in this thesis, which clinical experts then review to identify the most appropriate solution. Once the groups are defined, the same experimentation for general prediction models is replicated within the groups to evaluate the comparative performance between the general and group-based prediction models. Additionally, patients within each group are selected to develop personalized prediction models, allowing further comparison with the group-based prediction models and determining whether the latter represents a viable intermediate solution between general and personalized prediction models. Each of these steps and the final contributions of the thesis are detailed below.

A novel longitudinal dataset

This thesis contributes with T1DiabetesGranada, an open longitudinal dataset that provides continuous blood glucose measurements and includes demographic and clinical information about the patients. The dataset comprises 257 780 days of measurements collected over four years from 736 type 1 diabetes patients in Granada, Spain. This dataset surpasses the current state of the art by being one of the most temporally extensive and comprehensive open datasets of continuous blood glucose measurements, driving the development of new artificial intelligence models for characterizing and predicting blood glucose levels.

Understanding evaluation methods for prediction models

General prediction models based on artificial neural networks are developed for blood glucose prediction, and they are trained and tested using continuous glucose data from all patients. These included prediction algorithms like linear regression and more advanced neural network architectures such as LSTM and CNN. Predictions are made using two hours of historical values taken every 15 minutes, with six different prediction horizons ranging from 30 to 240 minutes. Clinical metrics (such as Clarke error grid analysis) and non-clinical metrics (RMSE, MSE, MAE, and MAPE) are used to evaluate the prediction models' performance, applied to the full glucose range and independently to clinically relevant ranges. The results showed slightly better performance from linear prediction algorithms than more complex prediction algorithms (LSTM and CNN), likely due to the concentration of data in a narrow glucose range (100-200 mg/dL), favoring simpler prediction models. The conclusion is that a holistic approach is key to properly evaluating these prediction models. Visualizations such as Clarke error grids help analyze the geometry of the predictions while evaluating metrics within specific glucose ranges, prevent biased conclusions, and more accurately reflect the prediction models' behavior in hypoglycemic and hyperglycemic ranges, which pose the most significant health risks.

Patient group identification

A key aspect of this thesis is identifying groups of patients with similar glucose patterns using unsupervised learning algorithms such as K-means, Gaussian Mixture Models, hierarchical clustering, and self-organizing maps. Features extracted from continuous glucose measurements (mean, standard deviation, minimum, and maximum) at different times of the day are used to represent each patient during the clustering process. The elbow method and dendrogram

analysis are applied to estimate the number of groups. The most promising results are selected using the Silhouette Coefficient and a customized method and are then presented to clinical experts. Ultimately, six groups with distinct glucose patterns are identified, which not only aid in the development of prediction models but also have the potential to influence medical care. These groups provide endocrinologists with the opportunity to design personalized treatments based on patient profiles. With continuous glucose monitors, new patients can be relatively quickly assigned to one of these groups, facilitating a more targeted therapeutic approach from the early stages of monitoring. The process also applies to patients with longer monitoring histories, provided their data is accessible.

Group-based prediction model evaluation

Once the patient groups are defined, blood glucose prediction models are developed for each group using the same experimental procedure and prediction algorithms applied to the general prediction models. To provide an additional point of comparison, personalized prediction models are created for a sample of patients, selecting those whose blood glucose is best and worst predicted by the group-based prediction models. These personalized prediction models are individually trained with each patient's data, replicating the training procedure applied to the general and group-based prediction models. The results showed that group-based prediction models outperformed general prediction models for certain patient groups and under specific conditions, such as in groups representing patients with better glucose control. In these cases, improvements in clinical metrics assessing the percentage of measurements within clinically acceptable zones became more pronounced as the prediction horizon increased, suggesting that these prediction models can capture long-term patterns more effectively. While improvements in hypoglycemic ranges are less significant, some improvements are observed in groups of patients with more frequent hypoglycemic events, particularly with LSTM and CNN prediction models. When comparing personalized prediction models to group-based prediction models, although the former offered improvements in some instances, they did not always outperform the group-based prediction models, with improvements seen in only 37.98% of cases. Therefore, group-based prediction models offer a balance between accuracy and practicality, outperforming many general prediction models and requiring less data for use in new patients, making them an effective solution for glucose prediction in type 1 diabetes patients.

Conclusions

Group-based prediction models are a promising intermediate solution between general and personalized prediction models for predicting blood glucose levels in type 1 diabetes patients. These prediction models outperform general prediction models, particularly for patients with better glucose control and higher proportions of hyperglycemia, balancing accuracy and practicality while requiring less data for implementation in new patients. Although personalized prediction models performed better in certain cases, group-based prediction models proved more effective in most situations, establishing themselves as a viable alternative for optimizing glucose prediction and providing personalized medical care in managing type 1 diabetes. The key contributions of this thesis include:

1. A large, multimodal longitudinal dataset of continuous glucose measurements collected using continuous glucose monitors, along with demographic and clinical information about type 1 diabetes patients.

2. A robust experimental methodology for applying prediction models to an extensive longitudinal dataset of continuous glucose measurements.
3. Three sets of prediction models for continuous glucose levels using artificial neural networks, namely general, group-based, and personalized prediction models.
4. A methodology for creating patient groups based on their continuous glucose measurements.
5. Various patient groups that enable endocrinologists to design personalized treatments based on unique patient profiles.
6. A codebase to support all experimental methodologies processes and the creation of the dataset, enabling reproducibility and scalability for future research.

Resumen

Introducción

La diabetes tipo 1 se caracteriza fundamentalmente por un severo problema de secreción de insulina. Los pacientes con diabetes tipo 1 se ven obligados a utilizar una fuente externa de insulina para equilibrar sus niveles de glucemia en sangre, que es una tarea muy compleja debido a la alta variabilidad de patrones en diferentes pacientes, influenciada por factores como el estilo de vida, metabolismo, o sexo, entre otros. Es por ello que es una práctica común que muchos pacientes con diabetes tipo 1 usen dispositivos de monitorización continua de glucemia para gestionar mejor la enfermedad, ya que les permite conocer los niveles de glucemia en todo momento. Sin embargo, contar con una aplicación que prediga niveles de glucemia sería muy útil, ayudando a los pacientes a tomar medidas preventivas y evitar complicaciones por niveles fuera de rango. La predicción de estos niveles de glucemia en sangre es una tarea compleja. Por un lado, los algoritmos de predicción generales, que utilizan datos de mediciones continuas de glucemia de múltiples pacientes para entrenar y evaluar, no logran capturar por completo las diferencias individuales en estos patrones. Por otro lado, la creación de modelos de predicción personalizados para cada paciente resulta poco práctica, ya que requiere una gran cantidad de datos de mediciones continuas de glucemia, lo que implica que los pacientes nuevos tendrían que esperar mucho para obtener predicciones precisas. Además, existe muy pocos conjuntos de datos de acceso abierto con suficiente cantidad de pacientes y longitudinalidad de mediciones de glucemia continua como para hacer experimentaciones robustas.

En este contexto, el objetivo de esta tesis es investigar técnicas inteligentes para apoyar la gestión de la diabetes mellitus tipo 1 en entornos del mundo real aprovechando los datos de mediciones continuas de glucemia recogidos de dispositivos móviles y vestibles. Para cumplir este objetivo principal se plantean los siguientes objetivos específicos: (1) crear un amplio conjunto de datos longitudinales de larga duración y de libre acceso consistente en mediciones de los niveles de glucemia en sangre recogidas mediante sensores de monitorización continua de la glucemia para desarrollar nuevos modelos inteligentes, (2) comprender la capacidad de los métodos de evaluación existentes para estimar el rendimiento de los modelos de predicción de los niveles de glucemia en sangre en entornos del mundo real, (3) identificar grupos de pacientes con características comunes a partir de las mediciones longitudinales de los niveles de glucemia en sangre de los pacientes, (4) evaluar el rendimiento de los modelos de predicción del nivel de glucemia en sangre basados en grupos en entornos del mundo real. Para dicha evaluación, se desarrollarán y compararán tres tipos de modelos de predicción: generales, basados en grupos y personalizados, utilizando métricas de evaluación clínicas y no clínicas. De este modo se determina la viabilidad de la propuesta realizada para su uso en predicción de niveles de glucemia en sangre en entornos realísticos.

Para abordar el problema, primeramente, se recopila un conjunto de datos con suficiente cantidad de mediciones continuas de glucemia y un número adecuado de pacientes, garantizando

así una base sólida para realizar la experimentación planteada. A continuación, se desarrollan modelos de predicción de glucemia generales, donde el entrenamiento y evaluación se realizan utilizando datos de mediciones de glucemia continua de todos los pacientes del conjunto de datos. Esto permite identificar las estrategias de evaluación más apropiadas para este tipo de modelos de predicción. Una vez comprendidas estas estrategias, se procede a la creación de grupos de pacientes mediante el uso de algoritmos de aprendizaje no supervisado de diversa naturaleza. Dado que se prueban múltiples configuraciones de tamaños de grupos, versiones de los datos y algoritmos, el conjunto de resultados de agrupamiento es amplio. Por ello, se seleccionan los resultados más prometedores utilizando una métrica de evaluación interna del agrupamiento, complementadas con un procedimiento diseñado en esta tesis, que posteriormente son revisados por expertos clínicos para identificar la solución más adecuada. Con los grupos definidos, se replica la experimentación realizada con los modelos de predicción generales para evaluar el rendimiento comparativo entre estos y los modelos de predicción basados en grupos. Además, se seleccionan pacientes dentro de cada grupo para desarrollar modelos de predicción personalizados, lo que permite realizar una comparación adicional con los modelos de predicción basados en grupos y así determinar si estos últimos representan una solución intermedia viable entre los modelos de predicción generales y los personalizados. A continuación se detalla cómo se realizaron cada uno de estos pasos y las contribuciones finales de la tesis.

Novel conjunto de datos longitudinal

Esta tesis contribuye con T1DiabetesGranada, un conjunto de datos longitudinales abierto que no sólo proporciona niveles continuos de glucemia en sangre, sino también información demográfica y clínica de los pacientes. El conjunto de datos incluye 257 780 días de mediciones que abarcan cuatro años de 736 pacientes con diabetes tipo 1 de la provincia de Granada, en España. Este conjunto de datos avanza más allá del estado del arte como uno de los conjuntos de datos abiertos más amplios temporalmente y extenso en mediciones continuas de glucemia en sangre, impulsando así el desarrollo de nuevos modelos de inteligencia artificial para la caracterización y predicción del nivel de glucemia en sangre.

Comprensión de los métodos de evaluación de los modelos de predicción

Se desarrollan modelos de predicción generales basados en redes neuronales artificiales para la predicción de glucemia, los cuales son entrenados y evaluados utilizando datos continuos de glucemia de todos los pacientes. Se incluyen 3 algoritmos de predicción, una regresión lineal, así como arquitecturas de redes neuronales más avanzadas como LSTM y CNN. La predicción se realiza a partir de dos horas de valores históricos tomados cada 15 minutos, con 6 diferentes horizontes de predicción de 30 a 240 minutos. Para evaluar su rendimiento se usan tanto métricas clínicas (análisis de la rejilla de error de Clarke) como no clínicas (RMSE, MSE, MAE y MAPE), aplicadas no solo en todo el rango de glucemia, sino también independientemente en rangos clínicamente relevantes. Los resultados muestran un desempeño ligeramente mejor de los modelos de predicción lineales frente a los más complejos (LSTM y CNN), probablemente debido a la concentración de datos en un rango reducido de glucemia (100-200 mg/dL), lo que favorece a los modelos de predicción más simples. Se concluye que un enfoque holístico es clave para evaluar correctamente estos modelos de predicción. Visualizaciones como la rejilla de error de Clarke permiten analizar la geometría de las predicciones, mientras que evaluar las métricas en rangos específicos de glucemia evita conclusiones sesgadas y refleja con mayor precisión el

comportamiento de los modelos de predicción en rangos de hipoglucemia e hiperglucemia que son los de más riesgo para la salud.

Identificación de grupo de pacientes

Un aspecto clave de la tesis es identificar grupos de pacientes con patrones similares de glucemia mediante algoritmos de aprendizaje no supervisados como K-means, Gaussian Mixture, agrupamiento jerárquico y mapas autoorganizados. Se utilizan características extraídas de las mediciones de glucemia (promedio, desviación estándar, mínimo y máximo) en diferentes momentos del día para representar a cada paciente en el proceso de agrupamiento. Para estimar el número de grupos, se aplican el método del codo y el análisis de dendrogramas. Los resultados más prometedores se seleccionan, utilizando el coeficiente de Silhouette y un método personalizado, para presentarlos a expertos clínicos. Finalmente, se identifican seis grupos con patrones diferenciados de glucemia, que no solo sirven para desarrollar modelos de predicción basados en ellos, sino que también pueden influir en la atención médica. Estos grupos brindan la oportunidad a los endocrinos de diseñar tratamientos personalizados según los perfiles de pacientes. Con el uso de monitores continuos de glucemia, es posible asignar relativamente rápido a nuevos pacientes a uno de estos grupos, facilitando un enfoque terapéutico más dirigido desde las primeras fases de monitorización. Además, el proceso es aplicable a pacientes con historiales más largos de monitoreo, siempre que sus datos sean accesibles

Evaluación de los modelos de predicción basados en grupos

Una vez definidos los grupos de pacientes, se procede a crear modelos de predicción de los niveles de glucemia en sangre para cada grupo utilizando el mismo procedimiento de experimentación y modelos de predicción utilizado para los modelos generales. Para tener un punto de comparación adicional, se crean modelos de predicción personalizados para una muestra de pacientes, se seleccionan a aquellos cuyos niveles de glucemia fueron mejor y peor predichos por los modelos de predicción basados en grupos. Estos modelos de predicción personalizados entrenaron individualmente con los datos de cada paciente, replicando el procedimiento de entrenamiento aplicado a los modelos de predicción generales y basados en grupos. Los resultados muestran que los modelos de predicción basados en grupos superan a los modelos de predicción generales en ciertos grupos de pacientes y condiciones específicas, como en los grupos que representan a pacientes con un mejor control de glucemia. En estos casos las mejoras en métricas clínicas que evalúan el porcentaje de mediciones dentro de áreas clínicamente aceptable son más pronunciadas a medida que aumenta el horizonte de predicción, lo que sugiere que estos modelos pueden capturar patrones a largo plazo de manera más efectiva. Si bien los avances en los rangos de hipoglucemia son menores, se observaron mejoras en algunos grupos de pacientes con más eventos hipoglucémicos sobre todo en los algoritmos de predicción LSTM y CNN. Al comparar los modelos de predicción personalizados con los basados en grupos, aunque los primeros ofrecen mejoras en ciertos casos, no siempre superan a los modelos de predicción basados en grupos, mejorando solo en el 37.98% de las ocasiones. Por lo que se puede decir que los modelos de predicción basados en grupos ofrecen un equilibrio entre precisión y practicidad, mejorando el rendimiento sobre muchos de los modelos de predicción generales y requiriendo menos datos para la utilización en nuevos pacientes, siendo una solución eficaz para la predicción de glucemia en pacientes con diabetes tipo 1.

Conclusiones

Los modelos de predicción basados en grupos resultan ser una solución intermedia prometedora entre los modelos generales y personalizados para la predicción de glucemia en pacientes con diabetes tipo 1. Estos modelos ofrecen mejoras sobre los modelos de predicción generales, particularmente en pacientes con mejor control de la glucemia y proporción elevada de hiperglucemias, equilibrando precisión y practicidad, y requiriendo menos datos para su implementación en nuevos pacientes. Aunque los modelos de predicción personalizados mostraron mejores resultados en algunos casos, los basados en grupos demostraron ser más eficaces en la mayoría de situaciones, consolidándose como una alternativa viable para optimizar la predicción y atención médica personalizada en el manejo de la diabetes tipo 1. Las principales contribuciones de la tesis son:

1. Un extenso conjunto de datos longitudinal multimodal de mediciones de glucemia continua, recopiladas utilizando medidores de glucemia continua, con información demográfica y clínica de los pacientes con diabetes tipo 1.
2. Una metodología de experimentación utilizando algoritmos de predicción aplicados a un conjunto de datos longitudinal extenso de mediciones de glucemia continua.
3. Tres conjuntos de modelos de predicción de niveles de glucemia continua basados en redes neuronales artificiales: generales, basados en grupos y personalizados.
4. Una metodología para crear grupos de pacientes basada en sus mediciones de glucemia continua.
5. Varios grupos de pacientes con diabetes tipo 1 que permiten a los endocrinos diseñar tratamientos personalizados según los perfiles únicos de los pacientes.
6. Una base de código para apoyar todos los procesos experimentales de las metodologías y la creación del conjunto de datos, permitiendo la reproducibilidad y la escalabilidad para futuras investigaciones.

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Chapter 1

Introduction

1.1 Diabetes mellitus

Diabetes mellitus (DM) is a metabolic disorder primarily characterized by high blood glucose levels (BGL). People with DM are more likely to have other major health problems. Therefore, their chances of requiring special medical attention increase as the patient's quality of life decreases [BD+16]. In 2021, the International Diabetes Federation (IDF) reported that 537 million adults worldwide had DM, resulting in an estimated 6.7 million deaths. Projections suggest a worrying increase to 643 million cases by 2030 and 783 million by 2045, reflecting a rise of 16.49% and 31.42%, respectively [Int21]. Such a continued increase in the prevalence of DM is mainly justified by the global rise in obesity, driven foremost by people's unhealthy lifestyles and urbanization [Zim+14]. The mortality rate from DM surpasses other diseases often considered more dangerous or more frequently addressed by health agencies [Int17].

DM is typically categorized into three groups, namely type 1 diabetes (T1D), type 2 diabetes (T2D), and gestational diabetes. T1D affects between 5% and 10% of patients with DM and most often occurs in young people [Org+19; Ass08]. T1D is fundamentally characterized by a severe problem of insulin secretion. Patients are required to use an external source of insulin to balance their BGLs. These multiple daily doses can be administered through injections or continuous insulin pumps. T2D affects between 90% and 95% of patients with DM, usually adults and senior citizens [Org+19; Ass08]. In this case, the pathophysiological mechanism is insulin resistance; over time, the body loses the ability to secrete the right amount of this hormone. In general, having control of the BGLs is easier for T2D patients than for T1D patients. To control their BGLs, T1D patients must keep strict control of the amount of carbohydrates ingested, physical activity performed, and insulin administered, which can become very complex [Gin+18; Chi+14].

Irrespective of the type of DM, low BGL (hypoglycemia) or too high BGL (hyperglycemia) in the blood for long periods can induce several complications in patients, leading to premature death in the worst cases. Critical hypoglycemia can cause comatose states and induce seizures. Chronic hyperglycemia can cause vascular damage, affect the heart, kidneys, eyes, and nerves, and lead to other serious complications [Org09; CV18]. Extensive tests have proven that appropriate metabolic control in all DM types can delay the onset and evolution of its complications [Wor22]. In addition, early diagnosis, continuous health care, and adequate self-monitoring of the disease by patients are vital for preventing or minimizing complications.

Moreover, several studies indicate that T2D can be prevented by maintaining a healthy lifestyle, attaining adequate nutrition, performing physical activity, and avoiding obesity [Hu+01].

1.2 Mobile and wearable technologies in diabetes mellitus

Monitoring specific parameters becomes crucial for patients with DM to manage their condition effectively. These parameters include body weight, BGLs, physical activity, blood pressure, low-density lipoprotein cholesterol, triglycerides, microalbuminuria, glycated hemoglobin levels [d'E+15], caloric intake, and the condition of their feet, eyes, and stress levels, among others [Zim+14; O'C+11]. By focusing on these factors, wearable devices offer significant potential to enhance the quality of life for individuals with DM by providing continuous, real-time health data.

The health community uses the term *diabetes technology* for devices and software that patients with DM use to aid their condition. According to this classification, diabetes technology has two main categories, namely insulin administration and blood glucose monitoring. Insulin pumps are the most popular devices used for insulin administration. Continuous glucose monitor (CGM) and flash glucose monitor (FGM) are most often used to monitor BGLs. In recent years, hybrid devices have been developed, including both functions. When this technology is used properly, it can improve patients' quality of life. However, the complexity and rapid changes in this field can be an obstacle to their widespread use by patients [Ass19]. Although this type of device has mostly dominated diabetes technologies, it is only recently that advances in mobile and wearable technologies have burst in to complement prior diabetes technology with a new generation of digital solutions at the reach of most people.

The widespread adoption of wearable and mobile technologies worldwide offers new opportunities for researchers to provide medical care and information in a portable and affordable way [KL17]. Smartphones stand out because of their strong computational features and pervasiveness. Even among older adults, smartphone ownership has increased significantly. By the beginning of 2019, approximately 350.4 million people were using wearable technology [Sta19], namely, devices worn directly on or loosely attached to a person [God+18], with a growing trend in the use of wrist-worn devices [Ric19]. This technology has distinctive applications in the healthcare field because of its capacity to gather, store, and transmit data and sometimes even process it. Patients and physicians can leverage these features to manage, treat, and assess their conditions. Despite those above mobile and wearable technology capabilities, these devices still need to be extensively used in clinical settings [God+18].

Several sensors are readily available on regular smartphones, such as the accelerometer (ACC), GPS, camera, ambient light, and microphone, among others. The data collected by these sensors can be used to determine the user context [Fel+19]. For example, the user's physical activity or calories burned can typically be measured using a smartphone's motion sensors (ACC and gyroscope) [Ban+16]. Wearables have features that are increasingly comparable to those of regular smartphones, including, in some cases, built-in GPS, barometer, heart rate (HR), ACC, or gyroscope sensors. In addition, wearables outmatch smartphones while sensing physiological signs, such as HR, electrocardiogram, or skin temperature, which are considered of particular interest for monitoring DM-related parameters. Some physiological measurement capabilities can also be instrumented in smartphones via external pluggable devices, although

only for occasional use [Lee+19]. By processing the collected data generated by the sensors on smartphones and wearables, it is possible to monitor many of the relevant parameters for patients with DM, such as BGL, blood pressure, calories, physical activity, feet condition, eye condition, and stress levels. In addition, one of the most relevant characteristics of this technology is its capacity to monitor in a continuous, passive, and unobtrusive way without necessarily interfering with people’s regular daily living.

Mobile and wearable devices generate an enormous amount of data, and their ability to process them is beyond human skills [CAR18]. As a result, sophisticated mechanisms such as artificial intelligence (AI) are most often used with these devices to digest and extract meaningful knowledge from the gathered data. AI is widely used to support advanced analytics and provide individualized medical assistance [YBK18]. In addition, a growing number of healthcare companies are applying AI algorithms to discover relevant clinical information from large amounts of data [Jia+17]. The main reasons for this growth include the explosive increase in the available data and the improved performance of intelligent methodologies capable of handling and processing it. AI is also attracting great attention to DM, as the amount of data acquired electronically by patients with DM has grown. Proper management of these large volumes of data is expected to increase patients with DM quality of life [Rum+20]. Thus, AI may play a key role in recognizing these systems as routine therapeutic aids for patients with DM.

1.3 Challenges in real-world blood glucose levels prediction

As previously discussed, DM is a pressing global health concern with potentially severe implications for those it affects. Among DM patients, those with T1D face the most daunting challenge in maintaining their BGLs within target ranges. This complexity is inherent to T1D and the multitude of factors that can influence BGLs fluctuations, underscoring the urgent need for more effective management strategies.

According to the IDF, the T1D patient population is rapidly growing. In 2022, there were 8.75 million T1D patients (more than 200.000 in Spain), projected to double to 17.5 million by 2045. The disease claimed 182.000 lives in 2022 alone, highlighting the urgency of the issue. The clinical costs associated with T1D have tripled in the last 15 years. This investigation focuses on T1D, a condition that significantly diminishes the quality of life for patients, primarily due to the challenges they face in managing their BGLs within an appropriate range, despite, in many cases, their best efforts in diet, physical activity, and medication adherence.

A major fear for T1D patients is the risk of hypoglycemic events, which can lead to immediate important consequences such as seizures, fainting, falls, or comatose states. Nighttime hypoglycemic events, affecting 30-60% of T1D patients [Zhu+21a], are particularly alarming as they may go unnoticed, potentially resulting in severe outcomes, even death. To mitigate these risks, patients often maintain elevated BGLs by eating carbohydrates or reducing insulin doses to set the glycemic baseline high enough, sometimes leading to hyperglycemia. This preventive approach has noticeable pernicious side effects, as it can diminish the body’s response to hyperglycemia to practically none, showing no longer any associated physical alerting discomfort, thus becoming a health-compromising practice.

CGM sensors have improved the management of these adverse glycemic events, as they can provide real-time data to inform when such an event is occurring. Despite the advantage of informing of their occurrence, these events require a rapid reaction to lessen their effect. Prolonged or frequent adverse glycemic events can result in the serious DM complications mentioned.

A practical solution to significantly enhance the quality of life for T1D patients would involve the development of prediction models capable of predicting BGLs well in advance. However, despite the advancements in AI and prediction models, including sophisticated artificial neural networks (ANN) and complex tools for managing T1D-related data, there is still a pressing need for further research and development to create models and applications that can effectively address these challenges for T1D patients. The subsequent sections explore the significant existing limitations that are hindering further progress in this area.

1.3.1 Lack of quality datasets

High-quality data sources are crucial for developing robust prediction models. Achieving reliable prediction models requires relevant, reliable, knowledgeable data about real-world conditions, which is comprehensive enough to support effective training and testing. However, obtaining such data can be challenging, especially in certain fields. In the context of T1D, objective data only became widely available with the development and increased use of CGM devices. Despite this advancement, many studies still rely on insufficient datasets to drive meaningful progress. The creation of high-quality datasets is often interfered with by challenges such as the need for large participant samples, significant infrastructure costs, and the extensive process of securing ethical approvals for working with human data.

On the one hand, some datasets appear to be of sufficient quality but are not publicly available, as they are used for specific studies by their authors and are not accessible to the broader scientific community. This lack of openness hinders innovation and the development of alternative solutions. On the other hand, some studies use artificially created (*in-silico*) datasets. While these datasets may be extensive, they only partially represent real-world conditions, making the resulting prediction models less realistic and unreliable for real-world use. Although the algorithms and applications used to create these *in-silico* datasets are well-crafted and the created dataset are functional for prototyping models, testing methodologies, and demonstrating tool use, their artificial nature makes them unreliable for sensitive medical applications on real-world settings [Wol+19; TKT22].

Finally, there are a few public datasets with real patient data from T1D cases, but these often have limitations that have led to stagnation in the development of models and applications. The main limitation is the need for sufficient data volume, primarily due to a limited number of patients and short data collection periods. A small sample size, sometimes fewer than ten patients, complicates realistic training and testing of models since each patient's BGL patterns can differ significantly, making the dataset inadequate for identifying meaningful trends. Additionally, if the dataset's longitudinal scope is limited, sometimes to just two weeks, it restricts the ability to capture seasonal patterns or lifestyle changes, such as holidays or weather seasons of the year, that may significantly impact patients' BGL [RL+23b].

1.3.2 Insufficient clinical evaluation of blood glucose prediction models

A critical aspect of developing prediction models is their proper evaluation. This process helps identify the best-performing prediction model from various experimental options and provides insight into how the prediction model will function in real-world applications. To this end, many metrics exist, varying by problem domain, data type, and other factors. In the context of predicting BGLs for T1D patients, this is treated as a regression problem, prompting many studies to use metrics such as Root Mean Square Error (RMSE), Mean Absolute Error (MAE), or Mean Absolute Percentage Error (MAPE).

However, these commonly used but non-clinical evaluation metrics do not account for errors in critical regions (hyperglycemia or hypoglycemia) crucial for patient intervention [Jac+24]. Some studies employ clinically relevant metrics, such as the Clarke Error Grid (CEG) [Cla+87] or the Parkes Consensus Grid (PCG) [Par+00], essential for a realistic clinical evaluation of the prediction models. Moreover, to achieve a thorough evaluation, analyzing results across various BGL ranges is essential, rather than focusing solely on the entire range. Neglecting this can lead to biased results, as the majority of measurements typically fall within the zone Time in Range (TIR), potentially overlooking more critical ranges where BGL falls into the Time Below Range (TBR) or rises into the Time Above Range (TAR), both of which pose a higher risk to patient health by exceeding the recommended thresholds.

1.3.3 Unpractical prediction approach

In the context of predicting BGL for T1D patients, the data are typically presented as time series. Generally higher data quality and volume result in better prediction model performance. Given the variability in BGL patterns among patients, many studies develop personalized prediction models for each patient using all available data to maximize performance metrics, as it is common in this research field. However, this approach poses significant practical challenges for real-world implementation. To create a prediction model for a new patient that starts to use a CGM, a substantial amount of data collection is required before the prediction model can be trained and deployed, causing a delay before the patient can benefit from the developed tool. This collection period may last from months to potentially years depending on the expected performance of the prediction models.

Another approach to this issue involves developing generalist prediction models, which, also due to the limited number of participants in existing public datasets, use the entire patient pool to create a single prediction model capable of predicting BGL for any patient. While this strategy would be ideal for real-world applications, it often proves overly ambitious and overlooks individual patient differences, leading to performance that falls short of expectations.

1.4 Objectives

In light of the challenges associated with managing diabetes mellitus, particularly for patients with type 1 diabetes mellitus, the potential offered by diabetes technologies, and the issues discussed previously in Section 1.3, the goal of this thesis is to investigate intelligent techniques to support the management of type 1 diabetes mellitus in real-world settings by leveraging con-

tinuous glucose measurements data collected from mobile and wearable devices. This research seeks to contribute new insights into the blood glucose level prediction process by emphasizing clinical evaluation of prediction models, targeting critical blood glucose level ranges (hypoglycemia and hyperglycemia), focusing on group-based prediction models, and ensuring that these prediction models are more applicable in real-world settings.

This thesis aims at achieving this goal via the following supporting objectives:

Objective 1: Create an extensive, long-term, open-access longitudinal dataset consisting of blood glucose level measurements collected through continuous glucose monitoring sensors to develop new intelligent models.

This objective aims to overcome the limitations of insufficient quality of the data mentioned in Section 1.3.1. The collected data will be composed of real data, providing the robustness needed for training and testing prediction algorithms. With substantial data volume per patient, based on the sampling frequency, long-term longitudinal data, and a large number of participants, the dataset has the potential to produce realistic prediction models, especially deep learning models that require large datasets for practical training. Furthermore, a dataset of this scale will enable more sophisticated experimental strategies that have been challenging to implement until now, such as dedicating complete patient data sets to training, validation, and testing, thereby reducing bias in prediction model evaluation. Additionally, incorporating demographic and clinical data may enhance the explainability of the models and provide a more holistic understanding of the patient's health status. The realization of this objective will be supported by the existing collaboration with experts of the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain and the access to T1D patients' data who regularly use CGM sensors in a daily basis.

Objective 2: Comprehend the capacity of existing evaluation methods for estimating the performance of blood glucose level prediction models in real-world settings.

To achieve this objective, models for predicting blood glucose levels will be developed and rigorously evaluated. The evaluation process includes non-clinical metrics like RMSE or MAPE, clinical metrics suited to this context like Clarke error grid, and evaluating these metrics across blood glucose level ranges defined by experts. Several strategies will be employed to ensure a comprehensive and unbiased comparison: using the blood glucose level measurements from the dataset created in the previous objective, partitioning data so training, validation, and testing patients are distinct, selecting diverse prediction models from state of the art, and applying a wide range of prediction horizons to explore different temporal predictions.

Objective 3: Identify patient groups with common characteristics based on patients' longitudinal blood glucose level measurements.

This objective aims to identify patient groups with common blood glucose levels patterns through a robust experimentation process using various unsupervised machine learning techniques, including distance-based, probabilistic, fuzzy logic, and neural network-based approaches. Optimal group numbers will be estimated computationally, and internal evaluation metrics and a custom method will help identify meaningful groups. Clinical experts of the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain, will then analyze these meaningful groups to select the most appropriate clustering. The chosen groups will serve as the foundation for further experimentation, testing the hypothesis that group-based prediction models offer a balance between general and personalized prediction models,

leading to improved accuracy. In practical applications, new patients could be matched to one of these profiles, allowing the corresponding prediction model to predict their blood glucose levels accurately.

Objective 4: Evaluate the performance of group-based blood glucose level prediction models in real-world settings.

To achieve this objective, the methodology used to create the general prediction models using the entire dataset will be used to create group-based prediction models, meaning that the same experimentation will be carried out but on each patient group. Later, a sample of patients from each group will be selected to develop personalized prediction models for each patient. This way, evaluation metrics results from group-based prediction models can be compared with the other two approaches, general and personalized. Using the same evaluation schemes for the three prediction model types will make it possible to compare them, minimizing biases.

1.5 Outline

This thesis is structured into seven chapters shortly described in the following.

Chapter 1 introduces the context of diabetes mellitus, focusing specifically on type 1 diabetes, its main characteristics, and how mobile and wearable technologies have aided patients. It also discusses the limitations that still exist in blood glucose prediction, followed by the presentation of the thesis objectives.

Chapter 2 delves deeper into advancements in mobile and wearable technologies for diabetes monitoring. Also, it explores existing continuous glucose monitoring datasets and the development of prediction models using these data types through traditional and clustering-based approaches.

Chapter 3 describes the process of creating the longitudinal dataset, explaining how the data were prepared, their key characteristics, limitations, and potential use cases.

Chapter 4 analyzes the methods for evaluating glucose prediction models by assessing three general prediction algorithms based on artificial neural networks using continuous glucose measurements from the generated longitudinal dataset.

Chapter 5 outlines the process of creating patient groups with T1D, utilizing continuous glucose measurements and unsupervised machine learning models.

Chapter 6 evaluates the performance of blood glucose prediction models based on the patient groups. It involves creating group-based and personalized prediction models and comparing the group-based prediction models against the general and personalized ones.

Finally, Chapter 7 presents the main achievements, contributions, and conclusions of this thesis while also presenting opportunities for future work stemming from these findings.

Chapter 2

State of the art

2.1 Advancements in Mobile and Wearable Technologies for Diabetes Monitoring

DM demands effective metabolic control, early diagnosis, continuous healthcare, and self-monitoring to prevent complications. Adopting a healthy lifestyle is crucial in preventing T2D and controlling type T1D, with essential monitoring of parameters like body weight, glucose levels, physical activity, blood pressure, cholesterol, triglycerides, and stress levels [AZ98; Hu+01]. Diabetes technology, such as insulin pumps and CGM, enhances patient quality of life, though the complexity of these tools may present challenges [Ass20]. Mobile and wearable technologies offer new opportunities for accessible, affordable care, utilizing sensors to track vital health indicators. These devices enable continuous, unobtrusive monitoring, supporting improved DM management and complementing traditional technologies to enhance patient outcomes [God+18; Lee+19]. By integrating these advanced tools, patients and healthcare providers can achieve more proactive and personalized care, ultimately leading to better management and outcomes for those with DM [Ban+16; Fel+19]. AI is crucial for processing the vast amounts of data generated by mobile and wearable devices. This enables advanced analytics and personalized medical assistance, which in turn improves the quality of life for patients with DM by effectively managing large volumes of data [Rum+20].

We conducted a systematic review to assess the potential of mobile and wearable technologies in managing DM through continuous, objective monitoring outside clinical settings [RL+21]. With seamless data collection, these technologies provide a wealth of information that surpasses traditional methods. Among the most groundbreaking used devices in recent years are CGM, which were employed in studies such as [Tur+17; Fac+18; Gro18; Mer+19; Ram+19; Ngu+19; Sev+19; LS+19]. Similarly, FGM, used in studies like [McM+18; RR+19; Whe+19], has also played a pivotal role in advancing BGL data collection. Many reviewed studies lacked specificity regarding the type of DM and focused more on technological performance than clinical validation in real-world contexts. Moreover, integrating mobile data with clinical data remains an area that requires further exploration to achieve a more comprehensive understanding of patient health.

Many of the studies reviewed also demonstrated areas for improvement in their experimental design, such as insufficient clinical trials, lack of detailed descriptions of devices and sensors used, and poor representation of diverse patient cohorts. These limitations suggest a need for more

rigorous research protocols and the inclusion of complementary clinical data to create more impactful and personalized DM management solutions. Furthermore, the studies frequently failed to address crucial aspects like data transparency, ethics, and privacy concerns, which are vital for the applicability and quality of the research outcomes.

Our findings call for the research community to address these challenges by ensuring better clinical validation, ethical standards, and mobile data integration with clinical records. The combination of advanced machine learning techniques with mobile and wearable sensor data presents a promising direction for future research, aiming to develop more robust and clinically relevant models that can significantly improve the management and prevention of DM, particularly T2D, which is preventable through early intervention and lifestyle changes.

Figure 2.1 summarizes our review’s key findings, highlighting the strengths, weaknesses, challenges, and recommendations related to studies on monitoring diabetes-related parameters. Strengths indicate areas where studies performed well and could be replicated, while weaknesses point to issues that need improvement in future research. Challenges are critical obstacles that the scientific community must address to advance this field, and recommendations offer guidance for enhancing research efforts in DM monitoring.

2.2 Longitudinal datasets in diabetes research

DM involves complex BGL management, particularly in T1D, where patients must meticulously balance diet, exercise, and insulin, unlike T2D, which generally allows for easier glucose control without insulin. In light of these challenges, scientists and technologists have recently focused on improving the quality of life for people with DM. The most notorious examples are the development of wearable devices such as insulin pumps, CGM, and FGM. In addition, mobile or wearable devices, such as wristbands or chest straps, are also used to measure other important variables for the disease, like physical activity [RL+21]. The use of CGM and FGM has led to a significant improvement in controlling BGLs in T1D patients [Dic+21]. The use of these devices by T1D patients is beneficial as it provides objective and continuous data that can help doctors treat more effectively. However, it also offers the opportunity to use AI and data science techniques to reveal interesting patterns from this data. In this regard, the most relevant applications would be to accurately predict patients’ BGLs in the short and mid-term and forecast the occurrence of hypoglycemia and hyperglycemia in advance. Comprehensive longitudinal datasets become essential to support this type of applications.

Despite the advent of the use of CGM and FGM in recent years, there is a clear lack of open, longitudinal datasets presenting data collected by these devices. A great deal of research in this area builds on private datasets, some of which obtain the data from real CGM or FGM sensors [Bia+17; Gad+19; Liu+21; Zul+21; Seo+21; RR+21; Pre+21], and others generate the data artificially (*in silico*) [AQA21; Cam+19; MDB21; Sam+17; Cap+19]. Few datasets are found in the literature that meets some of the necessary requirements for making realistic predictions: "REPLACE-BG" [Ale+17], a public dataset collecting real CGM data during 182 days from 226 T1D patients with well-controlled DM; "The D1NAMO Open Dataset" [Dub+18], an open dataset collecting real CGM data during approximately 30 days from 9 T1D patients; "The OhioT1DM Dataset" [MB20], an on-request dataset collecting real CGM data during 56 days from 12 T1D patients; and "ShanghaiT1DM" [Zha+23] a public dataset collecting real CGM data during 14 days from 12 T1D patients. However, these four datasets are characterized by a relatively small sample size and short study duration. Very recently, a contribution

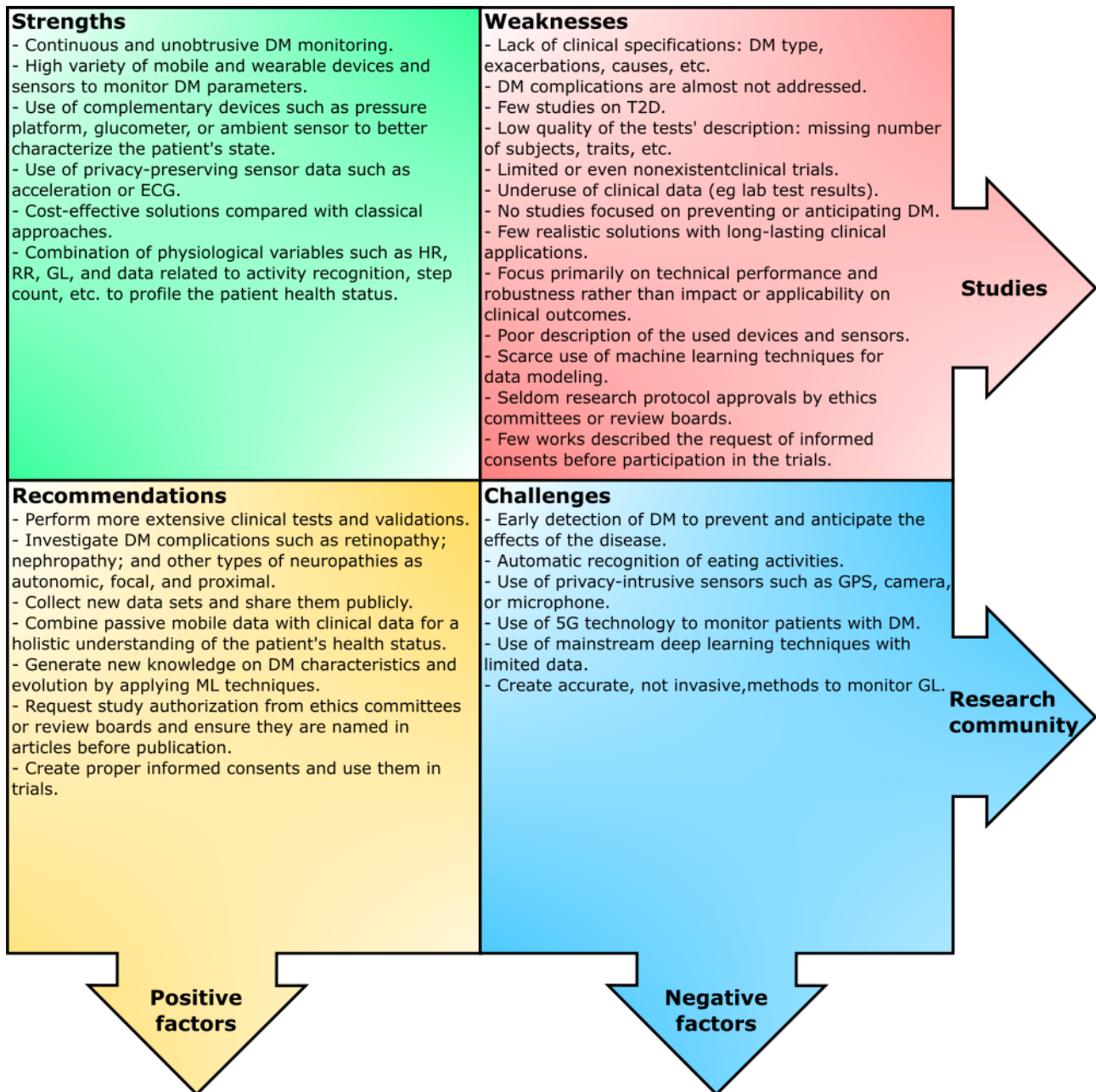


Figure 2.1: Summary of the principal findings of the reviewed manuscripts. List acronyms: DM: diabetes mellitus; ECG: electrocardiogram; GL: glucose level; HR: heart rate; ML: machine learning; RR: respiration rate; T2D: type 2 diabetes. Source: [RL+21].

has been made towards increasing the study duration, "DiaTrend" [Pri+23], a public dataset collecting real CGM data during an average of 510 days from 54 T1D patients.

Since no existing dataset meets our specific requirements, creating one that satisfies all established criteria while addressing previous limitations, such as including complementary clinical data, is essential. This dataset must also adhere to strict ethical standards and privacy policies. It will span several years and allow for the investigation of T1D disease evolution across different times of the year, such as comparing holidays to regular days or seasonal variations. Additionally, the dataset will be available to the scientific community to advance new AI models, enabling personalized treatment and predictive DM management strategies.

2.3 Evaluation metrics in prediction of blood glucose level measurements

2.3.1 Non-clinical evaluation metrics

Evaluation metrics are essential tools in machine learning (ML) used to assess the performance and effectiveness of prediction models. These metrics provide quantitative measures that help determine how well a prediction model performs, whether in making predictions, classifying data, or grouping similar items. One of the primary goals of evaluation metrics is to provide a standard way to compare different prediction models or approaches and guide the improvement of these prediction models by highlighting their strengths and weaknesses [Zho+21]. Supervised and unsupervised metrics play crucial roles in different scenarios. Supervised metrics, used when the data includes labeled outcomes, provide a clear benchmark for comparing model predictions. On the other hand, unsupervised metrics, applied to data without labels, evaluate prediction model quality based on inherent data structures or patterns. Supervised metrics are commonly applied in regression and classification problems, while unsupervised metrics are primarily used in clustering and dimensionality reduction tasks [NZS23].

Classification metrics are essential for evaluating models that predict categorical outcomes in supervised learning. Metrics such as accuracy, precision, recall, F1-score, and AUC-ROC provide distinct insights into different aspects of model performance. Accuracy measures the overall correctness of predictions, while precision focuses on the proportion of correctly predicted positive cases. Recall assesses the ability of the model to identify all relevant positive instances. The F1-score balances precision and recall, offering a combined measure, and AUC-ROC evaluates the model's ability to distinguish between classes across different thresholds, adding a layer of robustness to model evaluation [RTK24].

Regression metrics are essential for evaluating models that predict continuous outcomes, such as financial forecasts, weather predictions, and various healthcare analytics like BGL prediction. Key metrics include MAE, Mean Squared Error (MSE), R-squared, and RMSE. MAE, a minimization metric with values greater than or equal to 0, provides an average of absolute errors. MSE, a minimization metric ranging from 0 to infinity, squares the errors, making it more sensitive to larger discrepancies. R-squared, a maximization metric ranging from 0 to 1, indicates the proportion of variance explained by the model. RMSE, with a range starting from 0 upwards, is another minimization metric combining sensitivity to outliers with interpretability, as its values are expressed in the same units as the domain of the problem [Tat21]. These metrics are commonly used in the state of the art to evaluate the models to predict BGL

in patients with T1D. Throughout this thesis, these metrics will be referred to as non-clinical metrics.

Unsupervised evaluation metrics, such as those used in clustering, include the Silhouette Coefficient, Davies-Bouldin Index, Calinski–Harabasz index [CH74], and Adjusted Rand Index, among others. These metrics do not rely on labeled data but instead, measure clustering quality by evaluating intra-cluster cohesion and inter-cluster separation [Ami+09]. For example, the Silhouette Coefficient, assesses how similar data points are within their clusters compared to others [Rou87]. The Davies-Bouldin Index evaluates cluster separation by measuring the average similarity ratio between each cluster and its most similar counterpart [DB79]. The Adjusted Rand Index compares clustering results to reference clustering, accounting for chance, making it a robust metric for validating unsupervised models [Ran71].

Expert criteria play a significant role in clustering evaluation within unsupervised learning, especially in ensuring clusters are meaningful and practically relevant. This approach, which relies on domain experts to assess whether the resulting clusters make sense based on their specialized knowledge and experience, is crucial in fields like healthcare. The practical relevance of this approach ensures that the clusters produced are not only mathematically valid but also practically useful, aligning closely with the real-world needs and challenges of the domain in question [Weg+21].

While foundational and widely used, the evaluation metrics analyzed in this section must be carefully selected to match the specific problem domain and data characteristics. Applying these metrics correctly ensures that the created groups are cohesive and well-separated when assessed by unsupervised metrics and that prediction models are accurate and applicable to real-world settings as evaluated by regression metrics, which is particularly crucial in healthcare and other critical fields.

2.3.2 Clinical evaluation metrics

In classification problems, confusion matrices provide a more interpretative understanding of model performance by categorizing predictions into groups. Similarly, in the context of BGLs prediction, a regression problem, specialized tools enhance the clinical relevance of evaluation metrics. The CEG and PCG, among these tools, categorize the accuracy of BGL measurements into zones that reflect varying levels of clinical risk associated with prediction errors. This approach underscores the importance of considering the safety and health implications for patients with T1D, ensuring that evaluations go beyond numerical accuracy.

Traditionally, in predicting BGL for T1D patients, researchers have relied only on non-clinical evaluation metrics like MAE or RMSE to assess the numerical precision of model predictions [Rob+11; MS14; Geo+15; LF16; Rey+16; Jan+16; FTL16; Tom17; Mir+17; Ham+18]. However, these metrics, while providing a quantitative assessment of how closely predictions match actual values, fall short in offering the semantic context necessary to evaluate these predictions' clinical significance and safety. This inadequacy underscores the need for more clinically oriented evaluation metrics, such as the CEG, to provide a wider understanding of a prediction model's performance by accounting for the potential clinical consequences of prediction errors, thereby enhancing the prediction model's utility in real-world medical scenarios [Jac+24].

The CEG was initially developed in 1987 by William Clarke and colleagues to evaluate the clinical accuracy of blood glucose meters [Cla+87]. Its primary objective was to provide a framework that assesses the numerical accuracy of BGL measurements and interprets the potential

clinical outcomes of these measurements. Unlike traditional error metrics that merely quantify discrepancies between predicted and actual values, the CEG visually maps these discrepancies into zones representing varying clinical risk levels.

The CEG divides a scatterplot of predicted versus reference BGL measurements into five distinct zones (Fig. 2.2), each representing a different level of risk associated with clinical decision-making:

- **Zone A:** Represents clinically accurate predictions within 20% of the reference values or lower than 70 mg/dL. This zone represents clinically accurate predictions that have no expected impact on treatment decisions
- **Zone B:** Contains predictions not within the 20% accuracy range but would not lead to inappropriate clinical actions. Errors in this zone are minor and generally acceptable in a clinical setting.
- **Zone C:** Includes predictions that, although not critically incorrect, could lead to unnecessary adjustments in treatment that might confuse both patients and healthcare providers.
- **Zone D:** Reflects significantly inaccurate predictions that could lead to potentially dangerous treatment decisions, such as administering incorrect insulin doses.
- **Zone E:** Represents critical errors where the predictions are opposite to the actual values, posing a severe risk of incorrect treatment and potentially life-threatening consequences.

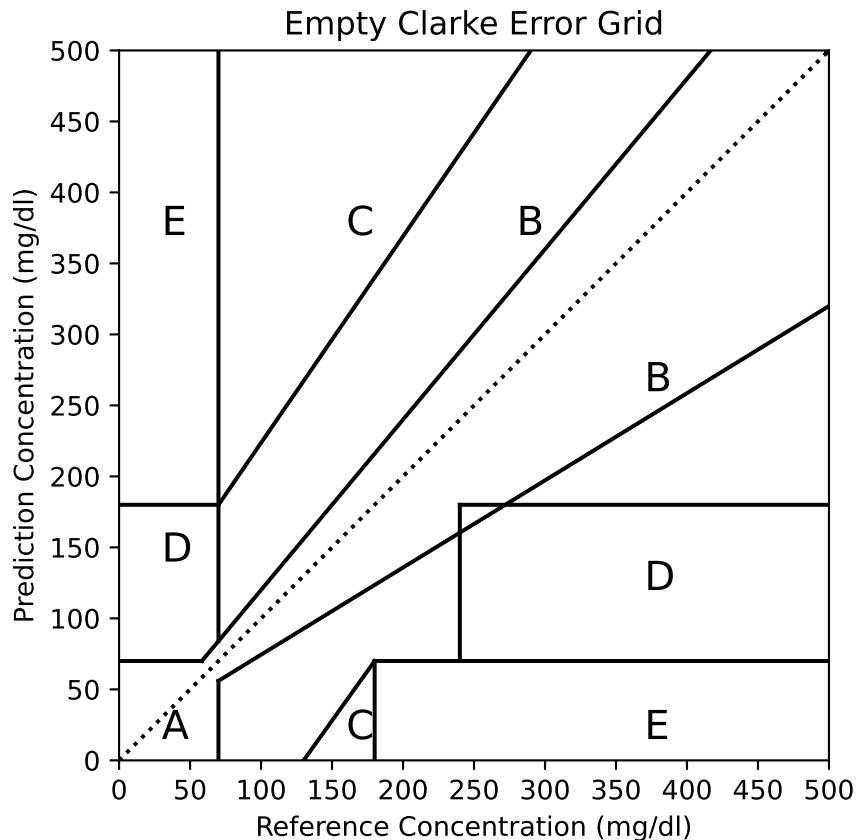


Figure 2.2: Empty Clarke Error Grid. Source: [Sue]

The CEG and other similar approaches have become increasingly relevant in the context of BGL prediction models in T1D, which is why some works have used it [All+11; Das+12;

WWM13; Zar+15; CV16; Con+17; Ali+18]. As prediction models, particularly those involving CGM data, have grown more sophisticated, the need for evaluation metrics that consider numerical accuracy and clinical relevance has become apparent. The CEG provides a valuable framework for evaluating these prediction models, helping to identify those that minimize numerical errors and avoid critical clinical errors. By applying the CEG to prediction model evaluation, researchers and clinicians gain a more comprehensive understanding of a prediction model’s effectiveness in real-world clinical settings. The grid not only helps identify prediction models likely to produce safe, reliable predictions (zones A and B) but also highlights those that could result in potentially harmful outcomes (zones C, D, and E). This approach underscores the importance of the CEG in ensuring that the evaluation of prediction models incorporates both traditional accuracy measures and a deeper consideration of patient safety, as using prediction models without proper evaluation could pose significant risks to T1D management.

2.4 Prediction of blood glucose levels

The prediction of BGLs is a fundamental aspect of DM management, as it allows individuals and healthcare providers to anticipate and mitigate potential fluctuations in BGL. Accurate BGL predictions enable proactive adjustments in medication, diet, and lifestyle, which are crucial for maintaining optimal glycemic control and preventing acute complications such as hypoglycemia and hyperglycemia. Advances in prediction models have significantly enhanced the ability to predict BGLs by analyzing complex patterns in CGM data and other relevant physiological and behavioral factors. These prediction models, which leverage large datasets and sophisticated algorithms, offer personalized insights into glucose dynamics, thereby improving treatment strategies and patient outcomes in DM care. Furthermore, ongoing research in this field focuses on integrating additional data sources, such as wearable and mobile devices, to further refine and enhance the capabilities of prediction models, ultimately aiming to provide more accurate and individualized DM management solutions [Jac+24].

Researchers have explored various techniques over the years to predict BGLs in individuals, achieving different levels of success. In [Bun+13], the authors propose a physiological model that uses mathematical equations to capture BGL trends. While equation-based approaches can provide acceptable results, they require significant cognitive effort to formulate and lack scalability, as new features necessitate redesigning the model. This mathematical model outperformed physicians’ predictions and demonstrated flexibility in combination with other methods. For example, in [Con+17], researchers combined it with a heuristic search algorithm to model the effects of carbohydrates and insulin on BGLs.

Statistical approaches have also been widely employed. Traditionally, AutoRegressive Integrated Moving Average (ARIMA) has been one of the most commonly used techniques in time series forecasting. In recent years, researchers have used variants of ARIMA for predicting BGLs, such as [Yan+19], which uses ARIMA with adaptive orders to try to capture the non-stationary changes of the BGLs over time. In [Pre+21], the investigators tested an ARIMA algorithm on the same dataset as thirty different linear and nonlinear prediction algorithms, including Long Short-Term Memory (LSTM) and feed-forward neural networks, outperformed them all with results of 22.15 (mg/dL) RMSE error for 30 minutes prediction. Several papers, such as those by [AAN22; ZG22; ZWY22], use other statistical methods. Remarkably, [AAN22] experimented with a long-term prediction horizon (PH) of 6 days, while most works use 30-to-60-minute PH, which are considered rigid and challenging to improve.

In recent years, researchers have primarily based their approaches on ANN. In [EII20], the authors suggest a 1-dimensional filter Convolutional Neural Network (CNN) and test it with five different forecasting strategies. The algorithm outperforms an LSTM algorithm also implemented by the author, obtaining an RMSE of 8.68 mg/dL for a 30-minute PH. In [Li+20b], the authors proposed a dilated CNN algorithm. Dilated CNNs can increase the receptive field of the network without increasing the number of parameters, allowing it to capture temporal patterns over a broader range of time steps. In addition, [Ali+19; Zhu+21b] examines ANN and Autoregressive Neural Networks.

However, among the various algorithms employed in BGL prediction, the Recurrent Neural Network (RNN) technique has gained significant popularity and is considered the leading approach. RNNs are a powerful technique that implements the concept of *memory* to ANN [Alh+22]. The main problem with classical RNN is the vanishing or exploding gradient problem [BSF94]. For this reason, most publications implement variations of classical RNN units such as LSTM [Mir+17; Ali+19; Mir+19; Aie+20; Mar+20; MO20; Nas+21] or dilated RNN [Zhu+20].

The work [Mir+17] creates a personalized LSTM prediction model per patient, improving the results of the previous work [Bun+13] using the same dataset. On the other hand, [Ali+19] utilizes the LSTM algorithm to study a large and heterogeneous cohort of patients and then applies it to completely new patients. The main objective of this work is to learn a generalizable prediction model that can easily be extrapolated to real-life applications. Several works have taken the theoretical base of LSTM and modified it to try to get more robust models that give better results. Examples include [Mir+19] with a Memory-Augmented LSTM that allows searching for similar BGL trends further back in time, [Aie+20] whose LSTM takes into account both past information and the suggested future information as inputs, or [Nas+21] that combines RNN with Restricted Boltzmann Machines, a type of artificial neural network that is used for unsupervised learning.

Another key parameter in BGL prediction models is the PH over which predictions will be made. The use of PH of 30 and 60 minutes is the more common one. According to the current state of the art, predicting BGL 15 minutes into the future is relatively easy, and for more than 60 minutes the results are usually too poor to be considered. Frequently, new publications improve the results for 30- and 60-minute PH, but few are venturing to increase these PH [TKT22]. Taking into account the papers from the state of the art that use data from real patients and have at least two weeks of data per patient, the best BGLs prediction models achieve an RMSE between 15 and 20 mg/dL for a 30-minute PH, and between 24 and 32 mg/dL for 60-minutes [Ali+19; Mir+19; Li+20a; Mar+20; Nas+21; Nem+22].

2.5 Clustering and prediction of blood glucose levels

Unsupervised learning involves building models using a dataset composed solely of input features without any information about categories or classifications of the examples. This form of learning relies on observation and discovery, where the learning system analyzes a series of entities and identifies common characteristics among them, allowing these entities to be grouped into conceptual clusters. Unsupervised learning aims to classify data in a way that enables the development of tools or models that would not make sense without this categorization. Moreover, only the classification can provide substantial insights, such as revealing patterns or relationships previously unknown to domain experts. For example, in a group of patients

suffering from the same disease, proper clustering could uncover risk factors or associations between symptoms that were not previously suspected [Mit97].

In BGL prediction, clustering algorithms, a category of unsupervised learning methods, have been explored to improve the accuracy and personalization of prediction models for DM management, particularly for T1D. This technique may uncover hidden patterns and structures in CGM data, which is valuable for predicting glucose trends and tailoring DM treatment to individual patients. The article [Con+17] is among the first to effectively explore the benefits of using clustering algorithms to create patient profiles for improving BGL prediction in T1D management. The study introduces a clinical decision support system that combines clustering techniques to identify characteristic glycemic profiles with predictive modeling to forecast BGLs based on these profiles. By simulating various patient scenarios and using a clustering approach based on the normalized compression distance (NCD), the researchers demonstrate that identifying distinct patient profiles allows for more tailored and accurate glucose prediction models.

In the study [Eis+20], clustering algorithms are employed to analyze and identify diurnal patterns in the daily routines of individuals with T1D. The primary objective of using clustering in this research is to improve the settings of bolus advisors (BA), which are decision support tools used to calculate insulin doses. The study uses K-means [REF] clustering on time-series data of daily glucose measurements and other related factors to automatically determine optimal time blocks for insulin administration. This approach addresses the limitations of current manual settings, enhancing personalization and accuracy in insulin dosing. By clustering the timestamps of routine measurements, the model suggests personalized adjustments to BA settings, helping to adapt to changes in patients' daily activities and improving glycemic control.

In the research [Lob+22], clustering algorithms are employed to classify daily CGM time series data into representative patterns. The primary goal of using clustering in this context is to reduce the complexity of CGM data by categorizing it into a finite set of daily profiles that can capture the typical glucose variability observed in patients with DM. This classification helps identify clinically relevant patterns and can be used to inform prediction models, decision support systems, and automated control systems, such as artificial pancreas devices. By grouping similar glucose patterns, the study aims to enhance the understanding of patient-specific glucose dynamics, crucial for developing personalized treatment plans and improving DM management strategies. The clustered profiles are a foundation for more robust and interpretable prediction modeling, particularly in capturing intra-patient variability and its impact on glucose levels.

By using clustering techniques, researchers have the potential to develop more accurate and individualized prediction models. This can lead to better management strategies tailored to the unique needs of T1D patients. For instance, the investigation [Con+19] investigates how clustering, specifically using the CHAID algorithm [Kas80], enhances the accuracy of Genetic Programming models for predicting BGLs in T1D patients. The study creates more tailored prediction models that capture specific glucose patterns by classifying glucose data into clusters based on time-related variables. The results show that models using clustered data provide significantly improved predictions, particularly for shorter prediction intervals, by better accounting for temporal and behavioral variations in BGLs. This approach demonstrates the potential for more personalized and clinically relevant predictions, ultimately supporting more effective DM management strategies.

Likewise, [Don+19] uses clustering algorithms to improve the accuracy of BGL predictions in DM patients. The authors introduce a novel approach, Clu-RNN, which integrates a clustering step using the K-means algorithm before applying a RNN. The clustering step groups patients based on their daily BGL fluctuation patterns, allowing the prediction model to account for variations in BGL dynamics more effectively. By preprocessing the data into clusters, using the K-means algorithm, capture different glycemic patterns, Clu-RNN enhances the prediction model's ability to provide more accurate and personalized glucose predictions compared to traditional methods like Support Vector Regression and standard RNNs. Finally, the article [Pre+22] discusses the use of fuzzy C-means clustering [Yan93] to improve BGL prediction T1D management. The researchers group similar postprandial glycemic profiles, which are particularly useful for handling overlapping data where patient glucose responses might not fit neatly into distinct categories. For each cluster identified, they develop a seasonal stochastic model (C-SARIMA) tailored to the specific glucose dynamics within that group.

Chapter 3

T1DiabetesGranada: a longitudinal dataset of continuous glucose measurements data of type 1 diabetes mellitus patients

3.1 Introduction

To conduct adequate research on intelligent techniques that support T1D patients in better managing their condition through continuous BGL monitoring, it is essential to have access to real, continuous BGL measurements. After an extensive search in Section 2.2 for datasets containing continuous BGL monitoring data from T1D patients and additional clinical and relevant information, it became evident that most studies rely on private or artificially generated data. Although some public datasets exist, they often lack the necessary quality regarding patient numbers, measurement intervals, and overall data volume required for comprehensive analysis. Consequently, the decision was made to create a new dataset incorporating all the required characteristics to support the research objectives effectively.

This chapter outlines the process of creating the "T1DiabetesGranada: a longitudinal multi-modal dataset of type 1 diabetes mellitus" [RL+23b; RL+23a]. It describes the criteria for participant onboarding, the methods used for data collection and processing, and the specific characteristics of the collected data. Additionally, it provides tools for using the dataset, as it is publicly available.

3.2 Methods

3.2.1 Ethical approval

Before starting the data collection process, approval from the Ethics Committee of Biomedical Research of the Province of Granada (CEIm/CEI GRANADA) was required due to the sensitive nature of the data to be collected. This study was reviewed and approved by the Ethics Committee of Biomedical Research of the Province of Granada (CEIm/CEI GRANADA) under Protocol Code: K134665CRL, Ethics Portal Code: 0698-N-21. The data has been authorized

for publication under a Data Usage Agreement, with the approval of the Ethics Committee serving as a testament to the ethical standards of the study.

3.2.2 Participant onboarding

Participants had to be patients at the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain. They had to be patients with T1D and be selected to wear a *FreeStyle Libre* device (*Abbott Diabetes Care, Inc., Alameda, CA, USA*). The study began on January 6th, 2018, and ended on March 21st, 2022, eventually involving 736 patients.

The enrolment into the study began when the patient was informed that had been selected to use the FGM, because they met the required eligibility criteria. Then, the patient visited the Clinical Unit of Endocrinology and Nutrition and received an explanation of how the sensor worked and, its potential for T1D management and the handling of the collected data. During this visit, patients were asked to give their consent to participate in the study and were informed of the possibility that their data would be shared anonymously. This was followed by a training session where the patient learnt how to wear and, operate the device and upload the data to the cloud platform. To upload the data, the patient had to register on the system and give consent for their BGL measurements and demographic information to be used for research purposes. They consented to access, use, and share the anonymized data. Should a participant wanted to withdraw from the study they had to unregister from the system or make a specific request. From then on, no further data was collected. However, the anonymized collected data was persisted. In any case, no participant withdrew from the study.

3.2.3 Data collection

The most commonly used FGM device during the study was *FreeStyle Libre 2*, although its first version, *FreeStyle Libre*, was also used in some cases at the beginning of the study. Both versions of the device are very similar and are manufactured by *Abbott Diabetes Care, Inc., Alameda, CA, USA* [Abb23]. These devices have a sensor in the form of a tiny needle that when introduced into the tissue measures the glucose level in the interstitial fluid. Each device has a service life of 14 days, during which it is not necessary to recharge the battery or perform any other action on it. After these 14 days, the device must be replaced with a new one.

Measurements of glucose in the interstitial fluid are recorded at 15-minute intervals. These measurements are stored in the device memory, which can hold a maximum of 8 hours of data. Before these 8 hours have elapsed, it is necessary to scan the FGM with a Near Field Communication (NFC) device, either a mobile phone or a *FreeStyle Libre Reader*. Once the scan takes place, the data is copied from the FGM device to the NFC device. Also, each time a patient performs an NFC scan, the current BGL measurement is added to the data as an extra measurement point. Then, when the NFC device used to collect the measurements is connected to the Internet, the data is transferred to the *LibreView* cloud platform.

In addition to BGLs, demographic and clinical information from patients were also collected in the study. The first time a patient visits the Clinical Unit of Endocrinology and Nutrition, data, such as birth date, pathological history of other diseases, home address and contact telephone numbers, are collected. For privacy reasons and relevance to T1D, only year of birth and additional diagnoses of other diseases were included in the dataset. The physicians of

the endocrinology unit schedule the following visits to the clinic considering the status of each patient (e.g. every three months or every six months) and request a series of biochemical tests for the days prior to the consultation to measure their biochemical parameters. The values of the patients' biochemical parameters obtained during the study period were also included as part of the dataset.

3.2.4 Data preparation

Independent technicians from the Information Technology Service of the San Cecilio University Hospital of Granada were designated for conducting the data anonymization process. They eliminated information that was confidential to the patients and irrelevant to the study such as name, e-mail, and medical record numbers. In addition, they assigned each patient a unique identifier to avoid revealing the identity of the patient.

Some basic data cleaning tasks were performed on the anonymized data, such as removal of duplicate rows, removal of rows with relevant missing values, and removal of irrelevant or empty columns. Furthermore, column names were translated from Spanish (local language) to English and some variables values were recoded into English, for example sex and the names of the biochemical parameters. Patients' diagnoses had an associated code and description following the standard of the Spanish government's Ministry of Health [Min14], so a mapping of the codes to the equivalent English version of the standard [Cen14] was performed. In addition, the values of some variables were reformatted. For instance the date fields in DD-MM-YYYY format were transformed to YYYY-MM-DD format to optimize tasks like sorting. Finally, all the files that compose the dataset were sorted by patient identifier and date if available.

3.3 Data records

The dataset is available for open access under specific permission via the Zenodo repository **T1DiabetesGranada: a longitudinal multi-modal dataset of type 1 diabetes mellitus** [RL+23a]. The data is stored in four comma-separated values (*CSV*) files which are presented in Table 3.1 and described in detail below.

Table 3.1: Overview of the T1DiabetesGranada dataset.

File Name	Number of records	Number of variables	Size (Bytes)	Lost values	Description
Patient_info.csv	736	11	8 096	Yes	File containing information about the patients.
Glucose_measurements.csv	22 671 708	4	90 686 832	No	File containing the continuous blood glucose level measurements of the patients.
Biochemical_parameters.csv	87 482	4	349 928	No	File containing data of the biochemical tests performed on patients to measure their biochemical parameters.
Diagnostics.csv	1 757	3	5 271	No	File containing diagnoses of diabetes mellitus complications or other diseases that patients have in addition to T1D mellitus.

3.3.1 Patient information

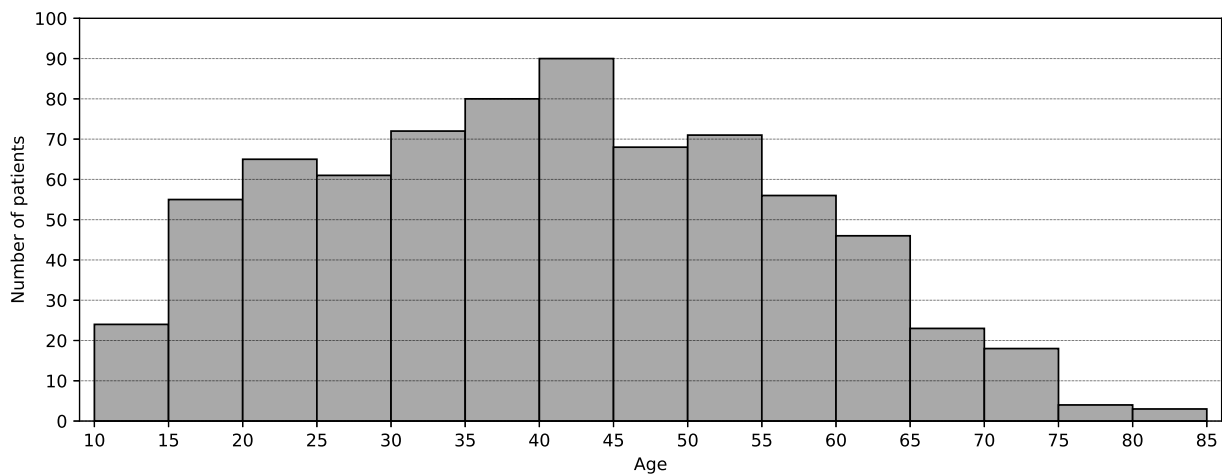
Patient_info.csv is the file containing information about the patients, such as demographic data, start and end dates of BGL measurements and biochemical parameters, number of biochemical parameters or number of diagnostics. This file is composed of 736 records, one for each patient in the dataset. Table 3.2 shows the detail of the eleven variables that make up the file *Patient_info.csv*. "Patient_ID" is an alphanumeric variable that uniquely identifies the patients in all files of the dataset. "Sex" codifies the sex of the patient and the distribution of this variable is balanced in the sample with 373 female patients (50.68%) and 363 male patients (49.32%). "Birth_year" indicates the year of birth of the patient and ranges from 1936 to 2005. The age of the patients at the beginning of the study (January 6th, 2018) was 40.34 ± 15.77 years and ranged from 12 to 81 years. The distribution of the patients' age is represented in Figure 3.1. "Initial_measurement_date" and "Final_measurement_date" mark the date of the first and the last BGL measurement of each patient in the study. This information is extracted from the file *Glucose_measurements.csv* by searching for the date of the earliest and the latest BGL measurement of each patient. "Number_of_days_with_measures" is the number of days with measurements per patient, this means the number of days in which the patient has at least one BGL measurement, with an average of 350.24 ± 284.15 days. This information is extracted from the file *Glucose_measurements.csv* and the histogram of this variable is shown in Figure 3.2. "Number_of_measurements" represents the total number of BGL measurements per patient, with an average of 30802.95 ± 25704.87 , and the information was extracted from the file *Glucose_measurements.csv*. Figure 3.3 depicts the number of patients participating in the study and the number of BGL measurements collected across time. Both the number of patients and the number of measurements have increased since the beginning of the study. "Initial_biochemical_parameters_date" and "Final_biochemical_parameters_date" are the dates of the first and the last time a biochemical parameter is measured for each patient. This information is extracted from the file *Biochemical_parameters.csv* by searching for the date of the earliest and the latest value of biochemical parameter of each patient. "Number_of_biochemical_parameters" represents the number of biochemical parameters values per patient. The average of this variable is 120.00 ± 87.83 calculated over the 723 patients that have available some values. This information is extracted from the file *Biochemical_parameters.csv*. "Number_of_diagnostics" represents the number of diagnostics per patient. The average of this variable is 3.44 ± 2.95 calculated over the 511 patients that have available some diagnostics. This information is extracted from the file *Diagnostics.csv*.

3.3.2 Glucose measurements

Glucose_measurements.csv is the file containing the continuous BGL measurements of the patients. The file is composed of more than 22.6 million records that constitute around 257 780 days of continuous BGL measurements. In this file there are multiple records with the same "Patient_ID" since each patient has several BGL measurements, usually one every 15 minutes. Table 3.3 describes the variables that make up the file *Glucose_measurements.csv*. "Measurement_date" and "Measurement_time" are the date and time in which the measurement of the BGL takes place. "Measurement" is the value of the BGLs of the patient measured in mg/dL and it is observed to be in average 164.78 ± 71.57 mg/dL. Figure 3.4a illustrates the distribution of the BGL measurements across the entire sample. Most of the values are between 100 mg/dL and 200 mg/dL with a median close to 150 mg/dL, and values above 350 mg/dL are considered extreme. It is also interesting to analyze the distribution of continuous BGL measurements in

Table 3.2: Variables detail from *Patient_info.csv* file.

Variable name	Type	Values	Description
Patient_ID	String	LIB19XXXX	Unique identifier of the patient.
Sex	String	One of {'F', 'M'}	Sex of the patient.
Birth_year	Date	YYYY	Year of birth of the patient.
Initial_measurement_date	Date	YYYY-MM-DD	Date of the first blood glucose level measurement of the patient in the <i>Glucose_measurements.csv</i> file.
Final_measurement_date	Date	YYYY-MM-DD	Date of the last blood glucose level measurement of the patient in the <i>Glucose_measurements.csv</i> file.
Number_of_days_with_measures	Integer	8 to 1 463	Number of days with blood glucose level measurements of the patient, extracted from the <i>Glucose_measurements.csv</i> file.
Number_of_measurements	Integer	400 to 137 292	Number of blood glucose level measurements of the patient, extracted from the <i>Glucose_measurements.csv</i> file.
Initial_biochemical_parameters_date	Date	YYYY-MM-DD	Date of the first biochemical test to measure some biochemical parameter of the patient, extracted from the <i>Biochemical_parameters.csv</i> file.
Final_biochemical_parameters_date	Date	YYYY-MM-DD	Date of the last biochemical test to measure some biochemical parameter of the patient, extracted from the <i>Biochemical_parameters.csv</i> file.
Number_of_biochemical_parameters	Integer	4 to 846	Number of biochemical parameters measured on the patient, extracted from the <i>Biochemical_parameters.csv</i> file.
Number_of_diagnostics	Integer	1 to 24	Number of diagnoses realized to the patient, extracted from the <i>Diagnostics.csv</i> file.

Figure 3.1: Distribution of the age of the patients at the start of the data collection (January 6th, 2018). Source: [RL+23b].

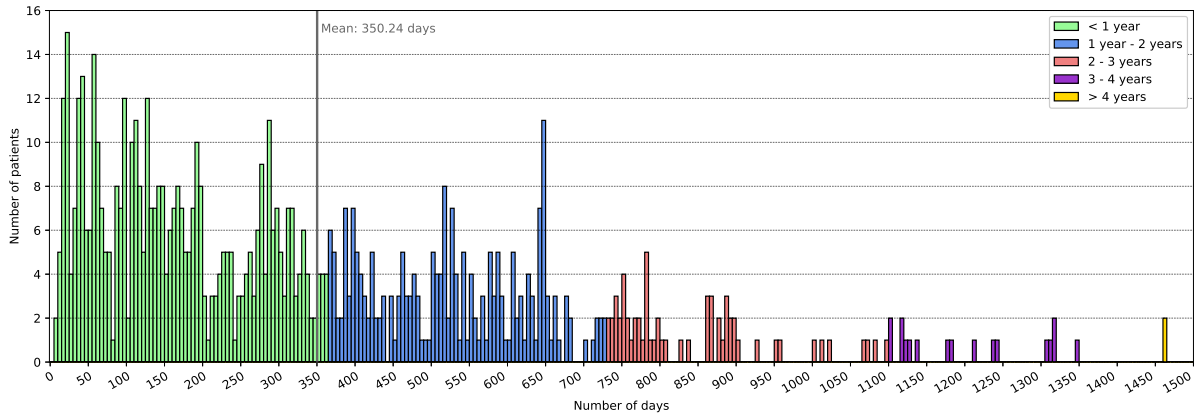


Figure 3.2: Number of patients by number of days with blood glucose level measurements. The colors depict periods of one year. The mean number of days is represented by a vertical line. Source: [RL+23b].

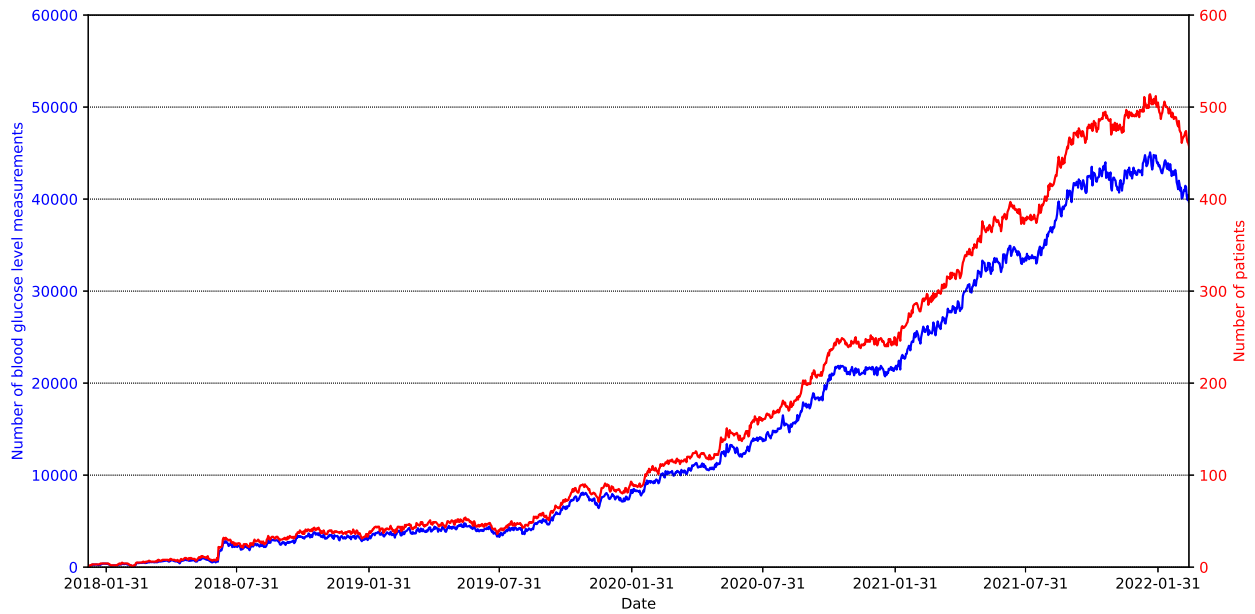


Figure 3.3: Number of patients and blood glucose level measurements by date. Source: [RL+23b].

relation to other variables. Figure 3.4b depicts the data distribution stratified by sex, while Figure 3.4c illustrates the distribution according to various age ranges. Both figures show that the distribution of BGL measurements exhibits minimal variation with respect to gender and age range, mirroring the overall sample pattern depicted in Figure 3.4a. Doctors normally consider some specific BGL ranges: time below range (TBR), time in range (TIR), and time above range (TAR). Standardized metrics for the use of CGM for clinical care compute the percentage of BGL measurements and time as [Els+23]: <54 mg/dL (TBR, level 2 hypoglycemia); 54–69 mg/dL (TBR, level 1 hypoglycemia); 70–180 mg/dL (TIR); 181–250 mg/dL (TAR, level 1 hyperglycemia); >250 mg/dL (TAR, level 2 hyperglycemia). Figure 3.5 displays the count of BGL measurements within specific BGL intervals and age groupings for the sampled population. The majority of the BGL measurements are in TIR, and the out-of-range measurements are mostly TAR. Finally, as previously noted, Figure 3.3 shows the connection between the count of participating patients and the quantity of BGL measurements over time. The blue plot clearly depicts an upward trend, signifying a growth in the daily count of continuous BGL measurements as time progresses. This phenomenon is largely attributable to the concurrent growth in the number of patients, as indicated by the red plot, hence resulting in the increase of the number of daily BGL measurements.

Table 3.3: Variables detail from *Glucose_measurements.csv* file.

Variable name	Type	Values	Description
Patient_ID	String	LIB19XXXX	Unique identifier of the patient.
Measurement_date	Date	YYYY-MM-DD	Date of the blood glucose level measurement.
Measurement_time	Time	HH:MM:SS	Time of the blood glucose level measurement.
Measurement	Integer	40 to 500	Value of the blood glucose level measurement in mg/dL.

3.3.3 Biochemical parameters

Biochemical_parameters.csv is the file containing data of the biochemical tests performed on patients to measure their biochemical parameters. This file is composed of 87 482 records. A patient, identified by their "Patient_ID", can have more than one record in this file, one for each biochemical parameter measured on the patient throughout the study. Table 3.4 explains the variables that make up the *Biochemical_parameters.csv* file. "Reception_date" is the date when the sample to measure the biochemical parameter is received in the laboratory. "Name" indicates the name of the measured biochemical parameter and "Value" the value of the biochemical parameter. Throughout the study, 17 different types of biochemical parameters were measured. Table 3.5 shows the measurement units of these biochemical parameters. Table 3.6 provides a summary of statistical information regarding the count of biochemical parameters per patient. The most prevalent biochemical parameters are "creatinine" with an average of 11.54 ± 12.05 occurrences and "glucose" with an average of 11.34 ± 11.63 occurrences. Conversely, the least frequently encountered parameters are "IA2 ANTIBODIES" with an average of 0.09 ± 0.30 occurrences and "insulin" with an average of 0.09 ± 0.41 occurrences. Furthermore, Table 3.7 presents a summary of statistical data pertaining to the values of these biochemical parameters. Figure 3.6 depicts the distribution in the sample of the values of the nine most common biochemical parameters.

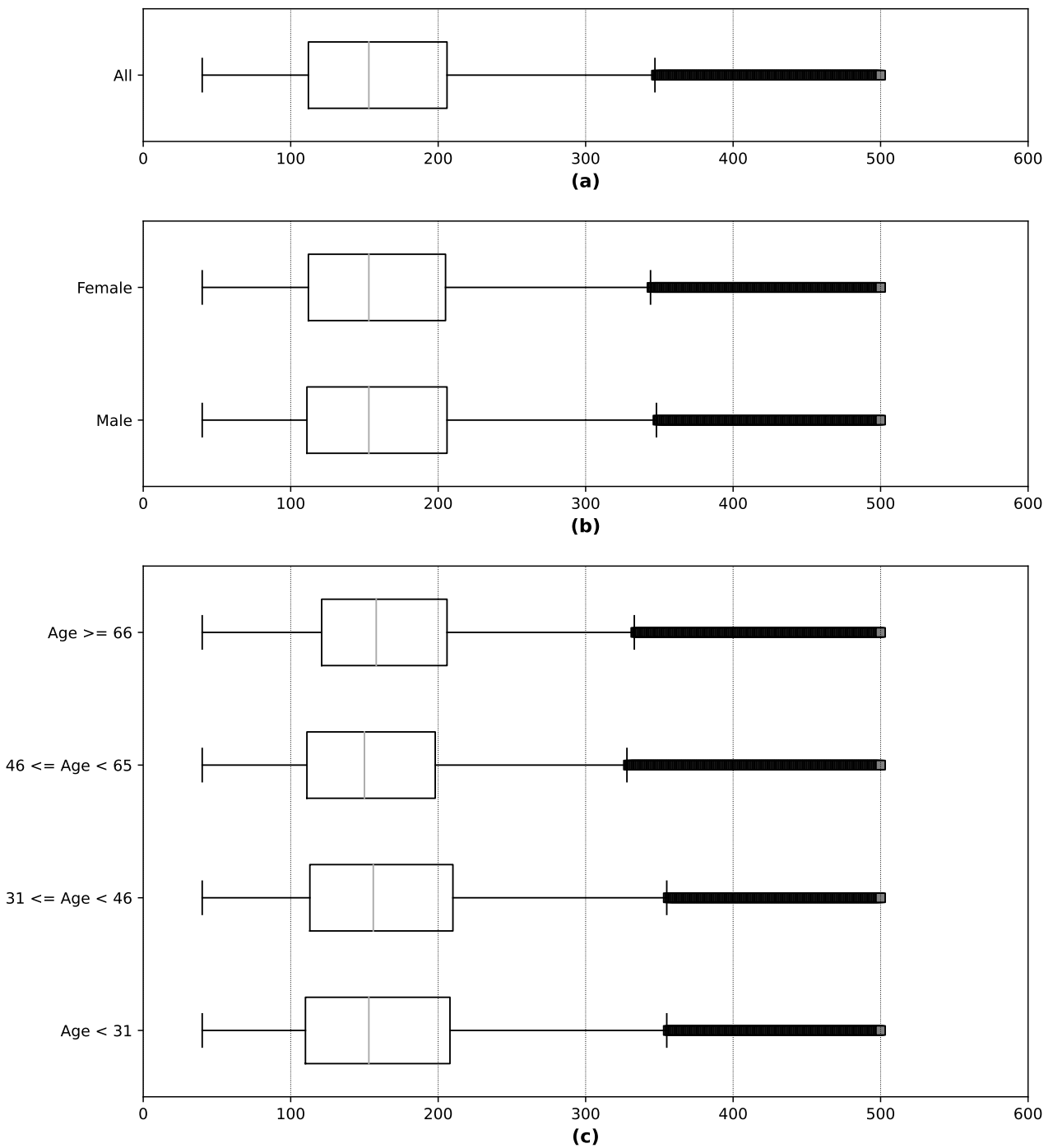


Figure 3.4: Data distribution of the blood glucose level measurements: (a) Overall; (b) By sex; and (c) By age. Source: [RL+23b].

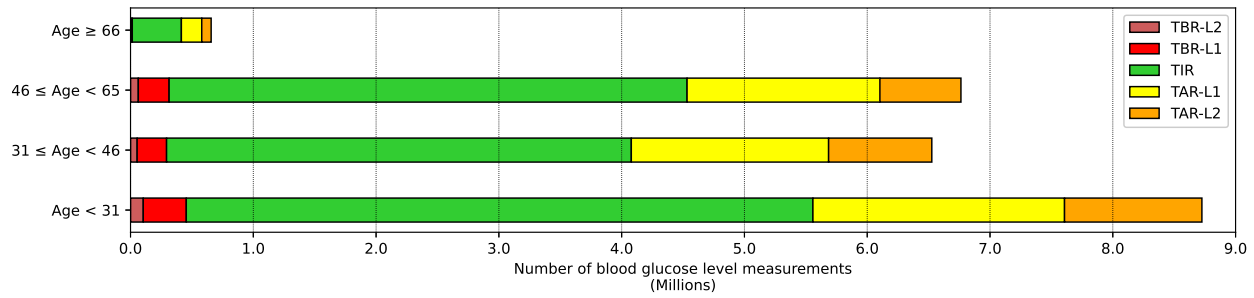


Figure 3.5: Percentage of blood glucose level measurements per level ranges and age ranges. Blood glucose level ranges are represented by colors and defined as: TBR-L2, time below range with level 2 hypoglycemia (< 54 mg/dL); TBR-L1, time below range with level 1 hypoglycemia (54 mg/dL - 69 mg/dL); TIR, time in range (70 mg/dL - 180 mg/dL); TAR-L1, time above range with level 1 hyperglycemia (181 mg/dL - 250 mg/dL). TAR-L2: time above range with level 2 hyperglycemia (≥ 251 mg/dL). Source: [RL+23b].

Table 3.4: Variables detail from *Biochemical_parameters.csv* file.

Variable name	Type	Values	Description
Patient_ID	String	LIB19XXXX	Unique identifier of the patient.
Reception_date	String	YYYY-MM-DD	Date of receipt in the laboratory of the sample to measure the biochemical parameter.
Name	String	One of {'Potassium', 'HDL cholesterol', 'Gamma-glutamyl Transferase (GGT)', 'Creatinine', 'Glucose', 'Uric acid', 'Triglycerides', 'Alanine transaminase (GPT)', 'Chlorine', 'Thyrotropin (TSH)', 'Sodium', 'Glycated hemoglobin (Ac)', 'Total cholesterol', 'Albumin (urine)', 'Creatinine (urine)', 'Insulin', 'IA ANTIBODIES'}	Name of the measured biochemical parameter.
Value	Float	-4.0 to 6446.74	Value of the biochemical parameter.

Table 3.5: Measurement unit of the biochemical parameters in *Biochemical_parameters.csv* file.

Biochemical parameter name	Measurement unit
Potassium	mEq/L
HDL cholesterol	mg/dL
Gamma-glutamyl Transferase (GGT)	U/L
Creatinine	mg/dL
Glucose	mg/dL
Uric acid	mg/dL
Triglycerides	mg/dL
Alanine transaminase (GPT)	U/L
Chlorine	mEq/L
Thyrotropin (TSH)	μ UI/mL
Sodium	mEq/L
Glycated hemoglobin (Ac)	%
Total cholesterol	mg/dL
Albumin (urine)	mg/dL
Creatinine (urine)	mg/dL
Insulin	μ UI/mL
IA ANTIBODIES	U/mL

Table 3.6: Summary of statistics of the number of biochemical parameters per patient.

Biochemical Parameter	Mean	STD	Median	Minimum	Maximum
Alanine transaminase (GPT)	9.69	8.85	8	0	90
Albumin (urine)	5.82	2.88	6	0	21
Chlorine	2.63	6.40	1	0	74
Creatinine	11.54	12.05	9	0	115
Creatinine (urine)	5.99	3.15	6	0	27
Gamma-glutamyl Transferase (GGT)	8.27	7.68	7	0	89
Glucose	11.34	11.63	9	0	111
Glycated hemoglobin (A1c)	6.49	2.76	7	0	16
HDL cholesterol	6.88	3.48	7	0	26
IA2 ANTIBODIES	0.09	0.30	0	0	2
Insulin	0.09	0.41	0	0	6
Potassium	10.67	11.72	8	0	108
Sodium	10.62	11.54	8	0	107
Thyrotropin (TSH)	6.21	3.13	6	0	17
Total cholesterol	8.09	4.92	7	0	40
Triglycerides	7.87	4.65	7	0	36
Uric acid	6.57	4.81	6	0	41

Table 3.7: Summary of statistics of the biochemical parameters values.

Biochemical Parameter	Mean	STD	Median	Min	Max
Alanine transaminase (GPT)	26.98	44.62	19.00	-4.00	868.00
Albumin (urine)	4.86	26.56	0.70	0.01	992.20
Chlorine	102.96	5.34	103.00	76.00	136.00
Creatinine	1.04	0.95	0.80	0.15	11.55
Creatinine (urine)	114.14	66.80	101.41	2.00	543.46
Gamma-glutamyl Transferase (GGT)	43.80	113.55	19.00	5.00	2051.00
Glucose	163.04	85.40	146.00	10.00	979.00
Glycated hemoglobin (A1c)	7.82	1.39	7.60	4.00	18.00
HDL cholesterol	56.63	14.37	55.00	7.00	137.00
IA2 ANTIBODIES	409.64	1237.70	1.15	0.21	6446.74
Insulin	22.69	40.54	10.24	0.74	298.50
Potassium	4.43	0.66	4.40	1.90	22.60
Sodium	138.16	3.47	138.00	117.00	168.00
Thyrotropin (TSH)	2.87	4.68	2.22	0.01	204.89
Total cholesterol	169.45	39.93	167.00	27.00	703.00
Triglycerides	102.97	94.69	81.00	23.00	3447.00
Uric acid	4.39	1.54	4.20	1.00	14.20

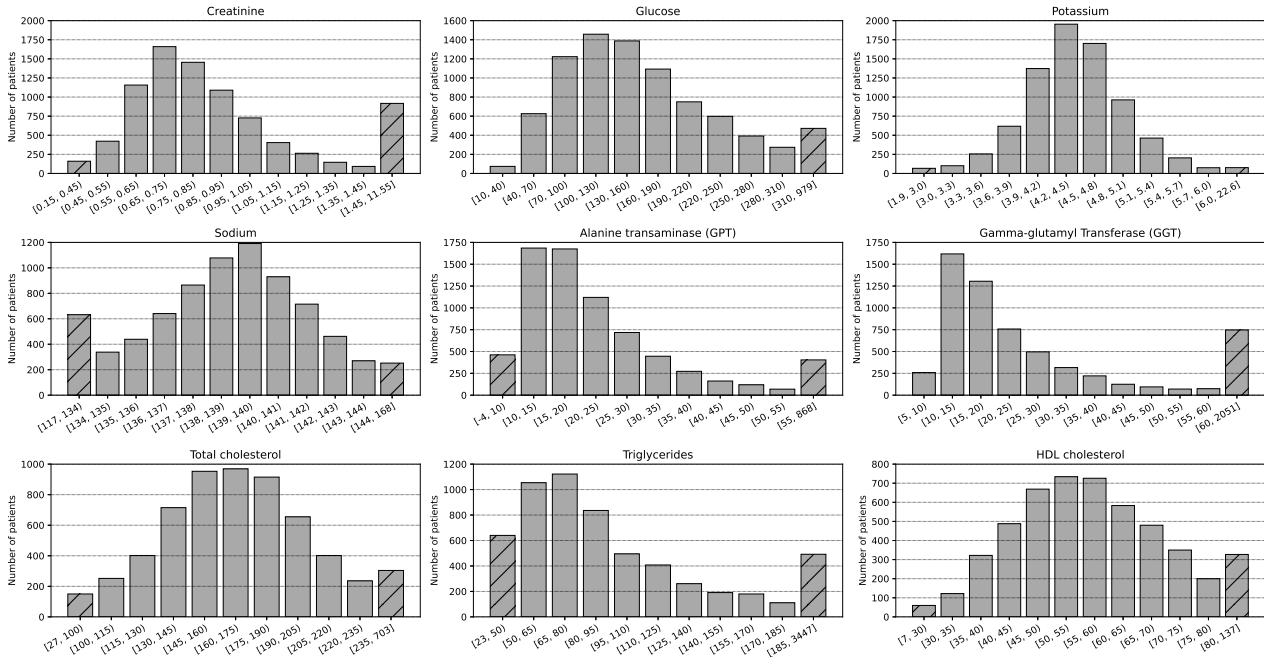


Figure 3.6: Distribution of the values of the most commonly measured biochemical parameters. The bars with lines do not have the same range breadth as the rest in each chart. Source: [RL+23b].

3.3.4 Diagnostics

Diagnostics.csv is the file containing diagnoses of DM complications or other diseases that patients have in addition to T1D. This file is composed of 1757 records. A patient, identified by their "Patient.ID", can have more than one record in this file, as many as diagnoses. Table 3.8 describes the variables that make up the file *Diagnosis.csv*. The diagnoses are represented by the ICD-9-CM standard code [Cen14] in the variable "Code" and the ICD-9-CM long description in "Description". In the *Diagnostics.csv* file there are 594 different types of diagnoses, Figure 3.7 shows the distribution of the ten most common ones.

Table 3.8: Variables detail from *Diagnostics.csv* file.

Variable name	Type	Values	Description
Patient.ID	String	LIB19XXXX	Unique identifier of the patient.
Code	String	594 unique values	ICD-9-CM diagnosis code.
Description	String	594 unique values	ICD-9-CM long description.

3.4 Technical validation

BGL measurements are collected using *FreeStyle Libre* devices, which are widely used for healthcare in patients with T1D. *Abbott Diabetes Care, Inc., Alameda, CA, USA*, the manufacturer company, has conducted validation studies of these devices concluding that the measurements made by their sensors compare to YSI analyzer devices (*Xylem Inc.*), the gold standard, yielding results of 99.9% of the time within zones A and B of the consensus error grid [Abb17]. In addi-

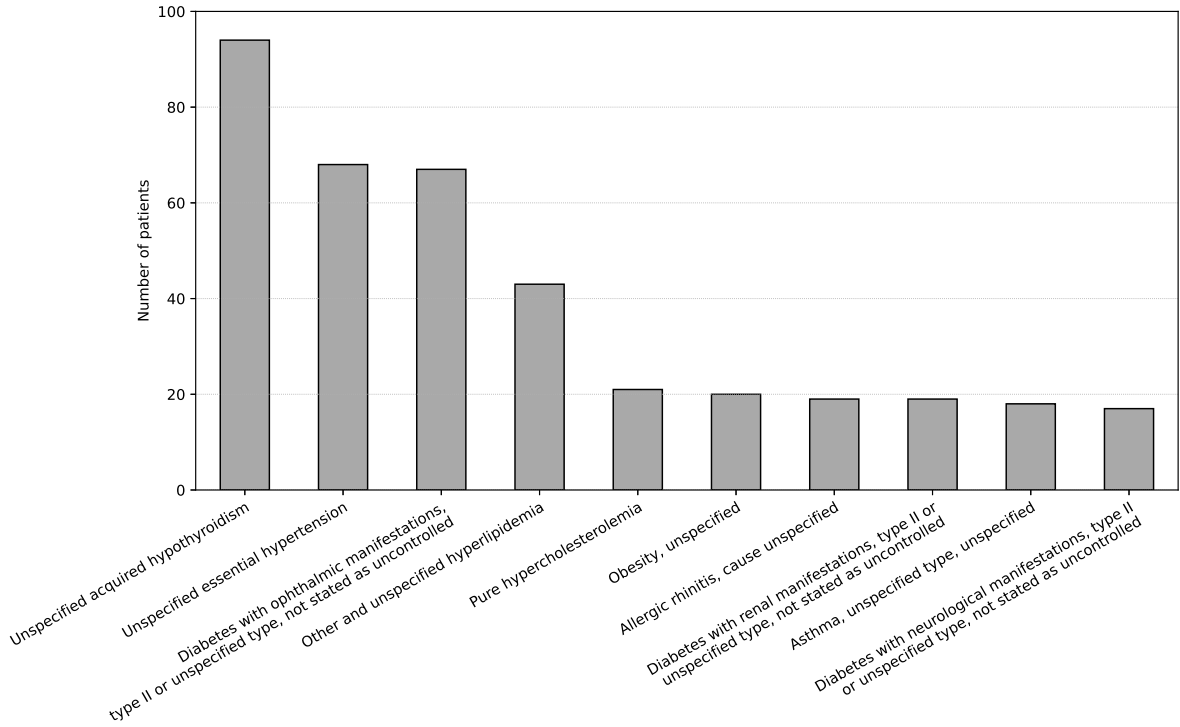


Figure 3.7: Number of patients per most common diagnoses of DM complications or other diseases. Source: [RL+23b].

tion, other studies external to the company concluded that the accuracy of the measurements is adequate [Tso+20].

Moreover, it was also checked in most cases the BGL measurements per patient were continuous (i.e. a sample at least every 15 minutes) in the *Glucose_measurements.csv* file as they should be.

3.5 Limitations

The current dataset faithfully represents the evolution of glucose levels over the time of the study. We firmly believe that these continuous glucose measurements are useful to researchers in the field, however there are some limitations to consider.

During the patient participation in the study there may be data gaps without BGL measurements due to two main reasons. The first reason is when the patient does not scan the FGM with an NFC device in less than 8 hours. Then, the BGL measurements are overwritten in the internal memory, thus losing the oldest data. The second reason is when the patient, after the 14-day life span of the FGM device, does not activate the replacement device early enough. Nonetheless these two situations were already considered in the protocol design in order to ensure that patients would proceed accordingly and do not lose data. Although BGL measurements are normally recorded every 15 minutes, there might be slight variations due to the tolerance of the device (± 1 min). Hence, measurement gaps are considered when the intervals are above 17 minutes. These gaps represent the 0.95% of the BGL measurements. Figure 3.8 shows the frequency of gaps of duration from 18 and 434 minutes as these represent statistically the majority of detected gaps.

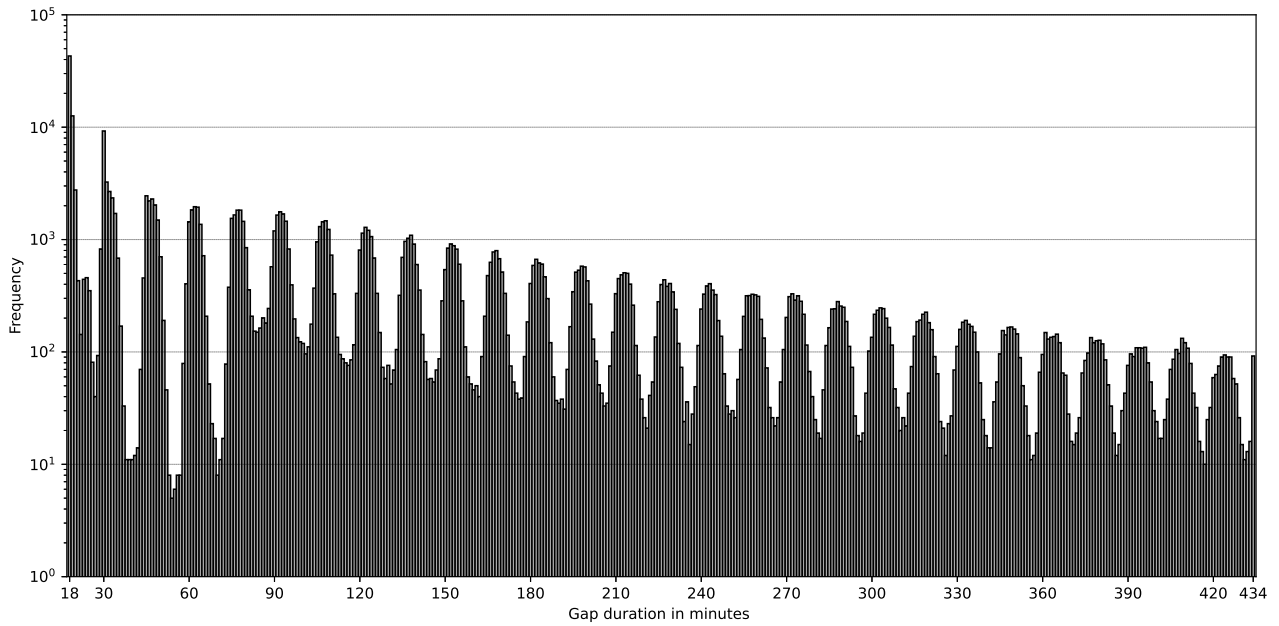


Figure 3.8: Logarithmic distribution of the gaps of blood glucose level measurements. Source: [RL+23b].

The duration of the participation of the patients varies due two main reasons. Firstly, the patients' enrolment in the study was progressive because the capacity to process all patients with T1D by the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada is limited. The enrolment was done in order of priority depending on the health status of the patients. Secondly, in seldom cases, the data collection ended due to different reasons, such as patients abandoned the use of the FGM device due to allergy to the glue used to attach it to the skin, death of the patient, transfer of the patient to another clinical unit, or the patient's personal decision to no longer use the FGM device.

3.6 Usage notes

The dataset is open under specific permission for research purposes in the Zenodo repository **T1DiabetesGranada: a longitudinal multi-modal dataset of type 1 diabetes mellitus** [RL+23a]. For data downloading, it is necessary to be authenticated on the Zenodo platform, accept the Data Usage Agreement and send a request specifying full name, email, and the justification of the data use. This request will be processed by the Secretary of the Department of Computer Engineering, Automatics, and Robotics of the University of Granada and access to the dataset will be granted.

The files that compose the dataset are CSV type files delimited by commas and are available in *T1DiabetesGranada.zip*. A Jupyter Notebook (Python v. 3.8) with code that may help to a better understanding of the dataset, with graphics and statistics, is available in *UsageNotes.zip*. Code availability details for generating the T1DiabetesGranada dataset are described in Appendix J, Section J.1.

Chapter 4

Understanding evaluation metrics for blood glucose level prediction

4.1 Introduction

Commonly used evaluation metrics for BGL prediction models in the literature tend to have a predominantly mathematical focus, meaning they are not clinically oriented, which is crucial in health-related tasks like these. Even in cases where clinical metrics are employed, the results are not analyzed separately across critical BGL ranges. Therefore, after creating a dataset with superior characteristics for conducting robust BGL prediction experimentation, this chapter will provide the necessary understanding to assess the evaluation capacity of existing methods. Besides, this research aims to improve the scenario of applying the resulting BGL prediction models in real-world settings, ensuring they are as objective and realistic as possible. Therefore, only BGL measurements are used as input for the prediction algorithms, as this is the most objective and easily obtainable measure when applying the results in a real-world environment. As discussed in Section 2.4, one of the most commonly used prediction algorithms in the state of the art for these tasks are ANNs, particularly RNNs. For this reason, the experimentation will employ two of the most representative prediction algorithms, an LSTM and a CNN, along with a simpler Linear model to establish a baseline for comparison.

4.2 Methods

4.2.1 Data preparation

The dataset file *Glucose_measurements.csv* with the BGL measurements, described in Section 3.3, must be transformed into a format suitable for supervised learning. This restructuring will allow prediction algorithms to use past BGL measurements to forecast future ones. Resampling is necessary because the time between consecutive samples varies due to both manual readings and issues such as delays (as comprehensively described in Section 3.5). Besides the prediction algorithms require consistent time intervals to ensure reliable predictions. After pre-processing, the dataset is adjusted to have one sample every 15 minutes. A possible strategy is to remove extra samples within intervals (downsampling) and fill in gaps by inserting empty measurements where data is missing (upsampling).

The downsampling process eliminates manual readings between the 15-minute automatic intervals and realigns measurements with slight time variations. The most recent record represents the BGL measurement when multiple occur within the same minute but at different seconds. In cases where manual readings fall between automatic ones, they are removed, while automatic measurements that closely align with the intended 15-minute intervals are kept and realigned. This ensures that the dataset maintains a consistent sampling rate. Figure 4.1 shows two examples of the resampling process. In example I, the pink circles represent four different measurements taken sequentially. A timestamp of 15 minutes is created from the first measurement. The first, second, and fourth measurements match the timestamp, so they are considered automatic measurements. The third measurement is a manual reading between the second and third marks of the timestamp. This third measurement is removed in the downsampling process, and the other three measurements are included in the dataset. Example II represents three automatic measurements, but the last two have deviations from the 15-minute timestamp and fall into the same interval. In this case, the strategy is to find the closest measurement to the timestamp. The second measurement is aligned to the timestamp at 15 minutes, and the third is assigned to the timestamp at 30 minutes; thus, the two measurements are realigned.

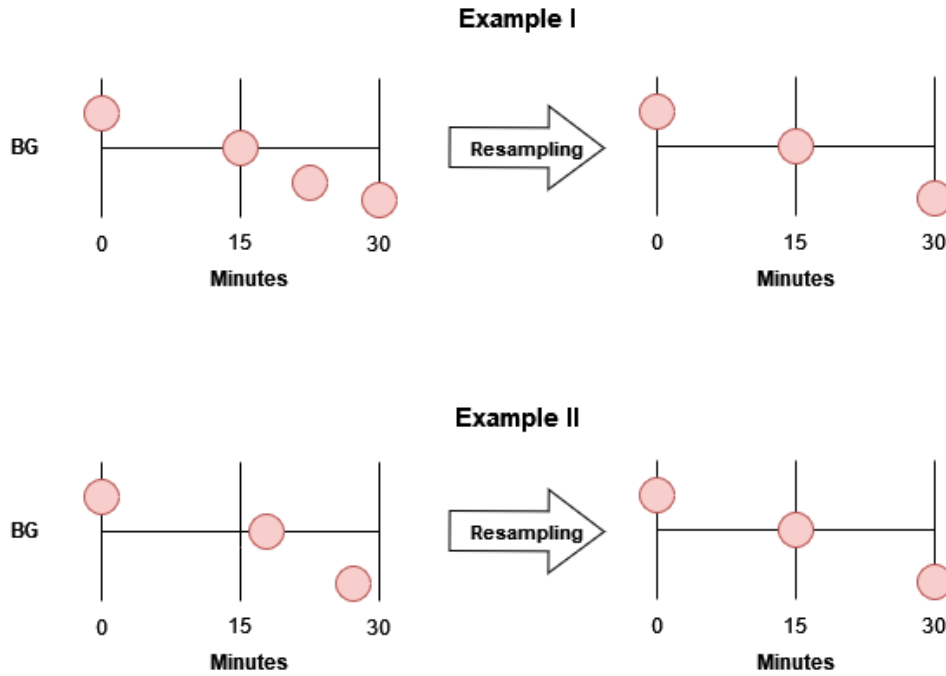


Figure 4.1: Examples of the resampling process. Source: own elaboration.

The upsampling process introduces significant challenges and potential biases due to the complexity of handling missing data. Simulating missing BGL measurements is unreliable because BGLs may change rapidly and non-linearly, leading to overfitting and poor predictions, especially over extended periods. Interpolation techniques are often imprecise and produce unrealistic trends, mainly when filling large gaps. Similarly, splitting the dataset into smaller segments disrupts the continuity of the data, complicating the prediction process and leading to multiple sub-datasets, which are harder to manage. Since both strategies often proved ineffective, it was decided to treat all missing data as unknown and discard sequences with gaps during the training of prediction algorithms. As a result, no upsampling was used in the end.

Only patients with an acceptable amount of data should be used in the experimentation process. Therefore, patients with at least one month (30 days) of continuous BGL measurements are selected. This period allows the model to capture a broader range of BGL variability, including daily, weekly, and monthly patterns influenced by lifestyle factors such as diet, exercise, professional life, or menstrual cycles in women’s cases. One month may provide enough data to train prediction algorithms like LSTM or CNN to avoid overfitting and improve generalization. Clinically, one month’s data reflects a more accurate picture of BGL management, capturing infrequent but critical events like hypoglycemia or hyperglycemia, which might not occur in shorter periods. Furthermore, this duration balances data sufficiency with practicality in real-world settings, supporting robust and meaningful model predictions. It should be noted that the number of measurements is not determined by directly examining the variable “Number_of_days_with_measures,” as described in Section 3.3.2. This is because it is possible for a patient to have more than 30 days of measurements with a low number of measurements. Instead, the focus is on ensuring the patient has at least the number of measurements equivalent to a complete month of monitoring. A complete day consists of 96 measurements (one every 15 minutes). Multiplying this by 30 days gives a total of 2880 measurements. Therefore, the criterion is that the “Number_of_measurements” described in Section 3.3.2 must match or exceed 2880. Following this process, 45 patients were excluded, leaving 691 patients for analysis.

Then, data must be reorganized as input sequences of measurements and their corresponding outputs or labels. The most straightforward strategy is to use all the measurements before the value to be predicted as input data and the value to be predicted as the output or label. Figure 4.2 shows an example of the technique, which uses a cumulative history length without maximum window size. Each cell in the figure represents a BGL measurement of the dataset. Each window is an input-output pair formed by the selected measurements, where the orange cells are the input sequence and the purple cell is the desired output. In this approach, where all past measurements are used before the prediction point, the input values, also called history length (HL), increase with each new prediction.

Windows / Time (min)	0'	15'	30'	45'	60'	75'	90'	105'	120'	135'
Window1										
Window2										
Window3										
Window4										
Window5										

History Length: All past values
Horizon Prediction: 2 samples (0.5 hours)

Figure 4.2: Sliding window scheme for a cumulative history length without maximum window size. Source: own elaboration.

The problem with the cumulative story length approach is that the input sequence length will be so long that the prediction cannot be calculated at some point. That is why it is necessary to set a common size for all the windows. The size of the window is determined by the HL plus the prediction horizon (PH). Some PHs are established based on the state of the

art, such as 30 and 60 minutes, also called short-term prediction, corresponding to 2 and 4 samples respectively. Extended PHs are also considered mid-term prediction, like 90 and 120 minutes, corresponding to 6 and 8 samples respectively, and finally, what is considered long-term prediction, such as 3 and 4 hours, corresponding to 12 and 16 samples, respectively. The selection of the HL was made by a tuning process that is explained in Section 4.3.2. The length of the input data (i.e., HL) will also determine the number of measurements required before the first prediction. During the data preparation process, windows containing empty measurements are discarded, either in the HL or the PH, which reduces the total number of windows. The selection of the HL was made by a tuning process that is explained in Section 4.3.2.

Another important decision is how the window slides along the time series data, i.e., how the samples are overlapped between one window and the next. Using a small scroll allows the creation of many windows, giving the prediction algorithm more opportunities to learn. On the other hand, overlapping measurements in different windows could cause overfitting problems, but the rapid changes in BGLs suggest that this is fine in this case. Therefore, the approach uses one sample shift for each new window, equivalent to a time interval between the windows of 15 minutes. Figure 4.3 shows an example for a window size of six samples, four as the history length and the other two as the PH, with a window shift of one sample.

Windows / Time (min)	0'	15'	30'	45'	60'	75'	90'	105'	120'	135'
Window1										
Window2										
Window3										
Window4										
Window5										

History Length: 4 samples (1 hour)
Horizon Prediction: 2 samples (0.5 hours)

Figure 4.3: Sliding window scheme for fixed window size. Source: own elaboration.

4.2.2 Single-output vs multi-output forecasting

The number of BGL measurements the prediction model can predict at each inference determines the output strategy. The single-output technique only predicts the value corresponding to the desired PH. In contrast, the multi-output technique can predict multiple BGL measurements. For example, Figure 4.3 shows windows for a PH of 2 samples. In a single-output approach, a prediction model only predicts the value at 75 minutes in the window "Window1". However, in a multi-output approach, the output also includes the prediction of other values in the PH. In the example of Window1, in addition to the 75 min prediction, the output also includes the value at 60 minutes. It is essential to consider that the implications of these approaches go further than the number of output values. Using a single-output strategy requires training a different prediction algorithm for each PH. On the other hand, a multi-output prediction model can predict the values of more than one PH in one inference, but this prediction is inherently more difficult because it requires modeling the joint probability of these future values.

Therefore, this thesis follows the single-output strategy, as in previous works like [BC20], with each prediction algorithm trained separately for each PH in the experiments.

4.2.3 Models architecture

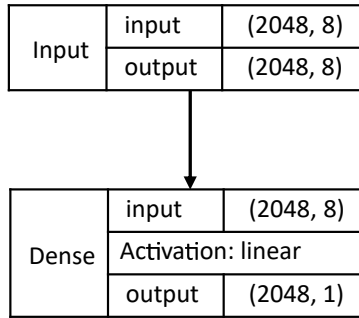
Three prediction algorithms were selected for the experiments, namely Linear, LSTM, and CNN. The work of [BC20] inspires the Linear and LSTM models, which achieved the top position in the Blood Glucose Level Prediction Challenge 2020 (BGLP) [Sma20]. On the other hand, the CNN model draws inspiration from [DA+22] due to its good performance. The referenced article used three types of inputs, namely CGM measurements, insulin-on-board, and ingested carbohydrates. However, the architecture has been adapted in the present thesis to use only CGM data as input.

The architectures that implement the three prediction algorithms offer different approaches to predicting outcomes based on input features. Their schemes are presented in Figure 4.4. The first architecture, a Linear, is shown in Figure 4.4a, is the simplest of the three, consisting of an input layer directly connected to a dense layer, which outputs a single prediction with a linear transformation. This structure focuses on simplicity and direct mapping of input to output without additional layers for feature extraction or temporal processing. The second architecture, an LSTM, is presented in Figure 4.4b, which starts with an input layer that feeds sequential data into an LSTM layer with 128 units, capturing temporal dependencies. The LSTM output is then passed to a dense layer that produces the final prediction. Finally, a CNN architecture is shown in Figure 4.4c, which begins with an input layer that processes time-series data, followed by two Conv1D layers with increasing filters and ReLU activations. Each convolutional layer is followed by MaxPooling1D layers that reduce the dimensionality of the data. The sequence is then flattened into a single vector and passed through a dense layer with 50 units and ReLU activation before reaching the output layer, which provides a single prediction with a linear activation. All architectures have an input layer of size 8 due to the HL selected in Section 4.3.2 and a batch size of 2048.

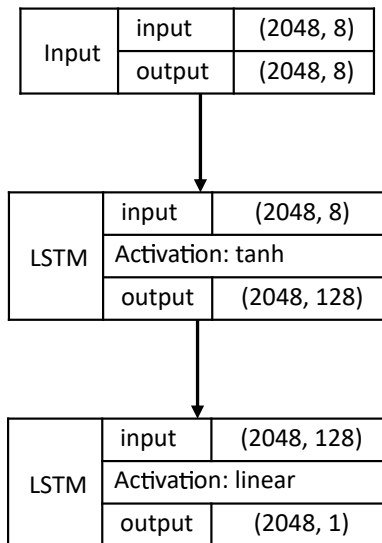
4.2.4 Evaluation metrics

As previously discussed in Section 2.3, two types of metrics are used to evaluate the performance of the models that predict BGL, one group with a non-clinical approach (Section 2.3.1) and another group with a clinical approach centered on the specific problem of predicting BGL (Section 2.3.2). Four non-clinical metrics, RMSE, MSE, MAE, and MAPE, are considered to evaluate the prediction models. For the clinical evaluation metrics, the percentage of BGL measurements located in each zone of the Clarke Error Grid (CEG) is calculated. Additionally, the percentage of BGL measurements in both zone A and zone B, hereafter named as zone 'A + B,' is used since these zones represent clinically acceptable BGL predictions.

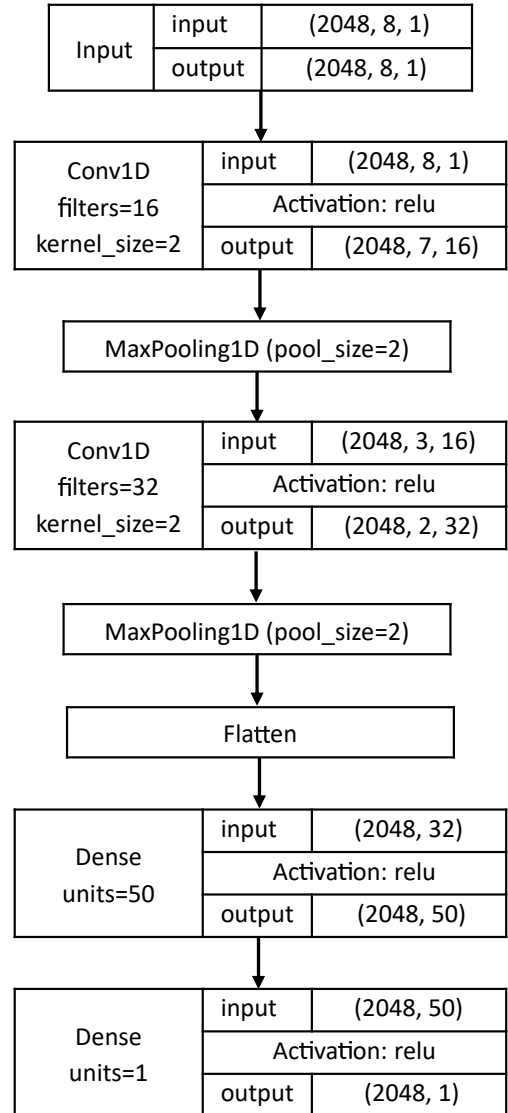
The evaluation of the BGL prediction models follows a traditional approach assessing the entire range of measurements in the evaluation set, but also analyzes performance in different BGL ranges. This novel method enables a more detailed comparison of metric performance within clinically significant ranges, which is crucial for understanding prediction model effectiveness. For instance, prediction model performance in hypoglycemic (TBR) or hyperglycemic (TAR) ranges is critical, as these ranges have the most significant impact on patient health.



(a) Linear model architecture schema



(b) LSTM model architecture schema.



(c) CNN model architecture schema.

Figure 4.4: Prediction algorithms architectures schemes. Source: own elaboration.

Therefore, each trained prediction model will generate a table like the sample Table 4.1. The rows represent different BGL ranges used for evaluation. The first row, labeled "ALL," covers the evaluation across the entire range of measurements (0-500 mg/dL), i.e., using the most common evaluation method in such tasks. The subsequent rows represent the proposed evaluation using the measurements divided by specific ranges, namely:

- TBR_2: Time below range with level 2 hypoglycemia ($\text{BGL} < 54\text{mg/dL}$);
- TBR_1: Time below range with level 1 hypoglycemia ($54\text{ mg/dL} \leq \text{BGL} \leq 69\text{ mg/dL}$);
- TIR: Time in range ($70\text{ mg/dL} \leq \text{BGL} \leq 180\text{ mg/dL}$);
- TAR_1: Time above range with level 1 hyperglycemia ($181\text{ mg/dL} \leq \text{BGL} \leq 250\text{ mg/dL}$);
- TAR_2: Time above range with level 2 hyperglycemia ($\text{BGL} \geq 251\text{ mg/dL}$);

The columns represent the different metrics. First, the percentage of BGL measurements in the five zones of the CEG (A, B, C, D, and E), then the percentage of BGL measurements in zone 'A + B,' followed by the non-clinical metrics (RMSE, MSE, MAE, and MAPE). This approach allows a clear comparison between non-clinical and clinical evaluation metrics across various BGL ranges.

Table 4.1: Evaluation metric template.

Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
ALL										
TBR_2										
TBR_1										
TIR										
TAR_1										
TAR_2										

4.3 Experimental setup

4.3.1 Data splitting

The data obtained from the preparation process described in Section 4.2.1 is split into training, validation, and testing sets. Table 4.2 shows the schema of the data division process. The training set consists of 484 patients, representing 70% of the total. The validation set consists of 69 patients, which is 10% of the total. The test set consists of the remaining 20% of the patients, 138. The selection of patients on each set was random, but it was ensured that the three sets contained patients with a similar number of measurements. To accomplish this distribution, the patients were sorted by their number of measurements and grouped into sets of patients with similar amounts of data.

Table 4.2: General prediction algorithm data split schema.

	Train	Validation	Test
Patient number	484	69	138
BGL measurments (Millions)	15.6	2.2	4.4

This separation implies that each patient is only used to train, validate, or test the prediction model. This approach in a general prediction model possibly creates a test set that is more

distant to the train set than the one created by other state-of-the-art research, as it is expected to have more variability between different patients than between different moments of the same patient. This is important to note because the metrics calculated on these test datasets will represent an estimation of the prediction model's performance and are used for comparisons. Also, this scenario is more similar to a real-world setting where the patients who use the prediction model are different from the patients used to train it.

4.3.2 History length tuning

The HL is a critical parameter that demands careful consideration. If the number of previous BGL measurements used for the prediction is too high, computational complexity can increase during training or execution. Additionally, a longer HL increases the likelihood of encountering missing measurements within the data sequence, which could disrupt the prediction process. Conversely, if the HL is too short, the prediction models may not perform well due to insufficient data to capture complex patterns. Hence, a tuning process is conducted to determine a good HL.

Data exploration showed that the persistence of the correlation between the BG measurements varied between 3 and 10 past measurements depending on the patient. Considering this result and the values suggested in the literature [BC20], the following values are selected to tune the history length: 30 minutes (2 samples), 1 hour (4 samples), 2 hours (8 samples), 2.5 hours (10 samples), 3 hours (12 samples), 3.5 hours (14 samples).

The tuning process consists of creating windows on each conformed split (Table 4.2) by each mentioned HL and a PH of 30 minutes, including all patients in these splits. Then, for each set of windows, an LSTM model is trained over 10 epochs and validated on the validation set of patients. A single prediction algorithm is selected to avoid adding complexity to the analysis, and an LSTM is preferred because it is one of the most widely used prediction models in the state of the art and has shown more promising results. Figure 4.5 shows the results of the HL tuning process. HL of 2 hours (8 samples) shows the best result. The results for values 10 and 12 samples are close, but using a HL of 8 samples is a more interesting choice because the total number of windows generated in the complete dataset will be higher. An HL of 8 samples means preparing the data so that the prediction model receives an input sequence of 8 past measurements to forecast the measurement in the PH. Then, the number of input units in the ANNs design for the experimentation is 8. The complete window size is set to 10 samples for the 30-minute PH, 12 samples for the 60-minute PH, and increases accordingly for subsequent PH. The process restructures all the patient data into windows of the 6 sizes defined for the following experiments.

4.3.3 Models training

For the experimentation process, each of the three selected prediction algorithms (Linear, LSTM, and CNN) is trained across the six PHs (2, 4, 6, 8, 12, and 16 samples), resulting in 18 prediction models. Each prediction algorithm undergoes training for up to 500 epochs, with early stopping applied after 50 epochs of no improvement. A batch size of 2048 is used, as the extensive training set requires a bigger batch to ensure memory efficiency. The Adam optimizer is selected due to its good performance in a reference study [BC20] and its balanced

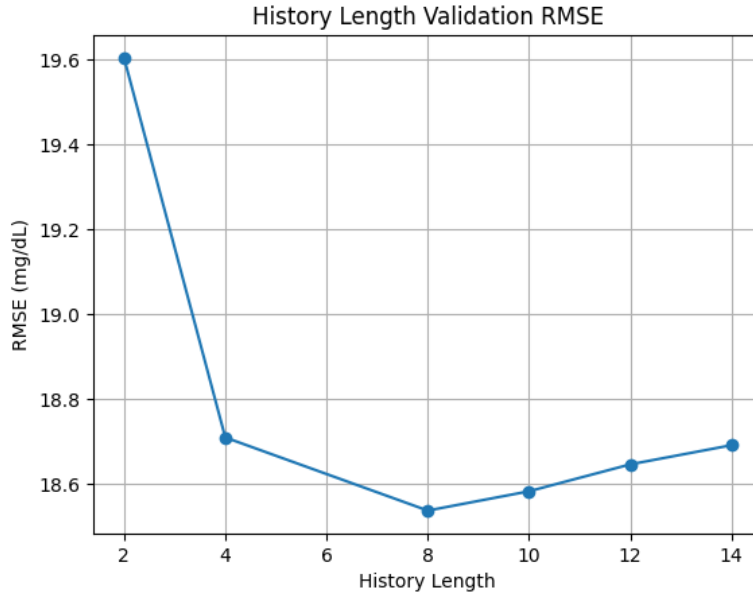


Figure 4.5: Validation results per history length. Source: own elaboration.

computational complexity. RMSE is chosen as the loss function to optimize prediction model performance.

4.4 Results

As explained in Section 4.2.4, each of the 18 trained prediction models is evaluated across 6 BGL ranges, resulting in a table of results with 108 rows. This extensive evaluation is detailed in Table A.1 in Appendix A. Table 4.3 presents the results of the proposed metrics for the three prediction algorithms and all their PH without considering the analysis of BGL ranges divisions, i.e., the standard approach commonly followed in the state of the art. A more detailed evaluation of these prediction models involves examining the results of the metrics within each of the different BGL ranges. Examples of such analyses are shown in Table 4.4 for a Linear prediction model at a PH of 8 samples and Table 4.5 for a LSTM prediction model at a PH of 4 samples. Appendix A provides the complete performance result for the general models in the different BGL ranges presented in Table A.1. The most noticeable pattern is that as the PH increases, the prediction models' performance decays, evident across all prediction algorithms and metrics.

Table 4.6 shows the ranking of the percentage of BGL measurements in zone 'A + B' marginalized by PHs. For each prediction algorithm and BGL range, the percentage of BGL measurements in zone 'A + B' is averaged for the different PHs. In the first half of the table, it is noticeable that the average results are less variable with respect to the PHs, as their standard deviations are small. However, in the second half of the table, a greater standard deviation in the calculated values are observed. This pattern occurs because the variation in PHs has little impact on the performance of the prediction algorithms in the BGL ranges with better performance, such as TIR and TAR_1. On the other hand, when the BGL ranges are those with the worst performance, such as TAR_2, TBR_1, and TBR_2, the variation in PHs does result in different model performance.

Table 4.3: Performance results for general prediction models in the entire BGL range assessed via both clinical and non-clinical metrics. The best results for the zone 'A + B' are highlighted in bold.

Algorithm	PH	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE ((mg/dL) ²)	MAE (%)	MAPE (mg/dL)
Linear	2	88.08	10.56	0.04	1.31	0.01	98.64	19.93	397.36	14.01	0.10
Linear	4	65.49	28.73	0.45	5.24	0.09	94.22	36.00	1295.96	26.44	0.19
Linear	6	53.27	38.59	0.90	7.00	0.23	91.86	46.63	2174.49	35.13	0.26
Linear	8	46.28	44.01	1.14	8.18	0.40	90.29	53.71	2884.81	41.21	0.31
Linear	12	39.55	48.48	1.14	10.21	0.62	88.03	61.28	3754.88	47.99	0.37
Linear	16	37.07	49.54	0.85	11.85	0.68	86.61	64.34	4139.32	50.83	0.40
LSTM	2	88.67	9.34	0.02	1.96	0.00	98.01	18.82	354.37	13.39	0.10
LSTM	4	67.63	26.21	0.34	5.77	0.04	93.84	34.60	1197.37	25.24	0.19
LSTM	6	55.10	36.65	0.80	7.29	0.16	91.75	45.25	2047.52	33.87	0.26
LSTM	8	47.64	42.61	1.13	8.29	0.32	90.25	52.54	2760.43	40.15	0.31
LSTM	12	40.36	47.56	1.21	10.34	0.53	87.92	60.48	3657.53	47.31	0.37
LSTM	16	37.57	48.93	1.01	11.88	0.62	86.50	63.87	4078.93	50.43	0.40
CNN	2	76.37	19.15	0.13	4.34	0.01	95.52	27.77	771.35	20.08	0.15
CNN	4	60.80	31.77	0.54	6.81	0.09	92.57	40.54	1643.78	29.86	0.22
CNN	6	50.84	40.05	0.91	7.97	0.23	90.89	49.29	2429.50	37.27	0.28
CNN	8	44.62	44.96	1.34	8.67	0.41	89.58	55.46	3075.43	42.89	0.34
CNN	12	39.51	47.87	1.15	10.93	0.54	87.38	61.62	3797.40	48.26	0.38
CNN	16	37.13	48.98	0.86	12.45	0.58	86.11	64.34	4139.97	50.85	0.40

Table 4.4: Performance results in the different BGL ranges for Linear prediction algorithm and PH of 8 samples assessed via both clinical and non-clinical metrics. The best results for the zone 'A + B' are highlighted in bold.

Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE ((mg/dL) ²)	MAE (%)	MAPE (mg/dL)
ALL	46.28	44.01	1.14	8.18	0.40	90.29	53.71	2884.81	41.21	0.31
TBR_2	0.27	0.00	0.00	93.25	6.48	0.27	77.47	6001.47	70.25	1.45
TBR_1	0.30	0.00	0.00	92.67	7.03	0.30	71.62	5128.83	64.51	1.05
TIR	47.03	50.65	1.78	0.50	0.04	97.68	42.48	1804.21	33.00	0.30
TAR_1	60.26	35.94	0.13	3.63	0.04	96.20	49.79	2478.73	39.69	0.19
TAR_2	33.99	43.71	0.02	22.26	0.03	77.70	96.27	9268.35	83.00	0.27

Table 4.5: Performance results in the different BGL ranges for LSTM prediction algorithm and PH of 4 samples assessed via both clinical and non-clinical metrics. The best results for the zone 'A + B' are highlighted in bold.

Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE ((mg/dL) ²)	MAE (%)	MAPE (mg/dL)
ALL	67.63	26.21	0.34	5.77	0.04	93.84	34.60	1197.37	25.24	0.19
TBR_2	14.36	0.00	0.00	85.18	0.46	14.36	42.77	1829.65	38.32	0.79
TBR_1	7.70	0.00	0.00	91.60	0.70	7.70	39.05	1524.54	33.77	0.55
TIR	67.71	31.36	0.47	0.46	0.01	99.07	28.77	827.77	21.02	0.18
TAR_1	76.94	21.57	0.19	1.29	0.01	98.51	37.92	1437.91	28.08	0.13
TAR_2	76.74	18.45	0.07	4.74	0.00	95.19	52.30	2735.75	40.09	0.13

Table 4.7 shows the ranking of the percentage of BGL measurements in zone 'A + B' marginalized by the prediction algorithm. For each PHs and BGL range, the percentage of BGL measurements in the zone 'A + B' is averaged for the different prediction algorithms. Analyzing the results of the standard deviation in this case, it is clear that, for the most part, the performance of the different prediction algorithms was similar for a given PH and BGL range, with the exception of three cases.

Table 4.8 shows the ranking of the percentage of BGL measurements in zone 'A + B' marginalized by PH and prediction algorithm. For each BGL range, the percentage of BGL measurements in zones 'A + B' is averaged for the different PHs and prediction algorithm. Similarly Table 4.9 shows the ranking of RMSE (mg/dL) marginalized by PHs and prediction algorithms. When analyzing these two tables, a discrepancy is observed between how non-clinical metrics evaluate the models compared to clinical ones. It is noticeable that the average RMSE in TAR_2 is 85.03; in TBR_1, it is 63.35, which might suggest a better result in TBR_1. However, when analyzing the 'A + B' averages from Table 4.8, it becomes clear that TAR_2 has a value of 75.50%, while TBR_1 only reaches 10.30%, indicating a much worse performance in TBR_1.

A marked difference among the performance becomes evident when comparing the metric results for the same prediction algorithm and the same PH and different BGL ranges. Table 4.4 presents the metrics for the Linear prediction algorithm and PH of 8 samples. Analyzing the first row, which corresponds to the entire BGL range, 90.29% of the measurements are within zones 'A + B,' with an RMSE of 53.71. Considering this is a two-hour prediction, these results can be considered acceptable. However, examining the rows corresponding to TBR_1 and TBR_2 reveals different outcomes, with 'A + B' metrics results near 0% and RMSE values of 77.47 and 71.62, respectively. In contrast, the values for TIR and TAR_1 show excellent 'A + B' metrics and better RMSE scores than those calculated for the entire BGL range. Table 4.5 shows a similar pattern where the 'A + B' metric result for the entire BGL range transcend 90%, and for TIR and TAR_1, they approach 100%. However, for TBR_1 and TBR_2, the values drop below 15%. In this second case, the results belong to a different prediction model, a LSTM with a shorter PH of 4 samples.

This pattern of different performance among different BGL ranges is consistently observed across all results as noticed in Table B.1 from Appendix B, which is sorted in descending order based on the percentage of measurements in the zones 'A + B'. The table shows a fairly consistent pattern of the ranges, with TIR, TAR_1, and TAR_2 appearing at the top, while TBR_1 and TBR_2 are at the bottom. However, it becomes even more evident when analyzing Tables 4.6, 4.7, and 4.8. In Table 4.6, which marginalized results by PHs, the highest metric values correspond to TIR, TAR_1, and the entire BGL ranges ranked in the first half of the table, with all entries surpassing 90%. Meanwhile, the second half of the table includes lower values for TBR_1, TBR_2, and TAR_2, ranging from 77.15% to 4.31%. A similar trend is seen in Table 4.7, where results are marginalized by prediction algorithm. Once again, TIR and most TAR_1 ranges are positioned at the top, while TBR ranges occupy the bottom, even results with PH shorter than some at the top of the table. Finally, in Table 4.8, which marginalized results by PHs and prediction algorithm, the same ranking order is observed, with TIR and TAR_1 ranges at the top and TBR_1 and TBR_2 at the bottom.

Testing the prediction models using clinical metrics also verifies whether the predictions fall outside the conceptually acceptable ranges for this problem, specifically BGL measurements below 0 mg/dL or above 500 mg/dL. This analysis determines the number of predictions that meet these conditions and the minimum and maximum values outside the acceptable range.

Table 4.6: Ranking of percentage of BGL measurements in zone 'A + B' marginalized by PHs.

Rank	Algorithm	Range	Mean	Std
1	LSTM	TIR	98.39	0.88
2	Linear	TIR	98.38	0.85
3	CNN	TIR	98.23	0.75
4	Linear	TAR_1	96.58	2.50
5	LSTM	TAR_1	96.54	2.51
6	CNN	TAR_1	96.00	2.38
7	Linear	ALL	91.61	4.38
8	LSTM	ALL	91.38	4.18
9	CNN	ALL	90.34	3.44
10	Linear	TAR_2	77.15	22.12
11	LSTM	TAR_2	76.78	21.94
12	CNN	TAR_2	72.58	22.58
13	Linear	TBR_2	20.54	37.33
14	LSTM	TBR_2	15.62	31.66
15	Linear	TBR_1	14.97	29.22
16	LSTM	TBR_1	11.63	24.83
17	CNN	TBR_2	6.20	14.60
18	CNN	TBR_1	4.31	9.99

Table 4.8: Ranking of percentage of BGL measurements in zone 'A + B' marginalized by PHs and prediction algorithms.

Rank	Range	Mean	Std
1	TIR	98.34	0.78
2	TAR_1	96.37	2.33
3	ALL	91.11	3.82
4	TAR_2	75.50	20.98
5	TBR_2	14.12	28.37
6	TBR_1	10.30	21.97

Table 4.7: Ranking of percentage of BGL measurements in zone 'A + B' marginalized by prediction algorithms.

Rank	PH	Range	Mean	Std
1	2	TIR	99.70	0.20
2	2	TAR_1	99.66	0.34
3	2	TAR_2	99.28	0.85
4	4	TIR	98.91	0.18
5	4	TAR_1	98.26	0.46
6	6	TIR	98.17	0.11
7	16	TIR	98.01	0.14
8	12	TIR	97.62	0.05
9	8	TIR	97.61	0.19
10	2	ALL	97.39	1.65
11	6	TAR_1	96.99	0.45
12	8	TAR_1	96.03	0.22
13	12	TAR_1	94.25	0.28
14	4	TAR_2	93.84	2.90
15	4	ALL	93.54	0.86
16	16	TAR_1	93.05	0.21
17	6	ALL	91.50	0.53
18	8	ALL	90.04	0.40
19	12	ALL	87.78	0.35
20	16	ALL	86.41	0.26
21	6	TAR_2	84.99	3.59
22	8	TAR_2	76.14	2.32
23	2	TBR_2	69.60	30.00
24	12	TAR_2	56.73	3.02
25	2	TBR_1	53.40	25.56
26	16	TAR_2	42.04	2.58
27	4	TBR_2	14.16	12.81
28	4	TBR_1	7.57	6.30
29	6	TBR_2	0.86	1.34
30	6	TBR_1	0.75	1.17
31	8	TBR_1	0.10	0.17
32	8	TBR_2	0.09	0.15
33	12	TBR_2	0.01	0.01
34	12	TBR_1	0.00	0.01
35	16	TBR_2	0.00	0.01
36	16	TBR_1	0.00	0.00

Table 4.9: Ranking of RMSE (mg/dL) marginalized by PHs and algorithms.

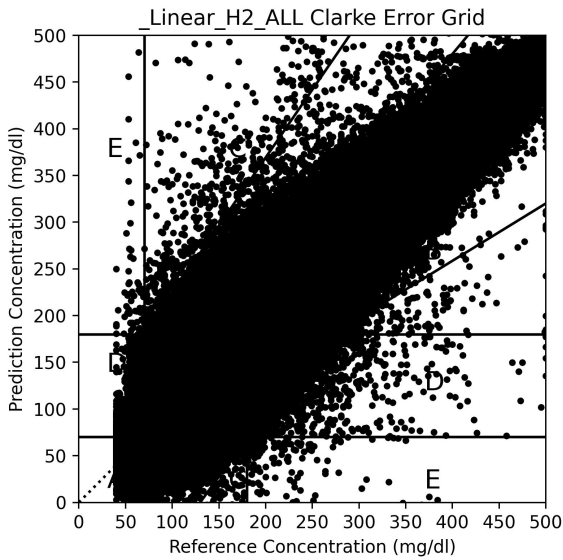
Rank	Range	Mean	Std
1	TIR	37.28	9.89
2	TAR_1	44.20	10.40
3	ALL	47.58	15.05
4	TBR_1	63.35	27.11
5	TBR_2	70.30	31.61
6	TAR_2	85.03	35.44

Table 4.10 presents these results. It is observed that Linear prediction algorithm produced far more out-of-range predictions during evaluation, as shown in Table 4.10, where LSTM and CNN prediction algorithms demonstrated superior performance.

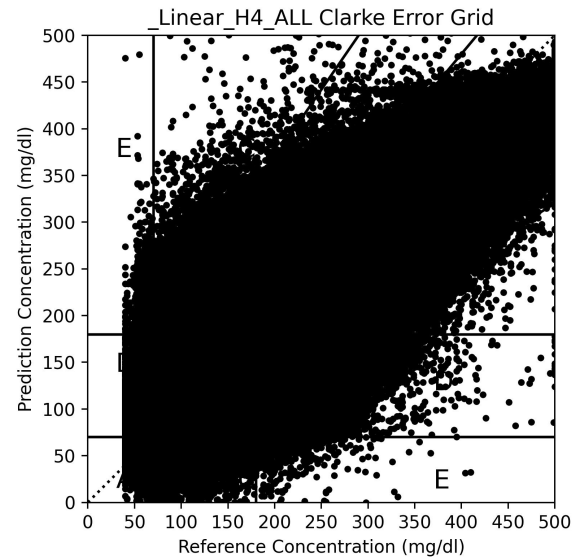
Table 4.10: Prediction outliers by prediction algorithm and PH.

	Linear			LSTM			CNN		
	Occurrences	Min	Max	Occurrences	Min	Max	Occurrences	Min	Max
PH 2	687	-627.18	1036.88	113	500.02	508.00	162	-18.51	546.67
PH 4	594	-677.08	1065.30	0			0		
PH 6	460	-613.21	983.44	0			0		
PH 8	310	-509.47	867.35	0			0		
PH 12	111	-298.00	646.98	0			0		
PH 16	23	-152.58	-0.11	0			1	-48.31	-48.31

In Appendix C there are Figures C.1, C.2, and C.3 that depict the CEG analyses for the three prediction algorithms across the six PH. Each figure is composed of six subfigures, corresponding to the PHs evaluated: 2, 4, 6, 8, 12, and 16 samples. Each subfigure shows the distribution of predicted BGL measurements within the defined zones, offering insight into the prediction model's clinical performance for each PH. The figures shows that for shorter PHs, such as 2 and 4 samples (showed in Figures 4.6, 4.7, and 4.8), a greater number of points align closely with the diagonal of the plot that represents a perfect prediction, while as PH increases, predictions deviate further. The three figures from Appendix C also reveal that as the PH grows, the prediction models increasingly lose their ability to predict values across the entire BGL range (0–500 mg/dL), with predictions becoming more condensed between 100 and 350 mg/dL. This tendency is more pronounced in the LSTM prediction model and slightly less so in the Linear prediction model.



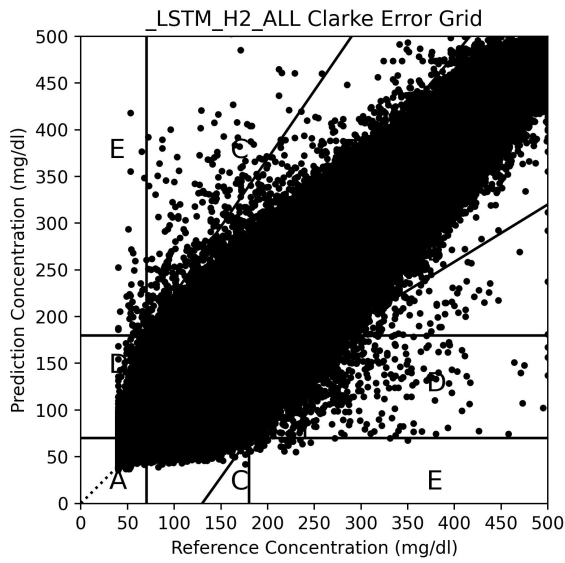
(a) PH of 2 samples.



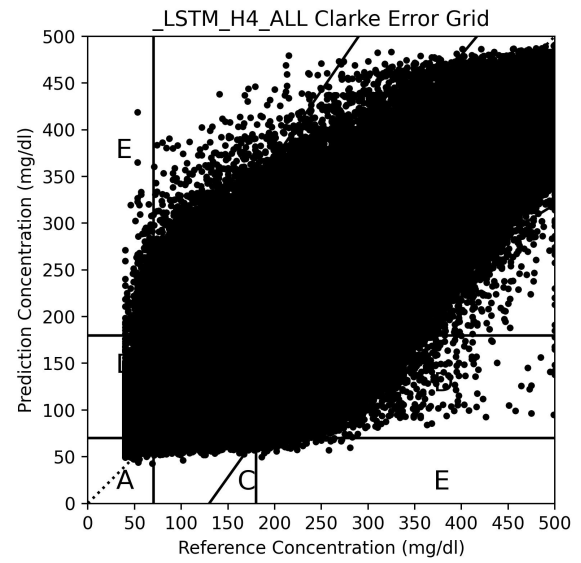
(b) PH of 4 samples.

Figure 4.6: CEG for Linear prediction models and PH of 2 and 4 samples. Source: own elaboration.

Figure 4.10 presents six subfigures, each displaying boxplots representing the results of the clinical evaluation metrics for the three prediction algorithms. The three boxplots within each

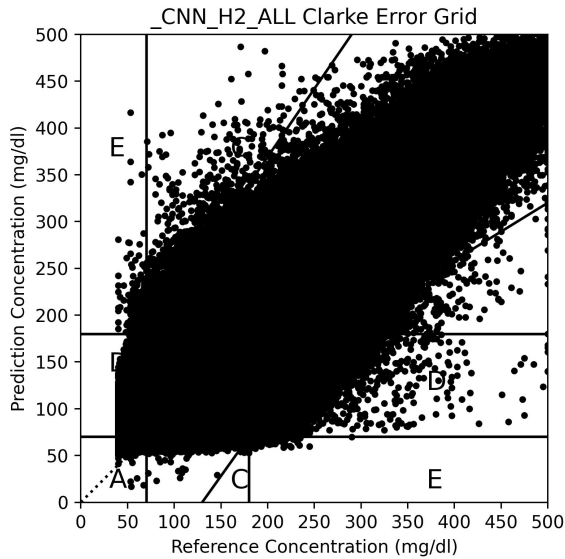


(a) PH of 2 samples.

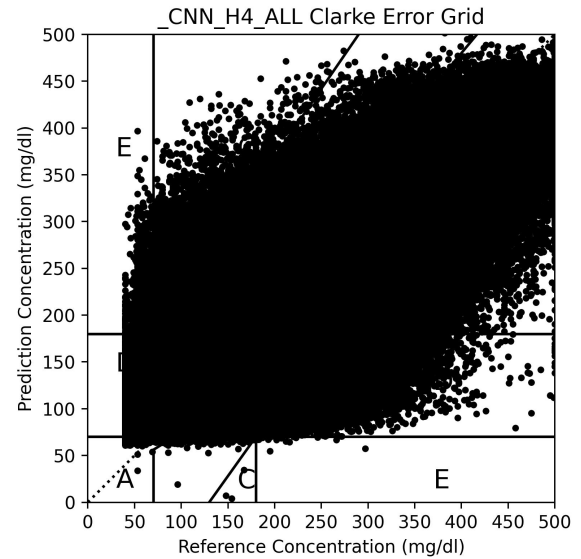


(b) PH of 4 samples.

Figure 4.7: CEG for LSTM prediction models and PH of 2 and 4 samples. Source: own elaboration.



(a) PH of 2 samples.



(b) PH of 4 samples.

Figure 4.8: CEG for CNN prediction models and PH of 2 and 4 samples. Source: own elaboration.

subfigure represent the performance of the prediction models in terms of the specific clinical metric. This visualization allows for a comparative analysis of the prediction models' clinical accuracy across different zones, providing insight into how each prediction model performs in critical and non-critical BGL ranges. Similarly, Figure 4.9 presents four subfigures with boxplots representing the non-clinical evaluation metrics across the three prediction algorithms. These boxplots provide a comparative view of the prediction models' accuracy based on non-clinical metrics.

Analyzing the general performance of the prediction algorithms reveals similar in the different BGL ranges and PH, especially between the Linear and LSTM prediction algorithms, with the CNN prediction algorithm performing slightly worse. However, a more detailed analysis shows the Linear to perform best, followed by the LSTM and CNN respectively. This trend is first observed in Figure 4.10. The mentioned ranking is evident in most subfigures, except for Subfigures 4.10c and 4.10e, where the LSTM prediction algorithm shows slightly better performance for zones C and E, respectively. Figure 4.9 reinforces these observations, as the non-clinical metrics reflect similar behavior between the Linear and LSTM prediction algorithms, with the CNN prediction algorithm consistently performing slightly worse.

Code availability for the experimentation process of general prediction models is described in Appendix J, Section J.2.

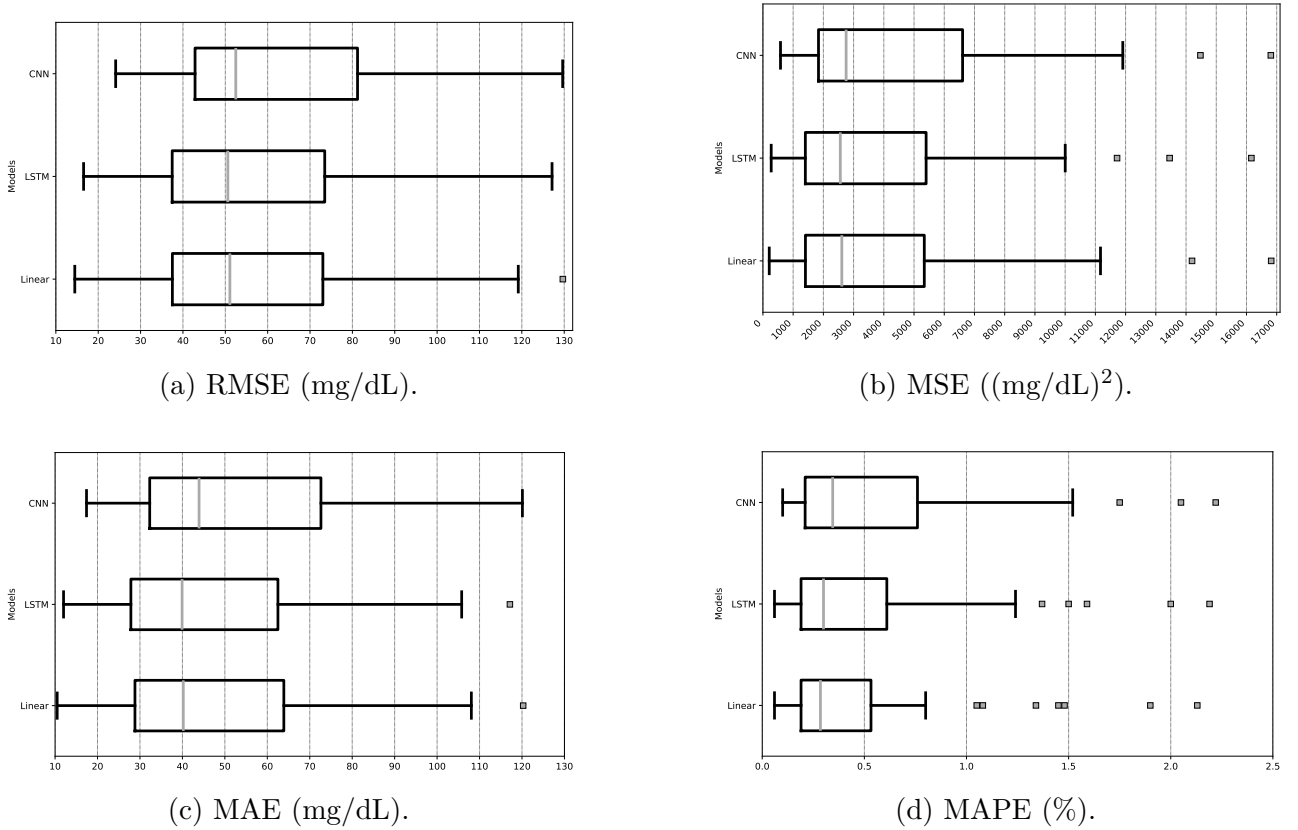
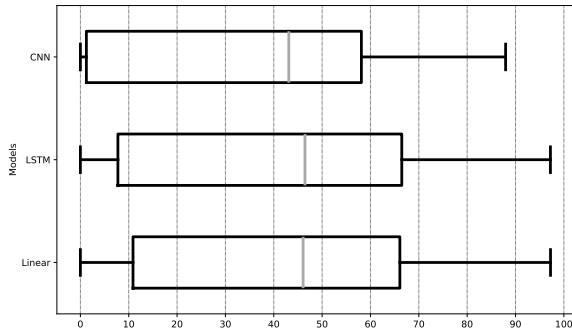
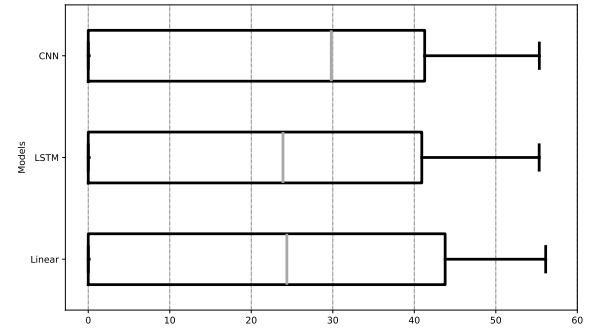


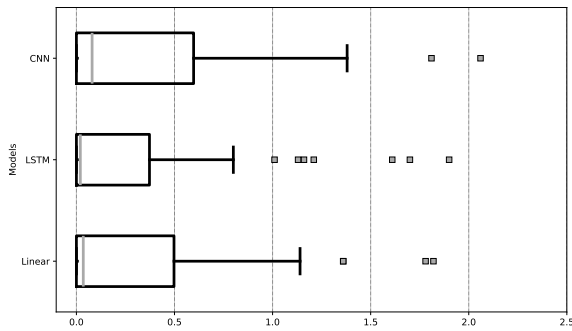
Figure 4.9: Performance result boxplots for general prediction models assessed via non-clinical metrics. Source: own elaboration.



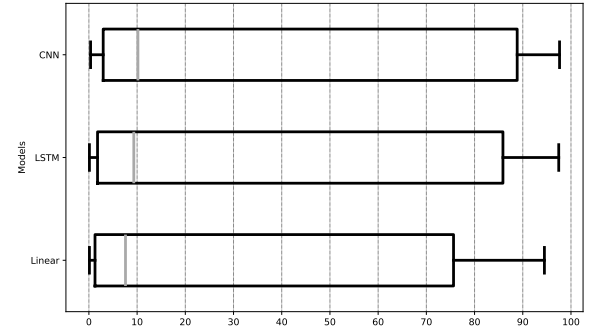
(a) percentage of BGL measurements in zone A.



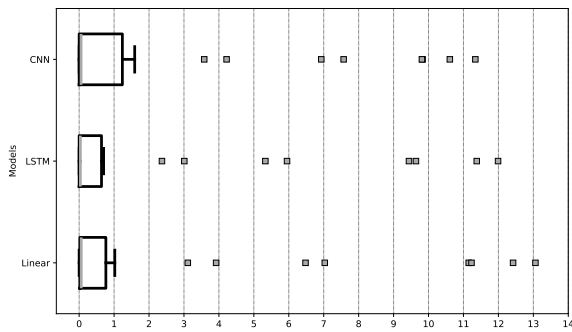
(b) percentage of BGL measurements in zone B.



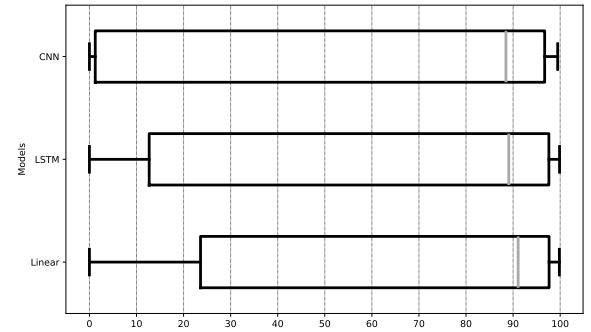
(c) percentage of BGL measurements in zone C.



(d) percentage of BGL measurements in zone D.



(e) percentage of BGL measurements in zone E.



(f) percentage of BGL measurements in zone 'A + B'.

Figure 4.10: Performance result boxplots for general prediction models assessed via clinical metrics. Source: own elaboration.

4.5 Discussion

As the PH increases, the performance of prediction models decays, which aligns with expectations and findings from the literature. This is likely because longer PHs introduce more significant variability in BGLs, making it more difficult for models to accurately predict future measurements based solely on historical data. Additionally, the CEG analysis indicates that with longer PHs, models tend to make predictions within a narrower range. A probable explanation is that as the prediction task becomes more complex for extended PHs, the models tend to revert to predicting more common measurements observed within the dataset, typically between 100 and 200 mg/dL, as illustrated in Figure 3.4.

Performance results of the BGL prediction models were unexpected because more complex prediction algorithms, such as LSTM or CNN, were presumed to perform better. However, the distribution of BGL measurements potentially influences the outcome. Since most data points are concentrated in a narrow range (approximately 100 and 200 mg/dL), which may correspond to periods of more stable and predictable glucose patterns, the Linear prediction algorithm may benefit from this. However, the more complex algorithm demonstrated superior performance related to the range of predictions, as they tended to remain within the expected range in most cases. This is likely because their complexity made them less sensitive to the non-linear and complex glucose patterns. In such cases, the linear model is less effective, as it needs to adapt to the intricacies of non-linear data.

A marked difference of the performance results is observed among the different BGL ranges. A possible explanation for this discrepancy in metric performance is the number of target measurements the prediction algorithms receive for each BGL range. As described in Figure 3.4, most BGL measurements in the dataset slide between 100 and 200 mg/dL, where the TIR and TAR₁ ranges are located. Figure 4.11 illustrates the density curve of BGL measurements for the patients used to train the prediction algorithms. This curve further confirms the trend, showing that the total number of TBR measurements is lower than TAR measurements. Therefore, there is a correlation between the number of BGL measurements in each range and the prediction model's accuracy, suggesting the potential for overfitting in ranges with more data and underfitting in ranges with fewer data points.

Analyzing the metrics across different BGL ranges proves essential, as neglecting this approach may result in a biased evaluation of the algorithms' prediction capabilities. This becomes particularly important when the ranges yielding the most unsatisfactory results correspond to those of the highest clinical relevance, namely hypoglycemia and hyperglycemia episodes. Based on the findings in this study, if only the entire BGL range were considered, it may seem that many algorithms perform adequately in a clinical setting. However, their actual performance in the most critical ranges is inadequate. This underscores not just the need, but the potential for detailed evaluation by the BGL ranges to improve algorithm performance.

The results further corroborate what has been observed in the state of the art that non-clinical metrics are insufficient for evaluating BGL prediction models. Relying solely on non-clinical metrics often leads to biased results. This discrepancy may occur in RMSE case because only measures the distance between predicted and actual points; in the case of TAR measurements, predictions, although more dispersed, can still fall within clinically acceptable zones. In contrast, predictions in TBR ranges may be closer to the actual measurements but fall into clinically risky zones.

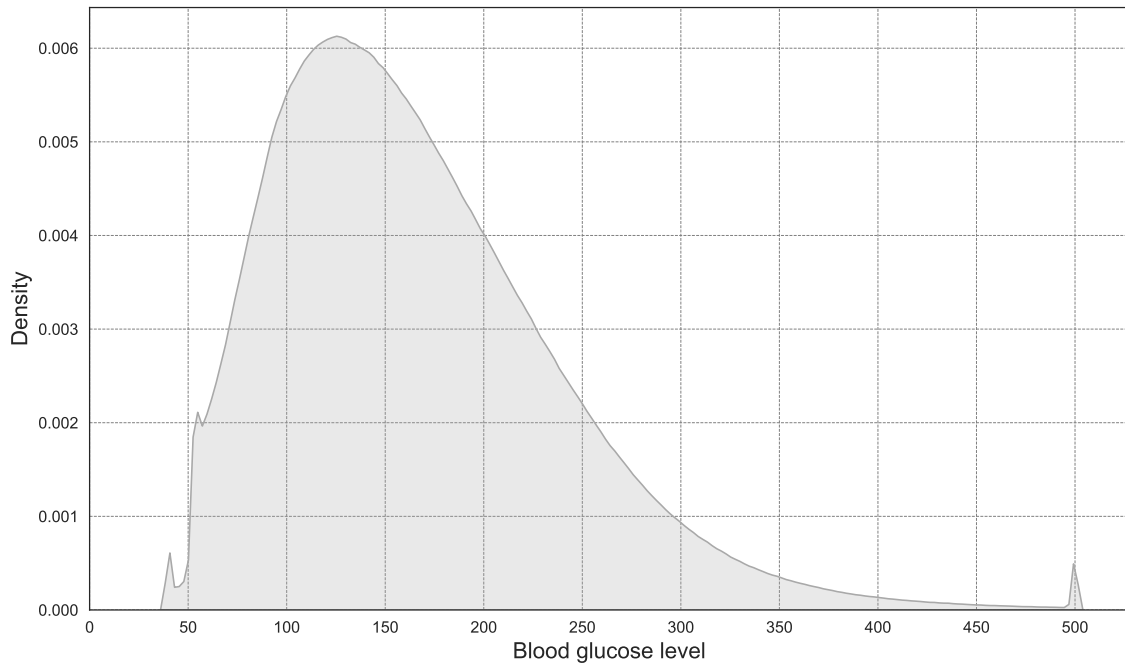


Figure 4.11: Density curve of the blood glucose level measurements used for training the prediction algorithms. Source: own elaboration.

In conclusion, a holistic approach is essential for adequately evaluating BGL prediction models. This means that results must be assessed and analyzed from multiple perspectives to avoid biased conclusions. Incorporating clinical metrics is crucial to provide the semantics in this context; otherwise, numerical results alone may convey little meaningful information. However, non-clinical metrics can add supplementary insights, such as understanding how compact the predictions are, among other characteristics. Analyzing visualizations like the CEG can offer additional information on the overall behavior of the prediction models and the geometry of their predictions. Nevertheless, this would only be sufficient for evaluating the metrics within defined BGL ranges, as metrics could be skewed by sample distribution, potentially leading to the underestimation of clinically critical ranges.

Despite the extensive experimentation, there are some limitations in understanding how to evaluate BGL predictions accurately. Firstly, while the data used is of a quality not previously available publicly, certain limitations arise regarding how it has been used in this chapter. For one, the distribution of data across different selected patients, both in quantity and temporal positioning, was not taken into account. The number of BGL measurements per patient varies significantly, and the distribution over time likely differs greatly, which may lead to abrupt changes in BGL patterns. This variability makes it more challenging for prediction models to adjust to these already complex patterns. Additionally, BGL measurements are imbalanced in their distribution within the admissible range of 0 to 500 mg/dL, as most measurements fall within a much narrower range. While this reflects intrinsic patient BGL measurement behavior rather than data collection issues, it poses a challenge for prediction algorithms during training, as it can lead to overfitting.

Moreover, although the experimental decisions were based on the state of the art of similar work, there are some limitations due to the computational complexity of the process and the time available to complete this thesis. One limitation is the decision to use only models based

on ANN, which means that prediction results from non-ANN-based models were not explored. It is possible that different types of models would have yielded different performance outcomes, adding depth to the understanding of the evaluation metrics. Additionally, while the HL used was based on experimental results, it remained the same for all PH. As the PH increases, BGL patterns become more complex, and the impact of increasing the HL proportionally to the PH on improving prediction model performance still needs to be investigated.

Chapter 5

Clustering patients based on blood glucose level measurements

5.1 Introduction

Predicting BGL in patients with T1D is inherently complex, and developing a general model that adequately performs this task can be challenging. Variability among patients' BGL patterns, influenced by factors such as lifestyle, metabolism, and sex, adds further complexity. On the other hand, creating personalized prediction models for each patient is often impractical, as a robust model requires a large amount of BGL measurements from patients. This implies that when a patient starts using a CGM, substantial time would be needed before they could benefit from an accurate prediction application. However, if patients could be grouped based on their BGL patterns, creating specialized BGL prediction models for each group could make the prediction task more practical and offer greater accuracy than a general model. Therefore, in this chapter, a clustering of T1D patients will be developed using clustering techniques based on their BGL measurements from CGM devices, enabling the prediction task to be carried out more practically while potentially improving the results of existing general models.

5.2 Methods

A series of steps were followed to identify the groups of T1D patients whose BGL patterns are most closely related. First, the data was prepared for the clustering process. The BGL measurements, initially in the form of time series data, are transformed into a feature matrix, a data format more commonly used in unsupervised ML problems. Information is extracted from each patient's time series, creating an instance for each patient in the new dataset. Then, outlier detection is performed using two methods, creating two versions of the modified dataset. Each of these datasets is then standardized, resulting in four versions of the dataset for experimentation.

Since the desired clustering is partitional, the number of groups had to be defined. Two methods were applied to determine this: analyzing the dendrograms from agglomerative hierarchical clustering and the elbow method. To ensure greater experimental variety, nearby values to the find partition value are also considered instead of selecting a single one. Six different clustering algorithms are trained with these configurations. Each resulting clustering is evaluated using clustering internal evaluation metrics and a custom procedure, which ultimately

highlights the most promising groupings for analysis by clinical experts, who select the final clustering solution.

5.2.1 Data preparation

Data transformation

The data used to create the patient groups consist of BGL measurements described in Section 3.3.2, stored in the file *Glucose_measurements.csv*. This file contains the patient’s BGL measurements in time series format. These time series are transformed for the clustering process to create a feature matrix dataset. For each patient, the mean, standard deviation, minimum, and maximum of their BGL measurements were calculated across five specific time ranges throughout the day. These time ranges are determined based on clinical criteria from experts of the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain. These ranges correspond to key moments in the day for T1D patients, reflecting typical lifestyle patterns in the geographic location from which the BGL data were collected, i.e., Granada, Spain, including sleep, work, and meal times. The final ranges, along with their corresponding semantics, are as follows:

- From 00:00 to 06:00: Early morning
- From 06:00 to 13:00: Morning
- From 13:00 to 16:00: Noon
- From 16:00 to 20:00: Afternoon
- From 20:00 to 24:00: Night

As a result, the final dataset contains 736 rows, one for each patient, and 20 variables representing the four calculated statistics for each of the five-time ranges.

Patients with very few days of measurements were removed from the sample, retaining those with 14 or more days of measurements. This decision was based on clinical criteria from experts of the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain, as they typically review at least 14 days of BGL data to assess a patient’s clinical status. Therefore, creating an accurate BGL profile for patients with fewer days of measurements is not considered practicable. The variable “Number_of_days_with_measures” from the *Patient_info.csv* file, described in Section 3.3.1, was used to perform this selection.

Outlier detection

The interquartile range (IQR) method detects and removes outliers from the created dataset through two different approaches. The first approach focuses on each variable individually, calculating the first (Q1) and third quartiles (Q3) and removing any values that fall outside the range of 1.5 times the IQR beyond Q1 and Q3. This process is repeated independently for each variable, ensuring that outliers in one variable do not affect others. In contrast, the second approach groups related variables, like variables of different time ranges but the same statistic like mean or minimum, and applies the IQR method to each variable but only removes rows identified as outliers in all variables within the same group. This approach retains more data by focusing on multivariate outliers across related variables, offering a more conservative and context-aware strategy. Both methods aim to enhance data quality by removing outliers,

but they differ in scope, with the first targeting individual variables and the second addressing multivariate outliers across variable groups.

Standardization

The dataset is then standardized, so all variables have a mean of 0 and a standard deviation of 1. As a result, four versions of the dataset are created, two for each outlier detection method, with one standardized version and one non-standardized version for each approach. At this stage, an analysis will determine whether all dataset versions should be used throughout the process. To do so, clustering is performed using two different methods, agglomerative and K-means. The clustering results are then compared using the Rand Index, which measures the similarity between two clustering solutions by calculating the proportion of correctly classified pairs of elements in both clusters. The Rand Index yields a score between 0 and 1, where 1 indicates perfect alignment between clusters and 0 indicates no similarity. If the clustering results show no significant differences, the non-standardized version of the dataset will be used, as there would be no additional value in using the standardized data. However, if significant differences are observed between the clusters, both dataset versions will be retained for further analysis. Regardless of the result of the procedure, the unstandardized dataset is retained to assign the labels, the product of the clustering process, based on the original data. Keep this version ensures that cluster centroids are calculated from unmodified data, providing a more accurate representation of the actual BGL measurement patterns without the influence of standardization

5.2.2 Estimating the number of clusters

One of the first steps in performing partitional clustering tasks is determining the number of clusters to create. There are several approaches to address this. In the first place, the dendrograms resulting from applying agglomerative hierarchical clustering to each version of the created dataset will be analyzed. This dendrogram analysis involves identifying an optimal cut point by observing changes in the distances between clusters as they merge, which can indicate how many groups should be formed. In some instances, a range of potential values may emerge rather than a single clear value. In the second place, the elbow method is used; this is another common approach employed to estimate the optimal number of clusters in partitional clustering. It plots the explained variance or within-cluster sum of squares (WCSS) as a function of the number of clusters. As the number of clusters increases, the WCSS decreases, but the rate of improvement slows down after a certain point. The "elbow" point on the plot, where the rate of decrease sharply diminishes, indicates the optimal number of clusters. This method helps to balance the trade-off between minimizing the WCSS and avoiding overfitting by choosing too many clusters.

5.2.3 Clustering methods

A diverse set of algorithms was chosen to cover a broad spectrum of clustering techniques and ensure comprehensive analysis. Each algorithm represents a different clustering methodology, providing distinctive advantages and insights into the data structure.

- **Hierarchical Clustering (Agglomerative, BIRCH):** agglomerative clustering is selected for its bottom-up approach, which repeatedly merges smaller clusters into larger ones, providing a hierarchical tree (dendrogram) that allows the flexibility to choose the optimal number of clusters at different levels of the tree. It works well for small to medium datasets and provides interpretable results. BIRCH (Balanced Iterative Reducing and Clustering using Hierarchies) is also used because is particularly effective for handling datasets with noise and outliers. Its hierarchical structure allows for identifying core patterns while minimizing the impact of anomalous data points. This makes it well-suited for ensuring precision in clustering, even when working with smaller datasets that require careful handling of variations and outliers.
- **Partitional Clustering (K-means):** the K-means algorithm is a classic and widely used partitional clustering technique. It partitions data into a predefined number of clusters by minimizing within-cluster variance. It is simple, computationally efficient, and performs well on datasets with compact and spherical clusters.
- **Probabilistic Clustering (Gaussian Mixture Models):** Gaussian Mixture Models introduce a probabilistic approach to clustering by assuming that the data is generated from a mixture of several Gaussian distributions. This method is especially useful when clusters have elliptical shapes and helps estimate the probability of each point belonging to different clusters, providing a more flexible representation of clusters.
- **Fuzzy Clustering (Fuzzy C-means):** Fuzzy C-means is chosen for its ability to assign data points to multiple clusters with varying degrees of membership. This method is beneficial when data points do not belong entirely to one cluster but share characteristics of multiple groups, offering a more distinct view of the data.
- **Neural Network-based Clustering (Self-Organizing Maps):** Self-organizing maps (SOM) are included as a neural network-based approach to clustering. SOM reduce the dimensionality of the data and group similar data points on a two-dimensional grid. They are effective for visualizing high-dimensional data and discovering intrinsic structures in datasets that traditional algorithms might overlook.

By leveraging these clustering methods, capturing different aspects of the data structure and ensuring that the most suitable clustering technique is applied, regardless of the underlying data distribution or characteristics, is possible. Each method brings unique strengths, from scalability (BIRCH) to soft clustering (Fuzzy C-means), making the clustering results more robust and applicable in real-world scenarios.

5.2.4 Evaluation procedure

The Silhouette Coefficient [Rou87] is employed as an internal evaluation metric to assess the quality of the clustering results. The Silhouette Coefficient measures how well-separated and cohesive the clusters are, providing insight into how well the data points within the same cluster are grouped and how distinct each cluster is from others. This metric is defined by Equation 5.1.

$$S(i) = \frac{b(i) - a(i)}{\max(a(i), b(i))} \quad (5.1)$$

Where:

- $S(i)$ is the silhouette score for a specific data point i .
- $a(i)$ is the average distance from point i to all other points within the same cluster.
- $b(i)$ is the minimum average distance from point i to all points in the next nearest cluster.

The value of $S(i)$ ranges from -1 to 1, where a score closer to 1 indicates that the data point is well-clustered, with a high separation from other clusters. A score near 0 suggests that the point is on or very close to the decision boundary between two clusters, and negative values indicate that the point might have been assigned to the wrong cluster. Using the Silhouette Coefficient allows for a quantitative assessment of how well the clustering algorithms perform, particularly ensuring that the clusters represent distinct patterns or groupings in the dataset.

A procedure is used to select the best clustering results to provide a more robust evaluation than simply relying on the highest Silhouette Coefficient score for a given value of K (the number of clusters). Instead of choosing the result with the best score outright, the algorithm first groups similar clustering results using the Rand Index, which measures the similarity between clustering labelings. This similarity threshold is controlled by a parameter alpha (α), which defines the minimum level of similarity required to group clustering results together.

Once the clustering results are grouped based on similarity, the algorithm selects the best result within each group by evaluating the Silhouette Coefficient. This procedure ensures that various clustering solutions are considered rather than discard potentially valuable groupings that offer different and maybe meaningful labelings while not having the highest Silhouette Coefficient.

The underlying principle of this procedure is to preserve the diversity of clustering solutions, acknowledging that different labelings with the same K can highlight distinct underlying structures within the data. This approach ensures that the final step in the evaluation process, presenting diverse and interesting clustering solutions to clinical experts for the ultimate selection of one, offers the richest possible set of options, avoiding the omission of potentially clinically relevant patterns or insights.

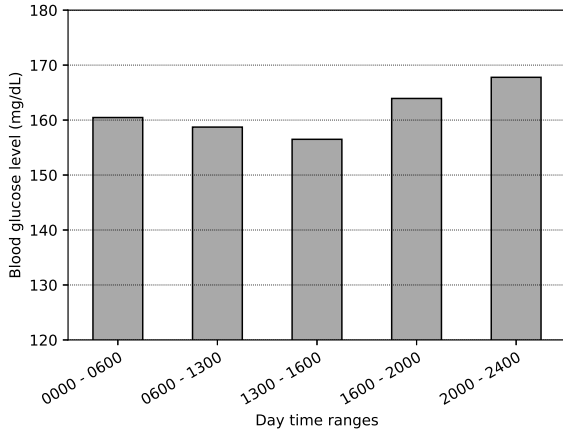
The cluster centroids or prototypes are generated from the previous clustering selection and presented to clinical experts of the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain, through representative charts to select a final clustering solution ultimately. Additionally, variables not used by the clustering methods but relevant for analysis are incorporated into this process. This allows for determining whether these variables correlate with the identified glucose patterns, even though the clustering algorithms did not process them. These variables include age, gender, the total number and ratio of hypoglycemic events, and the total number and ratio of hyperglycemic events.

5.3 Results

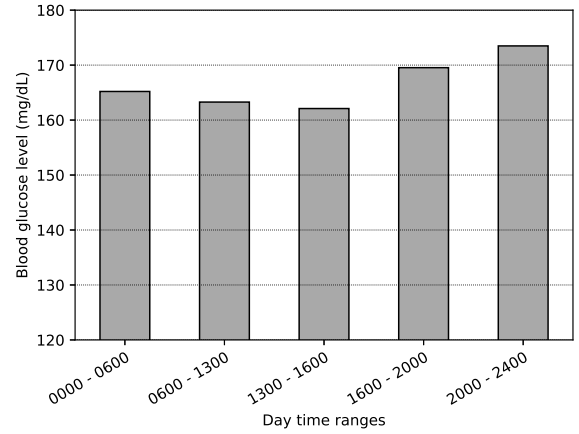
5.3.1 Data preparation

After removing patients with fewer than 14 days of BGL measurements, 731 remained, resulting from the exclusion of 5 patients.

The application of the outlier removal procedures yielded the following results. The first method, the column-by-column approach, removed 140 patients (19.15%), leaving 591 patients (80.85%). This dataset version will be referred to as V1. The second method, based on groups of columns, removed 15 patients (2.05%), leaving 716 patients (97.95%). This dataset version will be referred to as V2. Figures 5.1, 5.2, and 5.3 illustrate the behavior of certain variables within these dataset versions. Figure 5.1 presents the average BGL across daily time ranges. Figure 5.2 focuses on statistics related to hypoglycemic events. Figures 5.2a and 5.2b display the average number of hypoglycemic episodes for each time range corresponding to datasets V1 and V2, while Figures 5.2c and 5.2d show the average hypoglycemia ratio for the same datasets. These ratios are calculated for each patient as the total number of hypoglycemic events in a time range divided by the total number of days with measurements, providing an estimate of daily hypoglycemic episodes in these ranges. Figure 5.3 presents information similar to that of Figure 5.2, but it is related to hyperglycemic events.



(a) Dataset V1.

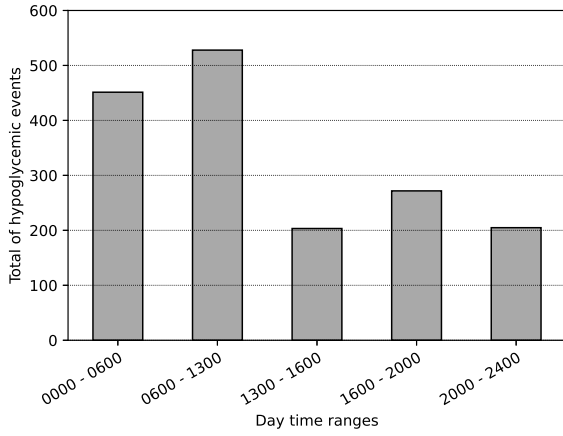


(b) Dataset V2.

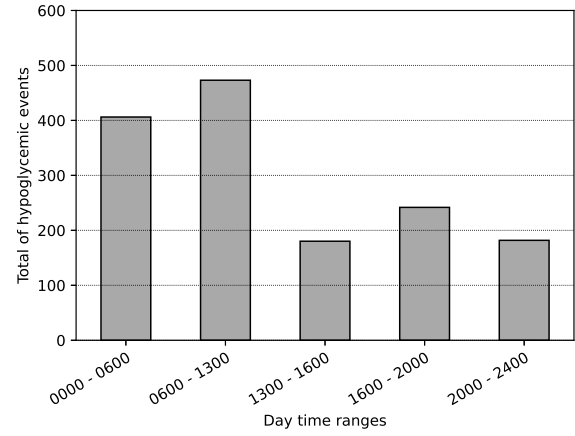
Figure 5.1: BGL average across day time ranges for both dataset versions. Source: own elaboration.

Standardization

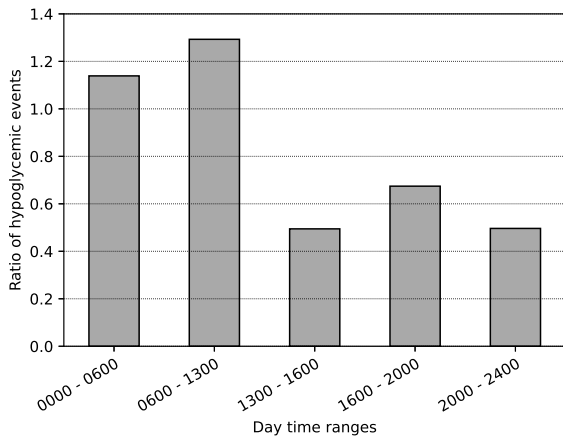
Two clustering methods, agglomerative clustering and K-means, were executed to determine whether the standardized versions of the two datasets should be retained. Tables 5.1 and 5.2 show the results of applying the Rand Index to equivalent clustering outcomes, i.e., using the same method and number of clusters, for datasets V1 and V2, respectively. The results are labeled using a structured naming convention with the format "`<Method>_K<Number>_data.V<Version>_<Standardization>`" indicating the method used, the number of clusters, the dataset version, and whether the dataset is standardized (0 for non-standardized and 1 for standardized). Upon analyzing the results and observing that the



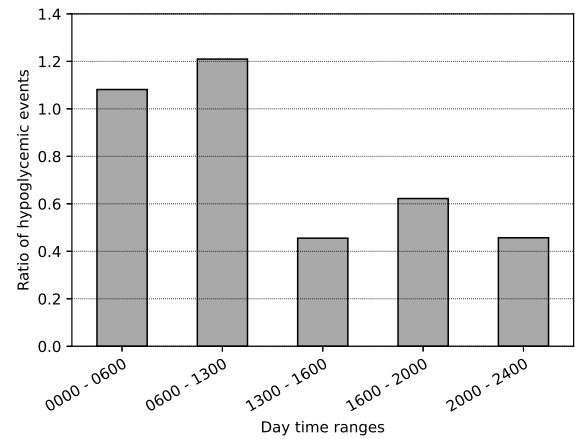
(a) Average of total hypoglycemic events for dataset V1.



(b) Average of total hypoglycemic events for dataset V2.

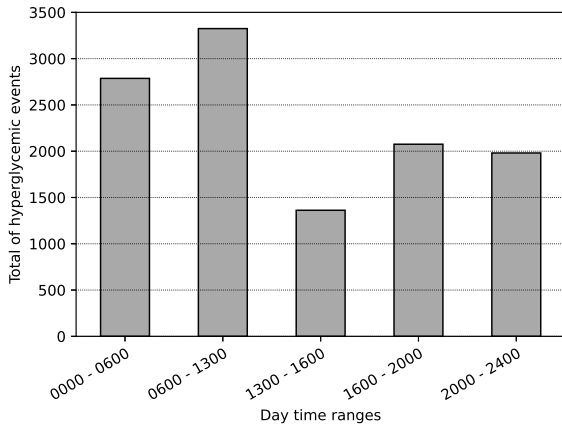


(c) Average of the ratio of hypoglycemic events for dataset V1.

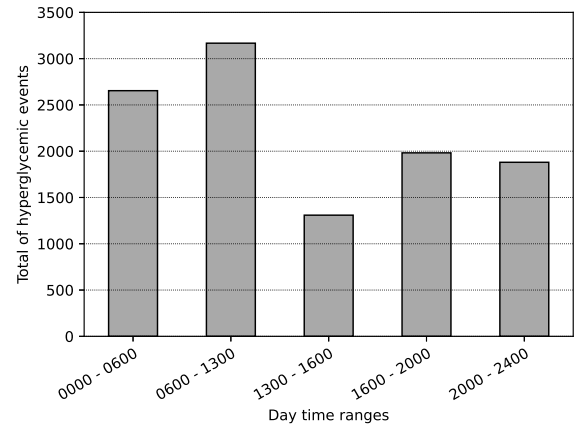


(d) Average of the ratio of hypoglycemic events for dataset V2.

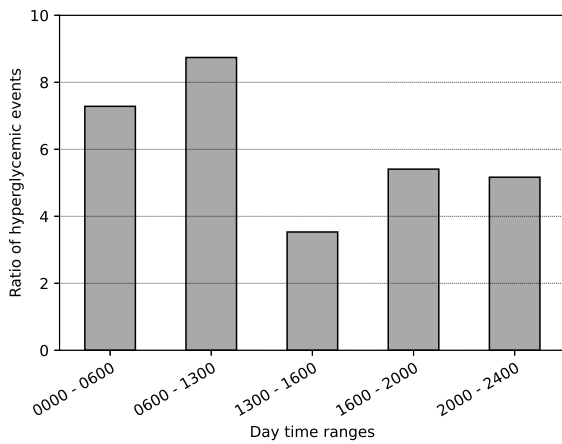
Figure 5.2: Hypoglycemia average stats across day time ranges for both dataset versions. Source: own elaboration.



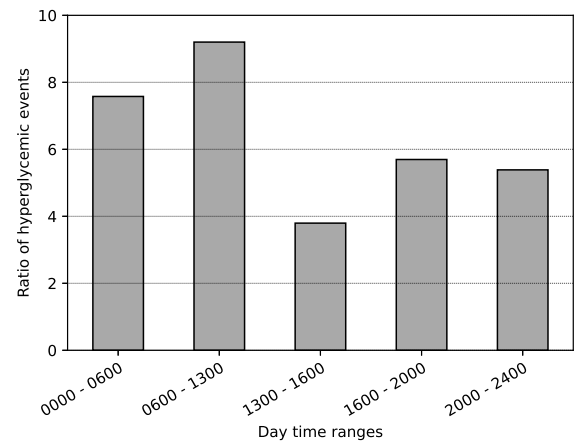
(a) Average of total hyperglycemic events for dataset V1.



(b) Average of total hyperglycemic events for dataset V2.



(c) Average of the ratio of hyperglycemic events for dataset V1.



(d) Average of the ratio of hyperglycemic events for dataset V2.

Figure 5.3: Hyperglycemia average stats across day time ranges for both dataset versions. Source: own elaboration.

calculated averages in both cases fall below the proposed threshold of 0.8, it is decided to use both versions because this indicates that the clustering outcomes for these algorithms are not very similar. Thus, further analysis should be conducted on both sets of results.

Table 5.1: Clustering similarity between V1 of the dataset unstandardized and standardize versions.

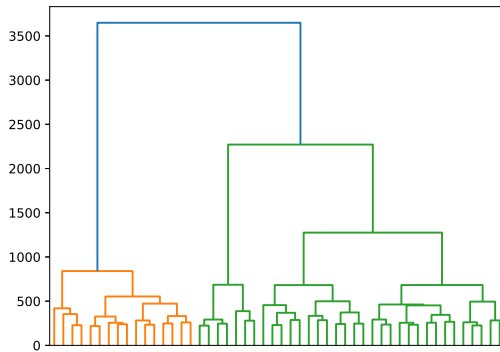
Unstandardize	Standardize	Similarity
Hier_K2_data_V1_0	Hier_K2_data_V1_1	0.74
Hier_K3_data_V1_0	Hier_K3_data_V1_1	0.71
Hier_K4_data_V1_0	Hier_K4_data_V1_1	0.74
Hier_K5_data_V1_0	Hier_K5_data_V1_1	0.75
Hier_K6_data_V1_0	Hier_K6_data_V1_1	0.75
Hier_K7_data_V1_0	Hier_K7_data_V1_1	0.79
Hier_K8_data_V1_0	Hier_K8_data_V1_1	0.81
Kmeans_K2_data_V1_0	Kmeans_K2_data_V1_1	0.81
Kmeans_K3_data_V1_0	Kmeans_K3_data_V1_1	0.70
Kmeans_K4_data_V1_0	Kmeans_K4_data_V1_1	0.74
Kmeans_K5_data_V1_0	Kmeans_K5_data_V1_1	0.77
Kmeans_K6_data_V1_0	Kmeans_K6_data_V1_1	0.78
Kmeans_K7_data_V1_0	Kmeans_K7_data_V1_1	0.81
Kmeans_K8_data_V1_0	Kmeans_K8_data_V1_1	0.82
Average		0.76

Table 5.2: Clustering similarity between V2 of the dataset unstandardized and standardize versions.

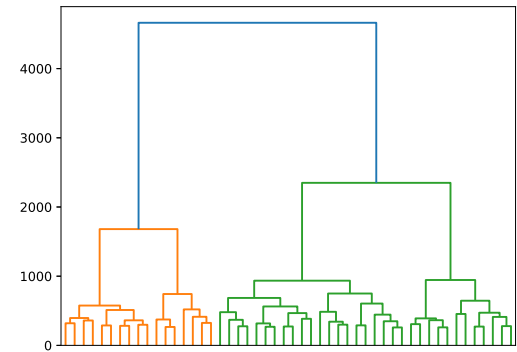
Group_0	Group_1	Similarity
Hier_K2_data_V2_0	Hier_K2_data_V2_1	0.84
Hier_K3_data_V2_0	Hier_K3_data_V2_1	0.75
Hier_K4_data_V2_0	Hier_K4_data_V2_1	0.72
Hier_K5_data_V2_0	Hier_K5_data_V2_1	0.74
Hier_K6_data_V2_0	Hier_K6_data_V2_1	0.74
Hier_K7_data_V2_0	Hier_K7_data_V2_1	0.80
Hier_K8_data_V2_0	Hier_K8_data_V2_1	0.81
Kmeans_K2_data_V2_0	Kmeans_K2_data_V2_1	0.82
Kmeans_K3_data_V2_0	Kmeans_K3_data_V2_1	0.79
Kmeans_K4_data_V2_0	Kmeans_K4_data_V2_1	0.75
Kmeans_K5_data_V2_0	Kmeans_K5_data_V2_1	0.75
Kmeans_K6_data_V2_0	Kmeans_K6_data_V2_1	0.81
Kmeans_K7_data_V2_0	Kmeans_K7_data_V2_1	0.83
Kmeans_K8_data_V2_0	Kmeans_K8_data_V2_1	0.81
Average		0.78

5.3.2 Estimating number of clusters

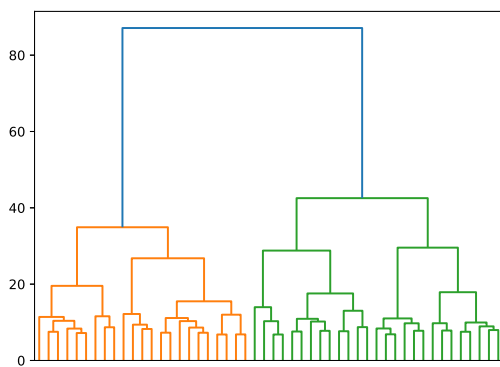
Figure 5.4 displays the dendrograms generated for the four versions of the datasets used for clustering. Upon analyzing these, the number of clusters possibly ranges from 2 to 5 in some cases, as shown in Figures 5.4a and 5.4b. In contrast, Figures 5.4c and 5.4d suggest a potential cluster count of up to 8. The elbow method, on the other hand, does not provide a definitive result, with estimates of K ranging between 2 and 5. Consequently, the decision was made to vary the value of K between 2 and 8, in line with conducting a comprehensive experimentation as outlined in the objectives of this thesis.



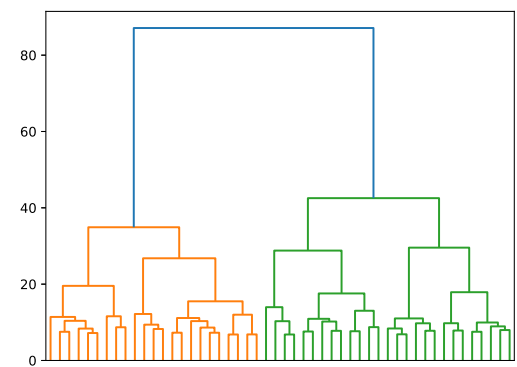
(a) Dendrogram of unstandardized V1 of the dataset.



(b) Dendrogram of unstandardized V2 of the dataset.

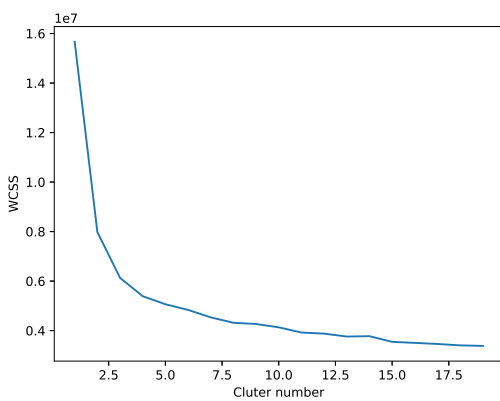


(c) Dendrogram of standardized V1 of the dataset.

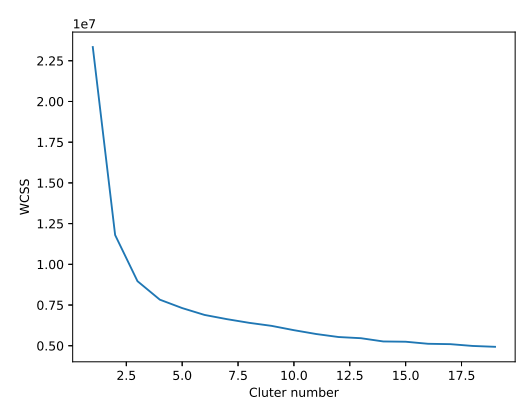


(d) Dendrogram of standardized V2 of the dataset.

Figure 5.4: Dendograms for estimation of number of clusters. Source: own elaboration.



(a) Unstandardized version of dataset V1.



(b) Unstandardized version of dataset V2.

Figure 5.5: Elbow method for estimation of number of clusters. Source: own elaboration.

5.3.3 Evaluation procedure

The 6 clustering methods chosen in Section 5.2.3 were executed using the four versions of the dataset created for this task and across the 7 selected partitions, from 2 to 8 partitions, giving a total of 168 clustering results. Each result group is evaluated independently based on the proposed methodology described in Section 5.2.4 to select each partition's representative models. The results of the selected models for dataset V1 are presented in Table 5.3. For the partition of size 2, two models were selected, a SOM and a Gaussian Mixture, with the latter being the only one created using the standardized dataset version. A single model, Kmeans, was chosen for the remaining partitions. The results of the selected models for dataset V2 are shown in Table 5.4, where, similar to the previous case, two models, SOM and Gaussian Mixture, appear for the partition of size 2. For the partition of size 3, there are also two models, a Kmeans and a Gaussian Mixture. The results for the rest of the partitions are represented by a single model, all of which are Kmeans. In this case, only results for the unstandardized version of the dataset are selected. These 17 clustering results, from the 168 total, are presented to the clinic expert for selecting the final groups of patients.

Table 5.3: Models selected for represent each group for dataset V1.

Name	Silhouette coefficient
SOM_K2_data_V1_0	0.38
Gauss_K2_data_V1_1	0.13
Kmeans_K3_data_V1_0	0.28
Kmeans_K4_data_V1_0	0.23
Kmeans_K5_data_V1_0	0.17
Kmeans_K6_data_V1_0	0.18
Kmeans_K7_data_V1_0	0.17
Kmeans_K8_data_V1_0	0.15

Table 5.4: Models selected for represent each group for dataset V2.

Name	Silhouette coefficient
SOM_K2_data_V2_0	0.39
Gauss_K2_data_V2_0	0.10
Kmeans_K3_data_V2_0	0.30
Gauss_K3_data_V2_0	0.07
Kmeans_K4_data_V2_0	0.24
Kmeans_K5_data_V2_0	0.18
Kmeans_K6_data_V2_0	0.18
Kmeans_K7_data_V2_0	0.16
Kmeans_K8_data_V2_0	0.16

The selected clusters underwent a comprehensive review by the clinical experts of the Clinical Unit of Endocrinology and Nutrition of the San Cecilio University Hospital of Granada, Spain. Their first conclusion was that the patterns derived from dataset V2, while generally similar to those from dataset V1, were smoother and less pronounced, leading them to focus primarily on the clusters from dataset V1. Ultimately, the clustering result from Kmeans_K6_data_V1_0 was identified as the most interesting, the Kmeans method using 6 partitions allows a characterization of each group with meaningful clinical insights. Figure 5.6 presents the centroids of the average BGL generated by this clustering, while Table 5.5 details the distribution of patients across each of the formed groups. In addition, Figures 5.7 and 5.8

provide an overview of the behavior of extreme BGL event ratios and the total extreme BGL events, respectively, for each group.

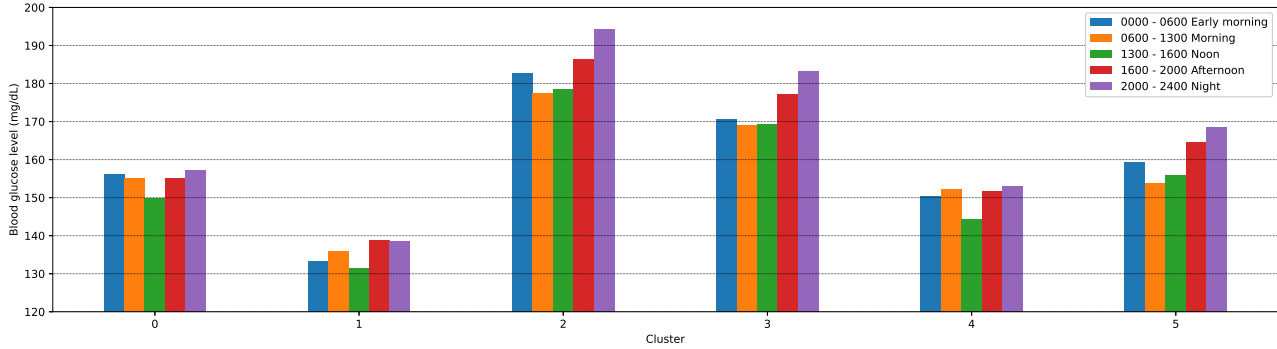


Figure 5.6: Kmeans_K6_data_V1_0 centroids of average BGL. Source: own elaboration. Source: own elaboration.

Table 5.5: Cluster Kmeans_K6_data_V1_0 patient distribution.

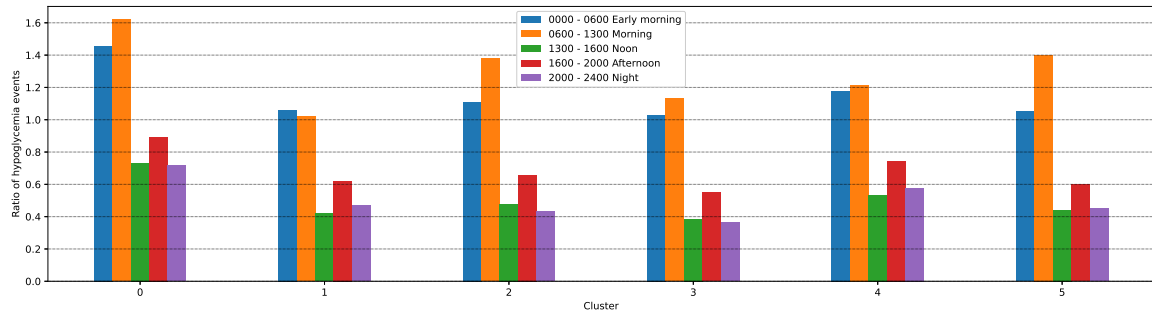
	Cluster 0	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Number of patients	72	71	124	93	133	98
Percentage of patients	12.18	12.01	20.98	15.74	22.50	16.58

Code availability for the clustering process is detailed in Appendix J, Section J.3.

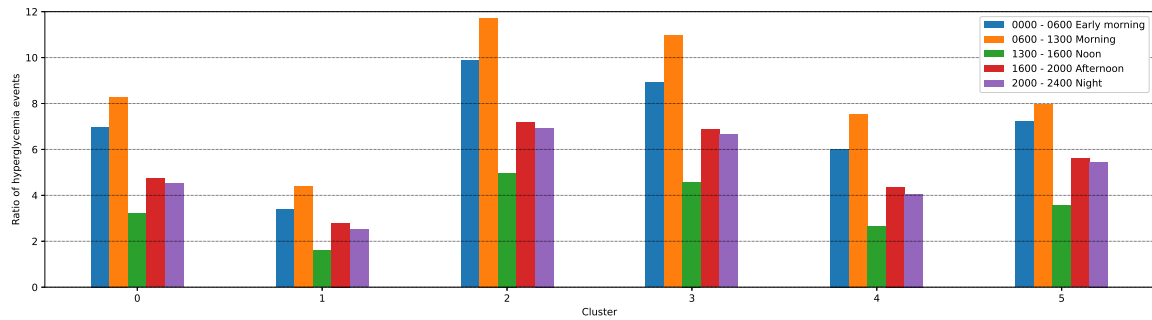
5.4 Discussion

From the resulting clustering, and in collaboration with the experts who selected it, the following characteristics can be identified for each group. These characteristics can be considered the semantics of the formed groups, a crucial element in a clustering process. Groups 0, 1, and 4 correspond to patients with better T1D management, where average BGL measurements remained within the TIR most of the time. These patients would typically achieve glycated hemoglobin levels of less than or equal to 7%, considered the threshold for good T1D management [d'E+15]. Group 1 represents patients with optimal management, as their BGLs remain in an acceptable range with the lowest ratios and totals of hypoglycemia events. Group 0 includes patients with good control but a higher risk of hypoglycemia, especially in the early morning and morning, as shown in the ratio and total hypoglycemia event charts (Figures 5.7a and 5.8a). Group 4 includes patients with good control but likely experience the dawn phenomenon. The dawn phenomenon in T1D refers to an early morning and morning rise in BGL, typically occurring between 4:00 and 8:00, due to the release of hormones like cortisol, adrenaline, glucagon, and growth hormone, which increase glucose production and reduce insulin sensitivity. In non-diabetic individuals, the body compensates by producing more insulin; however, in T1D patients, this mechanism is impaired, leading to elevated morning BGL levels. This is inferred from the BGL patterns in Group 4 (Figure 5.6), where a morning peak suggests the dawn phenomenon. Additionally, this group shows a high hyperglycemia ratio (Figure 5.7b).

Group 5 represents patients with moderate control, as their average BGLs are slightly above ideal values but do not exceed 180 mg/dL, the threshold for hyperglycemia. Groups 2 and 3

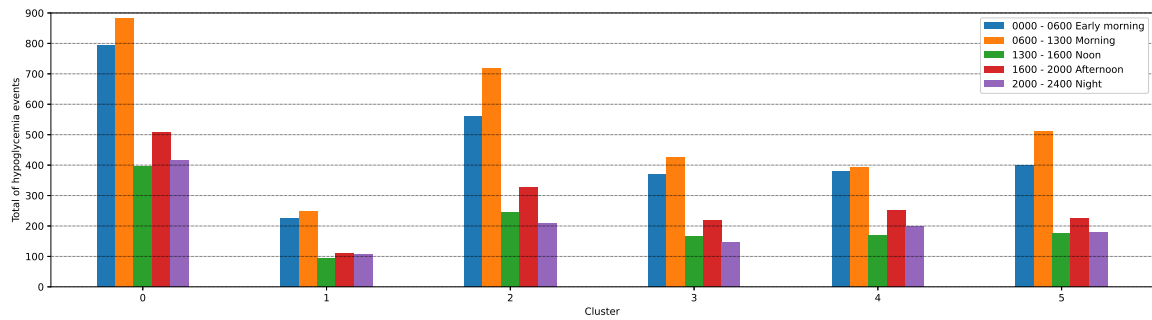


(a) Ratio of hypoglycemia events.

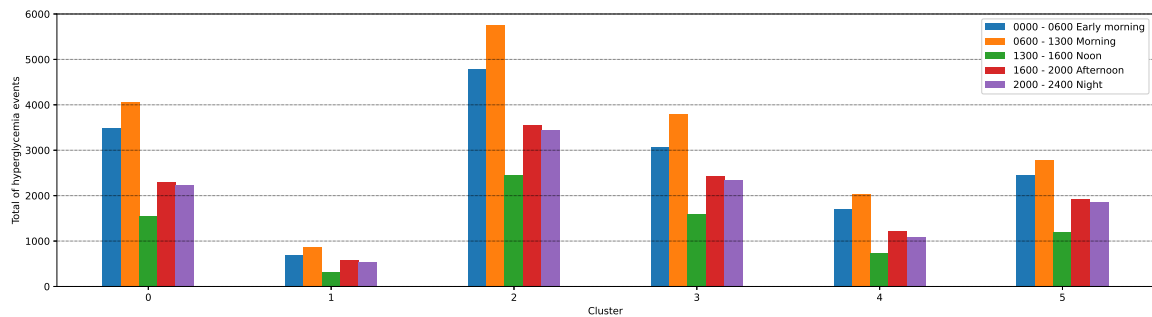


(b) Ratio of hyperglycemia events.

Figure 5.7: Ratio of extreme BGL events per day of Kmeans_K6_data_V1_0 on the centroids of each cluster. Source: own elaboration.



(a) Total hypoglycemia events.



(b) Total hyperglycemia events.

Figure 5.8: Total extreme BGL events of Kmeans_K6_data_V1_0 on the centroids of each cluster. Source: own elaboration.

reflect patients with the most deficient management. Group 2 is the worst overall, showing the highest incidence of hyperglycemia and likely experiencing the dawn phenomenon based on the elevated number and ratio of hyperglycemia in the early morning and morning seen on Figures 5.7b and 5.8b.

These findings not only have the potential to enhance the accuracy and real-world applicability of BGL prediction models but also hold the capacity to directly impact the health care of T1D patients. Firstly, by identifying distinct patient profiles with unique characteristics, endocrinologists can develop tailored treatment strategies for each group, leading to more personalized care. Additionally, due to the widespread use of CGM devices among T1D patients, a simple application could assign a patient to one of these predefined groups after a few days of monitoring, providing clinicians with early indications on the most effective strategies for managing that patient. This process could also be applied to patients using CGM for extended periods as long as their data is stored and accessible.

There are some limitations in the process of identifying the final groups. One of the main issues lies in the procedure used to transform the BGL measurement time series, as the selected daily time intervals are strongly linked to the population's lifestyle from which the T1DiabetesGranada dataset was collected. Using the same time ranges in different datasets might not yield equivalent results. Moreover, while the clustering process involved a variety of algorithms and data versions, and efforts were made to minimize bias during the evaluation process, the final clustering result, as well as its clinical interpretation, remains a subjective process, relying on expert analysis. This could introduce human bias, as different experts might interpret the results differently.

Chapter 6

Evaluating the performance of group-based blood glucose level prediction models

6.1 Introduction

Current approaches to developing prediction models for BGL in real-world scenarios require significant improvement to enhance their applicability. General prediction models often fail to capture the wide variability in BGL patterns among patients with T1D, making them less effective for personalized management. On the other hand, developing fully personalized prediction models for each patient is not only computationally demanding, requiring the creation of a prediction model for every individual, but also impractical for newly enrolled patients. These patients would need to wait for significant BGL data to accumulate before a reliable prediction application could be deployed. This delay makes such an approach less feasible in practice. As a potential solution, creating group-based prediction models through unsupervised learning techniques offers a promising middle ground.

To evaluate the usefulness of this approach, it is first necessary to develop prediction models for each group formed by the clustering solution identified in Chapter 5. After building these prediction models, a comparison must be conducted: first, with the general prediction models developed in Chapter 4, and second, with fully individualized prediction models. This comparison shows how much personalized prediction models improve predictions over group-based prediction models and if group-based prediction models are more valuable than general ones. Therefore, this chapter focuses on training and testing both types of prediction models to enable a comprehensive comparison.

6.2 Methods

6.2.1 Group-based prediction models

The same experimental procedure outlined in Chapter 4 is applied to create the prediction models based on the identified patient groups. The three prediction algorithms, Linear, LSTM, and CNN, are trained and tested using the same evaluation framework. This ensures consis-

tency across experiments and minimizes bias when comparing the performance of group-based prediction models with that of the previously developed general prediction models.

To perform a comparison based on the performance of the models evaluated through both clinical and non-clinical metrics, the process involved subtracting the performance results of the group-based prediction models from those of the general models obtained in Chapter 4. Specifically, the results from evaluating the group-based prediction models for each cluster are compiled into a table. Each of these tables is then subtracted from the table containing the results of the general prediction models to calculate the absolute differences in performance. These differences are evaluated across all the metrics to determine where the group-based models showed improvements or where the general models performed better. It is important to note that from the outcome of this comparison for the percentage of measurements in the zone 'A + B,' which is a maximization metric, positive values indicate that the group-based prediction models perform better, negative values indicate worse performance, and zero means equal performance between both types of models. The effect of minimization metrics (RMSE, MSE, MAE, and MAPE) is reversed, where positive values reflect worse performance for group-based models, negative values indicate better performance, and zero means equal results. Therefore, the tables generated from this subtraction process are formatted for a more explicit comparison. To improve clarity, the cells corresponding to these key metrics, particularly 'A + B' and all non-clinical metrics, are color-coded: green represents better results for group-based models, red represents worse results, and gray indicates equal performance for both model types.

The data from the preparation process outlined in Section 4.1.1 is used for this experiment. When creating the training, validation, and test sets, the same strategy of stratifying patients into equally sized subsets is applied to ensure the number of measurements in each subset corresponds as closely as possible to the division percentages of patients by sub-dataset, namely 70% for training, 10% for validation, and 20% for testing.

6.2.2 Personalized prediction models

The next step involves creating personalized prediction models for comparison with the group-based prediction models. Although personalized prediction has the potential to offer better prediction quality, it requires substantial data from individual patients, necessitating the use of CGM for significantly more extended periods. Although this approach may not present the most practical solution for predicting BGL in T1D patients, it has been included to evaluate how much accuracy might be lost when choosing a group-based solution.

Personalized prediction models are designed to train prediction algorithms based solely on an individual patient's data. Following the same experimental framework used in general and group-based prediction model development, each patient would require the training of 18 prediction models, 3 prediction algorithms (Linear, LSTM, and CNN) for each of the 6 defined PH. Given the considerable computational and organizational challenges involved in training 18 prediction models per patient for all 591 patients in the selected cluster solution, a more streamlined approach is adopted.

Two patients from each of the 6 groups are selected for modeling to ensure computational feasibility and ease of analysis. The selection criterion focuses on choosing the patients whose BGL predictions were best or worst at predicting using the group-based prediction models. This strategy helps mitigate potential biases in the comparison, including both well and poorly

predicted patients. Consequently, 36 prediction models are developed per group (18 per patient), resulting in 216 prediction models for comparative analysis across all 6 groups.

As mentioned in Section 6.2.1, the group-based prediction models are created by employing complete patient data for each subset of the generated split. Therefore, the set of patients assigned to each created group was distributed into training, validation, or testing sets in a stratified manner, based on the number of measurements for each patient. To ensure the comparison is as unbiased as possible, only the patients assigned to each cluster’s testing set are used to identify the best and worst-performing predictions of their BGLs. This comprises 113 patients distributed across the groups, as shown in Table 6.1.

Table 6.1: Number of patients by test set on each cluster.

Cluster	Patients
cluster0	14
cluster1	13
cluster2	24
cluster3	18
cluster4	25
cluster5	19

Each patient’s BGL data is split into 70%, 10%, and 20% for training, validation, and testing. The testing portion serves a dual purpose: first, it is used to evaluate the group-based prediction models to select the best and worst-predicted patients, and second, it is used to test the personalized prediction models created for those patients. This ensures fairness in the comparison process, as neither the group-based prediction models nor the personalized prediction models have used the testing data for training or validation, and both are evaluated on the same test set, minimizing biases in the comparison.

Then, each patient is tested on the 18 prediction models corresponding to their assigned group, and the best and worst cases are selected based on the ‘A + B’ metric, the most comprehensive clinical metric used. For each prediction model, the patient with the highest and lowest value for this metric is selected. Personalized prediction models are subsequently created for these selected patients. Upon obtaining these results, a comparison is conducted between the group-based prediction models and the personalized prediction models. In this comparison, the evaluation is not based on the original performance of the group-based models. Instead, the test split of each patient used during the training process of the personalized prediction models is also used to generate predictions for the corresponding group-based prediction models. This way, results for the same data partitions for each patient are obtained, both for the group-based models and the personalized prediction models. Once the predictions are available, the performance of the personalized models is subtracted from the performance of the group-based models. The resulting tables from this operation maintain the same semantics and color-coding format as described in Section 6.1.1, making the comparison straightforward and visually consistent.

6.3 Results

Code availability for the evaluation of group-based and personalized prediction models is provided in Appendix J, Section J.4.

6.3.1 Group-based prediction models

After training and evaluating the prediction models, the results are presented in a table formatted similarly to the results table for the general prediction models (Appendix A), containing 108 rows. However, in this case, there are results for each of the 6 groups, leading to a total of 648 rows, which can be found in Table D.1 from Appendix D. The results of this group-based prediction models are compared to those of the general prediction models by subtracting the equivalent metric values, and the outcomes of this comparison are presented in Table E.1 from Appendix E. When analyzing this table it may seem that no precise pattern appears immediately evident. However, filtering the results by BGL ranges reveals some interesting insights. For instance, when focusing on the entire BGL ranges, clusters 1, 3, and 4 consistently show better metric A results than the general prediction models. Similarly, metric 'A + B' shows improvements across these clusters, except for cluster 4 in the case of the Linear prediction model with a PH of 2. Additionally, there is an increase in the difference, meaning better performance, as the PH lengthens in clusters 1 and 4, where non-clinical metrics always outperform the general prediction models. These clusters, 1 and 4, represent the groups with the best BGL management overall. Table 6.2 shows the details of these observations.

Examining the hypoglycemia ranges, TBR_2 and TBR_1, reveals a slight improvement in clusters 4 and 5, particularly in the non-clinical metrics. The LSTM and CNN prediction algorithms outperform the Linear prediction algorithm in these cases. Table 6.3 provides a detailed breakdown of the results.

Table 6.4 presents the hyperglycemia ranges (TAR_2 and TAR_1) for clusters 2 and 3. In this case, it becomes much more apparent that group-based prediction models outperform general prediction models. For instance, the 'A + B' metric performs better in nearly all instances, with only 4 out of 72 cases showing worse results than general prediction models. This improvement is particularly pronounced in PH 8, 12, and 16 for the TAR_2 range. Additionally, most non-clinical metrics also show better results. Current results could be linked to these clusters having the highest ratios of hyperglycemia (Figure 5.7b) and total hyperglycemia events (Figure 5.8b), suggesting that more evident patterns within these groups allowed the prediction models to adjust more effectively.

The final filtering based on BGL ranges focuses on the TIR case. Here, the prediction models based on groups 0, 1, 4, and 5 outperform the general prediction models. The difference in performance becomes more pronounced as the PH increase. Non-clinical metrics also tend to be superior in most cases. These groups correspond to those identified as having better control (0, 1, and 4) and moderate control (5), indicating that most patients in these groups are more likely to remain within the TIR range. This trend suggests that the prediction models may have specialized in forecasting measurements within this range, leading to better performance. Table 6.5 provides further details on these findings.

Table 6.2: Absolute difference between group-based prediction models and general prediction models performance in the entire BGL range assessed via both clinical and non-clinical metrics for clusters 1, 3, and 4. Green: better for group-based models, red: worse, gray: equal. Bold: best result for 'A + B' metric.

Cluster	Algorithm	PH	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	2	4.26	-1.76	-0.10	-2.39	-0.01	2.50	-5.09	-256.93	-3.71	-0.02
cluster1	CNN	4	6.94	-2.49	-0.47	-3.92	-0.06	4.45	-9.27	-666.27	-6.87	-0.04
cluster1	CNN	6	8.55	-2.99	-0.84	-4.52	-0.19	5.56	-13.38	-1139.96	-10.18	-0.07
cluster1	CNN	8	10.43	-4.01	-1.32	-4.70	-0.39	6.42	-16.71	-1574.19	-13.44	-0.12
cluster1	CNN	12	10.94	-2.59	-1.15	-6.66	-0.54	8.35	-20.97	-2144.66	-16.56	-0.13
cluster1	CNN	16	12.60	-3.00	-0.86	-8.17	-0.58	9.60	-22.95	-2427.09	-18.57	-0.15
cluster1	LSTM	2	2.15	-1.15	-0.02	-0.97	0.00	1.00	-2.89	-100.65	-2.15	-0.01
cluster1	LSTM	4	6.07	-2.35	-0.29	-3.39	-0.03	3.72	-7.22	-447.75	-5.35	-0.04
cluster1	LSTM	6	8.03	-3.04	-0.71	-4.16	-0.12	4.99	-11.48	-907.03	-8.65	-0.07
cluster1	LSTM	8	9.29	-3.28	-1.08	-4.64	-0.29	6.01	-15.23	-1368.06	-11.79	-0.09
cluster1	LSTM	12	10.99	-3.17	-1.21	-6.09	-0.53	7.82	-20.06	-2024.04	-16.07	-0.13
cluster1	LSTM	16	12.50	-3.28	-1.01	-7.60	-0.62	9.22	-22.45	-2363.47	-18.34	-0.15
cluster1	Linear	2	2.17	-1.56	-0.03	-0.57	-0.01	0.61	-3.40	-124.10	-2.29	-0.01
cluster1	Linear	4	6.64	-3.39	-0.39	-2.79	-0.07	3.25	-7.91	-507.03	-5.78	-0.03
cluster1	Linear	6	8.43	-3.63	-0.83	-3.78	-0.19	4.80	-12.16	-986.39	-9.21	-0.06
cluster1	Linear	8	9.48	-3.60	-1.10	-4.43	-0.37	5.88	-15.86	-1452.36	-12.26	-0.09
cluster1	Linear	12	11.48	-3.78	-1.14	-5.95	-0.62	7.70	-20.66	-2104.60	-16.48	-0.13
cluster1	Linear	16	13.13	-4.03	-0.85	-7.57	-0.68	9.10	-22.77	-2411.13	-18.70	-0.15
cluster3	CNN	2	1.48	-0.67	0.02	-0.84	0.00	0.81	0.56	31.09	0.52	-0.01
cluster3	CNN	4	2.45	-1.04	-0.02	-1.41	0.00	1.41	0.56	45.27	0.67	-0.01
cluster3	CNN	6	2.47	-0.94	0.17	-1.75	0.04	1.53	0.37	36.92	0.81	0.00
cluster3	CNN	8	3.25	-1.83	-0.13	-1.31	0.03	1.42	-0.12	-12.80	0.17	-0.03
cluster3	CNN	12	2.79	-1.64	-0.15	-1.06	0.06	1.15	-0.06	-8.11	0.43	-0.03
cluster3	CNN	16	2.68	-2.63	-0.31	0.27	-0.02	0.05	-0.06	-8.36	0.29	-0.03
cluster3	LSTM	2	0.69	-0.21	-0.01	-0.46	0.00	0.48	0.58	21.87	0.44	-0.01
cluster3	LSTM	4	2.35	-1.04	0.01	-1.33	0.01	1.31	0.47	32.44	0.50	-0.01
cluster3	LSTM	6	2.69	-1.16	0.00	-1.55	0.02	1.53	0.28	25.91	0.58	-0.02
cluster3	LSTM	8	2.87	-1.40	-0.06	-1.43	0.02	1.47	0.10	10.47	0.43	-0.02
cluster3	LSTM	12	2.90	-1.52	-0.06	-1.40	0.07	1.38	-0.03	-2.77	0.43	-0.02
cluster3	LSTM	16	2.80	-1.89	-0.14	-0.86	0.08	0.91	-0.14	-16.95	0.43	-0.03
cluster3	Linear	2	0.39	-0.28	-0.02	-0.09	-0.01	0.11	0.20	7.98	0.49	0.00
cluster3	Linear	4	2.89	-1.86	-0.04	-1.00	0.00	1.03	0.24	17.38	0.36	-0.01

Continue on next page

Cluster	Algorithm	PH	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	6	3.14	-1.82	-0.10	-1.21	-0.01	1.32	0.26	24.19	0.52	-0.01
cluster3	Linear	8	2.97	-1.67	-0.03	-1.30	0.01	1.30	0.15	16.62	0.60	-0.01
cluster3	Linear	12	2.81	-1.80	-0.08	-0.96	0.03	1.01	0.04	5.40	0.61	-0.02
cluster3	Linear	16	2.70	-2.34	-0.18	-0.17	0.01	0.36	-0.10	-12.70	0.48	-0.03
cluster4	CNN	2	1.18	-0.92	-0.07	-0.19	0.00	0.26	-3.10	-162.88	-1.98	-0.01
cluster4	CNN	4	1.72	-0.64	-0.34	-0.72	-0.03	1.08	-5.44	-411.94	-3.47	-0.01
cluster4	CNN	6	3.09	-1.52	-0.69	-0.76	-0.12	1.57	-7.31	-666.91	-5.12	-0.03
cluster4	CNN	8	3.54	-1.45	-1.07	-0.74	-0.26	2.09	-9.17	-932.25	-6.63	-0.05
cluster4	CNN	12	3.65	-0.98	-1.03	-1.22	-0.42	2.67	-10.59	-1193.16	-7.73	-0.06
cluster4	CNN	16	3.75	-0.95	-0.84	-1.44	-0.53	2.80	-11.15	-1310.64	-8.28	-0.06
cluster4	LSTM	2	0.82	-0.73	-0.02	-0.06	0.00	0.09	-1.89	-67.60	-1.25	-0.01
cluster4	LSTM	4	2.04	-1.28	-0.21	-0.53	-0.01	0.76	-4.32	-280.32	-2.84	-0.02
cluster4	LSTM	6	2.54	-1.21	-0.59	-0.67	-0.07	1.33	-6.42	-539.93	-4.33	-0.03
cluster4	LSTM	8	3.17	-1.43	-0.90	-0.62	-0.20	1.74	-8.16	-791.07	-5.83	-0.04
cluster4	LSTM	12	3.81	-1.40	-1.04	-0.97	-0.40	2.41	-10.32	-1141.35	-7.71	-0.06
cluster4	LSTM	16	3.78	-1.21	-0.98	-1.03	-0.56	2.57	-11.06	-1290.25	-8.34	-0.06
cluster4	Linear	2	1.00	-1.06	-0.03	0.10	-0.01	-0.06	-2.35	-88.31	-1.34	0.00
cluster4	Linear	4	2.40	-2.04	-0.30	-0.02	-0.04	0.36	-4.71	-317.18	-3.05	-0.01
cluster4	Linear	6	2.78	-1.61	-0.65	-0.38	-0.12	1.17	-6.75	-583.96	-4.49	-0.02
cluster4	Linear	8	3.01	-1.35	-0.87	-0.55	-0.25	1.66	-8.40	-831.71	-5.73	-0.03
cluster4	Linear	12	3.63	-1.69	-1.03	-0.39	-0.51	1.94	-10.39	-1165.35	-7.53	-0.05
cluster4	Linear	16	3.83	-1.71	-0.84	-0.63	-0.65	2.12	-11.16	-1311.70	-8.38	-0.06

Table 6.3: Absolute difference between group-based prediction models and general prediction models performance in TBR_2 and TBR_1 BGL ranges assessed via both clinical and non-clinical metrics for clusters 4 and 5. Green: better for group-based models, red: worse, gray: equal. Bold: best result for 'A + B' metric.

Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	2	TBR_2	-0.36	0.00	0.00	0.30	0.05	-0.36	-0.24	-14.79	-0.53	-0.02
cluster4	CNN	2	TBR_1	-2.30	0.00	0.00	2.24	0.05	-2.30	-0.46	-26.02	-0.19	-0.01
cluster4	CNN	4	TBR_2	0.62	0.00	0.00	-0.64	0.03	0.62	-3.77	-388.93	-3.61	-0.09
cluster4	CNN	4	TBR_1	0.04	0.00	0.00	0.38	-0.42	0.04	-2.77	-258.21	-2.04	-0.03
cluster4	CNN	6	TBR_2	0.00	0.00	0.00	1.79	-1.79	0.00	-10.88	-1473.14	-9.88	-0.24
cluster4	CNN	6	TBR_1	0.01	0.00	0.00	2.17	-2.17	0.01	-9.03	-1092.14	-7.93	-0.13

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	8	TBR_2	0.00	0.00	0.00	4.29	-4.29	0.00	-14.76	-2419.11	-13.20	-0.31
cluster4	CNN	8	TBR_1	0.00	0.00	0.00	4.81	-4.81	0.00	-12.42	-1817.13	-10.78	-0.18
cluster4	CNN	12	TBR_2	0.00	0.00	0.00	7.95	-7.95	0.00	-16.56	-3107.30	-15.23	-0.36
cluster4	CNN	12	TBR_1	0.00	0.00	0.00	7.33	-7.33	0.00	-13.50	-2244.17	-12.27	-0.21
cluster4	CNN	16	TBR_2	0.00	0.00	0.00	10.32	-10.32	0.00	-16.70	-3366.42	-15.54	-0.38
cluster4	CNN	16	TBR_1	0.00	0.00	0.00	9.58	-9.58	0.00	-13.53	-2406.69	-12.42	-0.21
cluster4	LSTM	2	TBR_2	-1.25	0.00	0.00	1.27	-0.02	-1.25	-0.17	-6.02	-0.76	-0.03
cluster4	LSTM	2	TBR_1	0.14	0.00	0.00	-0.13	-0.01	0.14	0.01	0.07	-0.07	0.00
cluster4	LSTM	4	TBR_2	1.22	0.00	0.00	-1.41	0.19	1.22	-2.37	-197.37	-2.62	-0.07
cluster4	LSTM	4	TBR_1	1.02	0.00	0.00	-0.92	-0.09	1.02	-2.33	-175.93	-2.02	-0.04
cluster4	LSTM	6	TBR_2	0.72	0.00	0.00	0.15	-0.88	0.72	-8.24	-1000.76	-7.55	-0.18
cluster4	LSTM	6	TBR_1	0.35	0.00	0.00	0.96	-1.32	0.35	-6.75	-738.35	-5.68	-0.09
cluster4	LSTM	8	TBR_2	-0.01	0.00	0.00	3.15	-3.14	-0.01	-13.54	-2031.07	-12.06	-0.29
cluster4	LSTM	8	TBR_1	0.02	0.00	0.00	3.68	-3.70	0.02	-11.89	-1589.58	-10.30	-0.17
cluster4	LSTM	12	TBR_2	0.00	0.00	0.00	7.16	-7.16	0.00	-17.47	-3190.14	-15.95	-0.38
cluster4	LSTM	12	TBR_1	0.00	0.00	0.00	7.16	-7.16	0.00	-14.67	-2372.29	-13.23	-0.21
cluster4	LSTM	16	TBR_2	0.00	0.00	0.00	11.00	-11.00	0.00	-18.18	-3605.81	-16.73	-0.39
cluster4	LSTM	16	TBR_1	0.00	0.00	0.00	10.28	-10.28	0.00	-15.23	-2663.65	-13.88	-0.23
cluster4	Linear	2	TBR_2	-2.59	0.00	0.00	2.60	-0.01	-2.59	1.20	35.93	1.45	0.02
cluster4	Linear	2	TBR_1	-2.46	0.00	0.00	2.48	-0.01	-2.46	-0.08	-2.53	0.45	0.01
cluster4	Linear	4	TBR_2	-11.85	0.00	0.00	11.78	0.07	-11.85	0.23	17.33	1.56	0.02
cluster4	Linear	4	TBR_1	-4.52	0.00	0.00	4.85	-0.33	-4.52	-2.33	-173.09	-0.56	-0.01
cluster4	Linear	6	TBR_2	-1.40	0.00	0.00	2.77	-1.39	-1.40	-4.60	-532.84	-1.62	-0.06
cluster4	Linear	6	TBR_1	-1.17	0.00	0.00	3.13	-1.96	-1.17	-5.42	-595.43	-2.55	-0.04
cluster4	Linear	8	TBR_2	-0.22	0.00	0.00	3.85	-3.63	-0.22	-7.29	-1076.51	-3.87	-0.11
cluster4	Linear	8	TBR_1	-0.20	0.00	0.00	4.41	-4.21	-0.20	-7.39	-1003.94	-4.28	-0.07
cluster4	Linear	12	TBR_2	-0.02	0.00	0.00	9.34	-9.32	-0.02	-11.73	-2123.28	-8.87	-0.23
cluster4	Linear	12	TBR_1	-0.01	0.00	0.00	9.13	-9.13	-0.01	-11.15	-1817.27	-8.71	-0.14
cluster4	Linear	16	TBR_2	-0.01	0.00	0.00	12.32	-12.31	-0.01	-15.13	-2969.17	-13.17	-0.32
cluster4	Linear	16	TBR_1	0.00	0.00	0.00	11.79	-11.79	0.00	-13.66	-2384.75	-11.97	-0.19
cluster5	CNN	2	TBR_2	3.39	0.00	0.00	-3.33	-0.06	3.39	-0.75	-45.85	-0.50	0.00
cluster5	CNN	2	TBR_1	1.01	0.00	0.00	-0.90	-0.11	1.01	-2.12	-116.64	-1.37	-0.02
cluster5	CNN	4	TBR_2	-1.25	0.00	0.00	1.33	-0.08	-1.25	1.40	151.46	1.77	0.06
cluster5	CNN	4	TBR_1	-0.56	0.00	0.00	0.79	-0.23	-0.56	-0.61	-57.55	0.06	0.00
cluster5	CNN	6	TBR_2	0.00	0.00	0.00	-0.38	0.38	0.00	-0.56	-81.03	-0.30	0.02
cluster5	CNN	6	TBR_1	0.00	0.00	0.00	0.69	-0.69	0.00	-3.04	-385.86	-2.40	-0.04
cluster5	CNN	8	TBR_2	0.00	0.00	0.00	1.92	-1.92	0.00	-4.07	-710.83	-2.99	-0.02

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	8	TBR_1	0.00	0.00	0.00	2.41	-2.41	0.00	-5.57	-853.46	-4.30	-0.07
cluster5	CNN	12	TBR_2	0.00	0.00	0.00	6.75	-6.75	0.00	-8.75	-1709.65	-7.29	-0.10
cluster5	CNN	12	TBR_1	0.00	0.00	0.00	5.81	-5.81	0.00	-8.53	-1460.80	-7.15	-0.12
cluster5	CNN	16	TBR_2	0.00	0.00	0.00	9.05	-9.05	0.00	-8.83	-1849.87	-7.72	-0.11
cluster5	CNN	16	TBR_1	0.00	0.00	0.00	7.41	-7.41	0.00	-8.07	-1479.16	-7.05	-0.11
cluster5	LSTM	2	TBR_2	-1.38	0.00	0.00	1.42	-0.04	-1.38	0.49	17.74	0.39	0.01
cluster5	LSTM	2	TBR_1	2.06	0.00	0.00	-2.04	-0.02	2.06	-0.91	-29.45	-0.69	-0.01
cluster5	LSTM	4	TBR_2	2.64	0.00	0.00	-2.50	-0.14	2.64	-0.10	-9.33	0.04	0.02
cluster5	LSTM	4	TBR_1	2.71	0.00	0.00	-2.53	-0.19	2.71	-2.17	-164.76	-1.70	-0.03
cluster5	LSTM	6	TBR_2	0.53	0.00	0.00	-0.47	-0.07	0.53	-0.03	-3.85	0.02	0.03
cluster5	LSTM	6	TBR_1	0.39	0.00	0.00	0.34	-0.73	0.39	-2.89	-327.11	-2.11	-0.03
cluster5	LSTM	8	TBR_2	-0.01	0.00	0.00	0.98	-0.97	-0.01	-2.01	-325.39	-0.85	0.02
cluster5	LSTM	8	TBR_1	0.00	0.00	0.00	1.78	-1.78	0.00	-4.89	-688.10	-3.58	-0.05
cluster5	LSTM	12	TBR_2	0.00	0.00	0.00	5.19	-5.19	0.00	-6.97	-1346.62	-5.56	-0.07
cluster5	LSTM	12	TBR_1	0.00	0.00	0.00	4.48	-4.48	0.00	-7.72	-1303.08	-6.45	-0.10
cluster5	LSTM	16	TBR_2	0.00	0.00	0.00	9.12	-9.12	0.00	-9.07	-1880.94	-7.76	-0.10
cluster5	LSTM	16	TBR_1	0.00	0.00	0.00	7.24	-7.24	0.00	-8.41	-1527.42	-7.32	-0.11
cluster5	Linear	2	TBR_2	-0.30	0.00	0.00	0.35	-0.05	-0.30	-0.53	-15.20	1.15	0.02
cluster5	Linear	2	TBR_1	-1.17	0.00	0.00	1.19	-0.02	-1.17	-1.09	-32.80	0.10	0.01
cluster5	Linear	4	TBR_2	-7.19	0.00	0.00	7.44	-0.25	-7.19	0.11	8.16	2.04	0.06
cluster5	Linear	4	TBR_1	-6.47	0.00	0.00	6.77	-0.30	-6.47	-1.66	-124.25	0.35	0.01
cluster5	Linear	6	TBR_2	-1.58	0.00	0.00	1.59	-0.02	-1.58	1.29	158.18	3.15	0.09
cluster5	Linear	6	TBR_1	-1.46	0.00	0.00	2.41	-0.96	-1.46	-1.16	-132.41	1.24	0.03
cluster5	Linear	8	TBR_2	-0.21	0.00	0.00	1.92	-1.71	-0.21	-1.62	-247.93	0.83	0.05
cluster5	Linear	8	TBR_1	-0.23	0.00	0.00	2.82	-2.59	-0.23	-3.49	-487.62	-0.88	-0.01
cluster5	Linear	12	TBR_2	-0.02	0.00	0.00	6.68	-6.66	-0.02	-3.70	-699.22	-1.28	0.02
cluster5	Linear	12	TBR_1	-0.01	0.00	0.00	5.96	-5.96	-0.01	-4.25	-721.71	-2.05	-0.03
cluster5	Linear	16	TBR_2	-0.01	0.00	0.00	11.04	-11.03	-0.01	-6.10	-1251.62	-4.26	-0.04
cluster5	Linear	16	TBR_1	0.00	0.00	0.00	9.42	-9.42	0.00	-5.74	-1047.09	-4.15	-0.06

Table 6.4: Absolute difference between group-based prediction models and general prediction models performance in TAR_2 and TAR_1 BGL ranges assessed via both clinical and non-clinical metrics for clusters 2 and 3. Green: better for group-based models, red: worse, gray: equal. Bold: best result for 'A + B' metric.

Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	2	TAR_1	-0.30	0.17	0.01	0.12	0.01	-0.13	0.74	45.68	0.23	0.00
cluster2	CNN	2	TAR_2	0.30	-0.10	0.00	-0.20	0.00	0.20	0.18	13.69	0.55	0.00
cluster2	CNN	4	TAR_1	3.74	-3.71	0.16	-0.20	0.00	0.03	-2.03	-173.52	-2.30	-0.01
cluster2	CNN	4	TAR_2	5.25	-2.44	0.00	-2.81	0.00	2.81	-4.62	-592.50	-4.54	-0.02
cluster2	CNN	6	TAR_1	7.21	-6.88	0.00	-0.32	0.00	0.33	-4.81	-447.05	-4.80	-0.02
cluster2	CNN	6	TAR_2	2.50	2.71	-0.05	-5.16	0.00	5.21	-2.67	-456.82	-2.39	-0.01
cluster2	CNN	8	TAR_1	9.04	-8.55	-0.04	-0.46	0.00	0.49	-5.92	-551.68	-5.78	-0.03
cluster2	CNN	8	TAR_2	2.47	4.75	-0.03	-7.18	0.00	7.22	-3.02	-587.00	-2.96	-0.02
cluster2	CNN	12	TAR_1	17.62	-16.70	-0.06	-0.86	0.00	0.92	-9.46	-902.63	-9.56	-0.05
cluster2	CNN	12	TAR_2	0.14	13.29	0.00	-13.43	0.00	13.43	-3.74	-885.89	-3.62	-0.02
cluster2	CNN	16	TAR_1	21.96	-20.95	-0.01	-1.00	0.00	1.01	-10.64	-1003.23	-10.72	-0.05
cluster2	CNN	16	TAR_2	-1.42	18.65	0.00	-17.21	0.00	17.23	-4.46	-1134.82	-4.50	-0.02
cluster2	LSTM	2	TAR_1	-0.86	0.84	0.01	0.02	0.00	-0.02	1.00	42.57	0.62	0.00
cluster2	LSTM	2	TAR_2	0.31	-0.24	-0.01	-0.06	0.00	0.07	-0.82	-40.02	-0.40	0.00
cluster2	LSTM	4	TAR_1	1.26	-1.38	0.09	0.02	0.00	-0.12	-0.15	-11.70	-0.69	0.00
cluster2	LSTM	4	TAR_2	2.52	-1.54	0.01	-0.99	0.00	0.98	-1.86	-191.95	-1.57	0.00
cluster2	LSTM	6	TAR_1	4.08	-4.01	0.04	-0.11	0.00	0.07	-2.57	-230.14	-2.69	-0.02
cluster2	LSTM	6	TAR_2	3.09	0.10	-0.05	-3.14	0.00	3.19	-2.21	-329.73	-2.13	-0.01
cluster2	LSTM	8	TAR_1	6.86	-6.60	-0.06	-0.21	0.00	0.26	-4.27	-404.35	-4.33	-0.02
cluster2	LSTM	8	TAR_2	1.77	3.53	-0.04	-5.26	0.00	5.30	-1.43	-263.61	-1.38	-0.01
cluster2	LSTM	12	TAR_1	14.91	-13.99	-0.06	-0.86	0.00	0.92	-8.42	-799.29	-8.56	-0.04
cluster2	LSTM	12	TAR_2	2.81	9.66	0.00	-12.47	0.00	12.47	-4.51	-1026.08	-4.84	-0.02
cluster2	LSTM	16	TAR_1	22.69	-21.28	-0.01	-1.40	0.00	1.41	-11.51	-1066.99	-11.63	-0.06
cluster2	LSTM	16	TAR_2	1.09	18.04	0.00	-19.13	0.00	19.13	-6.32	-1566.29	-6.72	-0.04
cluster2	Linear	2	TAR_1	-0.94	0.94	-0.01	0.02	-0.01	0.00	0.82	35.59	0.59	0.00
cluster2	Linear	2	TAR_2	0.08	0.01	-0.01	-0.06	-0.01	0.09	-1.32	-66.94	-0.36	0.00
cluster2	Linear	4	TAR_1	0.77	-0.94	0.12	0.06	-0.02	-0.17	-0.24	-18.01	-0.51	0.00
cluster2	Linear	4	TAR_2	1.89	-1.18	0.01	-0.70	-0.02	0.71	-1.88	-194.31	-1.32	-0.01
cluster2	Linear	6	TAR_1	4.36	-4.34	0.13	-0.15	-0.01	0.02	-2.88	-255.24	-2.87	-0.02
cluster2	Linear	6	TAR_2	3.67	-0.54	-0.01	-3.11	-0.02	3.13	-3.33	-503.43	-3.13	-0.01
cluster2	Linear	8	TAR_1	8.49	-8.02	0.05	-0.50	-0.01	0.47	-5.68	-532.75	-5.46	-0.03
cluster2	Linear	8	TAR_2	4.62	1.76	-0.01	-6.37	-0.02	6.38	-4.53	-851.99	-4.65	-0.02
cluster2	Linear	12	TAR_1	16.88	-15.73	-0.02	-1.12	-0.01	1.15	-10.19	-962.82	-9.84	-0.05

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	12	TAR_2	3.28	10.70	0.00	-13.97	-0.01	13.98	-6.44	-1493.20	-6.75	-0.03
cluster2	Linear	16	TAR_1	21.46	-20.14	0.00	-1.31	0.00	1.32	-11.53	-1082.35	-11.25	-0.05
cluster2	Linear	16	TAR_2	0.01	18.77	0.00	-18.77	-0.01	18.78	-6.14	-1555.45	-6.34	-0.03
cluster3	CNN	2	TAR_1	2.21	-2.12	-0.02	-0.07	0.00	0.09	-1.52	-91.03	-1.38	-0.01
cluster3	CNN	2	TAR_2	1.46	-1.15	-0.01	-0.30	0.00	0.31	-2.93	-219.55	-2.35	-0.01
cluster3	CNN	4	TAR_1	4.86	-4.55	-0.12	-0.20	0.00	0.31	-3.47	-290.83	-3.11	-0.02
cluster3	CNN	4	TAR_2	0.64	0.76	-0.06	-1.34	0.00	1.40	-3.45	-446.90	-1.92	-0.01
cluster3	CNN	6	TAR_1	8.17	-7.39	-0.11	-0.66	0.00	0.78	-6.20	-567.85	-5.66	-0.02
cluster3	CNN	6	TAR_2	5.61	-0.64	-0.07	-4.90	0.00	4.97	-9.66	-1583.16	-8.38	-0.03
cluster3	CNN	8	TAR_1	7.62	-7.06	-0.20	-0.36	0.00	0.56	-5.02	-472.58	-4.80	-0.02
cluster3	CNN	8	TAR_2	-1.56	5.78	-0.05	-4.17	0.00	4.22	-6.09	-1163.09	-3.50	-0.01
cluster3	CNN	12	TAR_1	11.54	-10.96	-0.08	-0.50	0.00	0.58	-6.49	-638.09	-6.40	-0.03
cluster3	CNN	12	TAR_2	-3.27	10.43	0.00	-7.17	0.00	7.16	-9.10	-2105.41	-6.29	-0.02
cluster3	CNN	16	TAR_1	9.46	-9.62	-0.01	0.18	0.00	-0.16	-4.71	-472.26	-4.48	-0.02
cluster3	CNN	16	TAR_2	-4.01	7.02	0.00	-2.99	0.00	3.01	-8.30	-2080.97	-5.61	0.00
cluster3	LSTM	2	TAR_1	0.48	-0.47	0.00	0.00	0.00	0.01	-0.55	-22.33	-0.49	0.00
cluster3	LSTM	2	TAR_2	0.20	-0.13	-0.01	-0.06	0.00	0.07	-1.34	-64.87	-0.90	0.00
cluster3	LSTM	4	TAR_1	4.19	-3.91	-0.08	-0.21	0.01	0.28	-2.97	-216.53	-2.74	-0.01
cluster3	LSTM	4	TAR_2	2.17	-1.19	-0.04	-0.94	0.00	0.98	-3.52	-356.14	-2.46	0.00
cluster3	LSTM	6	TAR_1	6.15	-5.63	-0.17	-0.37	0.01	0.52	-4.66	-408.07	-4.24	-0.02
cluster3	LSTM	6	TAR_2	2.05	0.67	-0.11	-2.61	0.00	2.72	-5.47	-797.79	-3.63	-0.01
cluster3	LSTM	8	TAR_1	7.10	-6.43	-0.22	-0.45	0.00	0.67	-4.96	-466.74	-4.71	-0.03
cluster3	LSTM	8	TAR_2	0.48	3.63	-0.08	-4.03	0.00	4.11	-6.28	-1128.48	-4.16	-0.01
cluster3	LSTM	12	TAR_1	11.26	-10.43	-0.11	-0.71	0.00	0.83	-6.44	-624.62	-6.47	-0.03
cluster3	LSTM	12	TAR_2	-2.02	9.91	0.00	-7.89	0.00	7.89	-8.99	-2006.70	-6.40	-0.01
cluster3	LSTM	16	TAR_1	13.98	-13.40	-0.01	-0.57	0.00	0.58	-7.22	-700.33	-7.16	-0.03
cluster3	LSTM	16	TAR_2	-2.76	11.11	0.00	-8.35	0.00	8.35	-10.68	-2600.75	-8.17	-0.02
cluster3	Linear	2	TAR_1	0.54	-0.50	-0.02	0.00	-0.01	0.04	-0.90	-38.31	-0.58	0.00
cluster3	Linear	2	TAR_2	0.18	-0.07	-0.01	-0.08	-0.01	0.11	-2.39	-118.61	-1.14	0.00
cluster3	Linear	4	TAR_1	2.41	-2.27	-0.09	-0.04	-0.01	0.14	-1.99	-145.57	-1.44	-0.01
cluster3	Linear	4	TAR_2	-0.78	1.02	-0.04	-0.19	-0.02	0.24	-1.36	-140.72	0.11	0.00
cluster3	Linear	6	TAR_1	3.78	-3.58	-0.12	-0.06	-0.03	0.20	-3.18	-280.73	-2.40	-0.02
cluster3	Linear	6	TAR_2	-2.11	3.29	-0.06	-1.10	-0.03	1.18	-2.99	-452.82	-0.79	0.00
cluster3	Linear	8	TAR_1	6.63	-6.22	-0.09	-0.29	-0.03	0.41	-5.12	-483.39	-4.27	-0.02
cluster3	Linear	8	TAR_2	-0.74	4.05	-0.02	-3.28	-0.02	3.31	-6.47	-1203.63	-4.21	0.00
cluster3	Linear	12	TAR_1	9.75	-9.38	-0.03	-0.34	-0.01	0.37	-6.67	-653.65	-5.86	-0.03
cluster3	Linear	12	TAR_2	-2.39	7.92	0.00	-5.51	-0.01	5.53	-9.24	-2116.79	-6.72	-0.02

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	16	TAR_1	11.45	-11.41	0.00	-0.03	0.00	0.04	-6.86	-676.43	-6.15	-0.03
cluster3	Linear	16	TAR_2	-2.66	7.38	0.00	-4.71	-0.01	4.72	-10.37	-2583.44	-7.93	-0.02

Table 6.5: Absolute difference between group-based prediction models and general prediction models performance in TIR BGL ranges assessed via both clinical and non-clinical metrics for clusters 0, 1, 4 and 5. Green: better for group-based models, red: worse, gray: equal. Bold: best result for 'A + B' metric.

Cluster	Algorithm	PH	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	2	-1.61	1.66	-0.07	0.04	0.00	0.05	0.28	13.54	0.52	0.00
cluster0	CNN	4	-4.04	4.12	-0.14	0.06	0.00	0.08	1.09	71.17	1.61	0.01
cluster0	CNN	6	2.06	-1.47	-0.63	0.05	-0.01	0.59	-2.75	-202.13	-1.63	-0.02
cluster0	CNN	8	3.54	-2.65	-0.92	0.05	-0.01	0.89	-4.09	-343.05	-2.91	-0.03
cluster0	CNN	12	4.46	-3.21	-1.29	0.06	-0.02	1.25	-5.62	-481.67	-4.11	-0.04
cluster0	CNN	16	8.55	-7.24	-1.35	0.09	-0.05	1.31	-9.17	-775.96	-7.22	-0.07
cluster0	LSTM	2	-1.33	1.32	-0.01	0.02	0.00	-0.01	0.53	18.32	0.59	0.00
cluster0	LSTM	4	-1.38	1.47	-0.14	0.04	-0.01	0.09	0.28	16.01	0.50	0.00
cluster0	LSTM	6	1.48	-1.05	-0.46	0.04	-0.01	0.43	-2.00	-140.18	-1.17	-0.01
cluster0	LSTM	8	2.37	-1.62	-0.78	0.05	-0.01	0.75	-3.43	-270.58	-2.13	-0.02
cluster0	LSTM	12	5.36	-4.08	-1.31	0.06	-0.02	1.28	-6.41	-544.09	-4.79	-0.04
cluster0	LSTM	16	6.87	-5.43	-1.47	0.08	-0.04	1.44	-7.56	-656.14	-5.91	-0.06
cluster0	Linear	2	-0.83	0.83	-0.03	0.03	0.00	0.00	-0.04	-1.43	0.21	0.00
cluster0	Linear	4	0.78	-0.55	-0.29	0.06	0.00	0.23	-1.33	-82.82	-0.75	-0.01
cluster0	Linear	6	1.12	-0.65	-0.52	0.05	0.00	0.47	-1.93	-145.13	-1.03	-0.01
cluster0	Linear	8	3.90	-3.00	-0.94	0.05	-0.01	0.90	-4.35	-350.30	-3.06	-0.03
cluster0	Linear	12	5.08	-3.84	-1.28	0.06	-0.03	1.24	-5.54	-479.50	-4.21	-0.04
cluster0	Linear	16	7.53	-6.28	-1.29	0.09	-0.05	1.25	-7.62	-659.47	-6.14	-0.06
cluster1	CNN	2	6.46	-6.15	-0.14	-0.16	0.00	0.31	-4.20	-184.99	-2.92	-0.03
cluster1	CNN	4	9.99	-9.03	-0.68	-0.27	-0.01	0.96	-7.31	-417.28	-5.04	-0.05
cluster1	CNN	6	13.11	-11.53	-1.29	-0.27	-0.02	1.58	-10.99	-716.14	-7.83	-0.08
cluster1	CNN	8	17.82	-15.48	-2.04	-0.25	-0.04	2.34	-16.47	-1178.26	-12.37	-0.13
cluster1	CNN	12	15.23	-13.13	-1.81	-0.24	-0.05	2.10	-16.86	-1256.25	-12.70	-0.14
cluster1	CNN	16	16.65	-14.99	-1.38	-0.23	-0.06	1.66	-18.14	-1372.39	-14.13	-0.16
cluster1	LSTM	2	3.86	-3.77	-0.02	-0.08	0.00	0.09	-2.42	-76.42	-1.74	-0.02
cluster1	LSTM	4	8.58	-7.93	-0.41	-0.24	-0.01	0.65	-5.91	-305.36	-4.11	-0.04

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Cluster	Algorithm	PH	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	6	12.40	-11.05	-1.05	-0.27	-0.02	1.35	-9.73	-607.35	-6.87	-0.07
cluster1	LSTM	8	14.75	-12.82	-1.63	-0.26	-0.03	1.93	-13.44	-924.96	-9.77	-0.10
cluster1	LSTM	12	16.26	-14.07	-1.90	-0.24	-0.05	2.19	-17.29	-1278.66	-13.10	-0.13
cluster1	LSTM	16	17.37	-15.47	-1.61	-0.23	-0.06	1.90	-18.97	-1430.07	-14.71	-0.16
cluster1	Linear	2	4.86	-4.76	-0.03	-0.07	0.00	0.10	-3.24	-109.38	-2.26	-0.02
cluster1	Linear	4	11.76	-11.00	-0.57	-0.18	-0.01	0.76	-8.10	-448.02	-5.82	-0.05
cluster1	Linear	6	14.83	-13.29	-1.27	-0.25	-0.02	1.54	-11.79	-770.74	-8.57	-0.08
cluster1	Linear	8	15.82	-13.80	-1.73	-0.25	-0.04	2.02	-14.31	-1010.81	-10.60	-0.10
cluster1	Linear	12	17.13	-15.02	-1.82	-0.23	-0.06	2.11	-17.38	-1297.46	-13.38	-0.14
cluster1	Linear	16	18.22	-16.57	-1.36	-0.22	-0.06	1.65	-19.03	-1430.50	-14.99	-0.16
cluster4	CNN	2	2.19	-2.07	-0.09	-0.03	0.00	0.12	-2.06	-95.26	-1.14	-0.01
cluster4	CNN	4	2.42	-1.90	-0.48	-0.03	0.00	0.52	-3.50	-213.43	-1.92	-0.02
cluster4	CNN	6	5.98	-4.89	-1.05	-0.03	-0.01	1.09	-6.42	-447.94	-4.30	-0.04
cluster4	CNN	8	7.79	-6.06	-1.68	-0.02	-0.02	1.73	-9.18	-723.51	-6.60	-0.06
cluster4	CNN	12	7.76	-6.08	-1.64	0.00	-0.04	1.68	-9.53	-779.79	-7.17	-0.07
cluster4	CNN	16	9.23	-7.85	-1.35	0.02	-0.05	1.38	-10.14	-848.14	-8.05	-0.08
cluster4	LSTM	2	1.74	-1.72	-0.01	0.00	0.00	0.02	-1.30	-42.47	-0.79	-0.01
cluster4	LSTM	4	3.09	-2.77	-0.28	-0.04	-0.01	0.32	-3.08	-167.63	-1.83	-0.02
cluster4	LSTM	6	4.99	-4.08	-0.85	-0.03	-0.01	0.91	-5.69	-377.84	-3.62	-0.03
cluster4	LSTM	8	7.31	-5.89	-1.37	-0.02	-0.02	1.42	-8.36	-617.88	-5.79	-0.06
cluster4	LSTM	12	8.88	-7.19	-1.66	0.00	-0.04	1.69	-10.33	-835.98	-7.84	-0.07
cluster4	LSTM	16	10.23	-8.62	-1.57	0.02	-0.05	1.61	-11.39	-944.71	-8.96	-0.09
cluster4	Linear	2	2.41	-2.38	-0.03	0.00	0.00	0.03	-1.96	-68.68	-1.17	-0.01
cluster4	Linear	4	5.71	-5.28	-0.43	0.01	-0.01	0.43	-4.96	-289.72	-3.39	-0.03
cluster4	Linear	6	6.88	-5.85	-1.00	-0.02	-0.01	1.03	-6.99	-490.30	-4.86	-0.04
cluster4	Linear	8	7.43	-6.00	-1.39	-0.02	-0.02	1.43	-8.05	-618.57	-5.77	-0.05
cluster4	Linear	12	9.71	-8.01	-1.67	0.01	-0.05	1.70	-10.18	-833.65	-7.93	-0.08
cluster4	Linear	16	11.14	-9.76	-1.34	0.03	-0.06	1.38	-11.31	-937.56	-9.12	-0.09
cluster5	CNN	2	0.73	-0.62	-0.07	-0.03	0.00	0.11	-0.63	-30.12	-0.21	-0.01
cluster5	CNN	4	-1.78	1.98	-0.17	-0.03	0.00	0.20	0.02	0.72	0.69	0.00
cluster5	CNN	6	1.01	-0.58	-0.40	-0.04	0.00	0.43	-1.28	-96.04	-0.46	-0.01
cluster5	CNN	8	2.74	-1.70	-0.99	-0.04	-0.01	1.04	-3.49	-294.75	-2.05	-0.02
cluster5	CNN	12	6.28	-4.83	-1.40	-0.01	-0.03	1.45	-6.48	-549.99	-4.78	-0.05
cluster5	CNN	16	7.16	-5.92	-1.20	0.00	-0.04	1.24	-6.43	-561.85	-5.26	-0.06
cluster5	LSTM	2	0.36	-0.33	-0.01	-0.01	0.00	0.03	-0.25	-8.43	0.02	0.00
cluster5	LSTM	4	0.36	-0.20	-0.12	-0.04	-0.01	0.16	-0.63	-35.92	-0.18	-0.01

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Cluster	Algorithm	PH	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	6	1.17	-0.72	-0.40	-0.04	-0.01	0.45	-1.84	-129.21	-0.83	-0.01
cluster5	LSTM	8	2.91	-2.08	-0.77	-0.04	-0.01	0.83	-3.35	-264.54	-1.99	-0.02
cluster5	LSTM	12	5.42	-4.08	-1.29	-0.02	-0.03	1.34	-5.64	-482.71	-4.12	-0.04
cluster5	LSTM	16	7.02	-5.62	-1.36	-0.01	-0.04	1.40	-6.54	-573.88	-5.24	-0.06
cluster5	Linear	2	0.80	-0.77	-0.03	-0.01	0.00	0.03	-0.74	-26.85	-0.24	-0.01
cluster5	Linear	4	1.26	-1.03	-0.23	0.00	-0.01	0.23	-1.74	-107.36	-0.93	-0.01
cluster5	Linear	6	1.19	-0.67	-0.49	-0.02	0.00	0.52	-2.06	-154.91	-0.98	-0.01
cluster5	Linear	8	3.90	-2.90	-0.96	-0.03	-0.01	1.00	-4.11	-332.28	-2.68	-0.03
cluster5	Linear	12	5.50	-4.13	-1.33	-0.01	-0.03	1.37	-5.03	-437.65	-3.79	-0.04
cluster5	Linear	16	7.42	-6.13	-1.24	0.00	-0.04	1.29	-6.23	-547.64	-5.24	-0.05

6.3.2 Personalized prediction models

Following the evaluation of patients within the prediction models for each cluster, the best- and worst-predicted patients were identified. Despite having 18 prediction models per cluster, many patients were repeatedly selected within a cluster across multiple prediction models, both in the best- and worst-predicted categories. As a result, the final group of best-predicted patients comprised 17, while the worst-predicted group included 10. Table 6.6 displays the characteristics of these patients' BGL measurements.

Table 6.6: BGL measurements stats from best and worst classified patients.

Stats	Best patient	Worst patient
count	751 728.00	362 938.00
mean	162.80	147.14
std	58.25	69.80
min	40.00	40.00
25%	119.00	92.00
50%	153.00	135.00
75%	199.00	190.00
max	500.00	500.00
Hypoglucemia %	1.56	11.56
Hyperglucemia %	33.63	28.35

After completing the training and testing process for the personalized prediction models for each patient, the results are presented in Appendix F. Table F.1 follows a similar format to the results of the group-based prediction models (Table D.1) but includes two additional columns, "Patient," which identifies the specific patient, and "Type," which indicates whether the patient belongs to the group of best-predicted or worst-predicted cases. In this case, the table size is double because each group picked two patients and has 1 296 rows. The results of the comparison of the performance between the personalized prediction models and the group-based prediction models can be found in Appendix G. Table G.1 maintains the same structure and color-coding as the previous comparison between group-based and general prediction models. Green continues to indicate a better outcome for the group-based prediction models, while red represents a worse outcome, and gray equal performance.

Table 6.7 shows the distribution of the absolute differences between the performance of personalized and group-based prediction models, specifically focusing on the 'A + B' metric in the different BGL ranges. The table organizes the results into four categories, namely "Personalized better", which includes instances where the personalized models outperform group-based models, followed by columns for cases where personalized models perform equally, worse, or are missing from the comparison. The distribution percentages and the number of cases are presented for each category. Upon examining this distribution, it is observed that only 37.98% of the results in the different BGL ranges show an improvement in personalized prediction models over group-based prediction models. Meanwhile, 55.71% of the results do not outperform, meaning that performance is equal to or worse than the group-based prediction models. Some results, 6.4%, of the data entries are empty. These empty values correspond to cases where some test sets in the personalized prediction models lacked hypoglycemia measurements, as seen in the TBR column, which is the only one with missing data.

Table 6.8, a more detailed distribution of the personalized model prediction performance compared to group-based prediction models based on the 'A + B' metric by the different BGL ranges and marginalized by patient type, algorithm, and cluster. From the analysis of it can

Table 6.7: Distribution of the personalized model prediction performance compared to group-based prediction models based on the 'A + B' metric by the different BGL ranges. The higher results for column are highlighted in bold.

	Personalized better		Personalized equal		Personalized worse		Personalized NaN	
	Number	%	Number	%	Number	%	Number	%
ALL	114	8.80	12	0.93	90	6.94	0	0.00
TBR_2	62	4.78	73	5.63	8	0.62	73	5.63
TBR_1	102	7.87	91	7.02	13	1.00	10	0.77
TIR	91	7.02	37	2.85	88	6.79	0	0.00
TAR_1	58	4.48	25	1.93	133	10.26	0	0.00
TAR_2	64	4.94	41	3.16	111	8.56	0	0.00
Total	491	37.89	279	21.52	443	34.17	83	6.4

be concluded that prediction models of patients worse classified by the group-based prediction models generally show better performance compare to patients best classified, as the "worst" row contains the highest values in most cases for better category, except in the TAR_1 and TAR_2 range. Additionally, when examining prediction model performance, the Linear prediction algorithm shows better performance in the entire, TBR_2, and TBR_1 BGL ranges. The LSTM prediction algorithm performs better in the TIR and TAR_1 BGL ranges, and the CNN prediction algorithm stands out in TAR_1 and TAR_2 BGL ranges. This observation provides an interesting indication for scenarios involving personalized prediction models, suggesting which prediction models may be more effective depending on the BGL range characteristics.

A more detailed analysis of the behavior of group-based prediction models versus personalized prediction models reveals interesting insights when patients are divided into types ("best" or "worst") and their performance is analyzed across BGL ranges. Focusing first on the patients worst predicted by group-based prediction models, two important cases emerge. The first concerns BGL ranges in TBR, where, in most cases, personalized prediction models outperform group-based prediction models. Only in cluster 1 there are some exceptions where group-based prediction models perform better, with some cases showing equal results. Table H.1 from Appendix H shows the results filtered by these variables. The second with the worst predicted patients in hyperglycemic ranges in clusters 2, 3, and 4, where group-based prediction models outperform personalized ones presented in Table 6.9. This finding are related with the previous Section 6.3.1, where clusters 2 and 3 showed much better performance than the general prediction models (Table 6.4). Finally, the most notable finding for patients best predicted by group-based prediction models occurs in the TBR ranges, differences in the results of most clinical metric are zero, indicating that both prediction model types performed equally. Detailed results for this analysis are provided in Table I.1 from Appendix I.

Table 6.8: Distribution of the personalized model prediction performance compared to group-based prediction models based on the 'A + B' metric by the different BGL ranges and marginalized by patient type, algorithm, and cluster.

Range	Perfor- mance	Patient type				Algorithm						Cluster											
		Best Nº	%	Worst Nº	%	Linear Nº	%	LSTM Nº	%	CNN Nº	%	C0 Nº	%	C1 Nº	%	C2 Nº	%	C3 Nº	%	C4 Nº	%	C5 Nº	%
ALL	Better	40	3.09	74	5.71	40	3.09	36	2.78	38	2.93	19	1.47	20	1.54	24	1.85	9	0.69	13	1.00	29	2.24
	Equal	11	0.85	1	0.08	1	0.08	6	0.46	5	0.39	2	0.15	6	0.46	0	0.00	0	0.00	4	0.31	0	0.00
	Worse	57	4.40	33	2.55	31	2.39	30	2.31	29	2.24	15	1.16	10	0.77	12	0.93	27	2.08	19	1.47	7	0.54
	NaN	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
TBR_2	Better	0	0.00	62	4.78	28	2.16	14	1.08	20	1.54	16	1.23	1	0.08	10	0.77	9	0.69	12	0.93	14	1.08
	Equal	35	2.70	38	2.93	16	1.23	29	2.24	28	2.16	13	1.00	27	2.08	16	1.23	6	0.46	5	0.39	6	0.46
	Worse	0	0.00	8	0.62	3	0.23	5	0.39	0	0.00	0	0.00	2	0.15	1	0.08	3	0.23	1	0.08	1	0.08
	NaN	73	5.63	0	0.00	25	1.93	24	1.85	24	1.85	7	0.54	6	0.46	9	0.69	18	1.39	18	1.39	15	1.16
TBR_1	Better	22	1.70	80	6.17	55	4.24	20	1.54	27	2.08	20	1.54	15	1.16	14	1.08	16	1.23	16	1.23	21	1.62
	Equal	68	5.25	23	1.77	11	0.85	40	3.09	40	3.09	14	1.08	11	0.85	21	1.62	18	1.39	15	1.16	12	0.93
	Worse	8	0.62	5	0.39	3	0.23	8	0.62	2	0.15	2	0.15	4	0.31	1	0.08	2	0.15	1	0.08	3	0.23
	NaN	10	0.77	0	0.00	3	0.23	4	0.31	3	0.23	0	0.00	6	0.46	0	0.00	0	0.00	4	0.31	0	0.00
TIR	Better	27	2.08	64	4.94	19	1.47	41	3.16	31	2.39	16	1.23	11	0.85	17	1.31	20	1.54	17	1.31	10	0.77
	Equal	29	2.24	8	0.62	4	0.31	17	1.31	16	1.23	5	0.39	15	1.16	1	0.08	6	0.46	8	0.62	2	0.15
	Worse	52	4.01	36	2.78	49	3.78	14	1.08	25	1.93	15	1.16	10	0.77	18	1.39	10	0.77	11	0.85	24	1.85
	NaN	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
TAR_1	Better	39	3.01	19	1.47	11	0.85	20	1.54	27	2.08	10	0.77	12	0.93	10	0.77	1	0.08	3	0.23	22	1.70
	Equal	17	1.31	8	0.62	6	0.46	9	0.69	10	0.77	3	0.23	11	0.85	1	0.08	0	0.00	7	0.54	3	0.23
	Worse	52	4.01	81	6.25	55	4.24	43	3.32	35	2.70	23	1.77	13	1.00	25	1.93	35	2.70	26	2.01	11	0.85
	NaN	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
TAR_2	Better	36	2.78	28	2.16	22	1.70	20	1.54	22	1.70	13	1.00	8	0.62	10	0.77	2	0.15	8	0.62	23	1.77
	Equal	27	2.08	14	1.08	12	0.93	16	1.23	13	1.00	4	0.31	21	1.62	1	0.08	2	0.15	10	0.77	3	0.23
	Worse	45	3.47	66	5.09	38	2.93	36	2.78	37	2.85	19	1.47	7	0.54	25	1.93	32	2.47	18	1.39	10	0.77
	NaN	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00

Table 6.9: Absolute difference between group-based prediction models and personalized prediction models performance in TAR_2 and TAR_1 BGL ranges assessed via both clinical and non-clinical metrics for clusters 2, 3, and 4. Green: better for group-based models, red: worse, gray: equal. Bold: best result for 'A + B' metric.

Cluster	Algorithm	PH	Range	Patient	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	2	TAR_1	LIB194012	3.25	-2.78	0.21	-0.62	-0.05	0.47	-2.38	-0.01	-167.31	-2.27
cluster2	CNN	2	TAR_2	LIB194012	8.66	-6.69	0.00	-1.97	0.00	1.97	-9.56	-0.03	-838.89	-9.35
cluster2	CNN	4	TAR_1	LIB194012	1.93	-1.56	0.41	-0.78	0.00	0.37	-1.66	-0.01	-127.39	-1.39
cluster2	CNN	4	TAR_2	LIB194012	11.52	-6.97	0.13	-4.69	0.00	4.55	-13.52	-0.05	-1598.27	-11.03
cluster2	CNN	6	TAR_1	LIB193916	3.19	-2.36	0.32	-1.14	0.00	0.83	-2.67	-0.01	-244.16	-2.44
cluster2	CNN	6	TAR_2	LIB193916	15.89	-9.63	0.00	-6.25	0.00	6.26	-15.49	-0.05	-2615.61	-14.19
cluster2	CNN	8	TAR_1	LIB193916	8.73	-7.24	0.27	-1.76	0.00	1.49	-5.59	-0.02	-496.44	-4.79
cluster2	CNN	8	TAR_2	LIB193916	16.61	-4.52	0.00	-12.09	0.00	12.09	-19.47	-0.06	-3639.57	-17.08
cluster2	CNN	12	TAR_1	LIB193916	18.99	-16.07	0.00	-2.91	0.00	2.92	-12.09	-0.06	-1182.65	-10.98
cluster2	CNN	12	TAR_2	LIB193916	7.80	19.97	0.00	-27.78	0.00	27.77	-20.55	-0.07	-4913.99	-18.85
cluster2	CNN	16	TAR_1	LIB193916	16.42	-16.24	0.00	-0.17	0.00	0.18	-8.89	-0.04	-858.58	-8.80
cluster2	CNN	16	TAR_2	LIB193916	0.14	10.05	0.00	-10.19	0.00	10.19	-8.59	-0.03	-2252.39	-8.63
cluster2	Linear	2	TAR_1	LIB194012	1.14	-0.97	0.00	-0.15	0.00	0.17	-1.26	-0.01	-73.75	-1.44
cluster2	Linear	2	TAR_2	LIB194012	1.31	-1.05	0.00	-0.26	0.00	0.26	-2.87	-0.01	-168.29	-3.23
cluster2	Linear	4	TAR_1	LIB194012	8.20	-6.90	0.31	-0.73	-0.89	1.30	-5.98	-0.03	-628.09	-6.88
cluster2	Linear	4	TAR_2	LIB194012	10.18	-5.63	-0.13	-4.43	0.00	4.55	-8.30	-0.03	-1215.53	-10.46
cluster2	Linear	6	TAR_1	LIB194012	14.76	-11.74	0.00	-2.01	-1.01	3.02	-11.54	-0.06	-1437.24	-13.43
cluster2	Linear	6	TAR_2	LIB194012	9.29	0.28	0.00	-8.88	-0.68	9.57	-11.44	-0.04	-2442.24	-14.24
cluster2	Linear	8	TAR_1	LIB193916	19.90	-15.09	-0.68	-2.23	-1.90	4.81	-19.09	-0.09	-2648.68	-21.80
cluster2	Linear	8	TAR_2	LIB193916	-0.52	12.30	0.00	-10.94	-0.84	11.78	-9.38	-0.03	-2595.01	-12.68
cluster2	Linear	12	TAR_1	LIB193916	25.12	-20.14	0.00	-0.92	-4.06	4.98	-29.02	-0.14	-4332.63	-32.94
cluster2	Linear	12	TAR_2	LIB193916	-3.31	18.09	-0.24	-12.65	-1.89	14.78	-16.01	-0.06	-4897.78	-19.23
cluster2	Linear	16	TAR_1	LIB193916	27.97	-22.94	0.00	-0.09	-4.95	5.03	-32.67	-0.16	-4934.50	-37.84
cluster2	Linear	16	TAR_2	LIB193916	-6.66	19.43	-0.27	-10.05	-2.45	12.77	-15.69	-0.06	-5301.52	-19.50
cluster2	LSTM	2	TAR_1	LIB194012	1.34	-1.08	-0.05	-0.20	0.00	0.26	-1.25	-0.01	-92.85	-1.85
cluster2	LSTM	2	TAR_2	LIB194012	1.32	-1.18	0.00	-0.13	0.00	0.14	-2.29	-0.01	-134.04	-2.63
cluster2	LSTM	4	TAR_1	LIB194012	2.61	-2.45	0.52	-0.68	0.00	0.16	-1.80	-0.01	-138.34	-1.60
cluster2	LSTM	4	TAR_2	LIB194012	9.25	-5.49	0.00	-3.76	0.00	3.76	-10.08	-0.03	-1065.00	-9.30
cluster2	LSTM	6	TAR_1	LIB194012	3.61	-2.81	0.42	-1.22	0.00	0.80	-3.63	-0.02	-327.70	-3.40
cluster2	LSTM	6	TAR_2	LIB194012	18.99	-14.34	0.00	-4.64	0.00	4.65	-16.51	-0.06	-2065.26	-12.25
cluster2	LSTM	8	TAR_1	LIB193916	0.81	-0.27	0.47	-1.02	0.00	0.54	-1.01	0.00	-85.21	-0.83
cluster2	LSTM	8	TAR_2	LIB193916	16.61	-12.41	0.00	-4.20	0.00	4.20	-15.11	-0.05	-2574.26	-12.93

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Cluster	Algorithm	PH	Range	Patient	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	12	TAR_1	LIB193916	12.71	-11.41	0.08	-1.38	0.00	1.30	-8.37	-0.04	-856.03	-8.11
cluster2	LSTM	12	TAR_2	LIB193916	11.82	3.08	0.00	-14.90	0.00	14.90	-20.33	-0.07	-4491.63	-18.11
cluster2	LSTM	16	TAR_1	LIB193916	22.07	-21.20	0.00	-0.87	0.00	0.87	-11.63	-0.05	-1078.70	-10.91
cluster2	LSTM	16	TAR_2	LIB193916	5.16	15.49	0.00	-20.65	0.00	20.65	-16.85	-0.06	-4163.92	-15.97
cluster3	CNN	2	TAR_1	LIB193878	1.96	-1.78	0.00	-0.19	0.00	0.18	-1.90	-0.01	-145.78	-2.22
cluster3	CNN	2	TAR_2	LIB193878	1.04	-0.18	0.00	-0.86	0.00	0.86	-1.70	-0.01	-164.54	-2.25
cluster3	CNN	4	TAR_1	LIB193878	4.55	-3.89	-0.13	-0.46	-0.07	0.66	-2.86	-0.01	-270.18	-2.83
cluster3	CNN	4	TAR_2	LIB193878	0.09	0.82	0.00	-0.91	0.00	0.91	-0.44	0.00	-75.76	-0.57
cluster3	CNN	6	TAR_1	LIB193878	7.15	-5.77	0.13	-1.51	0.00	1.38	-6.68	-0.03	-762.56	-7.09
cluster3	CNN	6	TAR_2	LIB193878	8.88	-3.35	0.00	-5.54	0.00	5.53	-8.57	-0.03	-1385.04	-7.99
cluster3	CNN	8	TAR_1	LIB193878	12.81	-10.52	0.00	-2.31	0.00	2.29	-10.03	-0.05	-1043.15	-9.31
cluster3	CNN	8	TAR_2	LIB193878	13.18	-1.32	0.00	-11.87	0.00	11.86	-15.65	-0.05	-2838.22	-13.27
cluster3	CNN	12	TAR_1	LIB193878	14.84	-12.25	0.00	-2.58	0.00	2.59	-10.53	-0.05	-1066.46	-9.60
cluster3	CNN	12	TAR_2	LIB193878	7.45	14.44	0.00	-21.89	0.00	21.89	-15.64	-0.05	-3577.27	-14.01
cluster3	CNN	16	TAR_1	LIB193878	29.57	-26.53	0.00	-3.05	0.00	3.04	-16.50	-0.08	-1717.40	-14.75
cluster3	CNN	16	TAR_2	LIB193878	0.95	24.83	0.00	-25.78	0.00	25.78	-18.33	-0.06	-4685.39	-16.88
cluster3	Linear	2	TAR_1	LIB193878	1.14	-1.01	0.00	-0.12	0.00	0.13	-1.72	-0.01	-103.74	-2.24
cluster3	Linear	2	TAR_2	LIB193878	0.96	-1.04	0.00	0.09	0.00	-0.08	-1.37	0.00	-82.16	-1.72
cluster3	Linear	4	TAR_1	LIB193878	7.58	-6.07	-0.46	-0.46	-0.59	1.51	-6.36	-0.03	-699.46	-7.94
cluster3	Linear	4	TAR_2	LIB193878	2.54	-1.18	0.00	-1.36	0.00	1.36	0.10	0.00	-229.48	-2.14
cluster3	Linear	6	TAR_1	LIB193878	11.41	-7.22	-0.96	-0.21	-3.02	4.19	-10.44	-0.05	-1465.13	-13.03
cluster3	Linear	6	TAR_2	LIB193878	-4.02	7.83	0.00	-3.15	-0.67	3.81	-0.08	0.00	-690.49	-4.29
cluster3	Linear	8	TAR_1	LIB193878	15.40	-10.08	-0.58	-0.57	-4.18	5.32	-15.83	-0.08	-2393.51	-19.40
cluster3	Linear	8	TAR_2	LIB193878	-4.16	11.77	0.00	-5.48	-2.13	7.61	-4.83	-0.02	-2138.31	-10.43
cluster3	Linear	12	TAR_1	LIB193878	17.98	-10.48	-0.56	-1.05	-5.89	7.50	-25.00	-0.12	-4081.98	-30.56
cluster3	Linear	12	TAR_2	LIB193878	-5.23	16.76	0.00	-6.87	-4.66	11.53	-15.99	-0.06	-6251.19	-23.66
cluster3	Linear	16	TAR_1	LIB193878	20.61	-12.57	-0.46	0.19	-7.76	8.04	-30.90	-0.15	-5168.87	-37.66
cluster3	Linear	16	TAR_2	LIB193878	-8.68	13.57	0.00	3.93	-8.82	4.89	-23.67	-0.08	-9157.07	-31.49
cluster3	LSTM	2	TAR_1	LIB193878	0.77	-0.70	0.00	-0.07	0.00	0.07	-0.46	0.00	-31.94	-0.75
cluster3	LSTM	2	TAR_2	LIB193878	-0.17	0.17	0.00	0.00	0.00	0.00	-0.79	0.00	-39.01	-0.85
cluster3	LSTM	4	TAR_1	LIB193878	1.91	-1.59	0.00	-0.33	0.00	0.32	-2.73	-0.01	-219.25	-2.69
cluster3	LSTM	4	TAR_2	LIB193878	4.80	-3.63	0.09	-1.27	0.00	1.17	-5.30	-0.02	-480.78	-4.70
cluster3	LSTM	6	TAR_1	LIB193878	8.52	-7.77	0.34	-1.10	0.00	0.75	-5.98	-0.03	-573.73	-5.61
cluster3	LSTM	6	TAR_2	LIB193878	6.49	-4.21	0.10	-2.39	0.00	2.28	-5.95	-0.02	-869.89	-5.73
cluster3	LSTM	8	TAR_1	LIB193878	12.82	-11.73	0.22	-1.30	0.00	1.09	-9.30	-0.04	-952.33	-8.59
cluster3	LSTM	8	TAR_2	LIB193878	16.33	-7.61	0.00	-8.72	0.00	8.72	-15.27	-0.05	-2525.01	-12.76

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Cluster	Algorithm	PH	Range	Patient	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	12	TAR_1	LIB193878	16.85	-13.55	0.00	-3.30	0.00	3.30	-12.32	-0.06	-1257.78	-11.22
cluster3	LSTM	12	TAR_2	LIB193878	11.76	8.26	0.00	-20.02	0.00	20.02	-19.68	-0.07	-4176.28	-16.78
cluster3	LSTM	16	TAR_1	LIB193878	28.56	-24.30	0.00	-4.25	0.00	4.26	-16.55	-0.08	-1591.26	-14.36
cluster3	LSTM	16	TAR_2	LIB193878	3.26	32.84	0.00	-36.09	0.00	36.10	-20.54	-0.07	-5012.36	-18.53
cluster4	CNN	2	TAR_1	LIB193826	11.70	-11.09	0.00	-0.60	0.00	0.61	-7.88	-0.04	-620.81	-8.21
cluster4	CNN	2	TAR_2	LIB193826	9.16	-2.29	0.00	-6.87	0.00	6.87	-10.03	-0.03	-1552.36	-12.87
cluster4	CNN	4	TAR_1	LIB193826	15.36	-14.35	0.00	-1.03	0.00	1.01	-9.62	-0.05	-925.31	-9.17
cluster4	CNN	4	TAR_2	LIB193826	10.08	-3.87	0.00	-6.20	0.00	6.21	-14.17	-0.05	-2484.16	-13.90
cluster4	CNN	6	TAR_1	LIB193826	16.53	-15.90	0.00	-0.62	0.00	0.63	-11.34	-0.06	-1210.64	-10.03
cluster4	CNN	6	TAR_2	LIB193826	6.30	7.09	0.00	-13.39	0.00	13.39	-14.27	-0.05	-3205.92	-14.02
cluster4	CNN	8	TAR_1	LIB193826	19.40	-18.33	0.00	-1.06	0.00	1.07	-12.68	-0.06	-1437.99	-11.30
cluster4	CNN	8	TAR_2	LIB193826	7.94	11.11	0.00	-19.05	0.00	19.05	-20.16	-0.07	-4770.25	-18.17
cluster4	CNN	12	TAR_1	LIB193838	15.59	-12.54	0.00	-3.07	0.00	3.05	-5.79	-0.03	-479.47	-3.59
cluster4	CNN	12	TAR_2	LIB193838	1.07	33.57	0.00	-34.64	0.00	34.64	-15.60	-0.05	-3413.53	-12.73
cluster4	CNN	16	TAR_1	LIB193838	3.51	-2.90	0.00	-0.61	0.00	0.61	-0.45	0.00	7.40	0.06
cluster4	CNN	16	TAR_2	LIB193838	0.00	6.64	0.00	-6.64	0.00	6.64	-5.26	-0.02	-1205.46	-4.41
cluster4	Linear	2	TAR_1	LIB193838	4.18	-4.18	0.12	-0.12	0.00	0.00	-2.70	-0.01	-202.98	-3.70
cluster4	Linear	2	TAR_2	LIB193838	0.29	-0.29	0.00	0.00	0.00	0.00	-0.46	0.00	-62.10	-1.15
cluster4	Linear	4	TAR_1	LIB193826	8.19	-7.18	0.00	-0.62	-0.41	1.01	-5.45	-0.03	-634.65	-7.11
cluster4	Linear	4	TAR_2	LIB193826	-3.88	8.53	0.00	-4.65	0.00	4.65	-2.29	-0.01	-349.26	-2.49
cluster4	Linear	6	TAR_1	LIB193826	11.09	-7.11	0.00	-0.63	-3.35	3.98	-10.78	-0.05	-1613.86	-13.98
cluster4	Linear	6	TAR_2	LIB193826	-5.51	11.02	-0.79	-3.94	-0.79	5.51	-0.61	0.00	-1120.88	-5.73
cluster4	Linear	8	TAR_1	LIB193826	7.25	-1.70	0.00	0.42	-5.97	5.55	-14.94	-0.07	-2533.89	-19.01
cluster4	Linear	8	TAR_2	LIB193826	-15.08	16.67	0.00	2.38	-3.97	1.59	-0.97	0.00	-2722.57	-11.26
cluster4	Linear	12	TAR_1	LIB193838	4.73	4.87	-0.14	1.95	-11.42	9.60	-26.79	-0.13	-5137.56	-30.73
cluster4	Linear	12	TAR_2	LIB193838	-13.93	3.21	0.00	15.71	-5.00	-10.72	-7.35	-0.03	-4876.35	-17.61
cluster4	Linear	16	TAR_1	LIB193838	1.67	11.59	0.00	1.68	-14.94	13.26	-31.06	-0.15	-6245.67	-35.80
cluster4	Linear	16	TAR_2	LIB193838	-7.81	-9.37	0.00	22.26	-5.08	-17.18	-9.05	-0.03	-4981.99	-16.98
cluster4	LSTM	2	TAR_1	LIB193838	0.24	-0.12	0.00	-0.12	0.00	0.12	-0.89	0.00	-29.24	-0.58
cluster4	LSTM	2	TAR_2	LIB193838	2.35	-1.17	0.00	-1.18	0.00	1.18	-8.56	-0.03	-608.04	-10.21
cluster4	LSTM	4	TAR_1	LIB193826	2.46	-2.26	0.00	-0.20	0.00	0.20	-1.36	-0.01	-216.34	-2.61
cluster4	LSTM	4	TAR_2	LIB193826	37.21	-36.43	0.00	-0.78	0.00	0.78	-27.05	-0.09	-3289.89	-20.80
cluster4	LSTM	6	TAR_1	LIB193826	3.34	-3.14	0.00	-0.21	0.00	0.20	-4.05	-0.02	-472.45	-4.51
cluster4	LSTM	6	TAR_2	LIB193826	29.92	-27.56	0.00	-2.36	0.00	2.36	-23.89	-0.08	-3759.77	-18.22
cluster4	LSTM	8	TAR_1	LIB193826	13.00	-11.09	0.00	-1.92	0.00	1.91	-9.84	-0.05	-1036.71	-8.42
cluster4	LSTM	8	TAR_2	LIB193826	8.73	44.44	0.00	-53.17	0.00	53.17	-22.76	-0.08	-4817.62	-19.12

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Cluster	Algorithm	PH	Range	Patient	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	12	TAR_1	LIB193826	26.95	-26.28	0.00	-0.66	0.00	0.67	-18.30	-0.09	-2244.75	-16.12
cluster4	LSTM	12	TAR_2	LIB193826	0.84	27.73	0.00	-28.57	0.00	28.57	-27.71	-0.09	-7575.81	-24.68
cluster4	LSTM	16	TAR_1	LIB193838	14.18	-13.42	0.00	-0.76	0.00	0.76	-2.42	-0.01	-120.52	-0.89
cluster4	LSTM	16	TAR_2	LIB193838	0.00	10.55	0.00	-10.55	0.00	10.55	-10.11	-0.04	-2403.40	-8.66

6.4 Discussion

6.4.1 Group-based prediction models

Although group-based prediction models do not consistently outperform general prediction models, they exhibit promising results that highlight the feasibility of this approach. The improvements observed in specific clusters and PH suggest that, with further refinement, group-based prediction models could offer significant advantages in predicting BGL, especially for specific patient subgroups. The key strength of these prediction models lies in their ability to capture unique patterns within distinct groups, allowing for more tailored predictions that general prediction models might overlook. This potential for personalization makes the group-based approach a valuable complement to traditional general prediction models, particularly when considering real-world applications where patient variability is high. Therefore, while not a universal solution, this methodology presents a viable path forward in enhancing the accuracy and clinical relevance of BGL predictions in T1D management.

6.4.2 Personalized prediction models

In the comparative analysis of personalized versus group-based prediction models, a distinct contrast emerges, particularly regarding predicting BGL within the hypoglycemic range. Personalized prediction models have an advantage in managing patients prone to frequent hypoglycemic events. The performance results indicate that group-based prediction models often struggle to accurately capture these patients' BGL patterns. This limitation is likely attributable to the lower incidence of hypoglycemic events across the broader patient population, leading to reduced model effectiveness in predicting critical episodes for individuals with higher susceptibility to hypoglycemia. In contrast, personalized models are better equipped to adapt to individual patients' specific and unique patterns, resulting in superior performance in predicting hypoglycemic ranges.

Conversely, an opposite trend is observed in the hyperglycemic range. In cases where patients frequently experience hyperglycemia, group-based prediction models sometimes outperform personalized prediction models. This may be due to the more pronounced and consistent patterns of hyperglycemia across groups, which group-based prediction models can recognize with greater efficacy. Consequently, group-based prediction models' broader pattern recognition capabilities may enhance prediction accuracy in scenarios where hyperglycemic events predominate, offering an advantage over personalized models.

6.4.3 Overall findings

This chapter explored the feasibility of group-based BGL prediction models, comparing them with general and personalized prediction models. The goal was to assess how these group-based prediction models perform relative to the other approaches, particularly given their practicality for real-world settings. The results indicate that group-based prediction models outperform general prediction models for specific patient groups under certain conditions. Groups 1 and 4, representing patients with better BGL management, show consistent improvements in clinical metrics such as A and 'A + B' in entire BGL ranges. These improvements became more

pronounced as the PH prolonged, suggesting that group-based prediction models may capture longer-term BGL patterns more effectively in these patients.

Although improvements over general prediction models were less significant in the hypoglycemic ranges (TBR_2 and TBR_1), slight performance gains were observed for groups 4 and 5, especially when using LSTM and CNN prediction algorithms. This suggests that group-based prediction models may offer better BGL predictions for patients with a tendency towards hypoglycemic events, particularly in specific patient subsets using these two prediction algorithms.

Regarding hyperglycemic ranges (TAR_2 and TAR_1), groups 2 and 3 showed improved performance metrics compared to the general prediction models. These improvements were particularly notable for longer PHs (8, 12, and 16). This could be related to the fact that these groups contain patients with a higher proportion of hyperglycemic events, which seems to make it easier for group-based prediction models to capture more distinct patterns associated with these conditions.

When comparing personalized prediction models to group-based prediction models, it's clear that personalized prediction models offer performance improvements, especially for patients whose BGL was poorly predicted by group-based prediction models. However, they do not always outperform group-based prediction models. In fact, personalized prediction models only showed an improvement in the 'A + B' metric compared to group-based prediction models in 37.98% of cases. This indicates that while personalized prediction models may benefit certain patients, group-based prediction models effectively balance performance and practicality, instilling confidence in their overall effectiveness.

On the other hand, personalized prediction models showed more significant improvements in hypoglycemic ranges for patients whose BGL was worst predicted by group-based prediction models. This suggests that personalized prediction models may be more effective for patients with more atypical BGL patterns or frequent hypoglycemic events. However, group-based prediction models continued to perform better in hyperglycemic ranges, particularly in groups with a higher proportion of hyperglycemic events.

In conclusion, group-based prediction models emerge as a promising intermediate solution between general and personalized prediction models. While they may not achieve the same level of precision as personalized prediction models in all cases, they offer significant improvements over general prediction models. Moreover, they require less data from new patients for implementation, making them a practical and effective option for improving BGL prediction in T1D patients, particularly in environments where full personalization is not feasible. This reduced data requirement implies shorter periods of continuous glucose monitoring sensor use by T1D patients, a key advantage over the personalized approach, as the latter typically requires extensive BGL measurements spanning months or even years. The potential for enhancing the performance of group-based prediction models by incorporating more complex variables into the group formation process further underscores their promise for future applications.

The development of group-based prediction models shares limitations similar to those found in general prediction models, particularly regarding the nature of BGL measurements. Patients within the same group can show variability in both the quantity and timing of their BGL measurements. Furthermore, the BGL measurements are likely similarly imbalanced, which could affect model performance. Additionally, the comparison between group-based and personalized prediction models was conducted on a limited number of patients. While efforts were made to minimize bias by selecting patients with both the best and worst performance, patients with

intermediate performance may have exhibited different patterns and then get other conclusions about the comparison.

Chapter 7

Conclusions and future work

7.1 Achievements

The goal of this thesis was to investigate intelligent techniques to support the management of type 1 diabetes mellitus in real-world settings by leveraging continuous glucose measurements data collected from mobile and wearable devices. This research seeks to contribute new insights into the blood glucose level prediction process by emphasizing clinical evaluation of prediction models, targeting critical blood glucose level ranges (hypoglycemia and hyperglycemia), focusing on group-based prediction models, and ensuring that these prediction models are more applicable in real-world settings. To this end, group-based blood glucose prediction models were developed using a high-quality continuous glucose measurement dataset. Upon achieving a thorough understanding of evaluation methods suitable for these prediction models, the group-based prediction models were compared with general and personalized prediction models. Results reveal the potential of group-based prediction models as an intermediate solution, balancing personalized prediction models' accuracy and general prediction models' applicability in real-world settings. In the following, the achievement of the four objectives established to support this thesis goal are described.

Objective 1: Create an extensive, long-term, open-access longitudinal dataset consisting of blood glucose level measurements collected through continuous glucose monitoring sensors to develop new intelligent models.

This thesis presents T1DiabetesGranada, an open-access, longitudinal, and multimodal dataset about type 1 diabetes. T1DiabetesGranada comprises four comma separated files, one containing continuous blood glucose measurements for individuals with type 1 diabetes and the others demographic, clinical, and additional comorbidity data. Continuous glucose measurements were primarily collected using the *FreeStyle Libre 2* flash glucose monitor device, manufactured by *Abbott Diabetes Care, Inc., Alameda, CA, USA*, which registers blood glucose levels at 15-minute rates. The dataset spans 257 780 recorded days over four years, covering 736 patients from the province of Granada, Spain.

The principal demographic variables included in this dataset are sex, year of birth, and start and end dates for continuous glucose monitoring. Blood glucose measurements are presented as time series data, each entry providing a timestamp and glucose level in mg/dL. In addition, the dataset includes clinical data such as 17 different biochemical parameters, with creatinine, glucose, and potassium among the most frequently registered. Diagnoses of other medical

conditions are also captured, with unspecified acquired hypothyroidism and unspecified essential hypertension being among the most prevalent.

This dataset is available for research purposes under specific permissions in the Zenodo repository. Access requires acceptance of a data usage agreement, submission of researcher information, and justification of use. T1DiabetesGranada significantly advances beyond the state of the art as one of the most temporally extensive and comprehensive in number of measurements open-access datasets of continuous glucose monitoring data. It thus facilitates the development of advanced artificial intelligence models for blood glucose characterization and prediction.

Objective 2: Comprehend the capacity of existing evaluation methods for estimating the performance of blood glucose level prediction models in real-world settings.

This thesis developed general prediction models based on artificial neural networks to gain a comprehensive understanding of the evaluation methods for blood glucose level prediction models. These models were trained and evaluated using continuous glucose measurements from all patients within the T1DiabetesGranada dataset. Three prediction algorithms were employed: a Linear model and more advanced recurrent neural network architectures, including LSTM and CNN. The prediction process was based on two hours of historical values, comprising eight glucose measurement samples taken at 15-minute intervals and six different prediction horizons of 30, 60, 90, 120, 180, and 240 minutes.

The prediction model performance evaluation included clinical metrics, such as Clarke’s error grid analysis, and non-clinical metrics, including RMSE, MSE, MAE, and MAPE. These metrics were calculated not only across the entire blood glucose levels range, as is commonly done in the literature, but also independently within clinically relevant ranges such as hypoglycemia and hyperglycemia. Results showed that linear prediction models slightly outperformed more complex models, such as LSTM and CNN, likely due to the high concentration of data within a narrower glucose range (100-200 mg/dL), which favored simpler models. However, linear models tended to predict values outside the realistic blood glucose range (0-500 mg/dL) more frequently than LSTM and CNN models, which were likely more robust to the non-linear and complex patterns of glucose levels.

Evaluating performance independently across blood glucose measurement ranges proved crucial. Results varied within these ranges for the same model, underscoring that the model capabilities could be overestimated without this division. While results may appear clinically acceptable in the overall assessment, performance in the critical health ranges (hypoglycemia and hyperglycemia) was often considerably worse. This knowledge allows for strategies to improve prediction models, focusing especially on ranges where accuracy is most critical to patient health. Additionally, results corroborate observations in the literature that non-clinical metrics alone are insufficient for adequately evaluating prediction models. Instances arose in which non-clinical metrics suggested a performance order that clinical metrics ultimately contradicted.

Ultimately, a holistic approach is essential for adequately evaluating blood glucose level prediction models. This means that results must be assessed and analyzed from multiple perspectives to avoid biased conclusions. Incorporating clinical metrics is crucial for providing context-specific meaning; without this, numerical results may hold little clinical relevance. Nevertheless, non-clinical metrics can provide supplementary insights, such as the compactness of predictions. Nevertheless, this would only be sufficient for evaluating the metrics within de-

finer blood glucose level ranges, as metrics could be skewed by sample distribution, potentially leading to the underestimation of clinically critical ranges.

Objective 3: Identify patient groups with common characteristics based on patients' longitudinal blood glucose level measurements.

A key direction of this thesis was to identify groups of patients with similar blood glucose level patterns using unsupervised learning algorithms. Six distinct groups of type 1 diabetes patients from the T1DiabetesGranada dataset were identified through K-means clustering. However, extensive experimentation was conducted with other algorithms, such as Gaussian Mixture, hierarchical clustering, and self-organizing maps. Continuous glucose measurements were transformed into a feature matrix comprising statistics like the average, standard deviation, minimum, and maximum blood glucose level readings across various time ranges throughout the day. These time ranges were defined by clinical experts, reflecting the lifestyle patterns of patients from the specific geographic region represented in the dataset. Four versions of the extracted feature set were created to ensure robust experimentation using two distinct outlier removal methods and subsequent standardization of these two dataset versions. Of the 168 clustering results generated, the most promising were selected based on the internal evaluation metric silhouette coefficient. A customized selection procedure was implemented to prioritize diverse clustering solutions by grouping similar clustering results, thus preserving potentially clinically valuable structures.

The final selection of six clusters by the clinical experts from the Clinical Unit of Endocrinology and Nutrition at the San Cecilio University Hospital of Granada benefits not only as a foundation for developing group-based prediction models but also as a tool to influence patient care. These groups enable endocrinologists to design personalized treatment plans according to specific patient profiles. For example, groups 0, 1, and 4 encompass patients with generally acceptable diabetes management, while group 0 patients exhibit a greater tendency toward hypoglycemia. Conversely, groups 2 and 3 represent patients with poorer disease control, with group 2 characterized by high rates of hyperglycemia. This information, combined with continuous glucose monitoring, allows for the relatively fast classification of new patients into one of these groups, facilitating a more targeted therapeutic approach from the initial monitoring stages. Furthermore, this process is adaptable for patients with longer monitoring histories as long as their data remains accessible.

Objective 4: Evaluate the performance of group-based blood glucose level prediction models in real-world settings.

Once patient groups were identified, blood glucose level prediction models were created for each group, applying the same experimentation procedures and algorithms used in the general prediction models. As an additional comparison point, personalized prediction models were developed for a sample of patients, selecting those whose blood glucose levels were best and worst predicted by the group-based prediction models. This selection process yielded two patients per group-based prediction model. These personalized prediction models were trained using the same training process used for the general and group-based prediction models, with training, validation, and testing data splits exclusively from the individual patient. To ensure an unbiased comparison, only patients from each cluster's test set were selected for the personalized prediction models, and both types of models were tested using an identical test split for a fair performance assessment.

The results showed that group-based prediction models outperformed general prediction models in specific patient groups and under certain conditions, such as groups representing patients with better glucose control. In these cases, clinical metrics like 'A + B' showed more pronounced improvements as the prediction horizon increased, suggesting that these models could more effectively capture long-term patterns. Although progress in hypoglycemic ranges was more modest, improvements were noted in some patient groups with more hypoglycemic events, especially in LSTM and CNN prediction algorithms. When comparing personalized prediction models to group-based models, personalized models offered improvements in some instances. However, they did not consistently outperform group-based models, showing better results in only 37.98% of cases. Thus, group-based prediction models can be seen as a fair balance between precision and practicality, offering better performance over many general prediction models while requiring less data from new patients, making them an effective solution for predicting blood glucose levels in type 1 diabetes patients.

7.2 Contributions

In Section 7.1 it has been proven that the objectives of this thesis have been completely fulfilled. Now, the main contributions of this thesis are listed:

1. A large, multimodal longitudinal dataset of continuous glucose measurements collected using continuous glucose monitors, along with demographic and clinical information about type 1 diabetes patients.
2. A robust experimental methodology for applying prediction models to an extensive longitudinal dataset of continuous glucose measurements.
3. Three sets of prediction models for continuous glucose levels using artificial neural networks, namely general, group-based, and personalized prediction models.
4. A methodology for creating patient groups based on their continuous glucose measurements.
5. Various patient groups that enable endocrinologists to design personalized treatments based on unique patient profiles.
6. A codebase to support all experimental methodologies processes and the creation of the dataset, enabling reproducibility and scalability for future research.

7.3 Future work

This thesis has proposed a solution for predicting blood glucose levels in type 1 diabetes patients using continuous glucose monitors. However, while this field has been researched and improved over recent years, there remains room for enhancement; efforts for improvements must be made, especially in areas directly related to healthcare. The following outlines possible future directions for continuing and extending the work undertaken in this thesis.

Enhancing prediction models through balanced continuous glucose measurements

Training prediction models using balanced data across glucose ranges offers a valuable strategy for enhancing predictive performance in type 1 diabetes management. Blood glucose level datasets from continuous glucose monitors tend to concentrate within normal ranges, which can bias model performance, making it less reliable in critical ranges like hypoglycemia and hyperglycemia. By balancing data across these ranges, models can learn more representative patterns, ultimately improving prediction accuracy in low and high blood glucose level regions essential for patient safety.

This approach has challenges, such as sourcing sufficient data across extreme glucose levels, but the potential benefits make it worthwhile. It provides a more clinically relevant evaluation of model performance, offering insights into model behavior across all blood glucose ranges. Balanced blood glucose level data better prepares models for the variability in real-life applications, improving their robustness and practical utility in diverse patient scenarios.

Specialized blood glucose prediction models for specific clinically relevant ranges

An effective approach to improve blood glucose level prediction accuracy in type 1 diabetes management could involve developing specialized prediction models for distinct blood glucose level ranges. Each range, like hypoglycemia, euglycemia, and hyperglycemia, has unique characteristics that general models may overlook due to their broad training scope. By creating specific models that focus exclusively on one range, it may be possible to better capture patterns and variations associated with that range, enabling more precise predictions tailored to the patient's clinical needs. Models optimized for each blood glucose level range would likely have a higher predictive accuracy since they would be specialized for the narrow, unique patterns within each target range.

An effective way to implement this would involve an initial classification model that assesses input data and assigns it to the appropriate blood glucose level range, activating the specialized prediction model assigned to that range. This classifier would be trained to recognize early indicators from recent glucose trends and relevant features to anticipate the blood glucose level range most likely to occur. When a classifier predicts, for instance, an impending hyperglycemic event, the corresponding prediction model will provide a prediction using training data tailored to that specific range. This setup would enable each prediction model to focus on learning the range-specific characteristics without interference from data belonging to unrelated glucose ranges.

This method of modular prediction could result in improved accuracy, computational efficiency, and clinical relevance. Specialized models are less likely to overfit irrelevant data and can focus on accurately predicting values within their trained range. Additionally, since each range poses distinct risks, such a modular approach offers more meaningful insights, especially for values falling in critical ranges like hypoglycemia and hyperglycemia. This approach could make blood glucose level prediction models far more reliable and actionable, enhancing the quality of care for patients managing diabetes in real-world settings.

Clinical intervention study to evaluate the efficacy of prediction models in T1D management

A logical extension of this research is to conduct a clinical intervention study that directly assesses the impact of prediction blood glucose levels models on diabetes management outcomes in patients with type 1 diabetes. This study would monitor patients' blood glucose levels over a fixed period, with one group using a prediction-enhanced intervention (e.g., a mobile app or wearable device) and a control group receiving standard type 1 diabetes care. The primary objectives would include measuring improvements in patients' time in the target glucose range, reduction in adverse events (such as hypoglycemic and hyperglycemic events), and improvements in other health indicators relevant to type 1 diabetes management.

The intervention group would utilize a predictive model capable of generating alerts for anticipated blood glucose level fluctuations. When a model predicts a deviation from acceptable levels, it could notify patients or healthcare providers, allowing time for preemptive action. For example, if a model forecasts a high probability of hypoglycemia, the patient could receive guidance to consume carbohydrates to prevent an episode. The study would track various metrics such as time in range, frequency of hypoglycemic and hyperglycemic events, patient adherence to recommendations, and user feedback on the prediction tool's usability and reliability.

Results from this study would provide valuable insights into whether predictive models meaningfully enhance T1D management in clinical practice. If successful, this research could support the broader adoption of predictive technology in routine diabetes care, ultimately contributing to personalized and proactive type 1 diabetes management solutions. Such a study would also offer evidence for improving algorithms to maximize clinical benefit and patient safety, establishing a framework for assessing real-world effectiveness in chronic disease management.

Acronyms

ACC Accelerometer

AI Artificial Intelligence

ANN Artificial Neural Networks

BA Bolus Advisors

BGL Blood Glucose Level

BIRCH Balanced Iterative Reducing and Clustering using Hierarchies

CEG Clarke Error Grid

CGM Continuous Glucose Monitor

CNN Convolutional Neural Network

DM Diabetes Mellitus

FGM Flash Glucose Monitor

HL History Length

HR Heart Rate

IDF International Diabetes Federation

IQR Interquartile Range

LSTM Long Short-Term Memory

MAE Mean Absolute Error

MAPE Mean Absolute Percentage Error

ML Machine Learning

MSE Mean Squared Error

NFC Near Field Communication

PCG Parkes Consensus Grid

PH Prediction Horizon

RMSE Root Mean Square Error

RNN Recurrent Neural Network

SOM Self-Organizing Maps

T1D Type 1 Diabetes Mellitus

T2D Type 2 Diabetes Mellitus

TAR Time Above Range

TBR Time Below Range

TIR Time In Range

WCSS Within-Cluster Sum of Squares

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Appendices

Appendix A

Performance results for general prediction models in the different BGL ranges

Table A.1 presents the evaluation metrics results for the general BGL prediction models in the six different BGL ranges. Since there are three prediction models, six PH, and six BGL ranges, the table contains a total of 108 rows of results.

Table A.1: Performance results for general prediction models in the different BGL ranges assessed via both clinical and non-clinical metrics.

Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
Linear	2	ALL	88.08	10.56	0.04	1.31	0.01	98.64	19.93	397.36	14.01	0.10
Linear	2	TBR_2	93.64	0.00	0.00	6.31	0.05	93.64	14.47	209.47	10.50	0.22
Linear	2	TBR_1	73.61	0.00	0.00	26.36	0.02	73.61	15.49	240.05	11.29	0.18
Linear	2	TIR	85.35	14.47	0.04	0.14	0.00	99.82	18.46	340.91	12.99	0.11
Linear	2	TAR_1	93.94	5.89	0.04	0.11	0.02	99.83	21.53	463.71	15.24	0.07
Linear	2	TAR_2	97.24	2.52	0.02	0.20	0.01	99.76	26.07	679.52	19.03	0.06
Linear	4	ALL	65.49	28.73	0.45	5.24	0.09	94.22	36.00	1295.96	26.44	0.19
Linear	4	TBR_2	26.87	0.00	0.00	72.46	0.67	26.87	37.26	1388.07	30.77	0.63
Linear	4	TBR_1	13.80	0.00	0.00	85.18	1.02	13.80	38.30	1467.09	30.97	0.50
Linear	4	TIR	62.94	36.01	0.64	0.40	0.01	98.95	31.68	1003.82	23.39	0.20
Linear	4	TAR_1	78.52	20.01	0.21	1.14	0.12	98.53	37.59	1412.98	27.41	0.13
Linear	4	TAR_2	77.59	18.22	0.06	4.10	0.03	95.81	52.46	2752.19	40.73	0.14
Linear	6	ALL	53.27	38.59	0.90	7.00	0.23	91.86	46.63	2174.49	35.13	0.26
Linear	6	TBR_2	2.41	0.00	0.00	94.49	3.11	2.41	60.25	3629.47	52.45	1.08
Linear	6	TBR_1	2.10	0.00	0.00	93.99	3.92	2.10	57.65	3323.45	49.56	0.80
Linear	6	TIR	52.27	45.85	1.36	0.50	0.02	98.12	38.58	1488.34	29.29	0.26
Linear	6	TAR_1	67.85	29.46	0.20	2.42	0.08	97.31	45.78	2095.52	35.05	0.17
Linear	6	TAR_2	53.34	34.18	0.06	12.39	0.04	87.52	77.28	5971.50	63.69	0.21
Linear	8	ALL	46.28	44.01	1.14	8.18	0.40	90.29	53.71	2884.81	41.21	0.31
Linear	8	TBR_2	0.27	0.00	0.00	93.25	6.48	0.27	77.47	6001.47	70.25	1.45
Linear	8	TBR_1	0.30	0.00	0.00	92.67	7.03	0.30	71.62	5128.83	64.51	1.05
Linear	8	TIR	47.03	50.65	1.78	0.50	0.04	97.68	42.48	1804.21	33.00	0.30
Linear	8	TAR_1	60.26	35.94	0.13	3.63	0.04	96.20	49.79	2478.73	39.69	0.19
Linear	8	TAR_2	33.99	43.71	0.02	22.26	0.03	77.70	96.27	9268.35	83.00	0.27
Linear	12	ALL	39.55	48.48	1.14	10.21	0.62	88.03	61.28	3754.88	47.99	0.37
Linear	12	TBR_2	0.02	0.00	0.00	88.83	11.15	0.02	96.36	9285.67	91.69	1.90
Linear	12	TBR_1	0.01	0.00	0.00	88.76	11.23	0.01	87.07	7580.74	82.66	1.34
Linear	12	TIR	42.95	54.69	1.82	0.48	0.06	97.64	46.01	2117.35	36.86	0.35
Linear	12	TAR_1	50.89	43.56	0.03	5.51	0.01	94.45	52.37	2742.39	44.04	0.21
Linear	12	TAR_2	12.88	45.79	0.00	41.31	0.01	58.67	119.16	14198.27	108.07	0.36
Linear	16	ALL	37.07	49.54	0.85	11.85	0.68	86.61	64.34	4139.32	50.83	0.40
Linear	16	TBR_2	0.01	0.00	0.00	86.93	13.06	0.01	105.69	11169.67	102.80	2.13
Linear	16	TBR_1	0.00	0.00	0.00	87.58	12.42	0.00	94.07	8849.92	91.38	1.48
Linear	16	TIR	41.98	56.12	1.36	0.47	0.06	98.10	47.10	2218.15	38.28	0.37
Linear	16	TAR_1	45.86	47.29	0.00	6.84	0.00	93.15	52.71	2778.43	45.75	0.21

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Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
Linear	16	TAR_2	4.89	38.53	0.00	56.57	0.01	43.42	129.68	16817.93	120.28	0.40
LSTM	2	ALL	88.67	9.34	0.02	1.96	0.00	98.01	18.82	354.37	13.39	0.10
LSTM	2	TBR_2	79.18	0.00	0.00	20.78	0.04	79.18	17.84	318.29	14.79	0.31
LSTM	2	TBR_1	61.92	0.00	0.00	38.06	0.02	61.92	16.55	274.04	12.87	0.21
LSTM	2	TIR	87.24	12.58	0.02	0.16	0.00	99.82	16.99	288.67	12.00	0.10
LSTM	2	TAR_1	94.21	5.66	0.01	0.11	0.00	99.87	20.80	432.52	14.97	0.07
LSTM	2	TAR_2	97.22	2.56	0.01	0.21	0.00	99.78	24.90	619.90	18.47	0.06
LSTM	4	ALL	67.63	26.21	0.34	5.77	0.04	93.84	34.60	1197.37	25.24	0.19
LSTM	4	TBR_2	14.36	0.00	0.00	85.18	0.46	14.36	42.77	1829.65	38.32	0.79
LSTM	4	TBR_1	7.70	0.00	0.00	91.60	0.70	7.70	39.05	1524.54	33.77	0.55
LSTM	4	TIR	67.71	31.36	0.47	0.46	0.01	99.07	28.77	827.77	21.02	0.18
LSTM	4	TAR_1	76.94	21.57	0.19	1.29	0.01	98.51	37.92	1437.91	28.08	0.13
LSTM	4	TAR_2	76.74	18.45	0.07	4.74	0.00	95.19	52.30	2735.75	40.09	0.13
LSTM	6	ALL	55.10	36.65	0.80	7.29	0.16	91.75	45.25	2047.52	33.87	0.26
LSTM	6	TBR_2	0.18	0.00	0.00	97.46	2.37	0.18	64.86	4207.00	59.90	1.24
LSTM	6	TBR_1	0.14	0.00	0.00	96.85	3.01	0.14	58.09	3374.42	52.37	0.85
LSTM	6	TIR	55.59	42.70	1.16	0.52	0.02	98.29	36.09	1302.24	27.20	0.24
LSTM	6	TAR_1	66.09	31.09	0.29	2.54	0.00	97.18	46.09	2124.17	35.61	0.17
LSTM	6	TAR_2	55.88	30.69	0.12	13.31	0.00	86.57	75.61	5716.83	60.91	0.20
LSTM	8	ALL	47.64	42.61	1.13	8.29	0.32	90.25	52.54	2760.43	40.15	0.31
LSTM	8	TBR_2	0.01	0.00	0.00	94.66	5.33	0.01	81.76	6685.27	76.70	1.59
LSTM	8	TBR_1	0.00	0.00	0.00	94.05	5.95	0.00	72.76	5294.36	67.29	1.09
LSTM	8	TIR	48.82	48.93	1.70	0.51	0.03	97.75	41.13	1691.58	31.74	0.29
LSTM	8	TAR_1	58.91	37.19	0.28	3.62	0.00	96.10	49.54	2453.72	39.76	0.19
LSTM	8	TAR_2	39.67	37.57	0.08	22.68	0.00	77.24	92.98	8645.31	78.31	0.26
LSTM	12	ALL	40.36	47.56	1.21	10.34	0.53	87.92	60.48	3657.53	47.31	0.37
LSTM	12	TBR_2	0.00	0.00	0.00	90.56	9.44	0.00	100.01	10002.73	96.45	2.00
LSTM	12	TBR_1	0.00	0.00	0.00	90.36	9.64	0.00	88.21	7780.96	84.51	1.37
LSTM	12	TIR	43.89	53.67	1.90	0.49	0.05	97.56	45.62	2081.39	36.34	0.34
LSTM	12	TAR_1	49.69	44.69	0.11	5.51	0.00	94.38	51.65	2668.15	43.74	0.20
LSTM	12	TAR_2	17.90	40.36	0.00	41.74	0.00	58.26	116.00	13456.91	103.90	0.34
LSTM	16	ALL	37.57	48.93	1.01	11.88	0.62	86.50	63.87	4078.93	50.43	0.40
LSTM	16	TBR_2	0.00	0.00	0.00	88.01	11.99	0.00	108.25	11717.81	105.79	2.19
LSTM	16	TBR_1	0.00	0.00	0.00	88.62	11.38	0.00	95.04	9032.91	92.52	1.50
LSTM	16	TIR	42.53	55.32	1.61	0.48	0.06	97.85	47.19	2226.64	38.13	0.37
LSTM	16	TAR_1	45.27	47.92	0.01	6.80	0.00	93.19	52.12	2716.08	45.40	0.21
LSTM	16	TAR_2	7.78	35.85	0.00	56.37	0.00	43.63	127.13	16162.25	117.15	0.39

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Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
CNN	2	ALL	76.37	19.15	0.13	4.34	0.01	95.52	27.77	771.35	20.08	0.15
CNN	2	TBR_2	35.98	0.00	0.00	63.92	0.10	35.98	31.25	976.32	27.60	0.57
CNN	2	TBR_1	24.67	0.00	0.00	75.16	0.17	24.67	28.56	815.70	23.78	0.39
CNN	2	TIR	75.54	23.93	0.17	0.35	0.00	99.47	24.12	581.80	17.41	0.15
CNN	2	TAR_1	84.91	14.36	0.09	0.62	0.01	99.27	30.69	941.96	22.28	0.11
CNN	2	TAR_2	87.95	10.34	0.03	1.68	0.00	98.29	38.91	1514.06	29.26	0.10
CNN	4	ALL	60.80	31.77	0.54	6.81	0.09	92.57	40.54	1643.78	29.86	0.22
CNN	4	TBR_2	1.25	0.00	0.00	97.63	1.12	1.25	53.43	2854.88	49.01	1.01
CNN	4	TBR_1	1.20	0.00	0.00	97.21	1.59	1.20	48.00	2303.57	42.54	0.69
CNN	4	TIR	61.94	36.77	0.77	0.51	0.01	98.71	32.17	1035.16	23.81	0.21
CNN	4	TAR_1	69.87	27.86	0.23	2.05	0.00	97.73	43.63	1903.91	33.11	0.16
CNN	4	TAR_2	64.30	26.21	0.09	9.41	0.00	90.51	66.43	4413.39	52.61	0.18
CNN	6	ALL	50.84	40.05	0.91	7.97	0.23	90.89	49.29	2429.50	37.27	0.28
CNN	6	TBR_2	0.00	0.00	0.00	96.42	3.58	0.00	73.15	5350.93	68.44	1.42
CNN	6	TBR_1	0.00	0.00	0.00	95.78	4.22	0.00	65.00	4224.43	59.58	0.97
CNN	6	TIR	52.28	45.81	1.37	0.52	0.02	98.09	38.07	1449.59	29.08	0.26
CNN	6	TAR_1	61.00	35.48	0.24	3.27	0.00	96.48	48.90	2390.86	38.77	0.18
CNN	6	TAR_2	45.47	35.42	0.08	19.03	0.00	80.89	86.82	7537.34	72.08	0.24
CNN	8	ALL	44.62	44.96	1.34	8.67	0.41	89.58	55.46	3075.43	42.89	0.34
CNN	8	TBR_2	0.00	0.00	0.00	93.07	6.93	0.00	89.34	7981.45	84.76	1.75
CNN	8	TBR_1	0.00	0.00	0.00	92.43	7.57	0.00	79.35	6296.64	74.31	1.21
CNN	8	TIR	45.31	52.08	2.06	0.50	0.04	97.39	44.02	1937.39	34.45	0.32
CNN	8	TAR_1	57.23	38.55	0.25	3.98	0.00	95.78	49.57	2456.96	40.28	0.19
CNN	8	TAR_2	35.03	38.44	0.05	26.48	0.00	73.47	98.52	9706.61	83.90	0.28
CNN	12	ALL	39.51	47.87	1.15	10.93	0.54	87.38	61.62	3797.40	48.26	0.38
CNN	12	TBR_2	0.00	0.00	0.00	90.17	9.83	0.00	102.13	10429.53	99.03	2.05
CNN	12	TBR_1	0.00	0.00	0.00	90.19	9.81	0.00	89.84	8072.02	86.57	1.41
CNN	12	TIR	44.04	53.61	1.81	0.49	0.05	97.65	45.69	2087.17	36.47	0.35
CNN	12	TAR_1	47.02	46.91	0.08	5.99	0.00	93.93	52.46	2751.57	44.96	0.21
CNN	12	TAR_2	14.41	38.84	0.00	46.75	0.00	53.25	120.32	14476.30	108.81	0.36
CNN	16	ALL	37.13	48.98	0.86	12.45	0.58	86.11	64.34	4139.97	50.85	0.40
CNN	16	TBR_2	0.00	0.00	0.00	88.66	11.34	0.00	109.12	11907.31	107.06	2.22
CNN	16	TBR_1	0.00	0.00	0.00	89.39	10.61	0.00	95.66	9151.28	93.53	1.52
CNN	16	TIR	42.75	55.34	1.38	0.48	0.06	98.09	46.89	2198.81	37.99	0.37
CNN	16	TAR_1	43.46	49.35	0.01	7.18	0.00	92.81	52.48	2753.90	46.12	0.21
CNN	16	TAR_2	6.09	32.97	0.00	60.93	0.00	39.06	129.64	16805.27	120.10	0.39

Appendix B

Ranking of percentage of BGL measurements in zone 'A + B' for general prediction models

Table B.1 presents the 108 results from Table A.1 sorted in descending order based on the value of the percentage of BGL measurements in zone 'A + B'. The results are identified by their corresponding prediction model, PH, and BGL range. To ensure a more compact presentation, the results are grouped into three columns side by side.

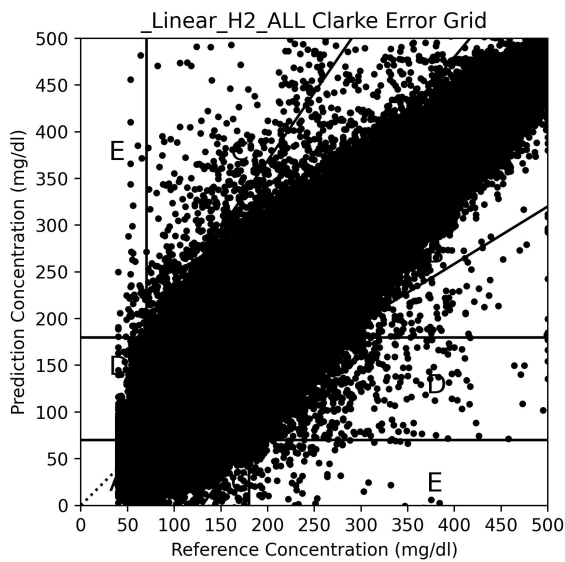
Table B.1: Ranking of percentage of BGL measurements in zone 'A + B' for general prediction models

Rank	Model	PH	Range	Rank	Model	PH	Range	Rank	Model	PH	Range
0	LSTM	2	TAR_1	36	CNN	2	ALL	72	CNN	12	TAR_2
1	Linear	2	TAR_1	37	LSTM	4	TAR_2	73	LSTM	16	TAR_2
2	Linear	2	TIR	38	Linear	12	TAR_1	74	Linear	16	TAR_2
3	LSTM	2	TIR	39	LSTM	12	TAR_1	75	CNN	16	TAR_2
4	LSTM	2	TAR_2	40	Linear	4	ALL	76	CNN	2	TBR_2
5	Linear	2	TAR_2	41	CNN	12	TAR_1	77	Linear	4	TBR_2
6	CNN	2	TIR	42	LSTM	4	ALL	78	CNN	2	TBR_1
7	CNN	2	TAR_1	43	Linear	2	TBR_2	79	LSTM	4	TBR_2
8	LSTM	4	TIR	44	LSTM	16	TAR_1	80	Linear	4	TBR_1
9	Linear	4	TIR	45	Linear	16	TAR_1	81	LSTM	4	TBR_1
10	CNN	4	TIR	46	CNN	16	TAR_1	82	Linear	6	TBR_2
11	Linear	2	ALL	47	CNN	4	ALL	83	Linear	6	TBR_1
12	Linear	4	TAR_1	48	Linear	6	ALL	84	CNN	4	TBR_2
13	LSTM	4	TAR_1	49	LSTM	6	ALL	85	CNN	4	TBR_1
14	LSTM	6	TIR	50	CNN	6	ALL	86	Linear	8	TBR_1
15	CNN	2	TAR_2	51	CNN	4	TAR_2	87	Linear	8	TBR_2
16	Linear	6	TIR	52	Linear	8	ALL	88	LSTM	6	TBR_2
17	Linear	16	TIR	53	LSTM	8	ALL	89	LSTM	6	TBR_1
18	CNN	6	TIR	54	CNN	8	ALL	90	Linear	12	TBR_2
19	CNN	16	TIR	55	Linear	12	ALL	91	Linear	16	TBR_2
20	LSTM	2	ALL	56	LSTM	12	ALL	92	Linear	12	TBR_1
21	LSTM	16	TIR	57	Linear	6	TAR_2	93	LSTM	8	TBR_2
22	LSTM	8	TIR	58	CNN	12	ALL	94	Linear	16	TBR_1
23	CNN	4	TAR_1	59	Linear	16	ALL	95	CNN	8	TBR_2
24	Linear	8	TIR	60	LSTM	6	TAR_2	96	LSTM	12	TBR_1
25	CNN	12	TIR	61	LSTM	16	ALL	97	LSTM	12	TBR_2
26	Linear	12	TIR	62	CNN	16	ALL	98	CNN	12	TBR_2
27	LSTM	12	TIR	63	CNN	6	TAR_2	99	CNN	12	TBR_1
28	CNN	8	TIR	64	LSTM	2	TBR_2	100	LSTM	16	TBR_2
29	Linear	6	TAR_1	65	Linear	8	TAR_2	101	CNN	6	TBR_1
30	LSTM	6	TAR_1	66	LSTM	8	TAR_2	102	CNN	6	TBR_2
31	CNN	6	TAR_1	67	Linear	2	TBR_1	103	LSTM	16	TBR_1
32	Linear	8	TAR_1	68	CNN	8	TAR_2	104	CNN	16	TBR_2
33	LSTM	8	TAR_1	69	LSTM	2	TBR_1	105	CNN	16	TBR_1
34	Linear	4	TAR_2	70	Linear	12	TAR_2	106	LSTM	8	TBR_1
35	CNN	8	TAR_1	71	LSTM	12	TAR_2	107	CNN	8	TBR_1

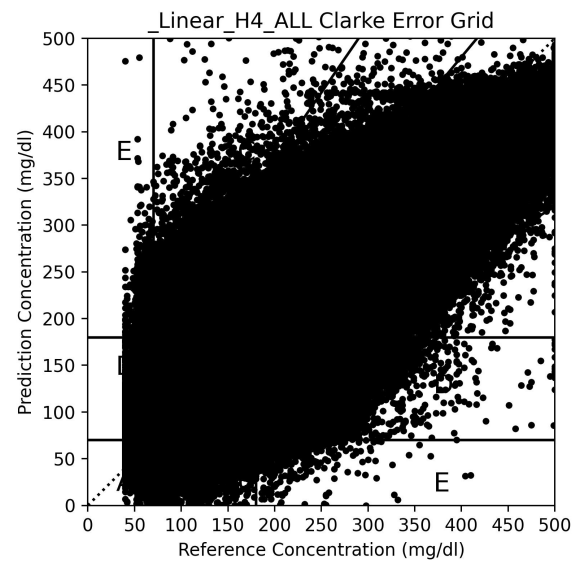
Appendix C

Complete CEG graphs for general prediction models

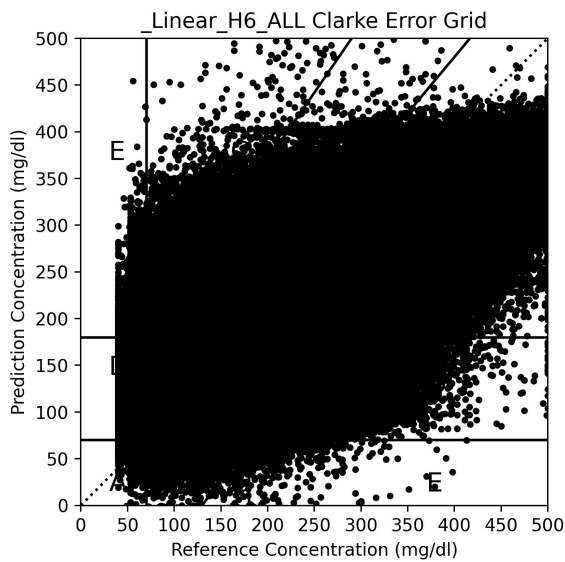
Figures C.1, C.2, and C.3 show the CEGs for the Linear, LSTM, and CNN prediction algorithms, respectively, for all PHs used in the experimentation.



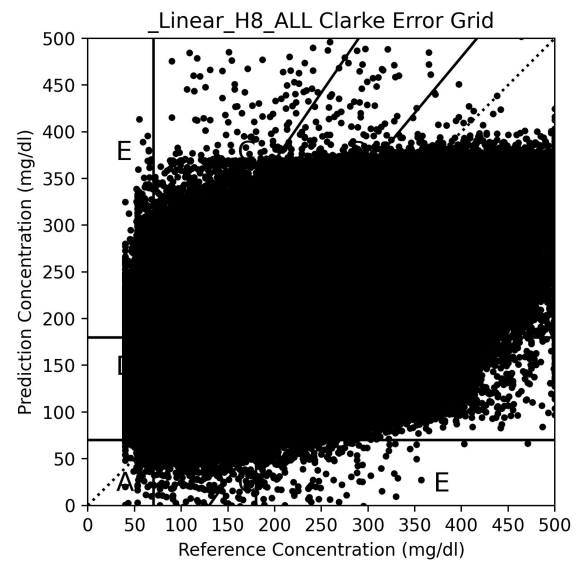
(a) PH of 2 samples.



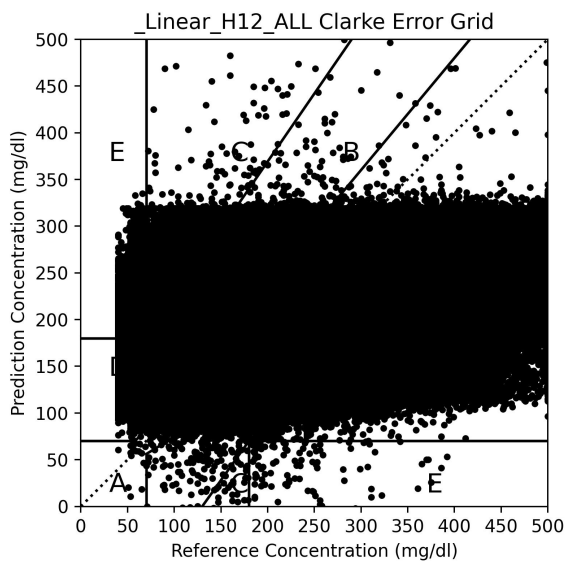
(b) PH of 4 samples.



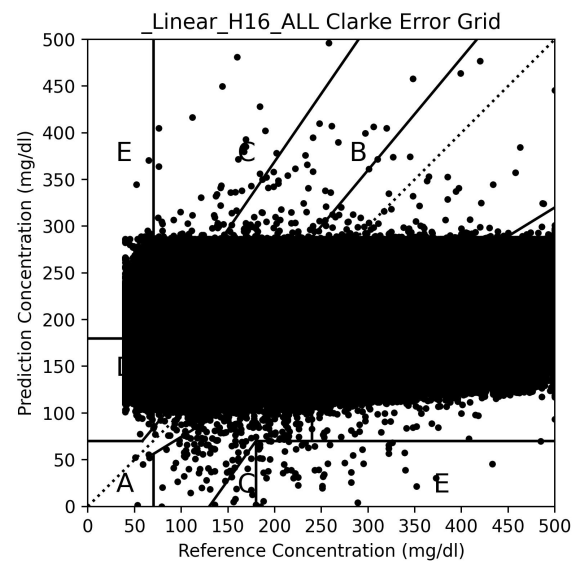
(c) PH of 6 samples.



(d) PH of 8 samples.

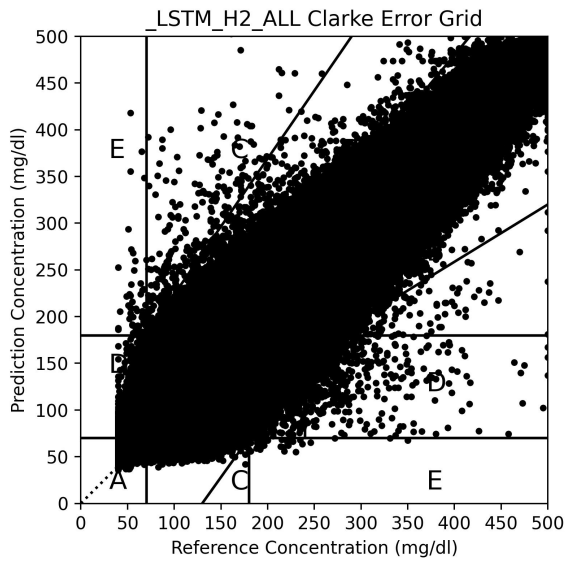


(e) PH of 12 samples.

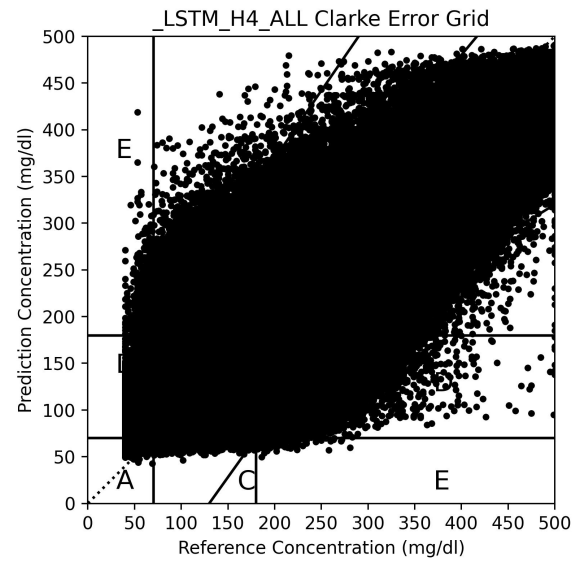


(f) PH of 16 samples.

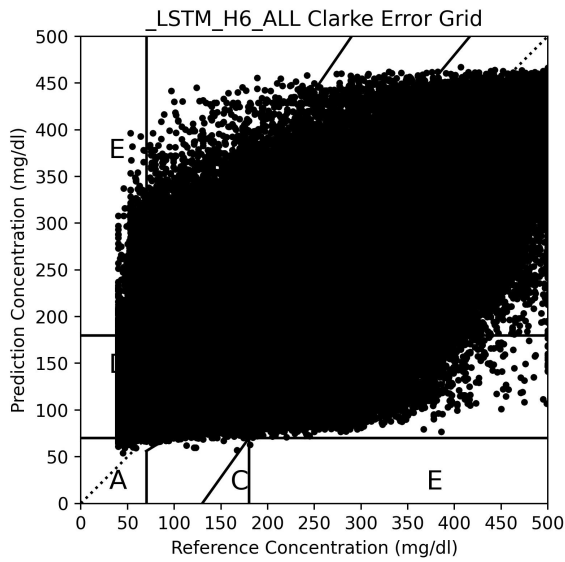
Figure C.1: CEG for Linear prediction models. Source: own elaboration.



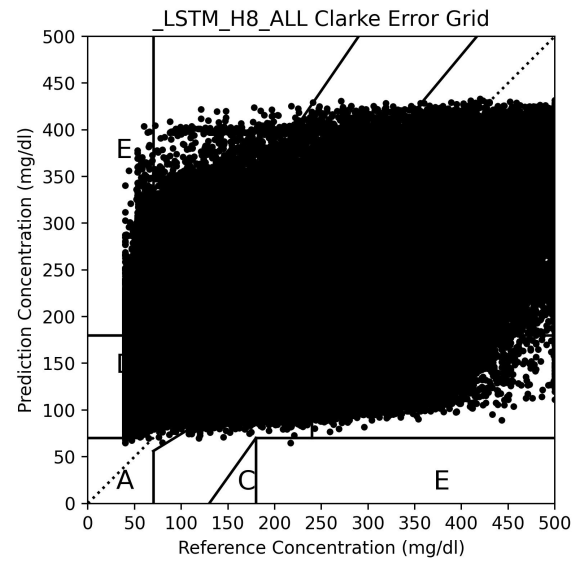
(a) PH of 2 samples.



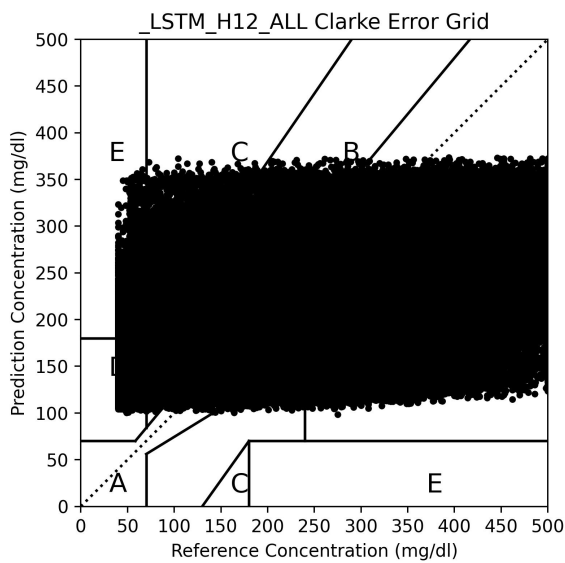
(b) PH of 4 samples.



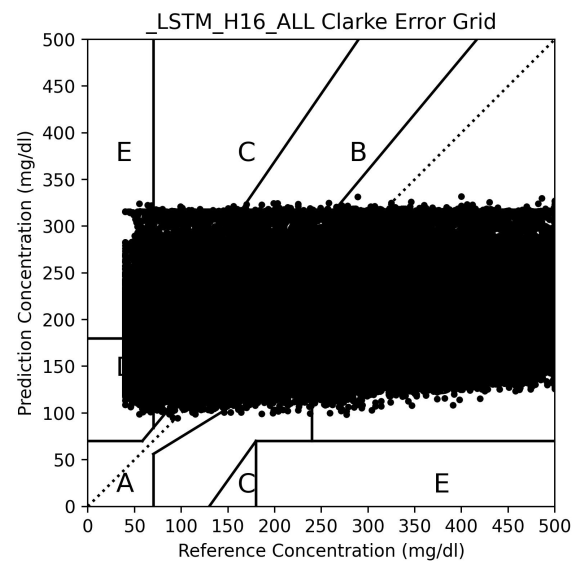
(c) PH of 6 samples.



(d) PH of 8 samples.

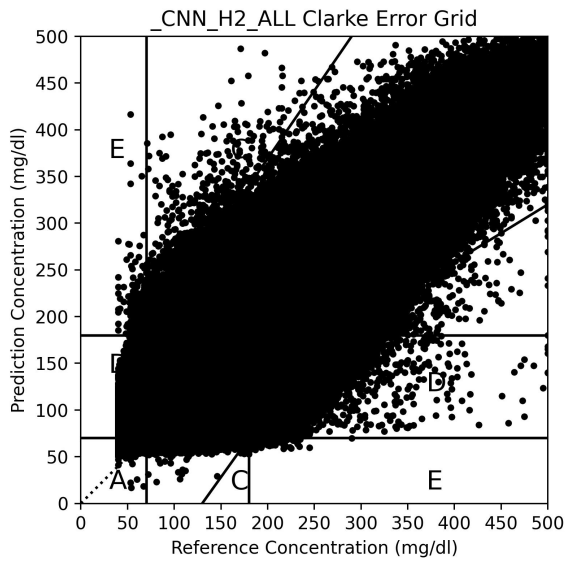


(e) PH of 12 samples.

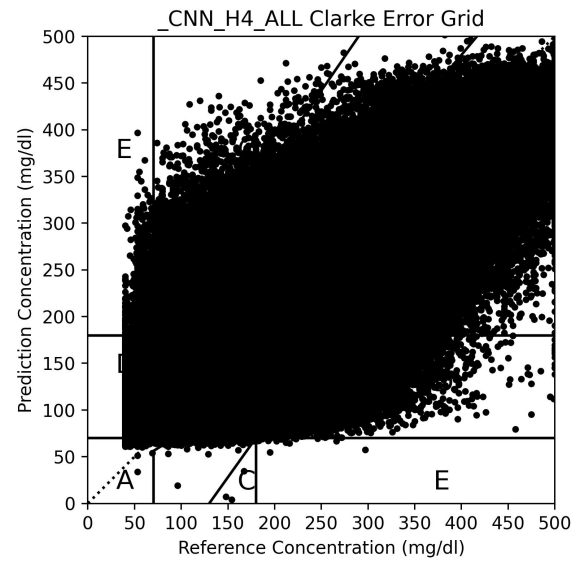


(f) PH of 16 samples.

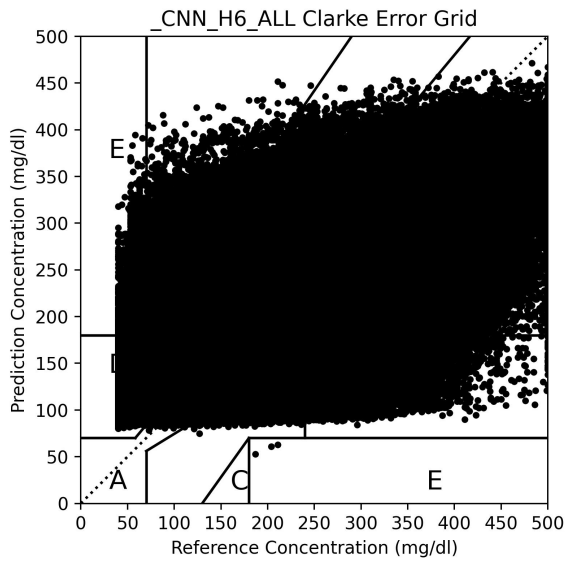
Figure C.2: CEG for LSTM prediction models. Source: own elaboration.



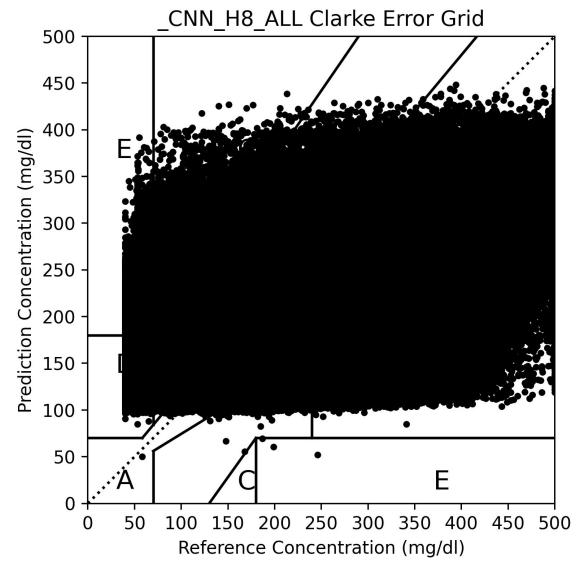
(a) PH of 2 samples.



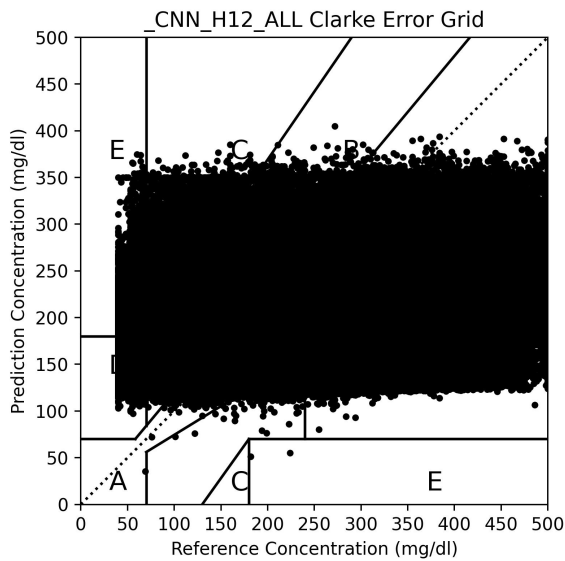
(b) PH of 4 samples.



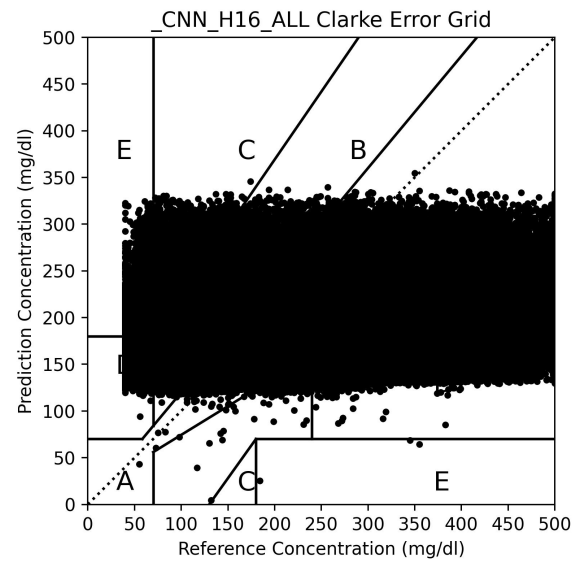
(c) PH of 6 samples.



(d) PH 8.



(e) PH of 12 samples.



(f) PH of 16 samples.

Figure C.3: CEG for CNN prediction models. Source: own elaboration.

Appendix D

Performance results for group-based prediction models in the different BGL ranges

Table D.1 presents the performance results for the group-based prediction models in the six different BGL ranges and six created groups. Since there are three prediction models, six PH, six BGL ranges, and six groups the table contains a total of 648 rows of results.

Table D.1: Performance results for group-based prediction models in the different BGL ranges assessed via both clinical and non-clinical metrics.

Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	Linear	2	ALL	87.18	11.19	0.01	1.61	0.00	98.37	19.89	395.65	14.39	0.10
cluster0	Linear	2	TBR_2	90.96	0.00	0.00	8.98	0.07	90.96	14.69	215.89	11.26	0.23
cluster0	Linear	2	TBR_1	69.62	0.00	0.00	30.37	0.01	69.62	15.74	247.73	11.92	0.19
cluster0	Linear	2	TIR	84.52	15.30	0.01	0.17	0.00	99.82	18.42	339.48	13.20	0.11
cluster0	Linear	2	TAR_1	93.53	6.31	0.01	0.15	0.01	99.84	21.87	478.47	15.91	0.08
cluster0	Linear	2	TAR_2	97.04	2.75	0.00	0.20	0.00	99.79	25.59	654.97	20.06	0.07
cluster0	Linear	4	ALL	64.45	29.22	0.23	6.04	0.07	93.67	36.14	1306.22	27.03	0.20
cluster0	Linear	4	TBR_2	17.93	0.00	0.00	81.58	0.49	17.93	37.01	1369.74	31.61	0.64
cluster0	Linear	4	TBR_1	11.37	0.00	0.00	88.06	0.58	11.37	37.17	1381.25	31.27	0.51
cluster0	Linear	4	TIR	63.72	35.46	0.35	0.46	0.01	99.18	30.35	921.00	22.64	0.19
cluster0	Linear	4	TAR_1	76.25	22.11	0.04	1.45	0.15	98.36	39.40	1552.34	29.75	0.14
cluster0	Linear	4	TAR_2	70.63	23.05	0.01	6.30	0.01	93.68	56.78	3224.25	47.00	0.16
cluster0	Linear	6	ALL	51.93	39.40	0.53	7.99	0.15	91.33	46.31	2144.34	35.63	0.27
cluster0	Linear	6	TBR_2	1.41	0.00	0.00	96.71	1.88	1.41	58.11	3376.50	52.76	1.06
cluster0	Linear	6	TBR_1	0.89	0.00	0.00	96.64	2.47	0.89	56.34	3174.25	50.57	0.82
cluster0	Linear	6	TIR	53.39	45.20	0.84	0.55	0.02	98.59	36.65	1343.21	28.26	0.25
cluster0	Linear	6	TAR_1	64.36	32.66	0.02	2.92	0.04	97.02	47.53	2259.38	37.67	0.18
cluster0	Linear	6	TAR_2	41.31	41.48	0.00	17.20	0.01	82.79	81.23	6597.88	70.76	0.24
cluster0	Linear	8	ALL	44.89	44.47	0.52	9.90	0.22	89.36	53.01	2809.86	41.32	0.31
cluster0	Linear	8	TBR_2	0.18	0.00	0.00	96.91	2.92	0.18	70.66	4992.63	66.60	1.34
cluster0	Linear	8	TBR_1	0.12	0.00	0.00	96.12	3.76	0.12	67.07	4498.89	62.38	1.01
cluster0	Linear	8	TIR	50.93	47.65	0.84	0.55	0.03	98.58	38.13	1453.91	29.94	0.27
cluster0	Linear	8	TAR_1	51.16	43.96	0.00	4.86	0.01	95.12	54.09	2926.10	45.46	0.21
cluster0	Linear	8	TAR_2	15.16	51.29	0.00	33.55	0.00	66.45	102.90	10588.57	94.39	0.32
cluster0	Linear	12	ALL	38.76	47.62	0.34	12.99	0.29	86.38	59.46	3535.72	47.23	0.36
cluster0	Linear	12	TBR_2	0.00	0.00	0.00	95.90	4.10	0.00	89.05	7930.64	86.91	1.75
cluster0	Linear	12	TBR_1	0.00	0.00	0.00	94.92	5.08	0.00	81.79	6688.88	79.32	1.29
cluster0	Linear	12	TIR	48.03	50.85	0.54	0.54	0.03	98.88	40.47	1637.85	32.65	0.31
cluster0	Linear	12	TAR_1	37.80	54.63	0.00	7.57	0.00	92.43	57.29	3282.62	50.89	0.24
cluster0	Linear	12	TAR_2	1.80	36.60	0.00	61.60	0.00	38.40	122.52	15011.73	116.49	0.40
cluster0	Linear	16	ALL	36.77	46.86	0.05	16.22	0.11	83.63	62.12	3859.00	49.44	0.38
cluster0	Linear	16	TBR_2	0.00	0.00	0.00	98.45	1.55	0.00	95.22	9067.21	94.27	1.90
cluster0	Linear	16	TBR_1	0.00	0.00	0.00	98.10	1.90	0.00	85.81	7364.04	84.70	1.38
cluster0	Linear	16	TIR	49.51	49.84	0.07	0.56	0.01	99.35	39.48	1558.68	32.14	0.31

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	Linear	16	TAR_1	25.91	64.29	0.00	9.80	0.00	90.20	60.47	3656.13	55.82	0.26
cluster0	Linear	16	TAR_2	0.03	10.17	0.00	89.80	0.00	10.20	133.18	17738.04	128.55	0.44
cluster0	LSTM	2	ALL	87.37	10.30	0.01	2.32	0.00	97.67	19.18	368.02	13.83	0.10
cluster0	LSTM	2	TBR_2	73.26	0.00	0.00	26.71	0.03	73.26	18.36	337.13	15.04	0.30
cluster0	LSTM	2	TBR_1	58.42	0.00	0.00	41.58	0.00	58.42	16.99	288.68	13.47	0.22
cluster0	LSTM	2	TIR	85.91	13.90	0.01	0.18	0.00	99.81	17.52	306.99	12.59	0.10
cluster0	LSTM	2	TAR_1	93.69	6.16	0.00	0.14	0.00	99.85	21.42	458.66	15.41	0.07
cluster0	LSTM	2	TAR_2	96.83	2.93	0.00	0.24	0.00	99.76	24.27	589.27	18.20	0.06
cluster0	LSTM	4	ALL	66.10	27.34	0.22	6.31	0.03	93.44	35.01	1225.85	25.79	0.19
cluster0	LSTM	4	TBR_2	11.13	0.00	0.00	88.48	0.39	11.13	41.71	1739.77	37.76	0.76
cluster0	LSTM	4	TBR_1	7.58	0.00	0.00	91.95	0.47	7.58	37.67	1419.11	33.15	0.54
cluster0	LSTM	4	TIR	66.33	32.83	0.33	0.50	0.00	99.16	29.05	843.78	21.52	0.18
cluster0	LSTM	4	TAR_1	75.86	22.63	0.07	1.43	0.01	98.49	39.21	1537.43	29.00	0.14
cluster0	LSTM	4	TAR_2	74.74	18.91	0.01	6.34	0.00	93.65	53.34	2845.60	41.30	0.14
cluster0	LSTM	6	ALL	54.13	37.06	0.44	8.26	0.10	91.19	45.28	2050.04	34.19	0.25
cluster0	LSTM	6	TBR_2	0.76	0.00	0.00	97.98	1.26	0.76	58.56	3428.78	54.48	1.10
cluster0	LSTM	6	TBR_1	0.55	0.00	0.00	97.73	1.72	0.55	52.94	2803.11	48.27	0.79
cluster0	LSTM	6	TIR	57.07	41.65	0.70	0.56	0.01	98.72	34.09	1162.06	26.03	0.23
cluster0	LSTM	6	TAR_1	62.21	34.61	0.04	3.13	0.00	96.82	49.08	2409.17	38.68	0.18
cluster0	LSTM	6	TAR_2	46.21	34.87	0.00	18.91	0.00	81.08	81.14	6584.34	68.45	0.24
cluster0	LSTM	8	ALL	46.74	42.88	0.57	9.62	0.18	89.62	51.79	2682.30	40.10	0.30
cluster0	LSTM	8	TBR_2	0.00	0.00	0.00	97.75	2.25	0.00	72.66	5279.10	69.39	1.40
cluster0	LSTM	8	TBR_1	0.00	0.00	0.00	96.77	3.22	0.00	66.66	4444.05	62.73	1.02
cluster0	LSTM	8	TIR	51.19	47.31	0.92	0.56	0.02	98.50	37.70	1421.00	29.61	0.27
cluster0	LSTM	8	TAR_1	54.27	41.33	0.02	4.38	0.00	95.60	52.71	2778.52	43.27	0.20
cluster0	LSTM	8	TAR_2	25.86	42.90	0.00	31.24	0.00	68.76	98.94	9788.39	88.36	0.30
cluster0	LSTM	12	ALL	39.76	46.90	0.36	12.72	0.26	86.66	58.83	3461.35	46.37	0.35
cluster0	LSTM	12	TBR_2	0.00	0.00	0.00	96.09	3.91	0.00	87.95	7735.46	85.88	1.73
cluster0	LSTM	12	TBR_1	0.00	0.00	0.00	95.49	4.51	0.00	79.26	6282.54	76.74	1.25
cluster0	LSTM	12	TIR	49.25	49.59	0.59	0.55	0.03	98.84	39.21	1537.30	31.55	0.30
cluster0	LSTM	12	TAR_1	37.98	54.90	0.00	7.12	0.00	92.88	58.13	3379.49	51.25	0.24
cluster0	LSTM	12	TAR_2	3.98	36.56	0.00	59.46	0.00	40.54	121.87	14852.92	115.01	0.39
cluster0	LSTM	16	ALL	37.19	47.11	0.09	15.45	0.16	84.30	61.78	3817.25	49.10	0.37
cluster0	LSTM	16	TBR_2	0.00	0.00	0.00	97.91	2.09	0.00	95.82	9181.02	94.84	1.91
cluster0	LSTM	16	TBR_1	0.00	0.00	0.00	97.12	2.88	0.00	85.72	7348.55	84.50	1.37
cluster0	LSTM	16	TIR	49.40	49.89	0.14	0.56	0.02	99.29	39.63	1570.50	32.22	0.31
cluster0	LSTM	16	TAR_1	27.98	62.78	0.00	9.24	0.00	90.76	59.83	3580.04	54.76	0.25

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	16	TAR_2	0.08	16.49	0.00	83.43	0.00	16.57	131.86	17387.95	126.91	0.44
cluster0	CNN	2	ALL	74.43	20.39	0.07	5.10	0.01	94.82	28.22	796.37	20.70	0.15
cluster0	CNN	2	TBR_2	23.54	0.00	0.00	76.38	0.08	23.54	31.72	1005.86	28.44	0.57
cluster0	CNN	2	TBR_1	18.62	0.00	0.00	81.28	0.10	18.62	28.80	829.48	24.70	0.40
cluster0	CNN	2	TIR	73.93	25.59	0.10	0.39	0.00	99.52	24.40	595.34	17.93	0.15
cluster0	CNN	2	TAR_1	84.01	15.20	0.03	0.74	0.01	99.21	31.70	1004.63	23.07	0.11
cluster0	CNN	2	TAR_2	86.58	11.08	0.00	2.34	0.00	97.66	39.68	1574.77	30.43	0.11
cluster0	CNN	4	ALL	57.95	34.21	0.41	7.36	0.07	92.16	40.81	1665.54	30.83	0.23
cluster0	CNN	4	TBR_2	0.05	0.00	0.00	99.04	0.91	0.05	52.71	2778.67	48.95	0.99
cluster0	CNN	4	TBR_1	0.36	0.00	0.00	98.37	1.27	0.36	48.64	2366.14	44.17	0.72
cluster0	CNN	4	TIR	57.90	40.89	0.63	0.57	0.01	98.79	33.26	1106.33	25.42	0.22
cluster0	CNN	4	TAR_1	70.13	27.69	0.09	2.09	0.00	97.82	43.45	1887.92	32.94	0.16
cluster0	CNN	4	TAR_2	62.20	26.56	0.01	11.23	0.00	88.76	66.21	4384.29	53.19	0.18
cluster0	CNN	6	ALL	49.63	40.52	0.46	9.26	0.12	90.15	49.18	2418.88	37.64	0.28
cluster0	CNN	6	TBR_2	0.00	0.00	0.00	98.26	1.74	0.00	65.13	4242.04	61.70	1.24
cluster0	CNN	6	TBR_1	0.00	0.00	0.00	97.81	2.18	0.00	59.37	3525.01	55.25	0.90
cluster0	CNN	6	TIR	54.34	44.34	0.74	0.57	0.01	98.68	35.32	1247.46	27.45	0.24
cluster0	CNN	6	TAR_1	55.74	40.19	0.02	4.05	0.00	95.93	52.44	2749.61	42.70	0.20
cluster0	CNN	6	TAR_2	32.43	40.22	0.00	27.35	0.00	72.65	93.32	8709.44	81.97	0.28
cluster0	CNN	8	ALL	44.49	44.48	0.71	10.06	0.26	88.97	54.09	2925.39	42.23	0.32
cluster0	CNN	8	TBR_2	0.00	0.00	0.00	96.85	3.15	0.00	79.07	6252.67	76.09	1.53
cluster0	CNN	8	TBR_1	0.00	0.00	0.00	95.27	4.73	0.00	72.41	5243.39	68.50	1.11
cluster0	CNN	8	TIR	48.85	49.43	1.14	0.55	0.03	98.28	39.93	1594.34	31.54	0.29
cluster0	CNN	8	TAR_1	52.20	42.96	0.01	4.83	0.00	95.16	53.12	2821.23	44.09	0.21
cluster0	CNN	8	TAR_2	22.33	41.87	0.00	35.80	0.00	64.20	103.23	10656.42	92.80	0.32
cluster0	CNN	12	ALL	38.94	47.34	0.32	13.11	0.29	86.28	59.74	3568.34	47.28	0.36
cluster0	CNN	12	TBR_2	0.00	0.00	0.00	95.99	4.01	0.00	91.29	8334.67	89.49	1.80
cluster0	CNN	12	TBR_1	0.00	0.00	0.00	94.82	5.18	0.00	82.05	6731.79	79.82	1.30
cluster0	CNN	12	TIR	48.50	50.40	0.52	0.55	0.03	98.90	40.07	1605.50	32.36	0.31
cluster0	CNN	12	TAR_1	37.07	55.49	0.00	7.44	0.00	92.56	57.83	3344.19	51.25	0.24
cluster0	CNN	12	TAR_2	2.45	34.35	0.00	63.20	0.00	36.80	123.95	15362.43	117.57	0.40
cluster0	CNN	16	ALL	36.66	46.53	0.02	16.74	0.05	83.19	62.55	3912.75	49.47	0.37
cluster0	CNN	16	TBR_2	0.00	0.00	0.00	99.59	0.41	0.00	94.28	8889.16	93.57	1.88
cluster0	CNN	16	TBR_1	0.00	0.00	0.00	99.10	0.90	0.00	83.74	7012.37	82.82	1.35
cluster0	CNN	16	TIR	51.30	48.10	0.03	0.57	0.01	99.40	37.72	1422.85	30.77	0.30
cluster0	CNN	16	TAR_1	20.70	69.25	0.00	10.06	0.00	89.95	62.89	3955.19	58.57	0.27

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	16	TAR_2	0.00	5.74	0.00	94.26	0.00	5.74	136.67	18679.75	132.19	0.45
cluster1	Linear	2	ALL	90.25	9.00	0.01	0.74	0.00	99.25	16.53	273.26	11.72	0.09
cluster1	Linear	2	TBR_2	83.50	0.00	0.00	16.50	0.00	83.50	16.41	269.25	13.21	0.26
cluster1	Linear	2	TBR_1	66.92	0.00	0.00	33.07	0.02	66.92	16.17	261.53	12.50	0.20
cluster1	Linear	2	TIR	90.21	9.71	0.01	0.07	0.00	99.92	15.22	231.53	10.73	0.09
cluster1	Linear	2	TAR_1	93.43	6.44	0.00	0.12	0.00	99.87	21.70	471.01	16.44	0.08
cluster1	Linear	2	TAR_2	94.07	5.31	0.00	0.61	0.00	99.38	29.42	865.77	23.82	0.09
cluster1	Linear	4	ALL	72.13	25.34	0.06	2.45	0.02	97.47	28.09	788.93	20.66	0.16
cluster1	Linear	4	TBR_2	7.71	0.00	0.00	91.79	0.50	7.71	42.23	1783.12	36.70	0.73
cluster1	Linear	4	TBR_1	7.72	0.00	0.00	91.65	0.63	7.72	37.58	1411.95	31.99	0.51
cluster1	Linear	4	TIR	74.70	25.01	0.07	0.22	0.00	99.71	23.58	555.80	17.57	0.15
cluster1	Linear	4	TAR_1	68.34	30.15	0.00	1.48	0.03	98.49	41.78	1745.52	33.87	0.16
cluster1	Linear	4	TAR_2	49.65	35.25	0.00	15.10	0.00	84.90	67.21	4517.85	59.23	0.22
cluster1	Linear	6	ALL	61.70	34.96	0.07	3.22	0.04	96.66	34.47	1188.10	25.92	0.20
cluster1	Linear	6	TBR_2	0.77	0.00	0.00	97.44	1.79	0.77	58.44	3415.54	53.51	1.06
cluster1	Linear	6	TBR_1	0.92	0.00	0.00	97.17	1.90	0.92	51.08	2609.42	45.83	0.73
cluster1	Linear	6	TIR	67.10	32.56	0.09	0.25	0.00	99.66	26.79	717.60	20.72	0.18
cluster1	Linear	6	TAR_1	42.87	53.79	0.00	3.33	0.02	96.66	55.08	3034.22	48.12	0.23
cluster1	Linear	6	TAR_2	12.58	43.18	0.00	44.17	0.08	55.76	96.37	9286.99	90.06	0.33
cluster1	Linear	8	ALL	55.76	40.41	0.04	3.75	0.03	96.17	37.85	1432.45	28.95	0.22
cluster1	Linear	8	TBR_2	0.00	0.00	0.00	98.41	1.59	0.00	68.54	4697.60	64.82	1.28
cluster1	Linear	8	TBR_1	0.07	0.00	0.00	98.38	1.55	0.07	59.08	3490.67	55.48	0.89
cluster1	Linear	8	TIR	62.85	36.85	0.05	0.25	0.00	99.70	28.17	793.40	22.40	0.20
cluster1	Linear	8	TAR_1	26.45	68.98	0.00	4.57	0.00	95.43	62.27	3877.12	56.77	0.27
cluster1	Linear	8	TAR_2	2.03	27.90	0.00	70.07	0.00	29.93	113.15	12804.03	108.69	0.40
cluster1	Linear	12	ALL	51.03	44.70	0.00	4.26	0.00	95.73	40.62	1650.28	31.51	0.24
cluster1	Linear	12	TBR_2	0.00	0.00	0.00	99.45	0.55	0.00	76.62	5870.54	75.08	1.48
cluster1	Linear	12	TBR_1	0.00	0.00	0.00	99.89	0.11	0.00	65.50	4290.83	64.08	1.02
cluster1	Linear	12	TIR	60.08	39.67	0.00	0.25	0.00	99.75	28.63	819.89	23.48	0.21
cluster1	Linear	12	TAR_1	9.18	85.31	0.00	5.50	0.00	94.49	69.21	4789.73	65.67	0.32
cluster1	Linear	12	TAR_2	0.00	2.62	0.00	97.38	0.00	2.62	128.89	16612.22	126.31	0.46
cluster1	Linear	16	ALL	50.20	45.51	0.00	4.28	0.00	95.71	41.57	1728.19	32.13	0.25
cluster1	Linear	16	TBR_2	0.00	0.00	0.00	100.00	0.00	0.00	78.67	6188.60	77.89	1.52
cluster1	Linear	16	TBR_1	0.00	0.00	0.00	100.00	0.00	0.00	67.05	4495.48	66.27	1.06
cluster1	Linear	16	TIR	60.20	39.55	0.00	0.25	0.00	99.75	28.07	787.65	23.29	0.21
cluster1	Linear	16	TAR_1	2.65	91.80	0.00	5.55	0.00	94.45	72.80	5299.29	70.01	0.34

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	Linear	16	TAR_2	0.00	0.00	0.00	100.00	0.00	0.00	136.71	18689.96	134.69	0.49
cluster1	LSTM	2	ALL	90.82	8.19	0.00	0.99	0.00	99.01	15.93	253.72	11.24	0.09
cluster1	LSTM	2	TBR_2	60.92	0.00	0.00	39.08	0.00	60.92	20.56	422.86	17.20	0.34
cluster1	LSTM	2	TBR_1	55.91	0.00	0.00	44.07	0.02	55.91	17.57	308.82	13.87	0.22
cluster1	LSTM	2	TIR	91.10	8.81	0.00	0.08	0.00	99.91	14.57	212.25	10.26	0.08
cluster1	LSTM	2	TAR_1	93.95	5.94	0.00	0.11	0.00	99.89	21.02	441.70	15.71	0.08
cluster1	LSTM	2	TAR_2	94.22	5.27	0.00	0.51	0.00	99.49	28.58	816.94	22.48	0.08
cluster1	LSTM	4	ALL	73.70	23.86	0.05	2.38	0.01	97.56	27.38	749.62	19.89	0.15
cluster1	LSTM	4	TBR_2	7.46	0.00	0.00	92.54	0.00	7.46	44.30	1962.27	39.46	0.78
cluster1	LSTM	4	TBR_1	10.86	0.00	0.00	88.68	0.46	10.86	37.29	1390.68	32.30	0.52
cluster1	LSTM	4	TIR	76.29	23.43	0.06	0.22	0.00	99.72	22.86	522.41	16.91	0.14
cluster1	LSTM	4	TAR_1	69.23	29.37	0.00	1.39	0.01	98.60	41.16	1694.41	32.60	0.16
cluster1	LSTM	4	TAR_2	54.57	30.83	0.00	14.60	0.00	85.40	64.64	4178.10	55.43	0.20
cluster1	LSTM	6	ALL	63.13	33.61	0.09	3.13	0.04	96.74	33.77	1140.49	25.22	0.19
cluster1	LSTM	6	TBR_2	0.00	0.00	0.00	98.47	1.53	0.00	60.00	3600.37	55.08	1.09
cluster1	LSTM	6	TBR_1	0.58	0.00	0.00	97.70	1.73	0.58	50.22	2522.25	45.37	0.72
cluster1	LSTM	6	TIR	67.99	31.65	0.11	0.25	0.00	99.64	26.36	694.89	20.33	0.17
cluster1	LSTM	6	TAR_1	47.20	49.79	0.00	3.01	0.00	96.99	53.84	2898.50	45.90	0.22
cluster1	LSTM	6	TAR_2	20.21	39.78	0.00	40.01	0.00	59.99	92.86	8623.22	85.37	0.31
cluster1	LSTM	8	ALL	56.93	39.33	0.05	3.65	0.03	96.26	37.31	1392.37	28.36	0.22
cluster1	LSTM	8	TBR_2	0.00	0.00	0.00	98.14	1.86	0.00	68.02	4626.19	64.27	1.27
cluster1	LSTM	8	TBR_1	0.00	0.00	0.00	98.50	1.50	0.00	57.18	3269.48	53.50	0.85
cluster1	LSTM	8	TIR	63.57	36.11	0.07	0.25	0.00	99.68	27.69	766.62	21.97	0.19
cluster1	LSTM	8	TAR_1	30.34	65.39	0.00	4.27	0.00	95.73	61.85	3825.52	55.59	0.27
cluster1	LSTM	8	TAR_2	5.01	29.78	0.00	65.21	0.00	34.79	110.95	12310.92	105.65	0.39
cluster1	LSTM	12	ALL	51.35	44.39	0.00	4.25	0.00	95.74	40.42	1633.49	31.24	0.24
cluster1	LSTM	12	TBR_2	0.00	0.00	0.00	100.00	0.00	0.00	75.22	5657.91	73.56	1.45
cluster1	LSTM	12	TBR_1	0.00	0.00	0.00	99.87	0.13	0.00	63.29	4006.17	61.56	0.98
cluster1	LSTM	12	TIR	60.15	39.60	0.00	0.25	0.00	99.75	28.33	802.73	23.24	0.21
cluster1	LSTM	12	TAR_1	11.04	83.50	0.00	5.46	0.00	94.54	69.36	4811.45	65.57	0.32
cluster1	LSTM	12	TAR_2	0.00	2.88	0.00	97.12	0.00	2.88	128.90	16614.48	126.26	0.46
cluster1	LSTM	16	ALL	50.07	45.65	0.00	4.28	0.00	95.72	41.42	1715.46	32.09	0.25
cluster1	LSTM	16	TBR_2	0.00	0.00	0.00	100.00	0.00	0.00	78.60	6178.23	77.73	1.52
cluster1	LSTM	16	TBR_1	0.02	0.00	0.00	99.98	0.00	0.02	66.79	4460.44	65.81	1.05
cluster1	LSTM	16	TIR	59.90	39.85	0.00	0.25	0.00	99.75	28.22	796.57	23.42	0.21
cluster1	LSTM	16	TAR_1	3.42	91.03	0.00	5.55	0.00	94.45	71.98	5181.71	69.08	0.33
cluster1	LSTM	16	TAR_2	0.00	0.00	0.00	100.00	0.00	0.00	135.86	18456.60	133.87	0.49

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	2	ALL	80.63	17.39	0.03	1.95	0.00	98.02	22.68	514.42	16.37	0.13
cluster1	CNN	2	TBR_2	22.82	0.00	0.00	77.18	0.00	22.82	35.67	1272.06	31.51	0.63
cluster1	CNN	2	TBR_1	18.99	0.00	0.00	80.94	0.07	18.99	29.81	888.48	25.65	0.41
cluster1	CNN	2	TIR	82.00	17.78	0.03	0.19	0.00	99.78	19.92	396.81	14.49	0.12
cluster1	CNN	2	TAR_1	81.89	17.50	0.00	0.61	0.00	99.39	31.85	1014.34	24.30	0.12
cluster1	CNN	2	TAR_2	76.34	19.08	0.00	4.58	0.00	95.42	45.96	2112.25	37.40	0.14
cluster1	CNN	4	ALL	67.74	29.28	0.07	2.89	0.03	97.02	31.27	977.51	22.99	0.18
cluster1	CNN	4	TBR_2	0.00	0.00	0.00	99.50	0.50	0.00	53.41	2852.16	48.94	0.97
cluster1	CNN	4	TBR_1	1.50	0.00	0.00	97.29	1.21	1.50	44.77	2004.26	39.74	0.64
cluster1	CNN	4	TIR	71.93	27.74	0.09	0.24	0.00	99.67	24.86	617.88	18.77	0.16
cluster1	CNN	4	TAR_1	55.52	42.17	0.00	2.31	0.00	97.69	49.43	2443.50	41.14	0.20
cluster1	CNN	4	TAR_2	33.77	37.22	0.00	29.01	0.00	70.99	81.86	6700.89	73.30	0.27
cluster1	CNN	6	ALL	59.39	37.06	0.07	3.45	0.04	96.45	35.91	1289.54	27.09	0.21
cluster1	CNN	6	TBR_2	0.00	0.00	0.00	97.44	2.56	0.00	65.34	4269.77	61.01	1.20
cluster1	CNN	6	TBR_1	0.02	0.00	0.00	98.27	1.71	0.02	54.43	2963.02	50.25	0.80
cluster1	CNN	6	TIR	65.39	34.28	0.08	0.25	0.00	99.67	27.08	733.45	21.25	0.18
cluster1	CNN	6	TAR_1	36.73	59.51	0.00	3.76	0.00	96.24	58.95	3475.21	52.03	0.25
cluster1	CNN	6	TAR_2	9.89	34.58	0.00	55.53	0.00	44.47	103.91	10796.70	97.70	0.36
cluster1	CNN	8	ALL	55.05	40.95	0.02	3.97	0.02	96.00	38.75	1501.24	29.45	0.22
cluster1	CNN	8	TBR_2	0.00	0.00	0.00	98.67	1.33	0.00	69.31	4803.36	66.39	1.31
cluster1	CNN	8	TBR_1	0.00	0.00	0.00	99.34	0.66	0.00	58.01	3365.32	55.14	0.88
cluster1	CNN	8	TIR	63.13	36.60	0.02	0.25	0.00	99.73	27.55	759.13	22.08	0.19
cluster1	CNN	8	TAR_1	19.71	75.37	0.00	4.92	0.00	95.08	66.63	4439.56	61.61	0.30
cluster1	CNN	8	TAR_2	1.13	17.68	0.00	81.19	0.00	18.81	120.30	14472.44	116.31	0.42
cluster1	CNN	12	ALL	50.45	45.28	0.00	4.27	0.00	95.73	40.65	1652.74	31.70	0.25
cluster1	CNN	12	TBR_2	0.00	0.00	0.00	99.45	0.55	0.00	77.59	6020.44	76.24	1.50
cluster1	CNN	12	TBR_1	0.00	0.00	0.00	99.93	0.07	0.00	66.22	4385.20	64.84	1.04
cluster1	CNN	12	TIR	59.27	40.48	0.00	0.25	0.00	99.75	28.83	830.92	23.77	0.21
cluster1	CNN	12	TAR_1	9.78	84.73	0.00	5.50	0.00	94.51	68.66	4714.15	65.12	0.31
cluster1	CNN	12	TAR_2	0.00	1.88	0.00	98.12	0.00	1.88	129.42	16749.60	126.97	0.46
cluster1	CNN	16	ALL	49.73	45.98	0.00	4.28	0.00	95.71	41.39	1712.88	32.28	0.25
cluster1	CNN	16	TBR_2	0.00	0.00	0.00	100.00	0.00	0.00	81.44	6631.69	80.62	1.58
cluster1	CNN	16	TBR_1	0.00	0.00	0.00	100.00	0.00	0.00	69.02	4764.27	68.15	1.09
cluster1	CNN	16	TIR	59.40	40.35	0.00	0.25	0.00	99.75	28.75	826.42	23.86	0.21
cluster1	CNN	16	TAR_1	4.01	90.44	0.00	5.55	0.00	94.45	70.50	4970.22	67.56	0.33
cluster1	CNN	16	TAR_2	0.00	0.00	0.00	100.00	0.00	0.00	134.71	18147.90	132.68	0.48
cluster2	Linear	2	ALL	88.11	10.64	0.03	1.20	0.01	98.75	21.67	469.72	15.55	0.10

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	2	TBR_2	93.92	0.00	0.00	6.04	0.04	93.92	14.78	218.38	11.77	0.25
cluster2	Linear	2	TBR_1	67.79	0.00	0.00	32.18	0.03	67.79	16.81	282.53	12.74	0.21
cluster2	Linear	2	TIR	83.01	16.79	0.05	0.15	0.00	99.80	20.41	416.73	14.50	0.12
cluster2	Linear	2	TAR_1	93.00	6.83	0.03	0.13	0.01	99.83	22.35	499.30	15.83	0.07
cluster2	Linear	2	TAR_2	97.32	2.53	0.01	0.14	0.00	99.85	24.75	612.58	18.67	0.06
cluster2	Linear	4	ALL	66.65	27.78	0.69	4.78	0.11	94.43	39.63	1570.31	29.32	0.19
cluster2	Linear	4	TBR_2	20.32	0.00	0.00	78.62	1.05	20.32	39.94	1595.29	33.98	0.71
cluster2	Linear	4	TBR_1	8.81	0.00	0.00	89.30	1.89	8.81	43.60	1900.88	35.81	0.58
cluster2	Linear	4	TIR	59.19	39.22	1.19	0.39	0.01	98.41	35.88	1287.12	26.50	0.22
cluster2	Linear	4	TAR_1	79.29	19.07	0.33	1.20	0.10	98.36	37.35	1394.97	26.90	0.13
cluster2	Linear	4	TAR_2	79.48	17.04	0.07	3.40	0.01	96.52	50.58	2557.88	39.41	0.13
cluster2	Linear	6	ALL	54.56	37.31	1.39	6.45	0.29	91.87	51.82	2685.65	39.35	0.27
cluster2	Linear	6	TBR_2	1.14	0.00	0.00	94.61	4.25	1.14	65.96	4350.67	58.81	1.23
cluster2	Linear	6	TBR_1	1.48	0.00	0.00	92.03	6.49	1.48	67.16	4510.51	58.69	0.96
cluster2	Linear	6	TIR	47.90	48.99	2.63	0.43	0.04	96.89	44.75	2002.87	34.07	0.29
cluster2	Linear	6	TAR_1	72.21	25.12	0.33	2.27	0.07	97.33	42.90	1840.28	32.18	0.15
cluster2	Linear	6	TAR_2	57.01	33.64	0.05	9.28	0.02	90.65	73.95	5468.07	60.56	0.20
cluster2	Linear	8	ALL	47.40	42.57	1.79	7.71	0.53	89.97	60.06	3607.45	46.45	0.32
cluster2	Linear	8	TBR_2	0.13	0.00	0.00	91.24	8.63	0.13	86.03	7400.61	79.84	1.67
cluster2	Linear	8	TBR_1	0.24	0.00	0.00	87.44	12.32	0.24	84.52	7143.22	77.44	1.26
cluster2	Linear	8	TIR	42.26	53.71	3.54	0.41	0.07	95.97	50.01	2501.15	39.15	0.35
cluster2	Linear	8	TAR_1	68.75	27.92	0.18	3.13	0.03	96.67	44.11	1945.98	34.23	0.16
cluster2	Linear	8	TAR_2	38.61	45.47	0.01	15.89	0.01	84.08	91.74	8416.36	78.35	0.25
cluster2	Linear	12	ALL	40.38	47.10	1.87	9.70	0.94	87.48	68.95	4753.89	54.42	0.38
cluster2	Linear	12	TBR_2	0.01	0.00	0.00	83.38	16.61	0.01	109.71	12035.69	106.36	2.23
cluster2	Linear	12	TBR_1	0.01	0.00	0.00	77.78	22.21	0.01	103.57	10727.44	99.88	1.63
cluster2	Linear	12	TIR	36.83	58.89	3.80	0.36	0.13	95.72	55.07	3032.35	44.95	0.41
cluster2	Linear	12	TAR_1	67.77	27.83	0.01	4.39	0.00	95.60	42.18	1779.57	34.20	0.16
cluster2	Linear	12	TAR_2	16.16	56.49	0.00	27.34	0.00	72.65	112.72	12705.07	101.32	0.33
cluster2	Linear	16	ALL	37.51	48.35	1.32	11.65	1.16	85.86	72.68	5282.95	57.75	0.41
cluster2	Linear	16	TBR_2	0.00	0.00	0.00	77.77	22.23	0.00	120.05	14411.98	118.47	2.49
cluster2	Linear	16	TBR_1	0.00	0.00	0.00	72.91	27.09	0.00	110.28	12161.05	108.54	1.77
cluster2	Linear	16	TIR	35.38	61.46	2.67	0.33	0.15	96.84	55.53	3083.55	46.17	0.43
cluster2	Linear	16	TAR_1	67.32	27.15	0.00	5.53	0.00	94.47	41.18	1696.08	34.50	0.16
cluster2	Linear	16	TAR_2	4.90	57.30	0.00	37.80	0.00	62.20	123.54	15262.48	113.94	0.37
cluster2	LSTM	2	ALL	88.66	9.64	0.02	1.68	0.00	98.30	20.83	433.81	14.90	0.09
cluster2	LSTM	2	TBR_2	79.93	0.00	0.00	20.02	0.04	79.93	17.98	323.33	14.37	0.30

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	2	TBR_1	57.38	0.00	0.00	42.59	0.03	57.38	17.98	323.44	13.92	0.23
cluster2	LSTM	2	TIR	84.81	15.00	0.03	0.16	0.00	99.81	19.10	364.89	13.40	0.11
cluster2	LSTM	2	TAR_1	93.35	6.50	0.02	0.13	0.00	99.85	21.80	475.09	15.59	0.07
cluster2	LSTM	2	TAR_2	97.53	2.32	0.00	0.15	0.00	99.85	24.08	579.88	18.07	0.06
cluster2	LSTM	4	ALL	68.97	25.33	0.56	5.07	0.07	94.30	38.52	1483.51	28.05	0.18
cluster2	LSTM	4	TBR_2	13.46	0.00	0.00	85.66	0.87	13.46	44.53	1983.35	39.43	0.83
cluster2	LSTM	4	TBR_1	5.59	0.00	0.00	92.89	1.51	5.59	43.24	1869.69	36.73	0.60
cluster2	LSTM	4	TIR	65.01	33.61	0.95	0.42	0.01	98.62	33.02	1090.42	23.77	0.20
cluster2	LSTM	4	TAR_1	78.20	20.19	0.28	1.31	0.01	98.39	37.77	1426.21	27.39	0.13
cluster2	LSTM	4	TAR_2	79.26	16.91	0.08	3.75	0.00	96.17	50.44	2543.80	38.52	0.13
cluster2	LSTM	6	ALL	56.36	35.41	1.25	6.74	0.24	91.77	50.74	2574.62	38.04	0.26
cluster2	LSTM	6	TBR_2	0.36	0.00	0.00	95.97	3.67	0.36	69.71	4859.75	63.81	1.34
cluster2	LSTM	6	TBR_1	0.17	0.00	0.00	94.15	5.68	0.17	66.65	4442.75	59.59	0.97
cluster2	LSTM	6	TIR	52.16	45.03	2.34	0.44	0.04	97.19	42.05	1767.92	31.46	0.27
cluster2	LSTM	6	TAR_1	70.17	27.08	0.33	2.43	0.00	97.25	43.52	1894.03	32.92	0.15
cluster2	LSTM	6	TAR_2	58.97	30.79	0.07	10.17	0.00	89.76	73.40	5387.10	58.78	0.19
cluster2	LSTM	8	ALL	49.00	40.76	1.64	8.14	0.45	89.76	59.13	3496.59	45.15	0.31
cluster2	LSTM	8	TBR_2	0.00	0.00	0.00	92.09	7.91	0.00	87.60	7674.62	82.30	1.73
cluster2	LSTM	8	TBR_1	0.00	0.00	0.00	89.31	10.69	0.00	82.64	6829.88	76.18	1.24
cluster2	LSTM	8	TIR	46.23	50.09	3.20	0.42	0.06	96.32	47.35	2241.75	36.34	0.32
cluster2	LSTM	8	TAR_1	65.77	30.59	0.22	3.41	0.00	96.36	45.27	2049.37	35.43	0.17
cluster2	LSTM	8	TAR_2	41.44	41.10	0.04	17.42	0.00	82.54	91.55	8381.70	76.93	0.25
cluster2	LSTM	12	ALL	41.42	45.51	2.00	10.21	0.86	86.93	68.34	4670.45	53.51	0.38
cluster2	LSTM	12	TBR_2	0.00	0.00	0.00	85.05	14.95	0.00	110.04	12109.04	106.91	2.24
cluster2	LSTM	12	TBR_1	0.00	0.00	0.00	79.74	20.26	0.00	102.60	10527.35	98.68	1.61
cluster2	LSTM	12	TIR	39.12	56.37	4.03	0.37	0.11	95.49	54.06	2922.38	43.43	0.40
cluster2	LSTM	12	TAR_1	64.60	30.70	0.05	4.65	0.00	95.30	43.23	1868.86	35.18	0.16
cluster2	LSTM	12	TAR_2	20.71	50.02	0.00	29.27	0.00	70.73	111.49	12430.83	99.06	0.32
cluster2	LSTM	16	ALL	38.21	47.38	1.73	11.50	1.18	85.59	72.29	5225.41	57.33	0.41
cluster2	LSTM	16	TBR_2	0.00	0.00	0.00	77.74	22.26	0.00	121.54	14773.00	119.81	2.51
cluster2	LSTM	16	TBR_1	0.00	0.00	0.00	72.36	27.64	0.00	111.56	12444.70	109.49	1.79
cluster2	LSTM	16	TIR	34.98	61.03	3.51	0.33	0.15	96.01	56.66	3210.82	46.91	0.44
cluster2	LSTM	16	TAR_1	67.96	26.64	0.00	5.40	0.00	94.60	40.61	1649.09	33.77	0.15
cluster2	LSTM	16	TAR_2	8.87	53.89	0.00	37.24	0.00	62.76	120.81	14595.96	110.43	0.35
cluster2	CNN	2	ALL	77.50	18.57	0.19	3.72	0.02	96.07	30.79	948.23	22.23	0.14
cluster2	CNN	2	TBR_2	38.34	0.00	0.00	61.45	0.21	38.34	31.80	1011.18	27.98	0.59
cluster2	CNN	2	TBR_1	21.16	0.00	0.00	78.49	0.34	21.16	30.68	941.10	25.38	0.41

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	2	TIR	73.76	25.59	0.31	0.33	0.00	99.35	26.64	709.89	18.93	0.15
cluster2	CNN	2	TAR_1	84.61	14.53	0.10	0.74	0.02	99.14	31.43	987.64	22.51	0.11
cluster2	CNN	2	TAR_2	88.25	10.24	0.03	1.48	0.00	98.49	39.09	1527.75	29.81	0.10
cluster2	CNN	4	ALL	61.48	31.37	1.01	6.00	0.14	92.85	45.36	2057.69	33.62	0.23
cluster2	CNN	4	TBR_2	0.02	0.00	0.00	97.72	2.26	0.02	58.84	3462.22	53.62	1.12
cluster2	CNN	4	TBR_1	0.14	0.00	0.00	96.40	3.47	0.14	56.35	3175.84	49.62	0.81
cluster2	CNN	4	TIR	56.64	41.09	1.80	0.45	0.02	97.73	38.69	1497.25	28.49	0.24
cluster2	CNN	4	TAR_1	73.61	24.15	0.39	1.85	0.00	97.76	41.60	1730.39	30.81	0.15
cluster2	CNN	4	TAR_2	69.55	23.77	0.09	6.60	0.00	93.32	61.81	3820.89	48.07	0.16
cluster2	CNN	6	ALL	51.94	38.86	1.40	7.47	0.34	90.80	55.45	3074.66	42.12	0.29
cluster2	CNN	6	TBR_2	0.00	0.00	0.00	94.48	5.52	0.00	80.45	6472.15	75.34	1.58
cluster2	CNN	6	TBR_1	0.00	0.00	0.00	91.96	8.04	0.00	76.32	5824.62	69.84	1.14
cluster2	CNN	6	TIR	48.36	48.46	2.70	0.43	0.05	96.82	44.85	2011.26	34.23	0.30
cluster2	CNN	6	TAR_1	68.21	28.60	0.24	2.95	0.00	96.81	44.09	1943.81	33.97	0.16
cluster2	CNN	6	TAR_2	47.97	38.13	0.03	13.87	0.00	86.10	84.15	7080.52	69.69	0.23
cluster2	CNN	8	ALL	46.04	42.99	2.01	8.35	0.61	89.03	62.20	3868.88	48.15	0.34
cluster2	CNN	8	TBR_2	0.00	0.00	0.00	89.60	10.40	0.00	98.03	9609.27	93.47	1.96
cluster2	CNN	8	TBR_1	0.00	0.00	0.00	85.63	14.37	0.00	92.01	8465.06	86.52	1.41
cluster2	CNN	8	TIR	41.36	54.20	3.96	0.40	0.08	95.56	51.63	2665.32	40.61	0.37
cluster2	CNN	8	TAR_1	66.27	30.00	0.21	3.52	0.00	96.27	43.65	1905.28	34.50	0.16
cluster2	CNN	8	TAR_2	37.50	43.19	0.02	19.30	0.00	80.69	95.50	9119.61	80.94	0.26
cluster2	CNN	12	ALL	40.30	46.08	1.69	11.04	0.89	86.38	69.70	4858.36	54.71	0.38
cluster2	CNN	12	TBR_2	0.00	0.00	0.00	84.02	15.98	0.00	112.39	12630.93	109.83	2.30
cluster2	CNN	12	TBR_1	0.00	0.00	0.00	79.03	20.97	0.00	104.11	10838.06	100.95	1.65
cluster2	CNN	12	TIR	39.06	57.03	3.43	0.37	0.12	96.09	53.49	2860.87	43.29	0.40
cluster2	CNN	12	TAR_1	64.64	30.21	0.02	5.13	0.00	94.85	43.00	1848.94	35.40	0.16
cluster2	CNN	12	TAR_2	14.55	52.13	0.00	33.32	0.00	66.68	116.58	13590.41	105.19	0.34
cluster2	CNN	16	ALL	37.51	47.23	1.19	13.00	1.06	84.74	72.95	5321.26	57.79	0.40
cluster2	CNN	16	TBR_2	0.00	0.00	0.00	79.49	20.51	0.00	121.20	14688.78	119.89	2.52
cluster2	CNN	16	TBR_1	0.00	0.00	0.00	75.33	24.67	0.00	110.32	12171.05	108.78	1.77
cluster2	CNN	16	TIR	36.57	60.53	2.41	0.35	0.13	97.10	54.54	2974.43	45.08	0.42
cluster2	CNN	16	TAR_1	65.42	28.40	0.00	6.18	0.00	93.82	41.84	1750.67	35.40	0.16
cluster2	CNN	16	TAR_2	4.67	51.62	0.00	43.72	0.00	56.29	125.18	15670.45	115.60	0.37
cluster3	Linear	2	ALL	88.47	10.28	0.02	1.22	0.00	98.75	20.13	405.34	14.50	0.10
cluster3	Linear	2	TBR_2	92.65	0.00	0.00	7.32	0.03	92.65	14.74	217.30	11.80	0.24
cluster3	Linear	2	TBR_1	65.43	0.00	0.00	34.55	0.02	65.43	16.80	282.16	12.90	0.21
cluster3	Linear	2	TIR	84.57	15.26	0.03	0.14	0.00	99.83	19.20	368.67	13.75	0.11

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	2	TAR_1	94.48	5.39	0.02	0.11	0.01	99.87	20.63	425.40	14.66	0.07
cluster3	Linear	2	TAR_2	97.42	2.45	0.01	0.12	0.00	99.87	23.68	560.91	17.89	0.06
cluster3	Linear	4	ALL	68.38	26.87	0.41	4.24	0.09	95.25	36.24	1313.34	26.80	0.18
cluster3	Linear	4	TBR_2	19.85	0.00	0.00	79.21	0.94	19.85	40.40	1631.86	33.86	0.70
cluster3	Linear	4	TBR_1	10.17	0.00	0.00	88.47	1.36	10.17	41.48	1720.99	34.15	0.55
cluster3	Linear	4	TIR	63.85	35.10	0.68	0.36	0.02	98.95	31.83	1013.02	23.52	0.20
cluster3	Linear	4	TAR_1	80.93	17.74	0.12	1.10	0.11	98.67	35.60	1267.41	25.97	0.12
cluster3	Linear	4	TAR_2	76.81	19.24	0.02	3.91	0.01	96.05	51.10	2611.47	40.84	0.14
cluster3	Linear	6	ALL	56.41	36.77	0.80	5.79	0.22	93.18	46.89	2198.68	35.65	0.25
cluster3	Linear	6	TBR_2	1.84	0.00	0.00	93.97	4.19	1.84	66.70	4449.46	59.11	1.23
cluster3	Linear	6	TBR_1	1.67	0.00	0.00	93.07	5.26	1.67	63.20	3994.71	55.39	0.90
cluster3	Linear	6	TIR	53.50	44.65	1.41	0.41	0.03	98.15	38.84	1508.24	29.57	0.26
cluster3	Linear	6	TAR_1	71.63	25.88	0.08	2.36	0.05	97.51	42.60	1814.79	32.65	0.15
cluster3	Linear	6	TAR_2	51.23	37.47	0.00	11.29	0.01	88.70	74.29	5518.68	62.90	0.21
cluster3	Linear	8	ALL	49.25	42.34	1.11	6.88	0.41	91.59	53.86	2901.43	41.81	0.30
cluster3	Linear	8	TBR_2	0.22	0.00	0.00	90.14	9.64	0.22	86.71	7518.83	80.06	1.67
cluster3	Linear	8	TBR_1	0.23	0.00	0.00	89.28	10.49	0.23	80.16	6426.29	73.74	1.20
cluster3	Linear	8	TIR	47.17	50.40	1.99	0.40	0.05	97.57	43.98	1934.56	34.40	0.31
cluster3	Linear	8	TAR_1	66.89	29.72	0.04	3.34	0.01	96.61	44.67	1995.34	35.42	0.17
cluster3	Linear	8	TAR_2	33.25	47.76	0.00	18.98	0.01	81.01	89.80	8064.72	78.79	0.27
cluster3	Linear	12	ALL	42.36	46.68	1.06	9.25	0.65	89.04	61.32	3760.28	48.60	0.35
cluster3	Linear	12	TBR_2	0.00	0.00	0.00	83.50	16.50	0.00	106.35	11309.83	102.67	2.14
cluster3	Linear	12	TBR_1	0.00	0.00	0.00	83.44	16.56	0.00	96.81	9373.07	93.49	1.52
cluster3	Linear	12	TIR	43.07	54.57	1.92	0.36	0.08	97.64	48.17	2320.49	38.81	0.36
cluster3	Linear	12	TAR_1	60.64	34.18	0.00	5.17	0.00	94.82	45.70	2088.74	38.18	0.18
cluster3	Linear	12	TAR_2	10.49	53.71	0.00	35.80	0.00	64.20	109.92	12081.48	101.35	0.34
cluster3	Linear	16	ALL	39.77	47.20	0.67	11.68	0.69	86.97	64.24	4126.62	51.31	0.37
cluster3	Linear	16	TBR_2	0.00	0.00	0.00	84.59	15.41	0.00	112.89	12743.04	111.22	2.32
cluster3	Linear	16	TBR_1	0.00	0.00	0.00	81.79	18.21	0.00	103.06	10622.08	101.46	1.65
cluster3	Linear	16	TIR	41.97	56.39	1.21	0.36	0.08	98.36	49.02	2403.40	39.96	0.38
cluster3	Linear	16	TAR_1	57.31	35.88	0.00	6.81	0.00	93.19	45.85	2102.00	39.60	0.18
cluster3	Linear	16	TAR_2	2.23	45.91	0.00	51.86	0.00	48.14	119.31	14234.49	112.35	0.38
cluster3	LSTM	2	ALL	89.36	9.13	0.01	1.50	0.00	98.49	19.40	376.24	13.83	0.09
cluster3	LSTM	2	TBR_2	76.40	0.00	0.00	23.55	0.05	76.40	18.39	338.21	14.69	0.31
cluster3	LSTM	2	TBR_1	60.22	0.00	0.00	39.78	0.00	60.22	17.32	299.87	13.28	0.22
cluster3	LSTM	2	TIR	86.56	13.29	0.02	0.13	0.00	99.85	17.96	322.62	12.66	0.10
cluster3	LSTM	2	TAR_1	94.69	5.19	0.01	0.11	0.00	99.88	20.25	410.19	14.48	0.07

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	2	TAR_2	97.42	2.43	0.00	0.15	0.00	99.85	23.56	555.03	17.57	0.06
cluster3	LSTM	4	ALL	69.98	25.17	0.35	4.44	0.05	95.15	35.07	1229.81	25.74	0.18
cluster3	LSTM	4	TBR_2	13.20	0.00	0.00	86.10	0.71	13.20	46.25	2138.80	41.16	0.86
cluster3	LSTM	4	TBR_1	5.49	0.00	0.00	93.41	1.10	5.49	42.51	1807.02	36.63	0.60
cluster3	LSTM	4	TIR	66.51	32.52	0.57	0.39	0.01	99.03	30.45	927.21	22.42	0.19
cluster3	LSTM	4	TAR_1	81.13	17.66	0.11	1.08	0.02	98.79	34.95	1221.38	25.34	0.12
cluster3	LSTM	4	TAR_2	78.91	17.26	0.03	3.80	0.00	96.17	48.78	2379.61	37.63	0.13
cluster3	LSTM	6	ALL	57.79	35.49	0.80	5.74	0.18	93.28	45.53	2073.43	34.45	0.24
cluster3	LSTM	6	TBR_2	0.91	0.00	0.00	95.49	3.60	0.91	70.62	4986.49	64.94	1.35
cluster3	LSTM	6	TBR_1	0.24	0.00	0.00	95.05	4.72	0.24	64.49	4158.60	58.40	0.95
cluster3	LSTM	6	TIR	54.24	43.94	1.37	0.42	0.03	98.18	38.12	1453.47	29.10	0.25
cluster3	LSTM	6	TAR_1	72.24	25.46	0.12	2.17	0.01	97.70	41.43	1716.10	31.37	0.15
cluster3	LSTM	6	TAR_2	57.93	31.36	0.01	10.70	0.00	89.29	70.14	4919.04	57.28	0.19
cluster3	LSTM	8	ALL	50.51	41.21	1.07	6.86	0.34	91.72	52.64	2770.90	40.58	0.29
cluster3	LSTM	8	TBR_2	0.08	0.00	0.00	91.84	8.08	0.08	87.12	7589.67	81.62	1.70
cluster3	LSTM	8	TBR_1	0.04	0.00	0.00	91.25	8.71	0.04	78.95	6233.19	73.39	1.19
cluster3	LSTM	8	TIR	48.34	49.31	1.91	0.40	0.04	97.65	42.87	1837.51	33.43	0.30
cluster3	LSTM	8	TAR_1	66.01	30.76	0.06	3.17	0.00	96.77	44.58	1986.98	35.05	0.16
cluster3	LSTM	8	TAR_2	40.15	41.20	0.00	18.65	0.00	81.35	86.70	7516.83	74.15	0.25
cluster3	LSTM	12	ALL	43.26	46.04	1.15	8.94	0.60	89.30	60.45	3654.76	47.74	0.35
cluster3	LSTM	12	TBR_2	0.00	0.00	0.00	85.83	14.17	0.00	106.71	11387.22	103.33	2.16
cluster3	LSTM	12	TBR_1	0.00	0.00	0.00	84.41	15.59	0.00	96.10	9234.65	92.73	1.50
cluster3	LSTM	12	TIR	43.32	54.17	2.07	0.37	0.07	97.49	47.99	2303.22	38.64	0.36
cluster3	LSTM	12	TAR_1	60.95	34.26	0.00	4.80	0.00	95.21	45.21	2043.53	37.27	0.17
cluster3	LSTM	12	TAR_2	15.88	50.27	0.00	33.85	0.00	66.15	107.01	11450.21	97.50	0.33
cluster3	LSTM	16	ALL	40.37	47.04	0.87	11.02	0.70	87.41	63.73	4061.98	50.86	0.37
cluster3	LSTM	16	TBR_2	0.00	0.00	0.00	85.29	14.71	0.00	114.03	13002.55	112.33	2.34
cluster3	LSTM	16	TBR_1	0.00	0.00	0.00	81.33	18.67	0.00	103.62	10737.23	101.84	1.65
cluster3	LSTM	16	TIR	41.43	56.56	1.57	0.36	0.08	97.99	49.75	2474.69	40.58	0.38
cluster3	LSTM	16	TAR_1	59.25	34.52	0.00	6.23	0.00	93.77	44.90	2015.75	38.24	0.18
cluster3	LSTM	16	TAR_2	5.02	46.96	0.00	48.02	0.00	51.98	116.45	13561.50	108.98	0.37
cluster3	CNN	2	ALL	77.85	18.48	0.15	3.50	0.01	96.33	28.33	802.44	20.60	0.14
cluster3	CNN	2	TBR_2	29.22	0.00	0.00	70.68	0.10	29.22	33.59	1128.21	29.94	0.63
cluster3	CNN	2	TBR_1	17.60	0.00	0.00	82.12	0.28	17.60	30.52	931.38	25.72	0.42
cluster3	CNN	2	TIR	74.42	25.05	0.23	0.31	0.00	99.47	25.56	653.51	18.60	0.15
cluster3	CNN	2	TAR_1	87.12	12.24	0.07	0.55	0.01	99.36	29.17	850.93	20.90	0.10
cluster3	CNN	2	TAR_2	89.41	9.19	0.02	1.38	0.00	98.60	35.98	1294.51	26.91	0.09

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	CNN	4	ALL	63.25	30.73	0.52	5.40	0.09	93.98	41.10	1689.05	30.53	0.21
cluster3	CNN	4	TBR_2	1.02	0.00	0.00	97.41	1.57	1.02	57.32	3285.03	52.13	1.09
cluster3	CNN	4	TBR_1	0.88	0.00	0.00	96.72	2.40	0.88	52.50	2756.04	46.34	0.75
cluster3	CNN	4	TIR	61.23	37.45	0.88	0.42	0.02	98.68	33.57	1126.79	25.02	0.21
cluster3	CNN	4	TAR_1	74.73	23.31	0.11	1.85	0.00	98.04	40.16	1613.08	30.00	0.14
cluster3	CNN	4	TAR_2	64.94	26.97	0.03	8.07	0.00	91.91	62.98	3966.49	50.69	0.17
cluster3	CNN	6	ALL	53.31	39.11	1.08	6.22	0.27	92.42	49.66	2466.42	38.08	0.28
cluster3	CNN	6	TBR_2	0.00	0.00	0.00	93.94	6.06	0.00	82.81	6858.21	77.41	1.61
cluster3	CNN	6	TBR_1	0.00	0.00	0.00	93.02	6.98	0.00	75.02	5627.88	69.28	1.12
cluster3	CNN	6	TIR	49.30	48.37	1.88	0.41	0.04	97.67	42.05	1767.86	32.55	0.29
cluster3	CNN	6	TAR_1	69.17	28.09	0.13	2.61	0.00	97.26	42.70	1823.01	33.11	0.16
cluster3	CNN	6	TAR_2	51.08	34.78	0.01	14.13	0.00	85.86	77.16	5954.18	63.70	0.21
cluster3	CNN	8	ALL	47.87	43.13	1.21	7.36	0.44	91.00	55.34	3062.63	43.06	0.31
cluster3	CNN	8	TBR_2	0.00	0.00	0.00	89.21	10.79	0.00	95.66	9150.87	90.76	1.89
cluster3	CNN	8	TBR_1	0.00	0.00	0.00	88.95	11.05	0.00	85.76	7355.27	80.76	1.31
cluster3	CNN	8	TIR	45.67	51.72	2.16	0.39	0.05	97.39	45.28	2050.37	35.75	0.32
cluster3	CNN	8	TAR_1	64.85	31.49	0.05	3.62	0.00	96.34	44.55	1984.38	35.48	0.17
cluster3	CNN	8	TAR_2	33.47	44.22	0.00	22.31	0.00	77.69	92.43	8543.52	80.40	0.27
cluster3	CNN	12	ALL	42.30	46.23	1.00	9.87	0.60	88.53	61.56	3789.29	48.69	0.35
cluster3	CNN	12	TBR_2	0.00	0.00	0.00	86.38	13.62	0.00	108.79	11834.91	106.05	2.21
cluster3	CNN	12	TBR_1	0.00	0.00	0.00	84.43	15.57	0.00	97.90	9583.44	95.12	1.54
cluster3	CNN	12	TIR	43.89	53.86	1.81	0.37	0.07	97.75	47.71	2276.03	38.38	0.36
cluster3	CNN	12	TAR_1	58.56	35.95	0.00	5.49	0.00	94.51	45.97	2113.48	38.56	0.18
cluster3	CNN	12	TAR_2	11.14	49.27	0.00	39.58	0.00	60.41	111.22	12370.89	102.52	0.34
cluster3	CNN	16	ALL	39.81	46.35	0.55	12.72	0.56	86.16	64.28	4131.61	51.14	0.37
cluster3	CNN	16	TBR_2	0.00	0.00	0.00	87.83	12.17	0.00	112.34	12619.50	110.99	2.32
cluster3	CNN	16	TBR_1	0.00	0.00	0.00	85.07	14.93	0.00	101.47	10295.78	100.03	1.62
cluster3	CNN	16	TIR	44.33	54.24	1.00	0.37	0.07	98.57	47.20	2227.54	38.20	0.36
cluster3	CNN	16	TAR_1	52.92	39.73	0.00	7.36	0.00	92.65	47.77	2281.64	41.64	0.19
cluster3	CNN	16	TAR_2	2.08	39.99	0.00	57.94	0.00	42.07	121.34	14724.30	114.49	0.39
cluster4	Linear	2	ALL	89.08	9.50	0.01	1.41	0.00	98.58	17.58	309.05	12.67	0.10
cluster4	Linear	2	TBR_2	91.05	0.00	0.00	8.91	0.04	91.05	15.67	245.40	11.95	0.24
cluster4	Linear	2	TBR_1	71.15	0.00	0.00	28.84	0.01	71.15	15.41	237.52	11.74	0.19
cluster4	Linear	2	TIR	87.76	12.09	0.01	0.14	0.00	99.85	16.50	272.23	11.82	0.10
cluster4	Linear	2	TAR_1	95.05	4.86	0.01	0.09	0.01	99.91	19.65	386.09	14.29	0.07
cluster4	Linear	2	TAR_2	97.49	2.35	0.00	0.16	0.00	99.84	24.00	575.82	18.79	0.07
cluster4	Linear	4	ALL	67.89	26.69	0.15	5.22	0.05	94.58	31.29	978.78	23.39	0.18

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	Linear	4	TBR_2	15.02	0.00	0.00	84.24	0.74	15.02	37.49	1405.40	32.33	0.65
cluster4	Linear	4	TBR_1	9.28	0.00	0.00	90.03	0.69	9.28	35.97	1294.00	30.41	0.49
cluster4	Linear	4	TIR	68.65	30.73	0.21	0.41	0.00	99.38	26.72	714.10	20.00	0.17
cluster4	Linear	4	TAR_1	78.33	20.44	0.01	1.17	0.05	98.77	36.40	1324.77	27.75	0.13
cluster4	Linear	4	TAR_2	70.20	23.50	0.00	6.30	0.00	93.70	54.46	2966.08	45.96	0.16
cluster4	Linear	6	ALL	56.05	36.98	0.25	6.62	0.11	93.03	39.88	1590.53	30.64	0.24
cluster4	Linear	6	TBR_2	1.01	0.00	0.00	97.26	1.72	1.01	55.65	3096.63	50.83	1.02
cluster4	Linear	6	TBR_1	0.93	0.00	0.00	97.12	1.96	0.93	52.23	2728.02	47.01	0.76
cluster4	Linear	6	TIR	59.15	40.00	0.36	0.48	0.01	99.15	31.59	998.04	24.43	0.22
cluster4	Linear	6	TAR_1	63.12	34.18	0.00	2.68	0.02	97.30	46.68	2179.47	37.86	0.18
cluster4	Linear	6	TAR_2	36.04	43.89	0.00	20.07	0.00	79.93	80.10	6415.89	71.71	0.25
cluster4	Linear	8	ALL	49.29	42.66	0.27	7.63	0.15	91.95	45.31	2053.10	35.48	0.28
cluster4	Linear	8	TBR_2	0.05	0.00	0.00	97.10	2.85	0.05	70.18	4924.96	66.38	1.34
cluster4	Linear	8	TBR_1	0.10	0.00	0.00	97.08	2.82	0.10	64.23	4124.89	60.23	0.98
cluster4	Linear	8	TIR	54.46	44.65	0.39	0.48	0.02	99.11	34.43	1185.64	27.23	0.25
cluster4	Linear	8	TAR_1	51.27	44.62	0.00	4.10	0.00	95.89	52.26	2731.56	44.34	0.21
cluster4	Linear	8	TAR_2	15.38	48.96	0.00	35.65	0.00	64.34	97.44	9495.16	90.27	0.32
cluster4	Linear	12	ALL	43.18	46.79	0.11	9.82	0.11	89.97	50.89	2589.53	40.46	0.32
cluster4	Linear	12	TBR_2	0.00	0.00	0.00	98.17	1.83	0.00	84.63	7162.39	82.82	1.67
cluster4	Linear	12	TBR_1	0.00	0.00	0.00	97.89	2.10	0.00	75.92	5763.47	73.95	1.20
cluster4	Linear	12	TIR	52.66	46.68	0.15	0.49	0.01	99.34	35.83	1283.70	28.93	0.27
cluster4	Linear	12	TAR_1	31.50	61.78	0.00	6.71	0.00	93.28	59.18	3502.46	53.67	0.25
cluster4	Linear	12	TAR_2	1.07	28.60	0.00	70.33	0.00	29.67	119.10	14185.39	114.32	0.40
cluster4	Linear	16	ALL	40.90	47.83	0.01	11.22	0.03	88.73	53.18	2827.62	42.45	0.34
cluster4	Linear	16	TBR_2	0.00	0.00	0.00	99.25	0.75	0.00	90.56	8200.50	89.63	1.81
cluster4	Linear	16	TBR_1	0.00	0.00	0.00	99.37	0.63	0.00	80.41	6465.17	79.41	1.29
cluster4	Linear	16	TIR	53.12	46.36	0.02	0.50	0.00	99.48	35.79	1280.59	29.16	0.28
cluster4	Linear	16	TAR_1	19.67	72.39	0.00	7.94	0.00	92.06	62.56	3913.94	58.48	0.28
cluster4	Linear	16	TAR_2	0.01	6.67	0.00	93.32	0.00	6.68	128.95	16627.65	125.32	0.44
cluster4	LSTM	2	ALL	89.49	8.61	0.00	1.90	0.00	98.10	16.93	286.77	12.14	0.09
cluster4	LSTM	2	TBR_2	77.93	0.00	0.00	22.05	0.02	77.93	17.67	312.27	14.03	0.28
cluster4	LSTM	2	TBR_1	62.06	0.00	0.00	37.93	0.01	62.06	16.56	274.11	12.80	0.21
cluster4	LSTM	2	TIR	88.98	10.86	0.01	0.16	0.00	99.84	15.69	246.20	11.21	0.09
cluster4	LSTM	2	TAR_1	95.25	4.67	0.00	0.08	0.00	99.92	19.20	368.49	13.84	0.07
cluster4	LSTM	2	TAR_2	97.51	2.36	0.00	0.13	0.00	99.87	22.83	521.16	17.25	0.06
cluster4	LSTM	4	ALL	69.67	24.93	0.13	5.24	0.03	94.60	30.28	917.05	22.40	0.17
cluster4	LSTM	4	TBR_2	15.58	0.00	0.00	83.77	0.65	15.58	40.40	1632.28	35.70	0.72

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	4	TBR_1	8.72	0.00	0.00	90.68	0.61	8.72	36.72	1348.61	31.75	0.51
cluster4	LSTM	4	TIR	70.80	28.59	0.19	0.42	0.00	99.39	25.69	660.14	19.19	0.16
cluster4	LSTM	4	TAR_1	78.99	19.87	0.01	1.11	0.01	98.86	35.47	1257.84	26.31	0.13
cluster4	LSTM	4	TAR_2	73.75	20.03	0.00	6.22	0.00	93.78	51.64	2666.81	41.49	0.15
cluster4	LSTM	6	ALL	57.64	35.44	0.21	6.62	0.09	93.08	38.83	1507.59	29.54	0.23
cluster4	LSTM	6	TBR_2	0.90	0.00	0.00	97.61	1.49	0.90	56.62	3206.24	52.35	1.06
cluster4	LSTM	6	TBR_1	0.49	0.00	0.00	97.81	1.69	0.49	51.34	2636.07	46.69	0.76
cluster4	LSTM	6	TIR	60.58	38.62	0.31	0.49	0.01	99.20	30.40	924.40	23.58	0.21
cluster4	LSTM	6	TAR_1	64.63	32.74	0.00	2.63	0.00	97.37	45.94	2110.91	36.28	0.17
cluster4	LSTM	6	TAR_2	42.41	37.87	0.00	19.71	0.00	80.28	78.18	6112.02	68.20	0.24
cluster4	LSTM	8	ALL	50.81	41.18	0.23	7.67	0.12	91.99	44.38	1969.36	34.32	0.27
cluster4	LSTM	8	TBR_2	0.00	0.00	0.00	97.81	2.19	0.00	68.22	4654.20	64.64	1.30
cluster4	LSTM	8	TBR_1	0.02	0.00	0.00	97.73	2.25	0.02	60.87	3704.78	56.99	0.92
cluster4	LSTM	8	TIR	56.13	43.04	0.33	0.49	0.01	99.17	32.77	1073.70	25.95	0.23
cluster4	LSTM	8	TAR_1	51.90	44.08	0.00	4.02	0.00	95.98	52.92	2801.01	44.07	0.21
cluster4	LSTM	8	TAR_2	20.36	43.40	0.00	36.25	0.00	63.76	97.28	9463.12	88.88	0.31
cluster4	LSTM	12	ALL	44.17	46.16	0.17	9.37	0.13	90.33	50.16	2516.18	39.60	0.31
cluster4	LSTM	12	TBR_2	0.00	0.00	0.00	97.72	2.28	0.00	82.54	6812.59	80.50	1.62
cluster4	LSTM	12	TBR_1	0.00	0.00	0.00	97.52	2.48	0.00	73.54	5408.67	71.28	1.16
cluster4	LSTM	12	TIR	52.77	46.48	0.24	0.49	0.01	99.25	35.29	1245.41	28.50	0.27
cluster4	LSTM	12	TAR_1	35.05	58.88	0.00	6.07	0.00	93.93	58.92	3471.55	52.38	0.25
cluster4	LSTM	12	TAR_2	4.58	31.34	0.00	64.08	0.00	35.92	117.02	13694.01	111.05	0.39
cluster4	LSTM	16	ALL	41.35	47.72	0.03	10.85	0.06	89.07	52.81	2788.68	42.09	0.34
cluster4	LSTM	16	TBR_2	0.00	0.00	0.00	99.01	0.99	0.00	90.07	8112.00	89.06	1.80
cluster4	LSTM	16	TBR_1	0.00	0.00	0.00	98.90	1.10	0.00	79.81	6369.26	78.64	1.27
cluster4	LSTM	16	TIR	52.76	46.70	0.04	0.50	0.01	99.46	35.80	1281.93	29.17	0.28
cluster4	LSTM	16	TAR_1	22.90	69.53	0.00	7.57	0.00	92.43	61.83	3822.95	57.28	0.27
cluster4	LSTM	16	TAR_2	0.00	12.22	0.00	87.78	0.00	12.22	127.64	16291.79	123.69	0.44
cluster4	CNN	2	ALL	77.55	18.23	0.06	4.15	0.01	95.78	24.67	608.47	18.10	0.14
cluster4	CNN	2	TBR_2	35.62	0.00	0.00	64.22	0.15	35.62	31.01	961.53	27.07	0.55
cluster4	CNN	2	TBR_1	22.37	0.00	0.00	77.40	0.22	22.37	28.10	789.68	23.59	0.38
cluster4	CNN	2	TIR	77.73	21.86	0.08	0.32	0.00	99.59	22.06	486.54	16.27	0.14
cluster4	CNN	2	TAR_1	87.17	12.33	0.01	0.48	0.00	99.50	28.04	786.18	20.33	0.10
cluster4	CNN	2	TAR_2	87.51	10.56	0.00	1.92	0.00	98.07	37.18	1382.62	28.69	0.10
cluster4	CNN	4	ALL	62.52	31.13	0.20	6.09	0.06	93.65	35.10	1231.84	26.39	0.21
cluster4	CNN	4	TBR_2	1.87	0.00	0.00	96.99	1.15	1.87	49.66	2465.95	45.40	0.92
cluster4	CNN	4	TBR_1	1.24	0.00	0.00	97.59	1.17	1.24	45.23	2045.36	40.50	0.66

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	4	TIR	64.36	34.87	0.29	0.48	0.01	99.23	28.67	821.73	21.89	0.19
cluster4	CNN	4	TAR_1	71.63	26.55	0.01	1.80	0.00	98.18	41.18	1695.44	31.42	0.15
cluster4	CNN	4	TAR_2	58.36	29.37	0.00	12.27	0.00	87.73	65.29	4263.44	54.45	0.19
cluster4	CNN	6	ALL	53.93	38.53	0.22	7.21	0.11	92.46	41.98	1762.59	32.15	0.25
cluster4	CNN	6	TBR_2	0.00	0.00	0.00	98.21	1.79	0.00	62.27	3877.79	58.56	1.18
cluster4	CNN	6	TBR_1	0.01	0.00	0.00	97.95	2.05	0.01	55.97	3132.29	51.65	0.84
cluster4	CNN	6	TIR	58.26	40.92	0.32	0.49	0.01	99.18	31.65	1001.65	24.78	0.22
cluster4	CNN	6	TAR_1	57.51	39.11	0.00	3.38	0.00	96.62	50.38	2538.00	40.94	0.19
cluster4	CNN	6	TAR_2	30.35	41.09	0.00	28.57	0.00	71.44	89.06	7931.06	79.58	0.28
cluster4	CNN	8	ALL	48.16	43.51	0.27	7.93	0.15	91.67	46.29	2143.18	36.26	0.29
cluster4	CNN	8	TBR_2	0.00	0.00	0.00	97.36	2.64	0.00	74.58	5562.34	71.56	1.44
cluster4	CNN	8	TBR_1	0.00	0.00	0.00	97.24	2.76	0.00	66.93	4479.51	63.53	1.03
cluster4	CNN	8	TIR	53.10	46.02	0.38	0.48	0.02	99.12	34.84	1213.88	27.85	0.26
cluster4	CNN	8	TAR_1	50.20	45.53	0.00	4.28	0.00	95.73	52.98	2806.48	44.54	0.21
cluster4	CNN	8	TAR_2	16.24	42.75	0.00	41.01	0.00	58.99	101.24	10250.32	93.28	0.33
cluster4	CNN	12	ALL	43.16	46.89	0.12	9.71	0.12	90.05	51.03	2604.24	40.53	0.32
cluster4	CNN	12	TBR_2	0.00	0.00	0.00	98.12	1.88	0.00	85.57	7322.23	83.80	1.69
cluster4	CNN	12	TBR_1	0.00	0.00	0.00	97.52	2.48	0.00	76.34	5827.85	74.30	1.20
cluster4	CNN	12	TIR	51.80	47.53	0.17	0.49	0.01	99.33	36.16	1307.38	29.30	0.28
cluster4	CNN	12	TAR_1	33.99	59.56	0.00	6.45	0.00	93.55	58.80	3457.88	52.72	0.25
cluster4	CNN	12	TAR_2	2.08	28.57	0.00	69.35	0.00	30.65	119.47	14272.48	114.19	0.40
cluster4	CNN	16	ALL	40.88	48.03	0.02	11.01	0.05	88.91	53.19	2829.33	42.57	0.34
cluster4	CNN	16	TBR_2	0.00	0.00	0.00	98.98	1.02	0.00	92.42	8540.89	91.52	1.84
cluster4	CNN	16	TBR_1	0.00	0.00	0.00	98.97	1.03	0.00	82.13	6744.59	81.11	1.31
cluster4	CNN	16	TIR	51.98	47.49	0.03	0.50	0.01	99.47	36.75	1350.67	29.94	0.29
cluster4	CNN	16	TAR_1	23.27	69.04	0.00	7.70	0.00	92.31	60.87	3705.75	56.49	0.27
cluster4	CNN	16	TAR_2	0.06	9.57	0.00	90.37	0.00	9.63	127.63	16289.50	123.80	0.44
cluster5	Linear	2	ALL	88.80	9.88	0.01	1.32	0.00	98.68	19.25	370.41	13.99	0.10
cluster5	Linear	2	TBR_2	93.34	0.00	0.00	6.66	0.00	93.34	13.94	194.27	11.65	0.24
cluster5	Linear	2	TBR_1	72.44	0.00	0.00	27.55	0.00	72.44	14.40	207.25	11.39	0.19
cluster5	Linear	2	TIR	86.15	13.70	0.01	0.13	0.00	99.85	17.72	314.06	12.75	0.10
cluster5	Linear	2	TAR_1	94.19	5.68	0.01	0.12	0.00	99.87	20.85	434.88	15.23	0.07
cluster5	Linear	2	TAR_2	97.01	2.85	0.00	0.14	0.00	99.86	25.14	632.10	19.70	0.07
cluster5	Linear	4	ALL	65.37	28.54	0.25	5.78	0.05	93.91	35.72	1276.08	26.77	0.19
cluster5	Linear	4	TBR_2	19.68	0.00	0.00	79.90	0.42	19.68	37.37	1396.23	32.81	0.69
cluster5	Linear	4	TBR_1	7.33	0.00	0.00	91.95	0.72	7.33	36.64	1342.84	31.32	0.51
cluster5	Linear	4	TIR	64.20	34.98	0.41	0.40	0.00	99.18	29.94	896.46	22.46	0.19

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	Linear	4	TAR_1	77.58	20.81	0.03	1.51	0.07	98.39	37.62	1415.47	28.27	0.13
cluster5	Linear	4	TAR_2	68.16	25.01	0.00	6.82	0.01	93.17	56.94	3242.32	47.23	0.16
cluster5	Linear	6	ALL	52.61	38.88	0.52	7.82	0.16	91.49	46.44	2156.48	35.76	0.26
cluster5	Linear	6	TBR_2	0.83	0.00	0.00	96.08	3.09	0.83	61.54	3787.65	55.60	1.17
cluster5	Linear	6	TBR_1	0.64	0.00	0.00	96.40	2.96	0.64	56.49	3191.04	50.80	0.83
cluster5	Linear	6	TIR	53.46	45.18	0.87	0.48	0.02	98.64	36.52	1333.43	28.31	0.25
cluster5	Linear	6	TAR_1	65.77	31.08	0.02	3.12	0.02	96.85	46.16	2130.58	36.37	0.17
cluster5	Linear	6	TAR_2	37.96	41.99	0.00	20.04	0.01	79.95	82.61	6824.87	72.61	0.25
cluster5	Linear	8	ALL	45.68	43.63	0.49	9.96	0.24	89.31	53.32	2843.21	41.72	0.30
cluster5	Linear	8	TBR_2	0.06	0.00	0.00	95.17	4.77	0.06	75.85	5753.54	71.08	1.50
cluster5	Linear	8	TBR_1	0.07	0.00	0.00	95.49	4.44	0.07	68.13	4641.21	63.63	1.04
cluster5	Linear	8	TIR	50.93	47.75	0.82	0.47	0.03	98.68	38.37	1471.93	30.32	0.27
cluster5	Linear	8	TAR_1	53.49	41.45	0.00	5.06	0.00	94.94	52.48	2754.63	43.80	0.20
cluster5	Linear	8	TAR_2	14.89	47.15	0.00	37.95	0.00	62.04	103.39	10689.51	95.43	0.33
cluster5	Linear	12	ALL	39.58	46.67	0.29	13.19	0.27	86.25	59.67	3560.95	47.61	0.35
cluster5	Linear	12	TBR_2	0.00	0.00	0.00	95.51	4.49	0.00	92.66	8586.45	90.41	1.92
cluster5	Linear	12	TBR_1	0.00	0.00	0.00	94.72	5.27	0.00	82.82	6859.03	80.61	1.31
cluster5	Linear	12	TIR	48.45	50.56	0.49	0.47	0.03	99.01	40.98	1679.70	33.07	0.31
cluster5	Linear	12	TAR_1	40.58	51.79	0.00	7.63	0.00	92.37	55.99	3135.21	49.43	0.23
cluster5	Linear	12	TAR_2	1.88	32.45	0.00	65.67	0.00	34.33	121.17	14683.25	115.56	0.40
cluster5	Linear	16	ALL	37.48	46.54	0.07	15.75	0.15	84.02	62.09	3855.49	49.76	0.37
cluster5	Linear	16	TBR_2	0.00	0.00	0.00	97.97	2.03	0.00	99.59	9918.05	98.54	2.09
cluster5	Linear	16	TBR_1	0.00	0.00	0.00	97.00	3.00	0.00	88.33	7802.83	87.23	1.42
cluster5	Linear	16	TIR	49.40	49.99	0.12	0.47	0.02	99.39	40.87	1670.51	33.04	0.32
cluster5	Linear	16	TAR_1	31.09	59.48	0.00	9.43	0.00	90.57	58.13	3378.52	53.18	0.25
cluster5	Linear	16	TAR_2	0.08	12.65	0.00	87.27	0.00	12.73	129.02	16646.23	124.54	0.43
cluster5	LSTM	2	ALL	89.27	8.92	0.00	1.80	0.00	98.19	18.54	343.67	13.40	0.09
cluster5	LSTM	2	TBR_2	77.80	0.00	0.00	22.20	0.00	77.80	18.33	336.03	15.18	0.32
cluster5	LSTM	2	TBR_1	63.98	0.00	0.00	36.02	0.00	63.98	15.64	244.59	12.18	0.20
cluster5	LSTM	2	TIR	87.60	12.25	0.01	0.15	0.00	99.85	16.74	280.24	12.02	0.10
cluster5	LSTM	2	TAR_1	94.61	5.29	0.00	0.10	0.00	99.90	20.21	408.49	14.72	0.07
cluster5	LSTM	2	TAR_2	96.94	2.93	0.00	0.14	0.00	99.87	24.60	605.29	18.81	0.07
cluster5	LSTM	4	ALL	67.83	26.23	0.22	5.69	0.03	94.06	34.61	1197.78	25.53	0.18
cluster5	LSTM	4	TBR_2	17.00	0.00	0.00	82.68	0.32	17.00	42.67	1820.32	38.36	0.81
cluster5	LSTM	4	TBR_1	10.41	0.00	0.00	89.07	0.51	10.41	36.88	1359.78	32.07	0.52
cluster5	LSTM	4	TIR	68.07	31.16	0.35	0.42	0.00	99.23	28.14	791.85	20.84	0.17
cluster5	LSTM	4	TAR_1	76.89	21.53	0.05	1.51	0.02	98.42	37.64	1416.52	28.08	0.13

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	4	TAR_2	70.79	22.39	0.02	6.81	0.00	93.18	54.92	3016.25	43.86	0.15
cluster5	LSTM	6	ALL	54.59	36.92	0.46	7.92	0.12	91.51	45.37	2058.66	34.46	0.25
cluster5	LSTM	6	TBR_2	0.71	0.00	0.00	96.99	2.30	0.71	64.83	4203.15	59.92	1.27
cluster5	LSTM	6	TBR_1	0.53	0.00	0.00	97.19	2.28	0.53	55.20	3047.31	50.26	0.82
cluster5	LSTM	6	TIR	56.76	41.98	0.76	0.48	0.01	98.74	34.25	1173.03	26.37	0.23
cluster5	LSTM	6	TAR_1	64.38	32.42	0.02	3.17	0.00	96.80	46.71	2182.23	36.61	0.17
cluster5	LSTM	6	TAR_2	42.15	37.39	0.00	20.47	0.00	79.54	81.68	6671.43	70.18	0.24
cluster5	LSTM	8	ALL	47.34	42.29	0.55	9.59	0.22	89.63	52.19	2723.50	40.48	0.30
cluster5	LSTM	8	TBR_2	0.00	0.00	0.00	95.64	4.36	0.00	79.75	6359.88	75.85	1.61
cluster5	LSTM	8	TBR_1	0.00	0.00	0.00	95.83	4.17	0.00	67.87	4606.26	63.71	1.04
cluster5	LSTM	8	TIR	51.73	46.85	0.93	0.47	0.02	98.58	37.78	1427.04	29.75	0.27
cluster5	LSTM	8	TAR_1	55.25	40.08	0.01	4.66	0.00	95.33	51.47	2649.64	42.12	0.20
cluster5	LSTM	8	TAR_2	22.70	42.34	0.00	34.96	0.00	65.04	99.74	9947.83	90.02	0.31
cluster5	LSTM	12	ALL	40.34	46.23	0.36	12.80	0.26	86.57	59.12	3495.52	46.85	0.35
cluster5	LSTM	12	TBR_2	0.00	0.00	0.00	95.75	4.25	0.00	93.04	8656.11	90.89	1.93
cluster5	LSTM	12	TBR_1	0.00	0.00	0.00	94.84	5.16	0.00	80.49	6477.88	78.06	1.27
cluster5	LSTM	12	TIR	49.31	49.59	0.61	0.47	0.02	98.90	39.98	1598.68	32.22	0.30
cluster5	LSTM	12	TAR_1	40.81	51.91	0.00	7.28	0.00	92.72	56.45	3186.19	49.31	0.23
cluster5	LSTM	12	TAR_2	3.95	33.59	0.00	62.45	0.00	37.54	120.47	14512.57	114.25	0.40
cluster5	LSTM	16	ALL	37.83	46.77	0.15	15.04	0.20	84.60	61.85	3825.40	49.41	0.36
cluster5	LSTM	16	TBR_2	0.00	0.00	0.00	97.13	2.87	0.00	99.18	9836.87	98.03	2.09
cluster5	LSTM	16	TBR_1	0.00	0.00	0.00	95.86	4.14	0.00	86.63	7505.49	85.20	1.39
cluster5	LSTM	16	TIR	49.55	49.70	0.25	0.47	0.02	99.25	40.65	1652.76	32.89	0.31
cluster5	LSTM	16	TAR_1	32.02	59.14	0.00	8.84	0.00	91.16	58.36	3405.47	52.84	0.24
cluster5	LSTM	16	TAR_2	0.20	17.85	0.00	81.95	0.00	18.05	128.44	16496.52	123.64	0.43
cluster5	CNN	2	ALL	76.85	18.87	0.07	4.21	0.01	95.72	27.69	766.48	20.23	0.14
cluster5	CNN	2	TBR_2	39.37	0.00	0.00	60.59	0.04	39.37	30.50	930.47	27.10	0.57
cluster5	CNN	2	TBR_1	25.68	0.00	0.00	74.26	0.06	25.68	26.44	699.06	22.41	0.37
cluster5	CNN	2	TIR	76.27	23.31	0.10	0.32	0.00	99.58	23.49	551.68	17.20	0.14
cluster5	CNN	2	TAR_1	84.71	14.53	0.02	0.74	0.01	99.24	30.54	932.58	22.33	0.11
cluster5	CNN	2	TAR_2	84.32	13.19	0.00	2.48	0.00	97.51	40.84	1667.75	31.78	0.11
cluster5	CNN	4	ALL	59.54	32.98	0.37	7.05	0.07	92.52	40.71	1657.40	30.63	0.22
cluster5	CNN	4	TBR_2	0.00	0.00	0.00	98.96	1.04	0.00	54.83	3006.34	50.78	1.07
cluster5	CNN	4	TBR_1	0.64	0.00	0.00	98.00	1.36	0.64	47.39	2246.02	42.60	0.69
cluster5	CNN	4	TIR	60.16	38.75	0.60	0.48	0.01	98.91	32.19	1035.88	24.50	0.21
cluster5	CNN	4	TAR_1	70.66	26.96	0.04	2.34	0.00	97.62	42.54	1809.97	32.38	0.15
cluster5	CNN	4	TAR_2	55.75	31.19	0.00	13.06	0.00	86.94	69.06	4769.89	57.26	0.20

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	6	ALL	50.54	39.99	0.58	8.69	0.19	90.53	49.23	2423.38	37.77	0.28
cluster5	CNN	6	TBR_2	0.00	0.00	0.00	96.04	3.96	0.00	72.59	5269.90	68.14	1.44
cluster5	CNN	6	TBR_1	0.00	0.00	0.00	96.47	3.53	0.00	61.96	3838.57	57.18	0.93
cluster5	CNN	6	TIR	53.29	45.23	0.97	0.48	0.02	98.52	36.79	1353.55	28.62	0.25
cluster5	CNN	6	TAR_1	60.16	35.94	0.02	3.88	0.00	96.10	49.41	2440.87	39.40	0.18
cluster5	CNN	6	TAR_2	33.08	39.71	0.00	27.21	0.00	72.79	90.81	8246.05	79.66	0.28
cluster5	CNN	8	ALL	44.45	44.50	0.63	10.14	0.28	88.95	54.54	2974.96	42.88	0.32
cluster5	CNN	8	TBR_2	0.00	0.00	0.00	94.99	5.01	0.00	85.27	7270.62	81.77	1.73
cluster5	CNN	8	TBR_1	0.00	0.00	0.00	94.84	5.16	0.00	73.78	5443.18	70.01	1.14
cluster5	CNN	8	TIR	48.05	50.38	1.07	0.46	0.03	98.43	40.53	1642.64	32.40	0.30
cluster5	CNN	8	TAR_1	54.20	40.66	0.00	5.14	0.00	94.86	51.24	2625.98	42.28	0.20
cluster5	CNN	8	TAR_2	17.99	42.00	0.00	40.02	0.00	59.99	104.31	10881.11	95.19	0.33
cluster5	CNN	12	ALL	39.31	46.32	0.24	13.93	0.20	85.63	60.22	3625.85	47.78	0.35
cluster5	CNN	12	TBR_2	0.00	0.00	0.00	96.92	3.08	0.00	93.38	8719.88	91.74	1.95
cluster5	CNN	12	TBR_1	0.00	0.00	0.00	96.00	4.00	0.00	81.31	6611.22	79.42	1.29
cluster5	CNN	12	TIR	50.32	48.78	0.41	0.48	0.02	99.10	39.21	1537.18	31.69	0.30
cluster5	CNN	12	TAR_1	35.28	56.68	0.00	8.04	0.00	91.96	58.30	3399.37	51.95	0.24
cluster5	CNN	12	TAR_2	2.09	26.19	0.00	71.72	0.00	28.28	124.99	15622.09	119.37	0.41
cluster5	CNN	16	ALL	37.45	46.64	0.11	15.65	0.16	84.09	62.21	3869.90	49.77	0.37
cluster5	CNN	16	TBR_2	0.00	0.00	0.00	97.71	2.29	0.00	100.29	10057.44	99.34	2.11
cluster5	CNN	16	TBR_1	0.00	0.00	0.00	96.80	3.20	0.00	87.59	7672.12	86.48	1.41
cluster5	CNN	16	TIR	49.91	49.42	0.18	0.48	0.02	99.33	40.46	1636.96	32.73	0.31
cluster5	CNN	16	TAR_1	29.80	60.93	0.00	9.27	0.00	90.73	58.79	3455.80	53.76	0.25
cluster5	CNN	16	TAR_2	0.14	13.14	0.00	86.72	0.00	13.28	129.75	16834.38	125.20	0.43

Appendix E

Absolute difference between group-based and general prediction models performance in the different BGL ranges

Table E.1 presents the absolute difference between the performance results for the group-based prediction models and the general prediction models. It is important to note that from the outcome of this comparison for the percentage of measurements in the zone 'A + B', which is a maximization metric, positive values indicate that the group-based prediction models perform better, negative values indicate worse performance, and zero means equal performance between both types of models. The effect of minimization metrics (RMSE, MSE, MAE, and MAPE) is reversed, where positive values reflect worse performance for group-based models, negative values indicate better performance, and zero means equal results. Therefore, the tables generated from this subtraction process are formatted for a more explicit comparison. To improve clarity, the cells corresponding to these key metrics, particularly 'A + B' and all non-clinical metrics, are color-coded: green represents better results for group-based models, red represents worse results, and gray indicates equal performance for both model types.

Table E.1: Absolute difference between group-based prediction models and general prediction models performance in the different BGL ranges assessed via both clinical and non-clinical metrics for all clusters. Green: better for group-based models, red: worse, gray: equal.

Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	2	ALL	-1.94	1.24	-0.06	0.76	0.00	-0.70	0.45	25.02	0.62	0.00
cluster0	CNN	2	TBR_2	-12.44	0.00	0.00	12.46	-0.02	-12.44	0.47	29.54	0.84	0.00
cluster0	CNN	2	TBR_1	-6.05	0.00	0.00	6.12	-0.07	-6.05	0.24	13.78	0.92	0.01
cluster0	CNN	2	TIR	-1.61	1.66	-0.07	0.04	0.00	0.05	0.28	13.54	0.52	0.00
cluster0	CNN	2	TAR_1	-0.90	0.84	-0.06	0.12	0.00	-0.06	1.01	62.67	0.79	0.00
cluster0	CNN	2	TAR_2	-1.37	0.74	-0.03	0.66	0.00	-0.63	0.77	60.71	1.17	0.01
cluster0	CNN	4	ALL	-2.85	2.44	-0.13	0.55	-0.02	-0.41	0.27	21.76	0.97	0.01
cluster0	CNN	4	TBR_2	-1.20	0.00	0.00	1.41	-0.21	-1.20	-0.72	-76.21	-0.06	-0.02
cluster0	CNN	4	TBR_1	-0.84	0.00	0.00	1.16	-0.32	-0.84	0.64	62.57	1.63	0.03
cluster0	CNN	4	TIR	-4.04	4.12	-0.14	0.06	0.00	0.08	1.09	71.17	1.61	0.01
cluster0	CNN	4	TAR_1	0.26	-0.17	-0.14	0.04	0.00	0.09	-0.18	-15.99	-0.17	0.00
cluster0	CNN	4	TAR_2	-2.10	0.35	-0.08	1.82	0.00	-1.75	-0.22	-29.10	0.58	0.00
cluster0	CNN	6	ALL	-1.21	0.47	-0.45	1.29	-0.11	-0.74	-0.11	-10.62	0.37	0.00
cluster0	CNN	6	TBR_2	0.00	0.00	0.00	1.84	-1.84	0.00	-8.02	-1108.89	-6.74	-0.18
cluster0	CNN	6	TBR_1	0.00	0.00	0.00	2.03	-2.04	0.00	-5.63	-699.42	-4.33	-0.07
cluster0	CNN	6	TIR	2.06	-1.47	-0.63	0.05	-0.01	0.59	-2.75	-202.13	-1.63	-0.02
cluster0	CNN	6	TAR_1	-5.26	4.71	-0.22	0.78	0.00	-0.55	3.54	358.75	3.93	0.02
cluster0	CNN	6	TAR_2	-13.04	4.80	-0.08	8.32	0.00	-8.24	6.50	1172.10	9.89	0.04
cluster0	CNN	8	ALL	-0.13	-0.48	-0.63	1.39	-0.15	-0.61	-1.37	-150.04	-0.66	-0.02
cluster0	CNN	8	TBR_2	0.00	0.00	0.00	3.78	-3.78	0.00	-10.27	-1728.78	-8.67	-0.22
cluster0	CNN	8	TBR_1	0.00	0.00	0.00	2.84	-2.84	0.00	-6.94	-1053.25	-5.81	-0.10
cluster0	CNN	8	TIR	3.54	-2.65	-0.92	0.05	-0.01	0.89	-4.09	-343.05	-2.91	-0.03
cluster0	CNN	8	TAR_1	-5.03	4.41	-0.24	0.85	0.00	-0.62	3.55	364.27	3.81	0.02
cluster0	CNN	8	TAR_2	-12.70	3.43	-0.05	9.32	0.00	-9.27	4.71	949.81	8.90	0.04
cluster0	CNN	12	ALL	-0.57	-0.53	-0.83	2.18	-0.25	-1.10	-1.88	-229.06	-0.98	-0.02
cluster0	CNN	12	TBR_2	0.00	0.00	0.00	5.82	-5.82	0.00	-10.84	-2094.86	-9.54	-0.25
cluster0	CNN	12	TBR_1	0.00	0.00	0.00	4.63	-4.63	0.00	-7.79	-1340.23	-6.75	-0.11
cluster0	CNN	12	TIR	4.46	-3.21	-1.29	0.06	-0.02	1.25	-5.62	-481.67	-4.11	-0.04
cluster0	CNN	12	TAR_1	-9.95	8.58	-0.08	1.45	0.00	-1.37	5.37	592.62	6.29	0.03
cluster0	CNN	12	TAR_2	-11.96	-4.49	0.00	16.45	0.00	-16.45	3.63	886.13	8.76	0.04
cluster0	CNN	16	ALL	-0.47	-2.45	-0.84	4.29	-0.53	-2.92	-1.79	-227.22	-1.38	-0.03
cluster0	CNN	16	TBR_2	0.00	0.00	0.00	10.93	-10.93	0.00	-14.84	-3018.15	-13.49	-0.34
cluster0	CNN	16	TBR_1	0.00	0.00	0.00	9.71	-9.71	0.00	-11.92	-2138.91	-10.71	-0.17
cluster0	CNN	16	TIR	8.55	-7.24	-1.35	0.09	-0.05	1.31	-9.17	-775.96	-7.22	-0.07

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	16	TAR_1	-22.76	19.90	-0.01	2.88	0.00	-2.86	10.41	1201.29	12.45	0.06
cluster0	CNN	16	TAR_2	-6.09	-27.23	0.00	33.33	0.00	-33.32	7.03	1874.48	12.09	0.06
cluster0	LSTM	2	ALL	-1.30	0.96	-0.01	0.36	0.00	-0.34	0.36	13.65	0.44	0.00
cluster0	LSTM	2	TBR_2	-5.92	0.00	0.00	5.93	-0.01	-5.92	0.52	18.84	0.25	-0.01
cluster0	LSTM	2	TBR_1	-3.50	0.00	0.00	3.52	-0.02	-3.50	0.44	14.64	0.60	0.01
cluster0	LSTM	2	TIR	-1.33	1.32	-0.01	0.02	0.00	-0.01	0.53	18.32	0.59	0.00
cluster0	LSTM	2	TAR_1	-0.52	0.50	-0.01	0.03	0.00	-0.02	0.62	26.14	0.44	0.00
cluster0	LSTM	2	TAR_2	-0.39	0.37	-0.01	0.03	0.00	-0.02	-0.63	-30.63	-0.27	0.00
cluster0	LSTM	4	ALL	-1.53	1.13	-0.12	0.54	-0.01	-0.40	0.41	28.48	0.55	0.00
cluster0	LSTM	4	TBR_2	-3.23	0.00	0.00	3.30	-0.07	-3.23	-1.06	-89.88	-0.56	-0.03
cluster0	LSTM	4	TBR_1	-0.12	0.00	0.00	0.35	-0.23	-0.12	-1.38	-105.43	-0.62	-0.01
cluster0	LSTM	4	TIR	-1.38	1.47	-0.14	0.04	-0.01	0.09	0.28	16.01	0.50	0.00
cluster0	LSTM	4	TAR_1	-1.08	1.06	-0.12	0.14	0.00	-0.02	1.29	99.52	0.92	0.01
cluster0	LSTM	4	TAR_2	-2.00	0.46	-0.06	1.60	0.00	-1.54	1.04	109.85	1.21	0.01
cluster0	LSTM	6	ALL	-0.97	0.41	-0.36	0.97	-0.06	-0.56	0.03	2.52	0.32	-0.01
cluster0	LSTM	6	TBR_2	0.58	0.00	0.00	0.52	-1.11	0.58	-6.30	-778.22	-5.42	-0.14
cluster0	LSTM	6	TBR_1	0.41	0.00	0.00	0.88	-1.29	0.41	-5.15	-571.31	-4.10	-0.06
cluster0	LSTM	6	TIR	1.48	-1.05	-0.46	0.04	-0.01	0.43	-2.00	-140.18	-1.17	-0.01
cluster0	LSTM	6	TAR_1	-3.88	3.52	-0.25	0.59	0.00	-0.36	2.99	285.00	3.07	0.01
cluster0	LSTM	6	TAR_2	-9.67	4.18	-0.12	5.60	0.00	-5.49	5.53	867.51	7.54	0.04
cluster0	LSTM	8	ALL	-0.90	0.27	-0.56	1.33	-0.14	-0.63	-0.75	-78.13	-0.05	-0.01
cluster0	LSTM	8	TBR_2	-0.01	0.00	0.00	3.09	-3.08	-0.01	-9.10	-1406.17	-7.31	-0.19
cluster0	LSTM	8	TBR_1	0.00	0.00	0.00	2.72	-2.73	0.00	-6.10	-850.31	-4.56	-0.07
cluster0	LSTM	8	TIR	2.37	-1.62	-0.78	0.05	-0.01	0.75	-3.43	-270.58	-2.13	-0.02
cluster0	LSTM	8	TAR_1	-4.64	4.14	-0.26	0.76	0.00	-0.50	3.17	324.80	3.51	0.01
cluster0	LSTM	8	TAR_2	-13.81	5.33	-0.08	8.56	0.00	-8.48	5.96	1143.08	10.05	0.04
cluster0	LSTM	12	ALL	-0.60	-0.66	-0.85	2.38	-0.27	-1.26	-1.65	-196.18	-0.94	-0.02
cluster0	LSTM	12	TBR_2	0.00	0.00	0.00	5.53	-5.53	0.00	-12.06	-2267.27	-10.57	-0.27
cluster0	LSTM	12	TBR_1	0.00	0.00	0.00	5.13	-5.13	0.00	-8.95	-1498.42	-7.77	-0.12
cluster0	LSTM	12	TIR	5.36	-4.08	-1.31	0.06	-0.02	1.28	-6.41	-544.09	-4.79	-0.04
cluster0	LSTM	12	TAR_1	-11.71	10.21	-0.11	1.61	0.00	-1.50	6.48	711.34	7.51	0.04
cluster0	LSTM	12	TAR_2	-13.92	-3.80	0.00	17.72	0.00	-17.72	5.87	1396.01	11.11	0.05
cluster0	LSTM	16	ALL	-0.38	-1.82	-0.92	3.57	-0.46	-2.20	-2.09	-261.68	-1.33	-0.03
cluster0	LSTM	16	TBR_2	0.00	0.00	0.00	9.90	-9.90	0.00	-12.43	-2536.79	-10.95	-0.28
cluster0	LSTM	16	TBR_1	0.00	0.00	0.00	8.50	-8.50	0.00	-9.32	-1684.36	-8.02	-0.13
cluster0	LSTM	16	TIR	6.87	-5.43	-1.47	0.08	-0.04	1.44	-7.56	-656.14	-5.91	-0.06
cluster0	LSTM	16	TAR_1	-17.29	14.86	-0.01	2.44	0.00	-2.43	7.71	863.96	9.36	0.04

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	16	TAR_2	-7.70	-19.36	0.00	27.06	0.00	-27.06	4.73	1225.70	9.76	0.05
cluster0	Linear	2	ALL	-0.90	0.63	-0.03	0.30	-0.01	-0.27	-0.04	-1.71	0.38	0.00
cluster0	Linear	2	TBR_2	-2.68	0.00	0.00	2.67	0.02	-2.68	0.22	6.42	0.76	0.01
cluster0	Linear	2	TBR_1	-3.99	0.00	0.00	4.01	-0.01	-3.99	0.25	7.68	0.63	0.01
cluster0	Linear	2	TIR	-0.83	0.83	-0.03	0.03	0.00	0.00	-0.04	-1.43	0.21	0.00
cluster0	Linear	2	TAR_1	-0.41	0.42	-0.03	0.04	-0.01	0.01	0.34	14.76	0.67	0.01
cluster0	Linear	2	TAR_2	-0.20	0.23	-0.02	0.00	-0.01	0.03	-0.48	-24.55	1.03	0.01
cluster0	Linear	4	ALL	-1.04	0.49	-0.22	0.80	-0.02	-0.55	0.14	10.26	0.59	0.01
cluster0	Linear	4	TBR_2	-8.94	0.00	0.00	9.12	-0.18	-8.94	-0.25	-18.33	0.84	0.01
cluster0	Linear	4	TBR_1	-2.43	0.00	0.00	2.88	-0.44	-2.43	-1.13	-85.84	0.30	0.01
cluster0	Linear	4	TIR	0.78	-0.55	-0.29	0.06	0.00	0.23	-1.33	-82.82	-0.75	-0.01
cluster0	Linear	4	TAR_1	-2.27	2.10	-0.17	0.31	0.03	-0.17	1.81	139.36	2.34	0.01
cluster0	Linear	4	TAR_2	-6.96	4.83	-0.05	2.20	-0.02	-2.13	4.32	472.06	6.27	0.02
cluster0	Linear	6	ALL	-1.34	0.81	-0.37	0.99	-0.08	-0.53	-0.32	-30.15	0.50	0.01
cluster0	Linear	6	TBR_2	-1.00	0.00	0.00	2.22	-1.23	-1.00	-2.14	-252.97	0.31	-0.02
cluster0	Linear	6	TBR_1	-1.21	0.00	0.00	2.65	-1.45	-1.21	-1.31	-149.20	1.01	0.02
cluster0	Linear	6	TIR	1.12	-0.65	-0.52	0.05	0.00	0.47	-1.93	-145.13	-1.03	-0.01
cluster0	Linear	6	TAR_1	-3.49	3.20	-0.18	0.50	-0.04	-0.29	1.75	163.86	2.62	0.01
cluster0	Linear	6	TAR_2	-12.03	7.30	-0.06	4.81	-0.03	-4.73	3.95	626.38	7.07	0.03
cluster0	Linear	8	ALL	-1.39	0.46	-0.62	1.72	-0.18	-0.93	-0.70	-74.95	0.11	0.00
cluster0	Linear	8	TBR_2	-0.09	0.00	0.00	3.66	-3.56	-0.09	-6.81	-1008.84	-3.65	-0.11
cluster0	Linear	8	TBR_1	-0.18	0.00	0.00	3.45	-3.27	-0.18	-4.55	-629.94	-2.13	-0.04
cluster0	Linear	8	TIR	3.90	-3.00	-0.94	0.05	-0.01	0.90	-4.35	-350.30	-3.06	-0.03
cluster0	Linear	8	TAR_1	-9.10	8.02	-0.13	1.23	-0.03	-1.08	4.30	447.37	5.77	0.02
cluster0	Linear	8	TAR_2	-18.83	7.58	-0.02	11.29	-0.03	-11.25	6.63	1320.22	11.39	0.05
cluster0	Linear	12	ALL	-0.79	-0.86	-0.80	2.78	-0.33	-1.65	-1.82	-219.16	-0.76	-0.01
cluster0	Linear	12	TBR_2	-0.02	0.00	0.00	7.07	-7.05	-0.02	-7.31	-1355.03	-4.78	-0.15
cluster0	Linear	12	TBR_1	-0.01	0.00	0.00	6.16	-6.15	-0.01	-5.28	-891.86	-3.34	-0.05
cluster0	Linear	12	TIR	5.08	-3.84	-1.28	0.06	-0.03	1.24	-5.54	-479.50	-4.21	-0.04
cluster0	Linear	12	TAR_1	-13.09	11.07	-0.03	2.06	-0.01	-2.02	4.92	540.23	6.85	0.03
cluster0	Linear	12	TAR_2	-11.08	-9.19	0.00	20.29	-0.01	-20.27	3.36	813.46	8.42	0.04
cluster0	Linear	16	ALL	-0.30	-2.68	-0.80	4.37	-0.57	-2.98	-2.22	-280.32	-1.39	-0.02
cluster0	Linear	16	TBR_2	-0.01	0.00	0.00	11.52	-11.51	-0.01	-10.47	-2102.46	-8.53	-0.23
cluster0	Linear	16	TBR_1	0.00	0.00	0.00	10.52	-10.52	0.00	-8.26	-1485.88	-6.68	-0.10
cluster0	Linear	16	TIR	7.53	-6.28	-1.29	0.09	-0.05	1.25	-7.62	-659.47	-6.14	-0.06
cluster0	Linear	16	TAR_1	-19.95	17.00	0.00	2.96	0.00	-2.95	7.76	877.70	10.07	0.05

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	Linear	16	TAR_2	-4.86	-28.36	0.00	33.23	-0.01	-33.22	3.50	920.11	8.27	0.04
cluster1	CNN	2	ALL	4.26	-1.76	-0.10	-2.39	-0.01	2.50	-5.09	-256.93	-3.71	-0.02
cluster1	CNN	2	TBR_2	-13.16	0.00	0.00	13.26	-0.10	-13.16	4.42	295.74	3.91	0.06
cluster1	CNN	2	TBR_1	-5.68	0.00	0.00	5.78	-0.10	-5.68	1.25	72.78	1.87	0.02
cluster1	CNN	2	TIR	6.46	-6.15	-0.14	-0.16	0.00	0.31	-4.20	-184.99	-2.92	-0.03
cluster1	CNN	2	TAR_1	-3.02	3.14	-0.09	-0.01	-0.01	0.12	1.16	72.38	2.02	0.01
cluster1	CNN	2	TAR_2	-11.61	8.74	-0.03	2.90	0.00	-2.87	7.05	598.19	8.14	0.04
cluster1	CNN	4	ALL	6.94	-2.49	-0.47	-3.92	-0.06	4.45	-9.27	-666.27	-6.87	-0.04
cluster1	CNN	4	TBR_2	-1.25	0.00	0.00	1.87	-0.62	-1.25	-0.02	-2.72	-0.07	-0.04
cluster1	CNN	4	TBR_1	0.30	0.00	0.00	0.08	-0.38	0.30	-3.23	-299.31	-2.80	-0.05
cluster1	CNN	4	TIR	9.99	-9.03	-0.68	-0.27	-0.01	0.96	-7.31	-417.28	-5.04	-0.05
cluster1	CNN	4	TAR_1	-14.35	14.31	-0.23	0.26	0.00	-0.04	5.80	539.59	8.03	0.04
cluster1	CNN	4	TAR_2	-30.53	11.01	-0.09	19.60	0.00	-19.52	15.43	2287.50	20.69	0.09
cluster1	CNN	6	ALL	8.55	-2.99	-0.84	-4.52	-0.19	5.56	-13.38	-1139.96	-10.18	-0.07
cluster1	CNN	6	TBR_2	0.00	0.00	0.00	1.02	-1.02	0.00	-7.81	-1081.16	-7.43	-0.22
cluster1	CNN	6	TBR_1	0.02	0.00	0.00	2.49	-2.51	0.02	-10.57	-1261.41	-9.33	-0.17
cluster1	CNN	6	TIR	13.11	-11.53	-1.29	-0.27	-0.02	1.58	-10.99	-716.14	-7.83	-0.08
cluster1	CNN	6	TAR_1	-24.27	24.03	-0.24	0.49	0.00	-0.24	10.05	1084.35	13.26	0.07
cluster1	CNN	6	TAR_2	-35.58	-0.84	-0.08	36.50	0.00	-36.42	17.09	3259.36	25.62	0.12
cluster1	CNN	8	ALL	10.43	-4.01	-1.32	-4.70	-0.39	6.42	-16.71	-1574.19	-13.44	-0.12
cluster1	CNN	8	TBR_2	0.00	0.00	0.00	5.60	-5.60	0.00	-20.03	-3178.09	-18.37	-0.44
cluster1	CNN	8	TBR_1	0.00	0.00	0.00	6.91	-6.91	0.00	-21.34	-2931.32	-19.17	-0.33
cluster1	CNN	8	TIR	17.82	-15.48	-2.04	-0.25	-0.04	2.34	-16.47	-1178.26	-12.37	-0.13
cluster1	CNN	8	TAR_1	-37.52	36.82	-0.25	0.94	0.00	-0.70	17.06	1982.60	21.33	0.11
cluster1	CNN	8	TAR_2	-33.90	-20.76	-0.05	54.71	0.00	-54.66	21.78	4765.83	32.41	0.14
cluster1	CNN	12	ALL	10.94	-2.59	-1.15	-6.66	-0.54	8.35	-20.97	-2144.66	-16.56	-0.13
cluster1	CNN	12	TBR_2	0.00	0.00	0.00	9.28	-9.28	0.00	-24.54	-4409.09	-22.79	-0.55
cluster1	CNN	12	TBR_1	0.00	0.00	0.00	9.74	-9.74	0.00	-23.62	-3686.82	-21.73	-0.37
cluster1	CNN	12	TIR	15.23	-13.13	-1.81	-0.24	-0.05	2.10	-16.86	-1256.25	-12.70	-0.14
cluster1	CNN	12	TAR_1	-37.24	37.82	-0.08	-0.49	0.00	0.58	16.20	1962.58	20.16	0.10
cluster1	CNN	12	TAR_2	-14.41	-36.96	0.00	51.37	0.00	-51.37	9.10	2273.30	18.16	0.10
cluster1	CNN	16	ALL	12.60	-3.00	-0.86	-8.17	-0.58	9.60	-22.95	-2427.09	-18.57	-0.15
cluster1	CNN	16	TBR_2	0.00	0.00	0.00	11.34	-11.34	0.00	-27.68	-5275.62	-26.44	-0.64
cluster1	CNN	16	TBR_1	0.00	0.00	0.00	10.61	-10.61	0.00	-26.64	-4387.01	-25.38	-0.43
cluster1	CNN	16	TIR	16.65	-14.99	-1.38	-0.23	-0.06	1.66	-18.14	-1372.39	-14.13	-0.16
cluster1	CNN	16	TAR_1	-39.45	41.09	-0.01	-1.63	0.00	1.64	18.02	2216.32	21.44	0.12

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	16	TAR_2	-6.09	-32.97	0.00	39.07	0.00	-39.06	5.07	1342.63	12.58	0.09
cluster1	LSTM	2	ALL	2.15	-1.15	-0.02	-0.97	0.00	1.00	-2.89	-100.65	-2.15	-0.01
cluster1	LSTM	2	TBR_2	-18.26	0.00	0.00	18.30	-0.04	-18.26	2.72	104.57	2.41	0.03
cluster1	LSTM	2	TBR_1	-6.01	0.00	0.00	6.01	0.00	-6.01	1.02	34.78	1.00	0.01
cluster1	LSTM	2	TIR	3.86	-3.77	-0.02	-0.08	0.00	0.09	-2.42	-76.42	-1.74	-0.02
cluster1	LSTM	2	TAR_1	-0.26	0.28	-0.01	0.00	0.00	0.02	0.22	9.18	0.74	0.01
cluster1	LSTM	2	TAR_2	-3.00	2.71	-0.01	0.30	0.00	-0.29	3.68	197.04	4.01	0.02
cluster1	LSTM	4	ALL	6.07	-2.35	-0.29	-3.39	-0.03	3.72	-7.22	-447.75	-5.35	-0.04
cluster1	LSTM	4	TBR_2	-6.90	0.00	0.00	7.36	-0.46	-6.90	1.53	132.62	1.14	-0.01
cluster1	LSTM	4	TBR_1	3.16	0.00	0.00	-2.92	-0.24	3.16	-1.76	-133.86	-1.47	-0.03
cluster1	LSTM	4	TIR	8.58	-7.93	-0.41	-0.24	-0.01	0.65	-5.91	-305.36	-4.11	-0.04
cluster1	LSTM	4	TAR_1	-7.71	7.80	-0.19	0.10	0.00	0.09	3.24	256.50	4.52	0.03
cluster1	LSTM	4	TAR_2	-22.17	12.38	-0.07	9.86	0.00	-9.79	12.34	1442.35	15.34	0.07
cluster1	LSTM	6	ALL	8.03	-3.04	-0.71	-4.16	-0.12	4.99	-11.48	-907.03	-8.65	-0.07
cluster1	LSTM	6	TBR_2	-0.18	0.00	0.00	1.01	-0.84	-0.18	-4.86	-606.63	-4.82	-0.15
cluster1	LSTM	6	TBR_1	0.44	0.00	0.00	0.85	-1.28	0.44	-7.87	-852.17	-7.00	-0.13
cluster1	LSTM	6	TIR	12.40	-11.05	-1.05	-0.27	-0.02	1.35	-9.73	-607.35	-6.87	-0.07
cluster1	LSTM	6	TAR_1	-18.89	18.70	-0.29	0.47	0.00	-0.19	7.75	774.33	10.29	0.05
cluster1	LSTM	6	TAR_2	-35.67	9.09	-0.12	26.70	0.00	-26.58	17.25	2906.39	24.46	0.11
cluster1	LSTM	8	ALL	9.29	-3.28	-1.08	-4.64	-0.29	6.01	-15.23	-1368.06	-11.79	-0.09
cluster1	LSTM	8	TBR_2	-0.01	0.00	0.00	3.48	-3.47	-0.01	-13.74	-2059.08	-12.43	-0.32
cluster1	LSTM	8	TBR_1	0.00	0.00	0.00	4.45	-4.45	0.00	-15.58	-2024.88	-13.79	-0.24
cluster1	LSTM	8	TIR	14.75	-12.82	-1.63	-0.26	-0.03	1.93	-13.44	-924.96	-9.77	-0.10
cluster1	LSTM	8	TAR_1	-28.57	28.20	-0.28	0.65	0.00	-0.37	12.31	1371.80	15.83	0.08
cluster1	LSTM	8	TAR_2	-34.66	-7.79	-0.08	42.53	0.00	-42.45	17.97	3665.61	27.34	0.13
cluster1	LSTM	12	ALL	10.99	-3.17	-1.21	-6.09	-0.53	7.82	-20.06	-2024.04	-16.07	-0.13
cluster1	LSTM	12	TBR_2	0.00	0.00	0.00	9.44	-9.44	0.00	-24.79	-4344.82	-22.89	-0.55
cluster1	LSTM	12	TBR_1	0.00	0.00	0.00	9.51	-9.51	0.00	-24.92	-3774.79	-22.95	-0.39
cluster1	LSTM	12	TIR	16.26	-14.07	-1.90	-0.24	-0.05	2.19	-17.29	-1278.66	-13.10	-0.13
cluster1	LSTM	12	TAR_1	-38.65	38.81	-0.11	-0.05	0.00	0.16	17.71	2143.30	21.83	0.12
cluster1	LSTM	12	TAR_2	-17.90	-37.48	0.00	55.38	0.00	-55.38	12.90	3157.57	22.36	0.12
cluster1	LSTM	16	ALL	12.50	-3.28	-1.01	-7.60	-0.62	9.22	-22.45	-2363.47	-18.34	-0.15
cluster1	LSTM	16	TBR_2	0.00	0.00	0.00	11.99	-11.99	0.00	-29.65	-5539.58	-28.06	-0.67
cluster1	LSTM	16	TBR_1	0.02	0.00	0.00	11.36	-11.38	0.02	-28.25	-4572.47	-26.71	-0.45
cluster1	LSTM	16	TIR	17.37	-15.47	-1.61	-0.23	-0.06	1.90	-18.97	-1430.07	-14.71	-0.16
cluster1	LSTM	16	TAR_1	-41.85	43.11	-0.01	-1.25	0.00	1.26	19.86	2465.63	23.68	0.12
cluster1	LSTM	16	TAR_2	-7.78	-35.85	0.00	43.63	0.00	-43.63	8.73	2294.35	16.72	0.10

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	Linear	2	ALL	2.17	-1.56	-0.03	-0.57	-0.01	0.61	-3.40	-124.10	-2.29	-0.01
cluster1	Linear	2	TBR_2	-10.14	0.00	0.00	10.19	-0.05	-10.14	1.94	59.78	2.71	0.04
cluster1	Linear	2	TBR_1	-6.69	0.00	0.00	6.71	0.00	-6.69	0.68	21.48	1.21	0.02
cluster1	Linear	2	TIR	4.86	-4.76	-0.03	-0.07	0.00	0.10	-3.24	-109.38	-2.26	-0.02
cluster1	Linear	2	TAR_1	-0.51	0.55	-0.04	0.01	-0.02	0.04	0.17	7.30	1.20	0.01
cluster1	Linear	2	TAR_2	-3.17	2.79	-0.02	0.41	-0.01	-0.38	3.35	186.25	4.79	0.03
cluster1	Linear	4	ALL	6.64	-3.39	-0.39	-2.79	-0.07	3.25	-7.91	-507.03	-5.78	-0.03
cluster1	Linear	4	TBR_2	-19.16	0.00	0.00	19.33	-0.17	-19.16	4.97	395.05	5.93	0.10
cluster1	Linear	4	TBR_1	-6.08	0.00	0.00	6.47	-0.39	-6.08	-0.72	-55.14	1.02	0.01
cluster1	Linear	4	TIR	11.76	-11.00	-0.57	-0.18	-0.01	0.76	-8.10	-448.02	-5.82	-0.05
cluster1	Linear	4	TAR_1	-10.18	10.14	-0.21	0.34	-0.09	-0.04	4.19	332.54	6.46	0.03
cluster1	Linear	4	TAR_2	-27.94	17.03	-0.06	11.00	-0.03	-10.91	14.75	1765.66	18.50	0.08
cluster1	Linear	6	ALL	8.43	-3.63	-0.83	-3.78	-0.19	4.80	-12.16	-986.39	-9.21	-0.06
cluster1	Linear	6	TBR_2	-1.64	0.00	0.00	2.95	-1.32	-1.64	-1.81	-213.93	1.06	-0.02
cluster1	Linear	6	TBR_1	-1.18	0.00	0.00	3.18	-2.02	-1.18	-6.57	-714.03	-3.73	-0.07
cluster1	Linear	6	TIR	14.83	-13.29	-1.27	-0.25	-0.02	1.54	-11.79	-770.74	-8.57	-0.08
cluster1	Linear	6	TAR_1	-24.98	24.33	-0.20	0.91	-0.06	-0.65	9.30	938.70	13.07	0.06
cluster1	Linear	6	TAR_2	-40.76	9.00	-0.06	31.78	0.04	-31.76	19.09	3315.49	26.37	0.12
cluster1	Linear	8	ALL	9.48	-3.60	-1.10	-4.43	-0.37	5.88	-15.86	-1452.36	-12.26	-0.09
cluster1	Linear	8	TBR_2	-0.27	0.00	0.00	5.16	-4.89	-0.27	-8.93	-1303.87	-5.43	-0.17
cluster1	Linear	8	TBR_1	-0.23	0.00	0.00	5.71	-5.48	-0.23	-12.54	-1638.16	-9.03	-0.16
cluster1	Linear	8	TIR	15.82	-13.80	-1.73	-0.25	-0.04	2.02	-14.31	-1010.81	-10.60	-0.10
cluster1	Linear	8	TAR_1	-33.81	33.04	-0.13	0.94	-0.04	-0.77	12.48	1398.39	17.08	0.08
cluster1	Linear	8	TAR_2	-31.96	-15.81	-0.02	47.81	-0.03	-47.77	16.88	3535.68	25.69	0.13
cluster1	Linear	12	ALL	11.48	-3.78	-1.14	-5.95	-0.62	7.70	-20.66	-2104.60	-16.48	-0.13
cluster1	Linear	12	TBR_2	-0.02	0.00	0.00	10.62	-10.60	-0.02	-19.74	-3415.13	-16.61	-0.42
cluster1	Linear	12	TBR_1	-0.01	0.00	0.00	11.13	-11.12	-0.01	-21.57	-3289.91	-18.58	-0.32
cluster1	Linear	12	TIR	17.13	-15.02	-1.82	-0.23	-0.06	2.11	-17.38	-1297.46	-13.38	-0.14
cluster1	Linear	12	TAR_1	-41.71	41.75	-0.03	-0.01	-0.01	0.04	16.84	2047.34	21.63	0.11
cluster1	Linear	12	TAR_2	-12.88	-43.17	0.00	56.07	-0.01	-56.05	9.73	2413.95	18.24	0.10
cluster1	Linear	16	ALL	13.13	-4.03	-0.85	-7.57	-0.68	9.10	-22.77	-2411.13	-18.70	-0.15
cluster1	Linear	16	TBR_2	-0.01	0.00	0.00	13.07	-13.06	-0.01	-27.02	-4981.07	-24.91	-0.61
cluster1	Linear	16	TBR_1	0.00	0.00	0.00	12.42	-12.42	0.00	-27.02	-4354.44	-25.11	-0.42
cluster1	Linear	16	TIR	18.22	-16.57	-1.36	-0.22	-0.06	1.65	-19.03	-1430.50	-14.99	-0.16
cluster1	Linear	16	TAR_1	-43.21	44.51	0.00	-1.29	0.00	1.30	20.09	2520.86	24.26	0.13
cluster1	Linear	16	TAR_2	-4.89	-38.53	0.00	43.43	-0.01	-43.42	7.03	1872.03	14.41	0.09
cluster2	CNN	2	ALL	1.13	-0.58	0.06	-0.62	0.01	0.55	3.02	176.88	2.15	-0.01

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	2	TBR_2	2.36	0.00	0.00	-2.47	0.11	2.36	0.55	34.86	0.38	0.02
cluster2	CNN	2	TBR_1	-3.51	0.00	0.00	3.33	0.17	-3.51	2.12	125.40	1.60	0.02
cluster2	CNN	2	TIR	-1.78	1.66	0.14	-0.02	0.00	-0.12	2.52	128.09	1.52	0.00
cluster2	CNN	2	TAR_1	-0.30	0.17	0.01	0.12	0.01	-0.13	0.74	45.68	0.23	0.00
cluster2	CNN	2	TAR_2	0.30	-0.10	0.00	-0.20	0.00	0.20	0.18	13.69	0.55	0.00
cluster2	CNN	4	ALL	0.68	-0.40	0.47	-0.81	0.05	0.28	4.82	413.91	3.76	0.01
cluster2	CNN	4	TBR_2	-1.23	0.00	0.00	0.09	1.14	-1.23	5.41	607.34	4.61	0.11
cluster2	CNN	4	TBR_1	-1.06	0.00	0.00	-0.81	1.88	-1.06	8.35	872.27	7.08	0.12
cluster2	CNN	4	TIR	-5.30	4.32	1.03	-0.06	0.01	-0.98	6.52	462.09	4.68	0.03
cluster2	CNN	4	TAR_1	3.74	-3.71	0.16	-0.20	0.00	0.03	-2.03	-173.52	-2.30	-0.01
cluster2	CNN	4	TAR_2	5.25	-2.44	0.00	-2.81	0.00	2.81	-4.62	-592.50	-4.54	-0.02
cluster2	CNN	6	ALL	1.10	-1.19	0.49	-0.50	0.11	-0.09	6.16	645.16	4.85	0.01
cluster2	CNN	6	TBR_2	0.00	0.00	0.00	-1.94	1.94	0.00	7.30	1121.22	6.90	0.16
cluster2	CNN	6	TBR_1	0.00	0.00	0.00	-3.82	3.82	0.00	11.32	1600.19	10.26	0.17
cluster2	CNN	6	TIR	-3.92	2.65	1.33	-0.09	0.03	-1.27	6.78	561.67	5.15	0.04
cluster2	CNN	6	TAR_1	7.21	-6.88	0.00	-0.32	0.00	0.33	-4.81	-447.05	-4.80	-0.02
cluster2	CNN	6	TAR_2	2.50	2.71	-0.05	-5.16	0.00	5.21	-2.67	-456.82	-2.39	-0.01
cluster2	CNN	8	ALL	1.42	-1.97	0.67	-0.32	0.20	-0.55	6.74	793.45	5.26	0.00
cluster2	CNN	8	TBR_2	0.00	0.00	0.00	-3.47	3.47	0.00	8.69	1627.82	8.71	0.21
cluster2	CNN	8	TBR_1	0.00	0.00	0.00	-6.80	6.80	0.00	12.66	2168.42	12.21	0.20
cluster2	CNN	8	TIR	-3.95	2.12	1.90	-0.10	0.04	-1.83	7.61	727.93	6.16	0.05
cluster2	CNN	8	TAR_1	9.04	-8.55	-0.04	-0.46	0.00	0.49	-5.92	-551.68	-5.78	-0.03
cluster2	CNN	8	TAR_2	2.47	4.75	-0.03	-7.18	0.00	7.22	-3.02	-587.00	-2.96	-0.02
cluster2	CNN	12	ALL	0.79	-1.79	0.54	0.11	0.35	-1.00	8.08	1060.96	6.45	0.00
cluster2	CNN	12	TBR_2	0.00	0.00	0.00	-6.15	6.15	0.00	10.26	2201.40	10.80	0.25
cluster2	CNN	12	TBR_1	0.00	0.00	0.00	-11.16	11.16	0.00	14.27	2766.04	14.38	0.24
cluster2	CNN	12	TIR	-4.98	3.42	1.62	-0.12	0.07	-1.56	7.80	773.70	6.82	0.05
cluster2	CNN	12	TAR_1	17.62	-16.70	-0.06	-0.86	0.00	0.92	-9.46	-902.63	-9.56	-0.05
cluster2	CNN	12	TAR_2	0.14	13.29	0.00	-13.43	0.00	13.43	-3.74	-885.89	-3.62	-0.02
cluster2	CNN	16	ALL	0.38	-1.75	0.33	0.55	0.48	-1.37	8.61	1181.29	6.94	0.00
cluster2	CNN	16	TBR_2	0.00	0.00	0.00	-9.17	9.17	0.00	12.08	2781.47	12.83	0.30
cluster2	CNN	16	TBR_1	0.00	0.00	0.00	-14.06	14.06	0.00	14.66	3019.77	15.25	0.25
cluster2	CNN	16	TIR	-6.18	5.19	1.03	-0.13	0.07	-0.99	7.65	775.62	7.09	0.05
cluster2	CNN	16	TAR_1	21.96	-20.95	-0.01	-1.00	0.00	1.01	-10.64	-1003.23	-10.72	-0.05
cluster2	CNN	16	TAR_2	-1.42	18.65	0.00	-17.21	0.00	17.23	-4.46	-1134.82	-4.50	-0.02
cluster2	LSTM	2	ALL	-0.01	0.30	0.00	-0.28	0.00	0.29	2.01	79.44	1.51	-0.01
cluster2	LSTM	2	TBR_2	0.75	0.00	0.00	-0.76	0.00	0.75	0.14	5.04	-0.42	-0.01

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	2	TBR_1	-4.54	0.00	0.00	4.53	0.01	-4.54	1.43	49.40	1.05	0.02
cluster2	LSTM	2	TIR	-2.43	2.42	0.01	0.00	0.00	-0.01	2.11	76.22	1.40	0.01
cluster2	LSTM	2	TAR_1	-0.86	0.84	0.01	0.02	0.00	-0.02	1.00	42.57	0.62	0.00
cluster2	LSTM	2	TAR_2	0.31	-0.24	-0.01	-0.06	0.00	0.07	-0.82	-40.02	-0.40	0.00
cluster2	LSTM	4	ALL	1.34	-0.88	0.22	-0.70	0.03	0.46	3.92	286.14	2.81	-0.01
cluster2	LSTM	4	TBR_2	-0.90	0.00	0.00	0.48	0.41	-0.90	1.76	153.70	1.11	0.04
cluster2	LSTM	4	TBR_1	-2.11	0.00	0.00	1.29	0.81	-2.11	4.19	345.15	2.96	0.05
cluster2	LSTM	4	TIR	-2.70	2.25	0.48	-0.04	0.00	-0.45	4.25	262.65	2.75	0.02
cluster2	LSTM	4	TAR_1	1.26	-1.38	0.09	0.02	0.00	-0.12	-0.15	-11.70	-0.69	0.00
cluster2	LSTM	4	TAR_2	2.52	-1.54	0.01	-0.99	0.00	0.98	-1.86	-191.95	-1.57	0.00
cluster2	LSTM	6	ALL	1.26	-1.24	0.45	-0.55	0.08	0.02	5.49	527.10	4.17	0.00
cluster2	LSTM	6	TBR_2	0.18	0.00	0.00	-1.49	1.30	0.18	4.85	652.75	3.91	0.10
cluster2	LSTM	6	TBR_1	0.03	0.00	0.00	-2.70	2.67	0.03	8.56	1068.33	7.22	0.12
cluster2	LSTM	6	TIR	-3.43	2.33	1.18	-0.08	0.02	-1.10	5.96	465.68	4.26	0.03
cluster2	LSTM	6	TAR_1	4.08	-4.01	0.04	-0.11	0.00	0.07	-2.57	-230.14	-2.69	-0.02
cluster2	LSTM	6	TAR_2	3.09	0.10	-0.05	-3.14	0.00	3.19	-2.21	-329.73	-2.13	-0.01
cluster2	LSTM	8	ALL	1.36	-1.85	0.51	-0.15	0.13	-0.49	6.59	736.16	5.00	0.00
cluster2	LSTM	8	TBR_2	-0.01	0.00	0.00	-2.57	2.58	-0.01	5.84	989.35	5.60	0.14
cluster2	LSTM	8	TBR_1	0.00	0.00	0.00	-4.74	4.74	0.00	9.88	1535.52	8.89	0.15
cluster2	LSTM	8	TIR	-2.59	1.16	1.50	-0.09	0.03	-1.43	6.22	550.17	4.60	0.03
cluster2	LSTM	8	TAR_1	6.86	-6.60	-0.06	-0.21	0.00	0.26	-4.27	-404.35	-4.33	-0.02
cluster2	LSTM	8	TAR_2	1.77	3.53	-0.04	-5.26	0.00	5.30	-1.43	-263.61	-1.38	-0.01
cluster2	LSTM	12	ALL	1.06	-2.05	0.79	-0.13	0.33	-0.99	7.86	1012.92	6.20	0.01
cluster2	LSTM	12	TBR_2	0.00	0.00	0.00	-5.51	5.51	0.00	10.03	2106.31	10.46	0.24
cluster2	LSTM	12	TBR_1	0.00	0.00	0.00	-10.62	10.62	0.00	14.39	2746.39	14.17	0.24
cluster2	LSTM	12	TIR	-4.77	2.70	2.13	-0.12	0.06	-2.07	8.44	840.99	7.09	0.06
cluster2	LSTM	12	TAR_1	14.91	-13.99	-0.06	-0.86	0.00	0.92	-8.42	-799.29	-8.56	-0.04
cluster2	LSTM	12	TAR_2	2.81	9.66	0.00	-12.47	0.00	12.47	-4.51	-1026.08	-4.84	-0.02
cluster2	LSTM	16	ALL	0.64	-1.55	0.72	-0.38	0.56	-0.91	8.42	1146.48	6.90	0.01
cluster2	LSTM	16	TBR_2	0.00	0.00	0.00	-10.27	10.27	0.00	13.29	3055.19	14.02	0.32
cluster2	LSTM	16	TBR_1	0.00	0.00	0.00	-16.26	16.26	0.00	16.52	3411.79	16.97	0.29
cluster2	LSTM	16	TIR	-7.55	5.71	1.90	-0.15	0.09	-1.84	9.47	984.18	8.78	0.07
cluster2	LSTM	16	TAR_1	22.69	-21.28	-0.01	-1.40	0.00	1.41	-11.51	-1066.99	-11.63	-0.06
cluster2	LSTM	16	TAR_2	1.09	18.04	0.00	-19.13	0.00	19.13	-6.32	-1566.29	-6.72	-0.04
cluster2	Linear	2	ALL	0.03	0.08	-0.01	-0.11	0.00	0.11	1.74	72.36	1.54	0.00
cluster2	Linear	2	TBR_2	0.28	0.00	0.00	-0.27	-0.01	0.28	0.31	8.91	1.27	0.03
cluster2	Linear	2	TBR_1	-5.82	0.00	0.00	5.82	0.01	-5.82	1.32	42.48	1.45	0.03

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	2	TIR	-2.34	2.32	0.01	0.01	0.00	-0.02	1.95	75.82	1.51	0.01
cluster2	Linear	2	TAR_1	-0.94	0.94	-0.01	0.02	-0.01	0.00	0.82	35.59	0.59	0.00
cluster2	Linear	2	TAR_2	0.08	0.01	-0.01	-0.06	-0.01	0.09	-1.32	-66.94	-0.36	0.00
cluster2	Linear	4	ALL	1.16	-0.95	0.24	-0.46	0.02	0.21	3.63	274.35	2.88	0.00
cluster2	Linear	4	TBR_2	-6.55	0.00	0.00	6.16	0.38	-6.55	2.68	207.22	3.21	0.08
cluster2	Linear	4	TBR_1	-4.99	0.00	0.00	4.12	0.87	-4.99	5.30	433.79	4.84	0.08
cluster2	Linear	4	TIR	-3.75	3.21	0.55	-0.01	0.00	-0.54	4.20	283.30	3.11	0.02
cluster2	Linear	4	TAR_1	0.77	-0.94	0.12	0.06	-0.02	-0.17	-0.24	-18.01	-0.51	0.00
cluster2	Linear	4	TAR_2	1.89	-1.18	0.01	-0.70	-0.02	0.71	-1.88	-194.31	-1.32	-0.01
cluster2	Linear	6	ALL	1.29	-1.28	0.49	-0.55	0.06	0.01	5.19	511.16	4.22	0.01
cluster2	Linear	6	TBR_2	-1.27	0.00	0.00	0.12	1.14	-1.27	5.71	721.20	6.36	0.15
cluster2	Linear	6	TBR_1	-0.62	0.00	0.00	-1.96	2.57	-0.62	9.51	1187.06	9.13	0.16
cluster2	Linear	6	TIR	-4.37	3.14	1.27	-0.07	0.02	-1.23	6.17	514.53	4.78	0.03
cluster2	Linear	6	TAR_1	4.36	-4.34	0.13	-0.15	-0.01	0.02	-2.88	-255.24	-2.87	-0.02
cluster2	Linear	6	TAR_2	3.67	-0.54	-0.01	-3.11	-0.02	3.13	-3.33	-503.43	-3.13	-0.01
cluster2	Linear	8	ALL	1.12	-1.44	0.65	-0.47	0.13	-0.32	6.35	722.64	5.24	0.01
cluster2	Linear	8	TBR_2	-0.14	0.00	0.00	-2.01	2.15	-0.14	8.56	1399.14	9.59	0.22
cluster2	Linear	8	TBR_1	-0.06	0.00	0.00	-5.23	5.29	-0.06	12.90	2014.39	12.93	0.21
cluster2	Linear	8	TIR	-4.77	3.06	1.76	-0.09	0.03	-1.71	7.53	696.94	6.15	0.05
cluster2	Linear	8	TAR_1	8.49	-8.02	0.05	-0.50	-0.01	0.47	-5.68	-532.75	-5.46	-0.03
cluster2	Linear	8	TAR_2	4.62	1.76	-0.01	-6.37	-0.02	6.38	-4.53	-851.99	-4.65	-0.02
cluster2	Linear	12	ALL	0.83	-1.38	0.73	-0.51	0.32	-0.55	7.67	999.01	6.43	0.01
cluster2	Linear	12	TBR_2	-0.01	0.00	0.00	-5.45	5.46	-0.01	13.35	2750.02	14.67	0.33
cluster2	Linear	12	TBR_1	0.00	0.00	0.00	-10.98	10.98	0.00	16.50	3146.70	17.22	0.29
cluster2	Linear	12	TIR	-6.12	4.20	1.98	-0.12	0.07	-1.92	9.06	915.00	8.09	0.06
cluster2	Linear	12	TAR_1	16.88	-15.73	-0.02	-1.12	-0.01	1.15	-10.19	-962.82	-9.84	-0.05
cluster2	Linear	12	TAR_2	3.28	10.70	0.00	-13.97	-0.01	13.98	-6.44	-1493.20	-6.75	-0.03
cluster2	Linear	16	ALL	0.44	-1.19	0.47	-0.20	0.48	-0.75	8.34	1143.63	6.92	0.01
cluster2	Linear	16	TBR_2	-0.01	0.00	0.00	-9.16	9.17	-0.01	14.36	3242.31	15.67	0.36
cluster2	Linear	16	TBR_1	0.00	0.00	0.00	-14.67	14.67	0.00	16.21	3311.13	17.16	0.29
cluster2	Linear	16	TIR	-6.60	5.34	1.31	-0.14	0.09	-1.26	8.43	865.40	7.89	0.06
cluster2	Linear	16	TAR_1	21.46	-20.14	0.00	-1.31	0.00	1.32	-11.53	-1082.35	-11.25	-0.05
cluster2	Linear	16	TAR_2	0.01	18.77	0.00	-18.77	-0.01	18.78	-6.14	-1555.45	-6.34	-0.03
cluster3	CNN	2	ALL	1.48	-0.67	0.02	-0.84	0.00	0.81	0.56	31.09	0.52	-0.01
cluster3	CNN	2	TBR_2	-6.76	0.00	0.00	6.76	0.00	-6.76	2.34	151.89	2.34	0.06
cluster3	CNN	2	TBR_1	-7.07	0.00	0.00	6.96	0.11	-7.07	1.96	115.68	1.94	0.03
cluster3	CNN	2	TIR	-1.12	1.12	0.06	-0.04	0.00	0.00	1.44	71.71	1.19	0.00

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	CNN	2	TAR_1	2.21	-2.12	-0.02	-0.07	0.00	0.09	-1.52	-91.03	-1.38	-0.01
cluster3	CNN	2	TAR_2	1.46	-1.15	-0.01	-0.30	0.00	0.31	-2.93	-219.55	-2.35	-0.01
cluster3	CNN	4	ALL	2.45	-1.04	-0.02	-1.41	0.00	1.41	0.56	45.27	0.67	-0.01
cluster3	CNN	4	TBR_2	-0.23	0.00	0.00	-0.22	0.45	-0.23	3.89	430.15	3.12	0.08
cluster3	CNN	4	TBR_1	-0.32	0.00	0.00	-0.49	0.81	-0.32	4.50	452.47	3.80	0.06
cluster3	CNN	4	TIR	-0.71	0.68	0.11	-0.09	0.01	-0.03	1.40	91.63	1.21	0.00
cluster3	CNN	4	TAR_1	4.86	-4.55	-0.12	-0.20	0.00	0.31	-3.47	-290.83	-3.11	-0.02
cluster3	CNN	4	TAR_2	0.64	0.76	-0.06	-1.34	0.00	1.40	-3.45	-446.90	-1.92	-0.01
cluster3	CNN	6	ALL	2.47	-0.94	0.17	-1.75	0.04	1.53	0.37	36.92	0.81	0.00
cluster3	CNN	6	TBR_2	0.00	0.00	0.00	-2.48	2.48	0.00	9.66	1507.28	8.97	0.19
cluster3	CNN	6	TBR_1	0.00	0.00	0.00	-2.76	2.76	0.00	10.02	1403.45	9.70	0.15
cluster3	CNN	6	TIR	-2.98	2.56	0.51	-0.11	0.02	-0.42	3.98	318.27	3.47	0.03
cluster3	CNN	6	TAR_1	8.17	-7.39	-0.11	-0.66	0.00	0.78	-6.20	-567.85	-5.66	-0.02
cluster3	CNN	6	TAR_2	5.61	-0.64	-0.07	-4.90	0.00	4.97	-9.66	-1583.16	-8.38	-0.03
cluster3	CNN	8	ALL	3.25	-1.83	-0.13	-1.31	0.03	1.42	-0.12	-12.80	0.17	-0.03
cluster3	CNN	8	TBR_2	0.00	0.00	0.00	-3.86	3.86	0.00	6.32	1169.42	6.00	0.14
cluster3	CNN	8	TBR_1	0.00	0.00	0.00	-3.48	3.48	0.00	6.41	1058.63	6.45	0.10
cluster3	CNN	8	TIR	0.36	-0.36	0.10	-0.11	0.01	0.00	1.26	112.98	1.30	0.00
cluster3	CNN	8	TAR_1	7.62	-7.06	-0.20	-0.36	0.00	0.56	-5.02	-472.58	-4.80	-0.02
cluster3	CNN	8	TAR_2	-1.56	5.78	-0.05	-4.17	0.00	4.22	-6.09	-1163.09	-3.50	-0.01
cluster3	CNN	12	ALL	2.79	-1.64	-0.15	-1.06	0.06	1.15	-0.06	-8.11	0.43	-0.03
cluster3	CNN	12	TBR_2	0.00	0.00	0.00	-3.79	3.79	0.00	6.66	1405.38	7.02	0.16
cluster3	CNN	12	TBR_1	0.00	0.00	0.00	-5.76	5.76	0.00	8.06	1511.42	8.55	0.13
cluster3	CNN	12	TIR	-0.15	0.25	0.00	-0.12	0.02	0.10	2.02	188.86	1.91	0.01
cluster3	CNN	12	TAR_1	11.54	-10.96	-0.08	-0.50	0.00	0.58	-6.49	-638.09	-6.40	-0.03
cluster3	CNN	12	TAR_2	-3.27	10.43	0.00	-7.17	0.00	7.16	-9.10	-2105.41	-6.29	-0.02
cluster3	CNN	16	ALL	2.68	-2.63	-0.31	0.27	-0.02	0.05	-0.06	-8.36	0.29	-0.03
cluster3	CNN	16	TBR_2	0.00	0.00	0.00	-0.83	0.83	0.00	3.22	712.19	3.93	0.10
cluster3	CNN	16	TBR_1	0.00	0.00	0.00	-4.32	4.32	0.00	5.81	1144.50	6.50	0.10
cluster3	CNN	16	TIR	1.58	-1.10	-0.38	-0.11	0.01	0.48	0.31	28.73	0.21	-0.01
cluster3	CNN	16	TAR_1	9.46	-9.62	-0.01	0.18	0.00	-0.16	-4.71	-472.26	-4.48	-0.02
cluster3	CNN	16	TAR_2	-4.01	7.02	0.00	-2.99	0.00	3.01	-8.30	-2080.97	-5.61	0.00
cluster3	LSTM	2	ALL	0.69	-0.21	-0.01	-0.46	0.00	0.48	0.58	21.87	0.44	-0.01
cluster3	LSTM	2	TBR_2	-2.78	0.00	0.00	2.77	0.01	-2.78	0.55	19.92	-0.10	0.00
cluster3	LSTM	2	TBR_1	-1.70	0.00	0.00	1.72	-0.02	-1.70	0.77	25.83	0.41	0.01
cluster3	LSTM	2	TIR	-0.68	0.71	0.00	-0.03	0.00	0.03	0.97	33.95	0.66	0.00
cluster3	LSTM	2	TAR_1	0.48	-0.47	0.00	0.00	0.00	0.01	-0.55	-22.33	-0.49	0.00

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	2	TAR_2	0.20	-0.13	-0.01	-0.06	0.00	0.07	-1.34	-64.87	-0.90	0.00
cluster3	LSTM	4	ALL	2.35	-1.04	0.01	-1.33	0.01	1.31	0.47	32.44	0.50	-0.01
cluster3	LSTM	4	TBR_2	-1.16	0.00	0.00	0.92	0.25	-1.16	3.48	309.15	2.84	0.07
cluster3	LSTM	4	TBR_1	-2.21	0.00	0.00	1.81	0.40	-2.21	3.46	282.48	2.86	0.05
cluster3	LSTM	4	TIR	-1.20	1.16	0.10	-0.07	0.00	-0.04	1.68	99.44	1.40	0.01
cluster3	LSTM	4	TAR_1	4.19	-3.91	-0.08	-0.21	0.01	0.28	-2.97	-216.53	-2.74	-0.01
cluster3	LSTM	4	TAR_2	2.17	-1.19	-0.04	-0.94	0.00	0.98	-3.52	-356.14	-2.46	0.00
cluster3	LSTM	6	ALL	2.69	-1.16	0.00	-1.55	0.02	1.53	0.28	25.91	0.58	-0.02
cluster3	LSTM	6	TBR_2	0.73	0.00	0.00	-1.97	1.23	0.73	5.76	779.49	5.04	0.11
cluster3	LSTM	6	TBR_1	0.10	0.00	0.00	-1.80	1.71	0.10	6.40	784.18	6.03	0.10
cluster3	LSTM	6	TIR	-1.35	1.24	0.21	-0.10	0.01	-0.11	2.03	151.23	1.90	0.01
cluster3	LSTM	6	TAR_1	6.15	-5.63	-0.17	-0.37	0.01	0.52	-4.66	-408.07	-4.24	-0.02
cluster3	LSTM	6	TAR_2	2.05	0.67	-0.11	-2.61	0.00	2.72	-5.47	-797.79	-3.63	-0.01
cluster3	LSTM	8	ALL	2.87	-1.40	-0.06	-1.43	0.02	1.47	0.10	10.47	0.43	-0.02
cluster3	LSTM	8	TBR_2	0.07	0.00	0.00	-2.82	2.75	0.07	5.36	904.40	4.92	0.11
cluster3	LSTM	8	TBR_1	0.04	0.00	0.00	-2.80	2.76	0.04	6.19	938.83	6.10	0.10
cluster3	LSTM	8	TIR	-0.48	0.38	0.21	-0.11	0.01	-0.10	1.74	145.93	1.69	0.01
cluster3	LSTM	8	TAR_1	7.10	-6.43	-0.22	-0.45	0.00	0.67	-4.96	-466.74	-4.71	-0.03
cluster3	LSTM	8	TAR_2	0.48	3.63	-0.08	-4.03	0.00	4.11	-6.28	-1128.48	-4.16	-0.01
cluster3	LSTM	12	ALL	2.90	-1.52	-0.06	-1.40	0.07	1.38	-0.03	-2.77	0.43	-0.02
cluster3	LSTM	12	TBR_2	0.00	0.00	0.00	-4.73	4.73	0.00	6.70	1384.49	6.88	0.16
cluster3	LSTM	12	TBR_1	0.00	0.00	0.00	-5.95	5.95	0.00	7.89	1453.69	8.22	0.13
cluster3	LSTM	12	TIR	-0.57	0.50	0.17	-0.12	0.02	-0.07	2.37	221.83	2.30	0.02
cluster3	LSTM	12	TAR_1	11.26	-10.43	-0.11	-0.71	0.00	0.83	-6.44	-624.62	-6.47	-0.03
cluster3	LSTM	12	TAR_2	-2.02	9.91	0.00	-7.89	0.00	7.89	-8.99	-2006.70	-6.40	-0.01
cluster3	LSTM	16	ALL	2.80	-1.89	-0.14	-0.86	0.08	0.91	-0.14	-16.95	0.43	-0.03
cluster3	LSTM	16	TBR_2	0.00	0.00	0.00	-2.72	2.72	0.00	5.78	1284.74	6.54	0.15
cluster3	LSTM	16	TBR_1	0.00	0.00	0.00	-7.29	7.29	0.00	8.58	1704.32	9.32	0.15
cluster3	LSTM	16	TIR	-1.10	1.24	-0.04	-0.12	0.02	0.14	2.56	248.05	2.45	0.01
cluster3	LSTM	16	TAR_1	13.98	-13.40	-0.01	-0.57	0.00	0.58	-7.22	-700.33	-7.16	-0.03
cluster3	LSTM	16	TAR_2	-2.76	11.11	0.00	-8.35	0.00	8.35	-10.68	-2600.75	-8.17	-0.02
cluster3	Linear	2	ALL	0.39	-0.28	-0.02	-0.09	-0.01	0.11	0.20	7.98	0.49	0.00
cluster3	Linear	2	TBR_2	-0.99	0.00	0.00	1.01	-0.02	-0.99	0.27	7.83	1.30	0.02
cluster3	Linear	2	TBR_1	-8.18	0.00	0.00	8.19	0.00	-8.18	1.31	42.11	1.61	0.03
cluster3	Linear	2	TIR	-0.78	0.79	-0.01	0.00	0.00	0.01	0.74	27.76	0.76	0.00
cluster3	Linear	2	TAR_1	0.54	-0.50	-0.02	0.00	-0.01	0.04	-0.90	-38.31	-0.58	0.00
cluster3	Linear	2	TAR_2	0.18	-0.07	-0.01	-0.08	-0.01	0.11	-2.39	-118.61	-1.14	0.00

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	4	ALL	2.89	-1.86	-0.04	-1.00	0.00	1.03	0.24	17.38	0.36	-0.01
cluster3	Linear	4	TBR_2	-7.02	0.00	0.00	6.75	0.27	-7.02	3.14	243.79	3.09	0.07
cluster3	Linear	4	TBR_1	-3.63	0.00	0.00	3.29	0.34	-3.63	3.18	253.90	3.18	0.05
cluster3	Linear	4	TIR	0.91	-0.91	0.04	-0.04	0.01	0.00	0.15	9.20	0.13	0.00
cluster3	Linear	4	TAR_1	2.41	-2.27	-0.09	-0.04	-0.01	0.14	-1.99	-145.57	-1.44	-0.01
cluster3	Linear	4	TAR_2	-0.78	1.02	-0.04	-0.19	-0.02	0.24	-1.36	-140.72	0.11	0.00
cluster3	Linear	6	ALL	3.14	-1.82	-0.10	-1.21	-0.01	1.32	0.26	24.19	0.52	-0.01
cluster3	Linear	6	TBR_2	-0.57	0.00	0.00	-0.52	1.08	-0.57	6.45	819.99	6.66	0.15
cluster3	Linear	6	TBR_1	-0.43	0.00	0.00	-0.92	1.34	-0.43	5.55	671.26	5.83	0.10
cluster3	Linear	6	TIR	1.23	-1.20	0.05	-0.09	0.01	0.03	0.26	19.90	0.28	0.00
cluster3	Linear	6	TAR_1	3.78	-3.58	-0.12	-0.06	-0.03	0.20	-3.18	-280.73	-2.40	-0.02
cluster3	Linear	6	TAR_2	-2.11	3.29	-0.06	-1.10	-0.03	1.18	-2.99	-452.82	-0.79	0.00
cluster3	Linear	8	ALL	2.97	-1.67	-0.03	-1.30	0.01	1.30	0.15	16.62	0.60	-0.01
cluster3	Linear	8	TBR_2	-0.05	0.00	0.00	-3.11	3.16	-0.05	9.24	1517.36	9.81	0.22
cluster3	Linear	8	TBR_1	-0.07	0.00	0.00	-3.39	3.46	-0.07	8.54	1297.46	9.23	0.15
cluster3	Linear	8	TIR	0.14	-0.25	0.21	-0.10	0.01	-0.11	1.50	130.35	1.40	0.01
cluster3	Linear	8	TAR_1	6.63	-6.22	-0.09	-0.29	-0.03	0.41	-5.12	-483.39	-4.27	-0.02
cluster3	Linear	8	TAR_2	-0.74	4.05	-0.02	-3.28	-0.02	3.31	-6.47	-1203.63	-4.21	0.00
cluster3	Linear	12	ALL	2.81	-1.80	-0.08	-0.96	0.03	1.01	0.04	5.40	0.61	-0.02
cluster3	Linear	12	TBR_2	-0.02	0.00	0.00	-5.33	5.35	-0.02	9.99	2024.16	10.98	0.24
cluster3	Linear	12	TBR_1	-0.01	0.00	0.00	-5.32	5.33	-0.01	9.74	1792.33	10.83	0.18
cluster3	Linear	12	TIR	0.12	-0.12	0.10	-0.12	0.02	0.00	2.16	203.14	1.95	0.01
cluster3	Linear	12	TAR_1	9.75	-9.38	-0.03	-0.34	-0.01	0.37	-6.67	-653.65	-5.86	-0.03
cluster3	Linear	12	TAR_2	-2.39	7.92	0.00	-5.51	-0.01	5.53	-9.24	-2116.79	-6.72	-0.02
cluster3	Linear	16	ALL	2.70	-2.34	-0.18	-0.17	0.01	0.36	-0.10	-12.70	0.48	-0.03
cluster3	Linear	16	TBR_2	-0.01	0.00	0.00	-2.34	2.35	-0.01	7.20	1573.37	8.42	0.19
cluster3	Linear	16	TBR_1	0.00	0.00	0.00	-5.79	5.79	0.00	8.99	1772.16	10.08	0.17
cluster3	Linear	16	TIR	-0.01	0.27	-0.15	-0.11	0.02	0.26	1.92	185.25	1.68	0.01
cluster3	Linear	16	TAR_1	11.45	-11.41	0.00	-0.03	0.00	0.04	-6.86	-676.43	-6.15	-0.03
cluster3	Linear	16	TAR_2	-2.66	7.38	0.00	-4.71	-0.01	4.72	-10.37	-2583.44	-7.93	-0.02
cluster4	CNN	2	ALL	1.18	-0.92	-0.07	-0.19	0.00	0.26	-3.10	-162.88	-1.98	-0.01
cluster4	CNN	2	TBR_2	-0.36	0.00	0.00	0.30	0.05	-0.36	-0.24	-14.79	-0.53	-0.02
cluster4	CNN	2	TBR_1	-2.30	0.00	0.00	2.24	0.05	-2.30	-0.46	-26.02	-0.19	-0.01
cluster4	CNN	2	TIR	2.19	-2.07	-0.09	-0.03	0.00	0.12	-2.06	-95.26	-1.14	-0.01
cluster4	CNN	2	TAR_1	2.26	-2.03	-0.08	-0.14	-0.01	0.23	-2.65	-155.78	-1.95	-0.01
cluster4	CNN	2	TAR_2	-0.44	0.22	-0.03	0.24	0.00	-0.22	-1.73	-131.44	-0.57	0.00
cluster4	CNN	4	ALL	1.72	-0.64	-0.34	-0.72	-0.03	1.08	-5.44	-411.94	-3.47	-0.01

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	4	TBR_2	0.62	0.00	0.00	-0.64	0.03	0.62	-3.77	-388.93	-3.61	-0.09
cluster4	CNN	4	TBR_1	0.04	0.00	0.00	0.38	-0.42	0.04	-2.77	-258.21	-2.04	-0.03
cluster4	CNN	4	TIR	2.42	-1.90	-0.48	-0.03	0.00	0.52	-3.50	-213.43	-1.92	-0.02
cluster4	CNN	4	TAR_1	1.76	-1.31	-0.22	-0.25	0.00	0.45	-2.45	-208.47	-1.69	-0.01
cluster4	CNN	4	TAR_2	-5.94	3.16	-0.09	2.86	0.00	-2.78	-1.14	-149.95	1.84	0.01
cluster4	CNN	6	ALL	3.09	-1.52	-0.69	-0.76	-0.12	1.57	-7.31	-666.91	-5.12	-0.03
cluster4	CNN	6	TBR_2	0.00	0.00	0.00	1.79	-1.79	0.00	-10.88	-1473.14	-9.88	-0.24
cluster4	CNN	6	TBR_1	0.01	0.00	0.00	2.17	-2.17	0.01	-9.03	-1092.14	-7.93	-0.13
cluster4	CNN	6	TIR	5.98	-4.89	-1.05	-0.03	-0.01	1.09	-6.42	-447.94	-4.30	-0.04
cluster4	CNN	6	TAR_1	-3.49	3.63	-0.24	0.11	0.00	0.14	1.48	147.14	2.17	0.01
cluster4	CNN	6	TAR_2	-15.12	5.67	-0.08	9.54	0.00	-9.45	2.24	393.72	7.50	0.04
cluster4	CNN	8	ALL	3.54	-1.45	-1.07	-0.74	-0.26	2.09	-9.17	-932.25	-6.63	-0.05
cluster4	CNN	8	TBR_2	0.00	0.00	0.00	4.29	-4.29	0.00	-14.76	-2419.11	-13.20	-0.31
cluster4	CNN	8	TBR_1	0.00	0.00	0.00	4.81	-4.81	0.00	-12.42	-1817.13	-10.78	-0.18
cluster4	CNN	8	TIR	7.79	-6.06	-1.68	-0.02	-0.02	1.73	-9.18	-723.51	-6.60	-0.06
cluster4	CNN	8	TAR_1	-7.03	6.98	-0.25	0.30	0.00	-0.05	3.41	349.52	4.26	0.02
cluster4	CNN	8	TAR_2	-18.79	4.31	-0.05	14.53	0.00	-14.48	2.72	543.71	9.38	0.05
cluster4	CNN	12	ALL	3.65	-0.98	-1.03	-1.22	-0.42	2.67	-10.59	-1193.16	-7.73	-0.06
cluster4	CNN	12	TBR_2	0.00	0.00	0.00	7.95	-7.95	0.00	-16.56	-3107.30	-15.23	-0.36
cluster4	CNN	12	TBR_1	0.00	0.00	0.00	7.33	-7.33	0.00	-13.50	-2244.17	-12.27	-0.21
cluster4	CNN	12	TIR	7.76	-6.08	-1.64	0.00	-0.04	1.68	-9.53	-779.79	-7.17	-0.07
cluster4	CNN	12	TAR_1	-13.03	12.65	-0.08	0.46	0.00	-0.38	6.34	706.31	7.76	0.04
cluster4	CNN	12	TAR_2	-12.33	-10.27	0.00	22.60	0.00	-22.60	-0.85	-203.82	5.38	0.04
cluster4	CNN	16	ALL	3.75	-0.95	-0.84	-1.44	-0.53	2.80	-11.15	-1310.64	-8.28	-0.06
cluster4	CNN	16	TBR_2	0.00	0.00	0.00	10.32	-10.32	0.00	-16.70	-3366.42	-15.54	-0.38
cluster4	CNN	16	TBR_1	0.00	0.00	0.00	9.58	-9.58	0.00	-13.53	-2406.69	-12.42	-0.21
cluster4	CNN	16	TIR	9.23	-7.85	-1.35	0.02	-0.05	1.38	-10.14	-848.14	-8.05	-0.08
cluster4	CNN	16	TAR_1	-20.19	19.69	-0.01	0.52	0.00	-0.50	8.39	951.85	10.37	0.06
cluster4	CNN	16	TAR_2	-6.03	-23.40	0.00	29.44	0.00	-29.43	-2.01	-515.77	3.70	0.05
cluster4	LSTM	2	ALL	0.82	-0.73	-0.02	-0.06	0.00	0.09	-1.89	-67.60	-1.25	-0.01
cluster4	LSTM	2	TBR_2	-1.25	0.00	0.00	1.27	-0.02	-1.25	-0.17	-6.02	-0.76	-0.03
cluster4	LSTM	2	TBR_1	0.14	0.00	0.00	-0.13	-0.01	0.14	0.01	0.07	-0.07	0.00
cluster4	LSTM	2	TIR	1.74	-1.72	-0.01	0.00	0.00	0.02	-1.30	-42.47	-0.79	-0.01
cluster4	LSTM	2	TAR_1	1.04	-0.99	-0.01	-0.03	0.00	0.05	-1.60	-64.03	-1.13	0.00
cluster4	LSTM	2	TAR_2	0.29	-0.20	-0.01	-0.08	0.00	0.09	-2.07	-98.74	-1.22	0.00
cluster4	LSTM	4	ALL	2.04	-1.28	-0.21	-0.53	-0.01	0.76	-4.32	-280.32	-2.84	-0.02
cluster4	LSTM	4	TBR_2	1.22	0.00	0.00	-1.41	0.19	1.22	-2.37	-197.37	-2.62	-0.07

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	4	TBR_1	1.02	0.00	0.00	-0.92	-0.09	1.02	-2.33	-175.93	-2.02	-0.04
cluster4	LSTM	4	TIR	3.09	-2.77	-0.28	-0.04	-0.01	0.32	-3.08	-167.63	-1.83	-0.02
cluster4	LSTM	4	TAR_1	2.05	-1.70	-0.18	-0.18	0.00	0.35	-2.45	-180.07	-1.77	0.00
cluster4	LSTM	4	TAR_2	-2.99	1.58	-0.07	1.48	0.00	-1.41	-0.66	-68.94	1.40	0.02
cluster4	LSTM	6	ALL	2.54	-1.21	-0.59	-0.67	-0.07	1.33	-6.42	-539.93	-4.33	-0.03
cluster4	LSTM	6	TBR_2	0.72	0.00	0.00	0.15	-0.88	0.72	-8.24	-1000.76	-7.55	-0.18
cluster4	LSTM	6	TBR_1	0.35	0.00	0.00	0.96	-1.32	0.35	-6.75	-738.35	-5.68	-0.09
cluster4	LSTM	6	TIR	4.99	-4.08	-0.85	-0.03	-0.01	0.91	-5.69	-377.84	-3.62	-0.03
cluster4	LSTM	6	TAR_1	-1.46	1.65	-0.29	0.09	0.00	0.19	-0.15	-13.26	0.67	0.00
cluster4	LSTM	6	TAR_2	-13.47	7.18	-0.12	6.40	0.00	-6.29	2.57	395.19	7.29	0.04
cluster4	LSTM	8	ALL	3.17	-1.43	-0.90	-0.62	-0.20	1.74	-8.16	-791.07	-5.83	-0.04
cluster4	LSTM	8	TBR_2	-0.01	0.00	0.00	3.15	-3.14	-0.01	-13.54	-2031.07	-12.06	-0.29
cluster4	LSTM	8	TBR_1	0.02	0.00	0.00	3.68	-3.70	0.02	-11.89	-1589.58	-10.30	-0.17
cluster4	LSTM	8	TIR	7.31	-5.89	-1.37	-0.02	-0.02	1.42	-8.36	-617.88	-5.79	-0.06
cluster4	LSTM	8	TAR_1	-7.01	6.89	-0.28	0.40	0.00	-0.12	3.38	347.29	4.31	0.02
cluster4	LSTM	8	TAR_2	-19.31	5.83	-0.08	13.57	0.00	-13.48	4.30	817.81	10.57	0.05
cluster4	LSTM	12	ALL	3.81	-1.40	-1.04	-0.97	-0.40	2.41	-10.32	-1141.35	-7.71	-0.06
cluster4	LSTM	12	TBR_2	0.00	0.00	0.00	7.16	-7.16	0.00	-17.47	-3190.14	-15.95	-0.38
cluster4	LSTM	12	TBR_1	0.00	0.00	0.00	7.16	-7.16	0.00	-14.67	-2372.29	-13.23	-0.21
cluster4	LSTM	12	TIR	8.88	-7.19	-1.66	0.00	-0.04	1.69	-10.33	-835.98	-7.84	-0.07
cluster4	LSTM	12	TAR_1	-14.64	14.19	-0.11	0.56	0.00	-0.45	7.27	803.40	8.64	0.05
cluster4	LSTM	12	TAR_2	-13.32	-9.02	0.00	22.34	0.00	-22.34	1.02	237.10	7.15	0.05
cluster4	LSTM	16	ALL	3.78	-1.21	-0.98	-1.03	-0.56	2.57	-11.06	-1290.25	-8.34	-0.06
cluster4	LSTM	16	TBR_2	0.00	0.00	0.00	11.00	-11.00	0.00	-18.18	-3605.81	-16.73	-0.39
cluster4	LSTM	16	TBR_1	0.00	0.00	0.00	10.28	-10.28	0.00	-15.23	-2663.65	-13.88	-0.23
cluster4	LSTM	16	TIR	10.23	-8.62	-1.57	0.02	-0.05	1.61	-11.39	-944.71	-8.96	-0.09
cluster4	LSTM	16	TAR_1	-22.37	21.61	-0.01	0.77	0.00	-0.76	9.71	1106.87	11.88	0.06
cluster4	LSTM	16	TAR_2	-7.78	-23.63	0.00	31.41	0.00	-31.41	0.51	129.54	6.54	0.05
cluster4	Linear	2	ALL	1.00	-1.06	-0.03	0.10	-0.01	-0.06	-2.35	-88.31	-1.34	0.00
cluster4	Linear	2	TBR_2	-2.59	0.00	0.00	2.60	-0.01	-2.59	1.20	35.93	1.45	0.02
cluster4	Linear	2	TBR_1	-2.46	0.00	0.00	2.48	-0.01	-2.46	-0.08	-2.53	0.45	0.01
cluster4	Linear	2	TIR	2.41	-2.38	-0.03	0.00	0.00	0.03	-1.96	-68.68	-1.17	-0.01
cluster4	Linear	2	TAR_1	1.11	-1.03	-0.03	-0.02	-0.01	0.08	-1.88	-77.62	-0.95	0.00
cluster4	Linear	2	TAR_2	0.25	-0.17	-0.02	-0.04	-0.01	0.08	-2.07	-103.70	-0.24	0.01
cluster4	Linear	4	ALL	2.40	-2.04	-0.30	-0.02	-0.04	0.36	-4.71	-317.18	-3.05	-0.01
cluster4	Linear	4	TBR_2	-11.85	0.00	0.00	11.78	0.07	-11.85	0.23	17.33	1.56	0.02
cluster4	Linear	4	TBR_1	-4.52	0.00	0.00	4.85	-0.33	-4.52	-2.33	-173.09	-0.56	-0.01

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	Linear	4	TIR	5.71	-5.28	-0.43	0.01	-0.01	0.43	-4.96	-289.72	-3.39	-0.03
cluster4	Linear	4	TAR_1	-0.19	0.43	-0.20	0.03	-0.07	0.24	-1.19	-88.21	0.34	0.00
cluster4	Linear	4	TAR_2	-7.39	5.28	-0.06	2.20	-0.03	-2.11	2.00	213.89	5.23	0.02
cluster4	Linear	6	ALL	2.78	-1.61	-0.65	-0.38	-0.12	1.17	-6.75	-583.96	-4.49	-0.02
cluster4	Linear	6	TBR_2	-1.40	0.00	0.00	2.77	-1.39	-1.40	-4.60	-532.84	-1.62	-0.06
cluster4	Linear	6	TBR_1	-1.17	0.00	0.00	3.13	-1.96	-1.17	-5.42	-595.43	-2.55	-0.04
cluster4	Linear	6	TIR	6.88	-5.85	-1.00	-0.02	-0.01	1.03	-6.99	-490.30	-4.86	-0.04
cluster4	Linear	6	TAR_1	-4.73	4.72	-0.20	0.26	-0.06	-0.01	0.90	83.95	2.81	0.01
cluster4	Linear	6	TAR_2	-17.30	9.71	-0.06	7.68	-0.04	-7.59	2.82	444.39	8.02	0.04
cluster4	Linear	8	ALL	3.01	-1.35	-0.87	-0.55	-0.25	1.66	-8.40	-831.71	-5.73	-0.03
cluster4	Linear	8	TBR_2	-0.22	0.00	0.00	3.85	-3.63	-0.22	-7.29	-1076.51	-3.87	-0.11
cluster4	Linear	8	TBR_1	-0.20	0.00	0.00	4.41	-4.21	-0.20	-7.39	-1003.94	-4.28	-0.07
cluster4	Linear	8	TIR	7.43	-6.00	-1.39	-0.02	-0.02	1.43	-8.05	-618.57	-5.77	-0.05
cluster4	Linear	8	TAR_1	-8.99	8.68	-0.13	0.47	-0.04	-0.31	2.47	252.83	4.65	0.02
cluster4	Linear	8	TAR_2	-18.61	5.25	-0.02	13.39	-0.03	-13.36	1.17	226.81	7.27	0.05
cluster4	Linear	12	ALL	3.63	-1.69	-1.03	-0.39	-0.51	1.94	-10.39	-1165.35	-7.53	-0.05
cluster4	Linear	12	TBR_2	-0.02	0.00	0.00	9.34	-9.32	-0.02	-11.73	-2123.28	-8.87	-0.23
cluster4	Linear	12	TBR_1	-0.01	0.00	0.00	9.13	-9.13	-0.01	-11.15	-1817.27	-8.71	-0.14
cluster4	Linear	12	TIR	9.71	-8.01	-1.67	0.01	-0.05	1.70	-10.18	-833.65	-7.93	-0.08
cluster4	Linear	12	TAR_1	-19.39	18.22	-0.03	1.20	-0.01	-1.17	6.81	760.07	9.63	0.04
cluster4	Linear	12	TAR_2	-11.81	-17.19	0.00	29.02	-0.01	-29.00	-0.06	-12.88	6.25	0.04
cluster4	Linear	16	ALL	3.83	-1.71	-0.84	-0.63	-0.65	2.12	-11.16	-1311.70	-8.38	-0.06
cluster4	Linear	16	TBR_2	-0.01	0.00	0.00	12.32	-12.31	-0.01	-15.13	-2969.17	-13.17	-0.32
cluster4	Linear	16	TBR_1	0.00	0.00	0.00	11.79	-11.79	0.00	-13.66	-2384.75	-11.97	-0.19
cluster4	Linear	16	TIR	11.14	-9.76	-1.34	0.03	-0.06	1.38	-11.31	-937.56	-9.12	-0.09
cluster4	Linear	16	TAR_1	-26.19	25.10	0.00	1.10	0.00	-1.09	9.85	1135.51	12.73	0.07
cluster4	Linear	16	TAR_2	-4.88	-31.86	0.00	36.75	-0.01	-36.74	-0.73	-190.28	5.04	0.04
cluster5	CNN	2	ALL	0.48	-0.28	-0.06	-0.13	0.00	0.20	-0.08	-4.87	0.15	-0.01
cluster5	CNN	2	TBR_2	3.39	0.00	0.00	-3.33	-0.06	3.39	-0.75	-45.85	-0.50	0.00
cluster5	CNN	2	TBR_1	1.01	0.00	0.00	-0.90	-0.11	1.01	-2.12	-116.64	-1.37	-0.02
cluster5	CNN	2	TIR	0.73	-0.62	-0.07	-0.03	0.00	0.11	-0.63	-30.12	-0.21	-0.01
cluster5	CNN	2	TAR_1	-0.20	0.17	-0.07	0.12	0.00	-0.03	-0.15	-9.38	0.05	0.00
cluster5	CNN	2	TAR_2	-3.63	2.85	-0.03	0.80	0.00	-0.78	1.93	153.69	2.52	0.01
cluster5	CNN	4	ALL	-1.26	1.21	-0.17	0.24	-0.02	-0.05	0.17	13.62	0.77	0.00
cluster5	CNN	4	TBR_2	-1.25	0.00	0.00	1.33	-0.08	-1.25	1.40	151.46	1.77	0.06
cluster5	CNN	4	TBR_1	-0.56	0.00	0.00	0.79	-0.23	-0.56	-0.61	-57.55	0.06	0.00
cluster5	CNN	4	TIR	-1.78	1.98	-0.17	-0.03	0.00	0.20	0.02	0.72	0.69	0.00

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	4	TAR_1	0.79	-0.90	-0.19	0.29	0.00	-0.11	-1.09	-93.94	-0.73	-0.01
cluster5	CNN	4	TAR_2	-8.55	4.98	-0.09	3.65	0.00	-3.57	2.63	356.50	4.65	0.02
cluster5	CNN	6	ALL	-0.30	-0.06	-0.33	0.72	-0.04	-0.36	-0.06	-6.12	0.50	0.00
cluster5	CNN	6	TBR_2	0.00	0.00	0.00	-0.38	0.38	0.00	-0.56	-81.03	-0.30	0.02
cluster5	CNN	6	TBR_1	0.00	0.00	0.00	0.69	-0.69	0.00	-3.04	-385.86	-2.40	-0.04
cluster5	CNN	6	TIR	1.01	-0.58	-0.40	-0.04	0.00	0.43	-1.28	-96.04	-0.46	-0.01
cluster5	CNN	6	TAR_1	-0.84	0.46	-0.22	0.61	0.00	-0.38	0.51	50.01	0.63	0.00
cluster5	CNN	6	TAR_2	-12.39	4.29	-0.08	8.18	0.00	-8.10	3.99	708.71	7.58	0.04
cluster5	CNN	8	ALL	-0.17	-0.46	-0.71	1.47	-0.13	-0.63	-0.92	-100.47	-0.01	-0.02
cluster5	CNN	8	TBR_2	0.00	0.00	0.00	1.92	-1.92	0.00	-4.07	-710.83	-2.99	-0.02
cluster5	CNN	8	TBR_1	0.00	0.00	0.00	2.41	-2.41	0.00	-5.57	-853.46	-4.30	-0.07
cluster5	CNN	8	TIR	2.74	-1.70	-0.99	-0.04	-0.01	1.04	-3.49	-294.75	-2.05	-0.02
cluster5	CNN	8	TAR_1	-3.03	2.11	-0.25	1.16	0.00	-0.92	1.67	169.02	2.00	0.01
cluster5	CNN	8	TAR_2	-17.04	3.56	-0.05	13.54	0.00	-13.48	5.79	1174.50	11.29	0.05
cluster5	CNN	12	ALL	-0.20	-1.55	-0.91	3.00	-0.34	-1.75	-1.40	-171.55	-0.48	-0.03
cluster5	CNN	12	TBR_2	0.00	0.00	0.00	6.75	-6.75	0.00	-8.75	-1709.65	-7.29	-0.10
cluster5	CNN	12	TBR_1	0.00	0.00	0.00	5.81	-5.81	0.00	-8.53	-1460.80	-7.15	-0.12
cluster5	CNN	12	TIR	6.28	-4.83	-1.40	-0.01	-0.03	1.45	-6.48	-549.99	-4.78	-0.05
cluster5	CNN	12	TAR_1	-11.74	9.77	-0.08	2.05	0.00	-1.97	5.84	647.80	6.99	0.03
cluster5	CNN	12	TAR_2	-12.32	-12.65	0.00	24.97	0.00	-24.97	4.67	1145.79	10.56	0.05
cluster5	CNN	16	ALL	0.32	-2.34	-0.75	3.20	-0.42	-2.02	-2.13	-270.07	-1.08	-0.03
cluster5	CNN	16	TBR_2	0.00	0.00	0.00	9.05	-9.05	0.00	-8.83	-1849.87	-7.72	-0.11
cluster5	CNN	16	TBR_1	0.00	0.00	0.00	7.41	-7.41	0.00	-8.07	-1479.16	-7.05	-0.11
cluster5	CNN	16	TIR	7.16	-5.92	-1.20	0.00	-0.04	1.24	-6.43	-561.85	-5.26	-0.06
cluster5	CNN	16	TAR_1	-13.66	11.58	-0.01	2.09	0.00	-2.08	6.31	701.90	7.64	0.04
cluster5	CNN	16	TAR_2	-5.95	-19.83	0.00	25.79	0.00	-25.78	0.11	29.11	5.10	0.04
cluster5	LSTM	2	ALL	0.60	-0.42	-0.02	-0.16	0.00	0.18	-0.28	-10.70	0.01	-0.01
cluster5	LSTM	2	TBR_2	-1.38	0.00	0.00	1.42	-0.04	-1.38	0.49	17.74	0.39	0.01
cluster5	LSTM	2	TBR_1	2.06	0.00	0.00	-2.04	-0.02	2.06	-0.91	-29.45	-0.69	-0.01
cluster5	LSTM	2	TIR	0.36	-0.33	-0.01	-0.01	0.00	0.03	-0.25	-8.43	0.02	0.00
cluster5	LSTM	2	TAR_1	0.40	-0.37	-0.01	-0.01	0.00	0.03	-0.59	-24.03	-0.25	0.00
cluster5	LSTM	2	TAR_2	-0.28	0.37	-0.01	-0.07	0.00	0.09	-0.30	-14.61	0.34	0.01
cluster5	LSTM	4	ALL	0.20	0.02	-0.12	-0.08	-0.01	0.22	0.01	0.41	0.29	-0.01
cluster5	LSTM	4	TBR_2	2.64	0.00	0.00	-2.50	-0.14	2.64	-0.10	-9.33	0.04	0.02
cluster5	LSTM	4	TBR_1	2.71	0.00	0.00	-2.53	-0.19	2.71	-2.17	-164.76	-1.70	-0.03
cluster5	LSTM	4	TIR	0.36	-0.20	-0.12	-0.04	-0.01	0.16	-0.63	-35.92	-0.18	-0.01
cluster5	LSTM	4	TAR_1	-0.05	-0.04	-0.14	0.22	0.01	-0.09	-0.28	-21.39	0.00	0.00

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	4	TAR_2	-5.95	3.94	-0.05	2.07	0.00	-2.01	2.62	280.50	3.77	0.02
cluster5	LSTM	6	ALL	-0.51	0.27	-0.34	0.63	-0.04	-0.24	0.12	11.14	0.59	-0.01
cluster5	LSTM	6	TBR_2	0.53	0.00	0.00	-0.47	-0.07	0.53	-0.03	-3.85	0.02	0.03
cluster5	LSTM	6	TBR_1	0.39	0.00	0.00	0.34	-0.73	0.39	-2.89	-327.11	-2.11	-0.03
cluster5	LSTM	6	TIR	1.17	-0.72	-0.40	-0.04	-0.01	0.45	-1.84	-129.21	-0.83	-0.01
cluster5	LSTM	6	TAR_1	-1.71	1.33	-0.27	0.63	0.00	-0.38	0.62	58.06	1.00	0.00
cluster5	LSTM	6	TAR_2	-13.73	6.70	-0.12	7.16	0.00	-7.03	6.07	954.60	9.27	0.04
cluster5	LSTM	8	ALL	-0.30	-0.32	-0.58	1.30	-0.10	-0.62	-0.35	-36.93	0.33	-0.01
cluster5	LSTM	8	TBR_2	-0.01	0.00	0.00	0.98	-0.97	-0.01	-2.01	-325.39	-0.85	0.02
cluster5	LSTM	8	TBR_1	0.00	0.00	0.00	1.78	-1.78	0.00	-4.89	-688.10	-3.58	-0.05
cluster5	LSTM	8	TIR	2.91	-2.08	-0.77	-0.04	-0.01	0.83	-3.35	-264.54	-1.99	-0.02
cluster5	LSTM	8	TAR_1	-3.66	2.89	-0.27	1.04	0.00	-0.77	1.93	195.92	2.36	0.01
cluster5	LSTM	8	TAR_2	-16.97	4.77	-0.08	12.28	0.00	-12.20	6.76	1302.52	11.71	0.05
cluster5	LSTM	12	ALL	-0.02	-1.33	-0.85	2.46	-0.27	-1.35	-1.36	-162.01	-0.46	-0.02
cluster5	LSTM	12	TBR_2	0.00	0.00	0.00	5.19	-5.19	0.00	-6.97	-1346.62	-5.56	-0.07
cluster5	LSTM	12	TBR_1	0.00	0.00	0.00	4.48	-4.48	0.00	-7.72	-1303.08	-6.45	-0.10
cluster5	LSTM	12	TIR	5.42	-4.08	-1.29	-0.02	-0.03	1.34	-5.64	-482.71	-4.12	-0.04
cluster5	LSTM	12	TAR_1	-8.88	7.22	-0.11	1.77	0.00	-1.66	4.80	518.04	5.57	0.03
cluster5	LSTM	12	TAR_2	-13.95	-6.77	0.00	20.71	0.00	-20.72	4.47	1055.66	10.35	0.06
cluster5	LSTM	16	ALL	0.26	-2.16	-0.86	3.16	-0.42	-1.90	-2.02	-253.53	-1.02	-0.04
cluster5	LSTM	16	TBR_2	0.00	0.00	0.00	9.12	-9.12	0.00	-9.07	-1880.94	-7.76	-0.10
cluster5	LSTM	16	TBR_1	0.00	0.00	0.00	7.24	-7.24	0.00	-8.41	-1527.42	-7.32	-0.11
cluster5	LSTM	16	TIR	7.02	-5.62	-1.36	-0.01	-0.04	1.40	-6.54	-573.88	-5.24	-0.06
cluster5	LSTM	16	TAR_1	-13.25	11.22	-0.01	2.04	0.00	-2.03	6.24	689.39	7.44	0.03
cluster5	LSTM	16	TAR_2	-7.58	-18.00	0.00	25.58	0.00	-25.58	1.31	334.27	6.49	0.04
cluster5	Linear	2	ALL	0.72	-0.68	-0.03	0.01	-0.01	0.04	-0.68	-26.95	-0.02	0.00
cluster5	Linear	2	TBR_2	-0.30	0.00	0.00	0.35	-0.05	-0.30	-0.53	-15.20	1.15	0.02
cluster5	Linear	2	TBR_1	-1.17	0.00	0.00	1.19	-0.02	-1.17	-1.09	-32.80	0.10	0.01
cluster5	Linear	2	TIR	0.80	-0.77	-0.03	-0.01	0.00	0.03	-0.74	-26.85	-0.24	-0.01
cluster5	Linear	2	TAR_1	0.25	-0.21	-0.03	0.01	-0.02	0.04	-0.68	-28.83	-0.01	0.00
cluster5	Linear	2	TAR_2	-0.23	0.33	-0.02	-0.06	-0.01	0.10	-0.93	-47.42	0.67	0.01
cluster5	Linear	4	ALL	-0.12	-0.19	-0.20	0.54	-0.04	-0.31	-0.28	-19.88	0.33	0.00
cluster5	Linear	4	TBR_2	-7.19	0.00	0.00	7.44	-0.25	-7.19	0.11	8.16	2.04	0.06
cluster5	Linear	4	TBR_1	-6.47	0.00	0.00	6.77	-0.30	-6.47	-1.66	-124.25	0.35	0.01
cluster5	Linear	4	TIR	1.26	-1.03	-0.23	0.00	-0.01	0.23	-1.74	-107.36	-0.93	-0.01
cluster5	Linear	4	TAR_1	-0.94	0.80	-0.18	0.37	-0.05	-0.14	0.03	2.49	0.86	0.00
cluster5	Linear	4	TAR_2	-9.43	6.79	-0.06	2.72	-0.02	-2.64	4.48	490.13	6.50	0.02

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Cluster	Algorithm	PH	Range	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	Linear	6	ALL	-0.66	0.29	-0.38	0.82	-0.07	-0.37	-0.19	-18.01	0.63	0.00
cluster5	Linear	6	TBR_2	-1.58	0.00	0.00	1.59	-0.02	-1.58	1.29	158.18	3.15	0.09
cluster5	Linear	6	TBR_1	-1.46	0.00	0.00	2.41	-0.96	-1.46	-1.16	-132.41	1.24	0.03
cluster5	Linear	6	TIR	1.19	-0.67	-0.49	-0.02	0.00	0.52	-2.06	-154.91	-0.98	-0.01
cluster5	Linear	6	TAR_1	-2.08	1.62	-0.18	0.70	-0.06	-0.46	0.38	35.06	1.32	0.00
cluster5	Linear	6	TAR_2	-15.38	7.81	-0.06	7.65	-0.03	-7.57	5.33	853.37	8.92	0.04
cluster5	Linear	8	ALL	-0.60	-0.38	-0.65	1.78	-0.16	-0.98	-0.39	-41.60	0.51	-0.01
cluster5	Linear	8	TBR_2	-0.21	0.00	0.00	1.92	-1.71	-0.21	-1.62	-247.93	0.83	0.05
cluster5	Linear	8	TBR_1	-0.23	0.00	0.00	2.82	-2.59	-0.23	-3.49	-487.62	-0.88	-0.01
cluster5	Linear	8	TIR	3.90	-2.90	-0.96	-0.03	-0.01	1.00	-4.11	-332.28	-2.68	-0.03
cluster5	Linear	8	TAR_1	-6.77	5.51	-0.13	1.43	-0.04	-1.26	2.69	275.90	4.11	0.01
cluster5	Linear	8	TAR_2	-19.10	3.44	-0.02	15.69	-0.03	-15.66	7.12	1421.16	12.43	0.06
cluster5	Linear	12	ALL	0.03	-1.81	-0.85	2.98	-0.35	-1.78	-1.61	-193.93	-0.38	-0.02
cluster5	Linear	12	TBR_2	-0.02	0.00	0.00	6.68	-6.66	-0.02	-3.70	-699.22	-1.28	0.02
cluster5	Linear	12	TBR_1	-0.01	0.00	0.00	5.96	-5.96	-0.01	-4.25	-721.71	-2.05	-0.03
cluster5	Linear	12	TIR	5.50	-4.13	-1.33	-0.01	-0.03	1.37	-5.03	-437.65	-3.79	-0.04
cluster5	Linear	12	TAR_1	-10.31	8.23	-0.03	2.12	-0.01	-2.08	3.62	392.82	5.39	0.02
cluster5	Linear	12	TAR_2	-11.00	-13.34	0.00	24.36	-0.01	-24.34	2.01	484.98	7.49	0.04
cluster5	Linear	16	ALL	0.41	-3.00	-0.78	3.90	-0.53	-2.59	-2.25	-283.83	-1.07	-0.03
cluster5	Linear	16	TBR_2	-0.01	0.00	0.00	11.04	-11.03	-0.01	-6.10	-1251.62	-4.26	-0.04
cluster5	Linear	16	TBR_1	0.00	0.00	0.00	9.42	-9.42	0.00	-5.74	-1047.09	-4.15	-0.06
cluster5	Linear	16	TIR	7.42	-6.13	-1.24	0.00	-0.04	1.29	-6.23	-547.64	-5.24	-0.05
cluster5	Linear	16	TAR_1	-14.77	12.19	0.00	2.59	0.00	-2.58	5.42	600.09	7.43	0.04
cluster5	Linear	16	TAR_2	-4.81	-25.88	0.00	30.70	-0.01	-30.69	-0.66	-171.70	4.26	0.03

Appendix F

Performance results for personalized prediction models in the different BGL range

Table F.1 presents the evaluation metric results for the personalized BGL prediction models. Performance results are shown for each selected pair of patients in each cluster, representing the best- and worst-predicted by the corresponding prediction model for that group. The table displays metric results across the different BGL ranges and the six established clusters. Since there are three prediction algorithms, six PH values, six BGL ranges, six groups, and two patients selected per model, the table contains a total of 1,296 rows of results. The "Patient" column indicates the identifier of the patient whose results are displayed, and the "Type" column specifies whether the patient was classified by the corresponding group-based model as best or worst. In cases where performance results are missing, this corresponds to instances where no BGL measurements were available for that specific test set, resulting in no performance data.

Table F.1: Performance results for personalized prediction models in the entire BGL ranges assessed via both clinical and non-clinical metrics. Missing results indicate cases with no available BGL measurements for the specific test set.

Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	12	ALL	LIB193914	best	42.05	52.23	0.01	5.72	0.00	94.28	46.02	2118.11	37.80	0.32
cluster0	CNN	12	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	97.06	9420.89	96.76	1.88
cluster0	CNN	12	TBR_1	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	79.44	6310.59	78.38	1.23
cluster0	CNN	12	TIR	LIB193914	best	49.13	50.37	0.01	0.49	0.00	99.50	37.13	1378.62	30.65	0.29
cluster0	CNN	12	TAR_1	LIB193914	best	20.25	73.64	0.00	6.11	0.00	93.89	59.47	3536.59	55.93	0.27
cluster0	CNN	12	TAR_2	LIB193914	best	0.00	8.26	0.00	91.74	0.00	8.26	117.15	13723.42	114.13	0.42
cluster0	CNN	16	ALL	LIB193914	best	40.76	53.31	0.00	5.93	0.00	94.07	47.28	2235.75	39.04	0.33
cluster0	CNN	16	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	100.61	10122.91	100.15	1.95
cluster0	CNN	16	TBR_1	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	84.04	7062.90	83.63	1.32
cluster0	CNN	16	TIR	LIB193914	best	47.78	51.72	0.00	0.50	0.00	99.50	38.55	1486.48	31.94	0.31
cluster0	CNN	16	TAR_1	LIB193914	best	18.86	74.74	0.00	6.40	0.00	93.60	59.34	3521.01	56.02	0.27
cluster0	CNN	16	TAR_2	LIB193914	best	0.00	0.29	0.00	99.71	0.00	0.29	120.79	14590.32	118.23	0.43
cluster0	CNN	2	ALL	LIB193859	best	75.40	23.67	0.15	0.78	0.00	99.07	33.08	1094.22	25.35	0.14
cluster0	CNN	2	TBR_2	LIB193859	best										
cluster0	CNN	2	TBR_1	LIB193859	best	0.00	0.00	0.00	100.00	0.00	0.00	51.78	2681.42	50.75	0.80
cluster0	CNN	2	TIR	LIB193859	best	69.18	30.60	0.22	0.00	0.00	99.78	27.56	759.30	21.36	0.17
cluster0	CNN	2	TAR_1	LIB193859	best	80.32	18.70	0.13	0.85	0.00	99.02	33.62	1130.63	25.47	0.12
cluster0	CNN	2	TAR_2	LIB193859	best	82.45	15.30	0.00	2.25	0.00	97.75	43.40	1883.39	35.31	0.12
cluster0	CNN	4	ALL	LIB193859	best	59.76	36.76	0.81	2.67	0.00	96.52	45.83	2100.06	35.51	0.20
cluster0	CNN	4	TBR_2	LIB193859	best										
cluster0	CNN	4	TBR_1	LIB193859	best	0.00	0.00	0.00	100.00	0.00	0.00	83.29	6937.30	82.50	1.32
cluster0	CNN	4	TIR	LIB193859	best	56.21	42.34	1.45	0.00	0.00	98.55	38.29	1465.96	29.45	0.24
cluster0	CNN	4	TAR_1	LIB193859	best	64.96	32.44	0.30	2.30	0.00	97.40	42.68	1821.77	34.16	0.16
cluster0	CNN	4	TAR_2	LIB193859	best	59.38	30.63	0.08	9.91	0.00	90.01	65.19	4250.22	53.59	0.18
cluster0	CNN	6	ALL	LIB193914	best	49.84	45.76	0.21	4.12	0.08	95.60	40.86	1669.59	32.66	0.27
cluster0	CNN	6	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	68.19	4650.42	66.04	1.28
cluster0	CNN	6	TBR_1	LIB193914	best	0.00	0.00	0.00	96.72	3.28	0.00	64.79	4197.10	59.82	0.94
cluster0	CNN	6	TIR	LIB193914	best	53.77	45.49	0.27	0.47	0.00	99.26	34.34	1179.34	27.40	0.26
cluster0	CNN	6	TAR_1	LIB193914	best	43.81	52.80	0.00	3.39	0.00	96.61	52.32	2737.67	46.43	0.22
cluster0	CNN	6	TAR_2	LIB193914	best	8.83	52.21	0.00	38.96	0.00	61.04	91.95	8455.09	86.99	0.32
cluster0	CNN	8	ALL	LIB193914	best	45.48	49.71	0.16	4.54	0.11	95.19	43.78	1916.28	35.56	0.30
cluster0	CNN	8	TBR_2	LIB193914	best	0.00	0.00	0.00	93.75	6.25	0.00	80.19	6430.36	78.41	1.51
cluster0	CNN	8	TBR_1	LIB193914	best	0.00	0.00	0.00	96.19	3.81	0.00	72.90	5314.28	69.63	1.10
cluster0	CNN	8	TIR	LIB193914	best	49.48	49.84	0.20	0.46	0.02	99.32	37.06	1373.72	30.09	0.28

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	8	TAR_1	LIB193914	best	38.45	57.31	0.00	4.24	0.00	95.76	54.23	2941.04	48.68	0.23
cluster0	CNN	8	TAR_2	LIB193914	best	4.83	41.55	0.00	53.62	0.00	46.38	100.10	10020.61	95.30	0.35
cluster0	Linear	12	ALL	LIB193914	best	41.89	52.63	0.77	4.38	0.33	94.52	51.95	2699.02	40.37	0.30
cluster0	Linear	12	TBR_2	LIB193914	best	0.00	0.00	0.00	78.57	21.43	0.00	90.86	8254.99	83.33	1.61
cluster0	Linear	12	TBR_1	LIB193914	best	6.44	0.00	0.00	89.60	3.96	6.44	58.00	3363.69	50.02	0.79
cluster0	Linear	12	TIR	LIB193914	best	46.57	52.04	0.98	0.38	0.04	98.61	41.47	1719.44	32.74	0.28
cluster0	Linear	12	TAR_1	LIB193914	best	27.88	66.84	0.00	4.19	1.10	94.72	75.97	5771.38	66.37	0.32
cluster0	Linear	12	TAR_2	LIB193914	best	20.51	20.23	0.00	59.26	0.00	40.74	118.15	13960.13	105.65	0.38
cluster0	Linear	16	ALL	LIB193914	best	39.23	54.55	1.02	4.81	0.40	93.78	54.67	2988.48	42.68	0.32
cluster0	Linear	16	TBR_2	LIB193914	best	0.00	0.00	0.00	78.57	21.43	0.00	92.17	8495.30	82.56	1.61
cluster0	Linear	16	TBR_1	LIB193914	best	4.68	0.00	0.00	91.69	3.64	4.68	60.10	3612.08	53.63	0.84
cluster0	Linear	16	TIR	LIB193914	best	44.28	53.96	1.29	0.41	0.06	98.24	43.17	1863.34	34.23	0.30
cluster0	Linear	16	TAR_1	LIB193914	best	24.01	69.95	0.00	4.65	1.40	93.96	80.08	6413.08	70.93	0.34
cluster0	Linear	16	TAR_2	LIB193914	best	11.50	14.75	0.00	73.16	0.59	26.25	130.40	17004.51	119.97	0.43
cluster0	Linear	2	ALL	LIB193859	best	86.45	13.37	0.03	0.13	0.01	99.82	24.38	594.45	18.39	0.11
cluster0	Linear	2	TBR_2	LIB193859	best										
cluster0	Linear	2	TBR_1	LIB193859	best	20.00	0.00	0.00	80.00	0.00	20.00	29.91	894.83	25.98	0.41
cluster0	Linear	2	TIR	LIB193859	best	79.32	20.62	0.06	0.00	0.00	99.94	23.56	555.22	17.78	0.13
cluster0	Linear	2	TAR_1	LIB193859	best	90.61	9.22	0.00	0.13	0.04	99.83	24.57	603.45	18.22	0.09
cluster0	Linear	2	TAR_2	LIB193859	best	97.26	2.58	0.00	0.16	0.00	99.84	26.03	677.43	20.25	0.07
cluster0	Linear	4	ALL	LIB193859	best	63.39	34.40	0.75	1.43	0.03	97.79	43.28	1873.05	33.34	0.19
cluster0	Linear	4	TBR_2	LIB193859	best										
cluster0	Linear	4	TBR_1	LIB193859	best	0.00	0.00	0.00	100.00	0.00	0.00	59.27	3512.63	53.69	0.86
cluster0	Linear	4	TIR	LIB193859	best	55.73	43.16	1.11	0.00	0.00	98.89	38.78	1503.75	30.02	0.23
cluster0	Linear	4	TAR_1	LIB193859	best	67.69	30.23	0.61	1.43	0.04	97.92	44.73	2000.71	34.34	0.16
cluster0	Linear	4	TAR_2	LIB193859	best	75.35	19.74	0.08	4.75	0.08	95.09	50.82	2582.20	39.96	0.14
cluster0	Linear	6	ALL	LIB193859	best	49.55	44.34	2.05	4.03	0.03	93.89	56.78	3223.75	44.36	0.25
cluster0	Linear	6	TBR_2	LIB193859	best										
cluster0	Linear	6	TBR_1	LIB193859	best	0.00	0.00	0.00	60.00	40.00	0.00	98.65	9732.23	91.35	1.48
cluster0	Linear	6	TIR	LIB193859	best	44.28	52.10	3.62	0.00	0.00	96.38	49.70	2469.71	38.32	0.30
cluster0	Linear	6	TAR_1	LIB193859	best	54.91	40.86	0.88	3.35	0.00	95.77	55.77	3110.25	44.53	0.21
cluster0	Linear	6	TAR_2	LIB193859	best	53.29	30.94	0.17	15.60	0.00	84.23	73.31	5374.16	59.57	0.20
cluster0	Linear	8	ALL	LIB193914	best	48.44	47.14	0.65	3.43	0.34	95.58	47.21	2229.17	35.94	0.27
cluster0	Linear	8	TBR_2	LIB193914	best	0.00	0.00	0.00	93.75	6.25	0.00	59.99	3598.23	51.35	0.99
cluster0	Linear	8	TBR_1	LIB193914	best	18.57	0.00	0.00	75.00	6.43	18.57	56.66	3210.14	43.83	0.69
cluster0	Linear	8	TIR	LIB193914	best	51.68	47.18	0.83	0.26	0.05	98.86	38.85	1508.99	29.99	0.26
cluster0	Linear	8	TAR_1	LIB193914	best	39.64	55.99	0.00	3.51	0.86	95.63	67.57	4565.13	56.68	0.27

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	Linear	8	TAR_2	LIB193914	best	33.51	28.95	0.00	37.53	0.00	62.46	96.20	9254.25	82.59	0.30
cluster0	LSTM	12	ALL	LIB193914	best	41.60	52.84	0.01	5.55	0.00	94.44	46.17	2131.77	38.27	0.33
cluster0	LSTM	12	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	101.48	10298.79	101.17	1.96
cluster0	LSTM	12	TBR_1	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	81.86	6701.41	80.81	1.27
cluster0	LSTM	12	TIR	LIB193914	best	47.13	52.38	0.01	0.49	0.00	99.51	38.81	1506.37	32.10	0.31
cluster0	LSTM	12	TAR_1	LIB193914	best	26.91	67.04	0.00	6.04	0.00	93.95	55.87	3120.90	52.28	0.25
cluster0	LSTM	12	TAR_2	LIB193914	best	0.00	15.95	0.00	84.05	0.00	15.95	111.52	12435.68	108.54	0.39
cluster0	LSTM	16	ALL	LIB193914	best	41.01	53.13	0.00	5.86	0.00	94.14	46.91	2200.46	38.70	0.33
cluster0	LSTM	16	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	100.07	10013.52	99.79	1.94
cluster0	LSTM	16	TBR_1	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	82.11	6741.67	81.60	1.29
cluster0	LSTM	16	TIR	LIB193914	best	48.25	51.25	0.00	0.50	0.00	99.50	37.82	1430.49	31.40	0.30
cluster0	LSTM	16	TAR_1	LIB193914	best	18.14	75.60	0.00	6.26	0.00	93.74	60.09	3610.39	56.78	0.27
cluster0	LSTM	16	TAR_2	LIB193914	best	0.00	2.65	0.00	97.35	0.00	2.65	121.04	14649.71	118.58	0.43
cluster0	LSTM	2	ALL	LIB193859	best	89.88	9.98	0.03	0.12	0.00	99.86	22.28	496.50	16.38	0.09
cluster0	LSTM	2	TBR_2	LIB193859	best										
cluster0	LSTM	2	TBR_1	LIB193859	best	0.00	0.00	0.00	100.00	0.00	0.00	38.94	1516.05	38.54	0.62
cluster0	LSTM	2	TIR	LIB193859	best	84.75	15.19	0.06	0.00	0.00	99.94	19.21	368.97	14.40	0.11
cluster0	LSTM	2	TAR_1	LIB193859	best	93.71	6.16	0.00	0.13	0.00	99.87	21.44	459.47	15.88	0.08
cluster0	LSTM	2	TAR_2	LIB193859	best	96.22	3.78	0.00	0.00	0.00	100.00	29.86	891.72	22.33	0.07
cluster0	LSTM	4	ALL	LIB193859	best	69.01	29.37	0.27	1.34	0.00	98.38	38.38	1472.86	29.34	0.16
cluster0	LSTM	4	TBR_2	LIB193859	best										
cluster0	LSTM	4	TBR_1	LIB193859	best	0.00	0.00	0.00	100.00	0.00	0.00	66.18	4380.16	65.75	1.05
cluster0	LSTM	4	TIR	LIB193859	best	66.41	33.02	0.57	0.00	0.00	99.43	30.66	940.27	23.44	0.19
cluster0	LSTM	4	TAR_1	LIB193859	best	70.42	28.15	0.00	1.43	0.00	98.57	38.65	1493.93	30.39	0.14
cluster0	LSTM	4	TAR_2	LIB193859	best	73.38	22.36	0.00	4.26	0.00	95.74	52.93	2801.65	42.48	0.14
cluster0	LSTM	6	ALL	LIB193914	best	53.40	42.66	0.32	3.50	0.11	96.06	39.10	1528.43	30.73	0.25
cluster0	LSTM	6	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	64.95	4218.37	60.65	1.17
cluster0	LSTM	6	TBR_1	LIB193914	best	1.87	0.00	0.00	94.15	3.98	1.87	62.04	3848.76	54.13	0.85
cluster0	LSTM	6	TIR	LIB193914	best	54.98	44.17	0.41	0.42	0.02	99.15	34.36	1180.74	26.93	0.25
cluster0	LSTM	6	TAR_1	LIB193914	best	56.48	41.17	0.00	2.35	0.00	97.65	47.25	2232.83	39.84	0.19
cluster0	LSTM	6	TAR_2	LIB193914	best	29.61	47.53	0.00	22.86	0.00	77.14	78.45	6155.16	72.12	0.26
cluster0	LSTM	8	ALL	LIB193914	best	47.77	47.61	0.17	4.34	0.12	95.38	42.62	1816.60	34.28	0.28
cluster0	LSTM	8	TBR_2	LIB193914	best	0.00	0.00	0.00	100.00	0.00	0.00	66.64	4440.28	64.08	1.23
cluster0	LSTM	8	TBR_1	LIB193914	best	0.00	0.00	0.00	96.19	3.81	0.00	69.26	4796.92	63.89	1.01
cluster0	LSTM	8	TIR	LIB193914	best	51.61	47.70	0.22	0.44	0.04	99.31	36.29	1317.28	29.13	0.27
cluster0	LSTM	8	TAR_1	LIB193914	best	42.09	53.84	0.00	4.07	0.00	95.93	52.70	2777.26	46.78	0.22

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	8	TAR_2	LIB193914	best	5.09	49.33	0.00	45.58	0.00	54.42	96.77	9363.68	92.15	0.34
cluster1	CNN	12	ALL	LIB193385	best	66.83	32.57	0.00	0.60	0.00	99.40	26.96	726.64	20.63	0.17
cluster1	CNN	12	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	68.71	4720.97	68.66	1.30
cluster1	CNN	12	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	54.47	2967.25	54.15	0.84
cluster1	CNN	12	TIR	LIB193385	best	69.71	30.18	0.00	0.11	0.00	99.89	22.69	514.89	18.37	0.16
cluster1	CNN	12	TAR_1	LIB193385	best	0.00	98.81	0.00	1.19	0.00	98.81	76.48	5848.86	74.84	0.38
cluster1	CNN	12	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	134.68	18137.49	134.59	0.52
cluster1	CNN	16	ALL	LIB193385	best	66.28	33.15	0.00	0.56	0.00	99.43	27.06	732.26	20.84	0.17
cluster1	CNN	16	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	73.11	5344.41	73.10	1.39
cluster1	CNN	16	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	57.68	3326.70	57.44	0.89
cluster1	CNN	16	TIR	LIB193385	best	69.15	30.76	0.00	0.09	0.00	99.91	22.88	523.69	18.59	0.16
cluster1	CNN	16	TAR_1	LIB193385	best	0.00	98.79	0.00	1.21	0.00	98.79	75.40	5685.44	73.75	0.37
cluster1	CNN	16	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	136.35	18590.51	136.23	0.52
cluster1	CNN	2	ALL	LIB193736	best	88.90	11.05	0.00	0.05	0.00	99.95	18.28	334.13	13.43	0.09
cluster1	CNN	2	TBR_2	LIB193736	best										
cluster1	CNN	2	TBR_1	LIB193736	best										
cluster1	CNN	2	TIR	LIB193736	best	88.72	11.23	0.00	0.06	0.00	99.95	16.23	263.27	11.92	0.09
cluster1	CNN	2	TAR_1	LIB193736	best	90.51	9.49	0.00	0.00	0.00	100.00	23.48	551.10	18.56	0.09
cluster1	CNN	2	TAR_2	LIB193736	best	80.56	19.44	0.00	0.00	0.00	100.00	37.92	1438.16	31.91	0.12
cluster1	CNN	4	ALL	LIB193736	best	77.34	22.42	0.00	0.24	0.00	99.76	25.23	636.77	19.16	0.13
cluster1	CNN	4	TBR_2	LIB193736	best										
cluster1	CNN	4	TBR_1	LIB193736	best										
cluster1	CNN	4	TIR	LIB193736	best	78.04	21.90	0.00	0.06	0.00	99.94	21.32	454.68	16.67	0.13
cluster1	CNN	4	TAR_1	LIB193736	best	75.60	23.86	0.00	0.54	0.00	99.46	34.69	1203.50	27.72	0.13
cluster1	CNN	4	TAR_2	LIB193736	best	61.76	32.35	0.00	5.88	0.00	94.11	59.09	3491.91	49.42	0.18
cluster1	CNN	6	ALL	LIB193385	best	70.10	29.25	0.00	0.64	0.00	99.35	25.28	639.23	19.22	0.16
cluster1	CNN	6	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	64.10	4109.43	63.90	1.21
cluster1	CNN	6	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	50.29	2528.98	49.26	0.77
cluster1	CNN	6	TIR	LIB193385	best	72.88	27.01	0.00	0.11	0.00	99.89	21.66	469.17	17.26	0.15
cluster1	CNN	6	TAR_1	LIB193385	best	6.53	92.32	0.00	1.16	0.00	98.85	68.95	4753.47	66.18	0.33
cluster1	CNN	6	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	125.14	15660.15	124.44	0.48
cluster1	CNN	8	ALL	LIB193385	best	67.53	31.84	0.00	0.63	0.00	99.37	26.07	679.66	20.05	0.17
cluster1	CNN	8	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	66.19	4381.76	66.16	1.26
cluster1	CNN	8	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	54.01	2917.20	53.39	0.83
cluster1	CNN	8	TIR	LIB193385	best	70.42	29.47	0.00	0.11	0.00	99.89	22.15	490.44	17.95	0.15
cluster1	CNN	8	TAR_1	LIB193385	best	0.32	98.51	0.00	1.17	0.00	98.83	72.51	5258.06	70.46	0.35

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	8	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	128.65	16551.49	128.42	0.49
cluster1	Linear	12	ALL	LIB193385	best	60.66	38.77	0.00	0.57	0.00	99.43	32.10	1030.27	24.34	0.19
cluster1	Linear	12	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	71.01	5042.89	71.00	1.35
cluster1	Linear	12	TBR_1	LIB193385	best	6.73	0.00	0.00	93.27	0.00	6.73	46.66	2177.36	40.98	0.64
cluster1	Linear	12	TIR	LIB193385	best	62.96	36.93	0.00	0.10	0.00	99.89	28.34	803.00	22.20	0.18
cluster1	Linear	12	TAR_1	LIB193385	best	7.36	91.45	0.00	1.19	0.00	98.81	81.58	6655.97	77.36	0.39
cluster1	Linear	12	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	147.03	21617.41	146.49	0.56
cluster1	Linear	16	ALL	LIB193385	best	58.83	40.57	0.04	0.54	0.00	99.40	32.72	1070.86	25.04	0.20
cluster1	Linear	16	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	88.15	7770.13	87.20	1.65
cluster1	Linear	16	TBR_1	LIB193385	best	4.17	0.00	0.00	95.83	0.00	4.17	50.18	2517.79	44.63	0.70
cluster1	Linear	16	TIR	LIB193385	best	61.13	38.74	0.05	0.09	0.00	99.87	29.03	842.83	22.89	0.19
cluster1	Linear	16	TAR_1	LIB193385	best	6.15	92.65	0.00	1.21	0.00	98.80	81.33	6615.03	77.37	0.39
cluster1	Linear	16	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	148.88	22165.02	148.34	0.57
cluster1	Linear	2	ALL	LIB193736	best	95.87	4.13	0.00	0.00	0.00	100.00	13.15	172.89	9.23	0.06
cluster1	Linear	2	TBR_2	LIB193736	best										
cluster1	Linear	2	TBR_1	LIB193736	best										
cluster1	Linear	2	TIR	LIB193736	best	95.44	4.56	0.00	0.00	0.00	100.00	11.95	142.80	8.26	0.06
cluster1	Linear	2	TAR_1	LIB193736	best	97.44	2.56	0.00	0.00	0.00	100.00	16.71	279.36	12.69	0.06
cluster1	Linear	2	TAR_2	LIB193736	best	100.00	0.00	0.00	0.00	0.00	100.00	22.05	486.24	18.83	0.07
cluster1	Linear	4	ALL	LIB193736	best	83.67	16.33	0.00	0.00	0.00	100.00	23.19	537.68	16.59	0.11
cluster1	Linear	4	TBR_2	LIB193736	best										
cluster1	Linear	4	TBR_1	LIB193736	best										
cluster1	Linear	4	TIR	LIB193736	best	84.65	15.35	0.00	0.00	0.00	100.00	20.40	415.96	14.59	0.11
cluster1	Linear	4	TAR_1	LIB193736	best	79.89	20.11	0.00	0.00	0.00	100.00	31.41	986.33	24.01	0.12
cluster1	Linear	4	TAR_2	LIB193736	best	76.47	23.53	0.00	0.00	0.00	100.00	41.00	1680.62	34.73	0.13
cluster1	Linear	6	ALL	LIB193385	best	71.49	28.01	0.01	0.48	0.01	99.50	26.90	723.65	19.48	0.15
cluster1	Linear	6	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	48.43	2345.61	48.29	0.92
cluster1	Linear	6	TBR_1	LIB193385	best	26.27	0.00	0.00	72.88	0.85	26.27	36.69	1346.46	29.44	0.46
cluster1	Linear	6	TIR	LIB193385	best	73.46	26.44	0.01	0.09	0.00	99.90	23.94	573.17	17.85	0.15
cluster1	Linear	6	TAR_1	LIB193385	best	26.00	72.95	0.00	0.95	0.11	98.95	67.07	4499.05	60.14	0.30
cluster1	Linear	6	TAR_2	LIB193385	best	0.00	14.29	0.00	85.71	0.00	14.29	118.32	14000.77	115.05	0.44
cluster1	Linear	8	ALL	LIB193385	best	65.98	33.51	0.00	0.51	0.00	99.49	29.83	890.03	22.06	0.17
cluster1	Linear	8	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	67.00	4489.47	66.15	1.26
cluster1	Linear	8	TBR_1	LIB193385	best	20.87	0.00	0.00	79.13	0.00	20.87	39.19	1536.07	32.88	0.52
cluster1	Linear	8	TIR	LIB193385	best	68.20	31.72	0.00	0.08	0.00	99.92	26.29	691.03	20.11	0.17
cluster1	Linear	8	TAR_1	LIB193385	best	13.77	85.06	0.00	1.17	0.00	98.83	76.80	5898.61	71.27	0.36
cluster1	Linear	8	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	140.74	19808.82	140.06	0.54

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	12	ALL	LIB193385	best	66.41	32.99	0.00	0.60	0.00	99.40	26.94	725.62	20.71	0.17
cluster1	LSTM	12	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	70.44	4962.29	70.36	1.34
cluster1	LSTM	12	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	56.19	3157.41	55.95	0.87
cluster1	LSTM	12	TIR	LIB193385	best	69.27	30.62	0.00	0.11	0.00	99.89	22.73	516.74	18.47	0.16
cluster1	LSTM	12	TAR_1	LIB193385	best	0.00	98.81	0.00	1.19	0.00	98.81	75.83	5750.12	74.16	0.37
cluster1	LSTM	12	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	134.99	18221.58	134.88	0.52
cluster1	LSTM	16	ALL	LIB193385	best	66.33	33.11	0.00	0.56	0.00	99.44	27.06	732.39	20.83	0.17
cluster1	LSTM	16	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	72.48	5253.29	72.48	1.38
cluster1	LSTM	16	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	56.80	3225.69	56.53	0.88
cluster1	LSTM	16	TIR	LIB193385	best	69.20	30.71	0.00	0.09	0.00	99.91	22.86	522.45	18.58	0.16
cluster1	LSTM	16	TAR_1	LIB193385	best	0.00	98.79	0.00	1.21	0.00	98.79	75.71	5731.44	73.98	0.37
cluster1	LSTM	16	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	136.50	18632.82	136.36	0.52
cluster1	LSTM	2	ALL	LIB193736	best	97.71	2.25	0.00	0.05	0.00	99.96	11.49	131.96	8.04	0.06
cluster1	LSTM	2	TBR_2	LIB193736	best										
cluster1	LSTM	2	TBR_1	LIB193736	best										
cluster1	LSTM	2	TIR	LIB193736	best	97.44	2.51	0.00	0.06	0.00	99.95	10.12	102.33	7.14	0.06
cluster1	LSTM	2	TAR_1	LIB193736	best	98.72	1.28	0.00	0.00	0.00	100.00	13.94	194.41	10.53	0.05
cluster1	LSTM	2	TAR_2	LIB193736	best	100.00	0.00	0.00	0.00	0.00	100.00	30.00	899.78	24.97	0.09
cluster1	LSTM	4	ALL	LIB193736	best	83.96	15.94	0.00	0.10	0.00	99.90	21.18	448.43	16.01	0.11
cluster1	LSTM	4	TBR_2	LIB193736	best										
cluster1	LSTM	4	TBR_1	LIB193736	best										
cluster1	LSTM	4	TIR	LIB193736	best	83.65	16.29	0.00	0.06	0.00	99.94	18.67	348.61	14.40	0.12
cluster1	LSTM	4	TAR_1	LIB193736	best	86.86	13.14	0.00	0.00	0.00	100.00	26.76	715.83	20.63	0.10
cluster1	LSTM	4	TAR_2	LIB193736	best	67.65	29.41	0.00	2.94	0.00	97.06	49.88	2488.04	45.36	0.17
cluster1	LSTM	6	ALL	LIB193385	best	74.00	25.35	0.00	0.64	0.00	99.35	24.06	578.92	17.91	0.15
cluster1	LSTM	6	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	56.53	3195.27	56.42	1.07
cluster1	LSTM	6	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	45.51	2071.54	43.94	0.68
cluster1	LSTM	6	TIR	LIB193385	best	76.66	23.23	0.00	0.11	0.00	99.89	20.70	428.54	16.08	0.14
cluster1	LSTM	6	TAR_1	LIB193385	best	14.11	84.74	0.00	1.16	0.00	98.85	65.13	4242.50	61.82	0.31
cluster1	LSTM	6	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	116.56	13585.64	115.58	0.44
cluster1	LSTM	8	ALL	LIB193385	best	69.50	29.87	0.00	0.63	0.00	99.37	25.63	656.71	19.50	0.16
cluster1	LSTM	8	TBR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	66.11	4370.57	66.07	1.25
cluster1	LSTM	8	TBR_1	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	51.20	2621.80	50.33	0.78
cluster1	LSTM	8	TIR	LIB193385	best	72.47	27.42	0.00	0.11	0.00	99.89	21.78	474.17	17.43	0.15
cluster1	LSTM	8	TAR_1	LIB193385	best	0.53	98.29	0.00	1.17	0.00	98.82	71.38	5094.45	69.06	0.35
cluster1	LSTM	8	TAR_2	LIB193385	best	0.00	0.00	0.00	100.00	0.00	0.00	127.58	16276.76	127.09	0.49
cluster2	CNN	12	ALL	LIB194050	best	54.08	43.12	0.98	1.77	0.05	97.20	48.94	2395.41	39.35	0.25

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	12	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	118.64	14075.13	118.64	2.24
cluster2	CNN	12	TBR_1	LIB194050	best	0.00	0.00	0.00	68.00	32.00	0.00	110.23	12150.91	109.17	1.71
cluster2	CNN	12	TIR	LIB194050	best	31.80	66.17	1.95	0.05	0.03	97.97	54.06	2922.68	46.76	0.37
cluster2	CNN	12	TAR_1	LIB194050	best	87.87	10.84	0.00	1.30	0.00	98.71	27.97	782.60	22.14	0.10
cluster2	CNN	12	TAR_2	LIB194050	best	25.42	62.08	0.00	12.49	0.00	87.50	81.49	6641.19	75.29	0.27
cluster2	CNN	16	ALL	LIB194050	best	54.09	42.91	0.42	2.51	0.08	97.00	49.07	2408.07	39.47	0.25
cluster2	CNN	16	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	100.00	0.00	136.06	18510.99	136.06	2.57
cluster2	CNN	16	TBR_1	LIB194050	best	0.00	0.00	0.00	54.55	45.45	0.00	114.58	13127.69	113.88	1.79
cluster2	CNN	16	TIR	LIB194050	best	37.54	61.56	0.83	0.03	0.04	99.10	50.49	2549.31	43.28	0.35
cluster2	CNN	16	TAR_1	LIB194050	best	85.71	12.36	0.00	1.92	0.00	98.07	30.25	915.18	24.14	0.11
cluster2	CNN	16	TAR_2	LIB194050	best	4.89	77.02	0.00	18.09	0.00	81.91	90.15	8127.06	85.78	0.31
cluster2	CNN	2	ALL	LIB194030	best	86.86	12.72	0.04	0.38	0.00	99.58	26.58	706.34	19.94	0.11
cluster2	CNN	2	TBR_2	LIB194030	best										
cluster2	CNN	2	TBR_1	LIB194030	best	0.00	0.00	0.00	100.00	0.00	0.00	35.81	1282.68	30.67	0.47
cluster2	CNN	2	TIR	LIB194030	best	79.67	20.17	0.03	0.13	0.00	99.84	22.77	518.68	16.82	0.13
cluster2	CNN	2	TAR_1	LIB194030	best	91.18	8.47	0.08	0.27	0.00	99.65	25.26	638.19	18.82	0.09
cluster2	CNN	2	TAR_2	LIB194030	best	93.29	6.30	0.00	0.41	0.00	99.59	33.12	1096.61	26.40	0.09
cluster2	CNN	4	ALL	LIB194030	best	70.37	27.98	0.32	1.33	0.00	98.35	40.22	1617.44	30.67	0.16
cluster2	CNN	4	TBR_2	LIB194030	best										
cluster2	CNN	4	TBR_1	LIB194030	best	0.00	0.00	0.00	100.00	0.00	0.00	56.66	3209.86	53.32	0.82
cluster2	CNN	4	TIR	LIB194030	best	61.38	37.85	0.61	0.16	0.00	99.23	33.20	1102.55	25.47	0.21
cluster2	CNN	4	TAR_1	LIB194030	best	80.41	18.24	0.20	1.15	0.00	98.65	34.77	1209.23	26.49	0.12
cluster2	CNN	4	TAR_2	LIB194030	best	72.16	24.91	0.00	2.94	0.00	97.07	54.66	2987.59	44.54	0.15
cluster2	CNN	6	ALL	LIB194030	best	58.72	37.95	1.04	2.25	0.04	96.67	51.45	2646.91	40.00	0.22
cluster2	CNN	6	TBR_2	LIB194030	best										
cluster2	CNN	6	TBR_1	LIB194030	best	0.00	0.00	0.00	80.00	20.00	0.00	92.44	8544.73	88.05	1.35
cluster2	CNN	6	TIR	LIB194030	best	45.97	51.64	2.23	0.13	0.03	97.61	46.69	2180.36	36.85	0.30
cluster2	CNN	6	TAR_1	LIB194030	best	75.01	22.70	0.32	1.97	0.00	97.71	39.38	1550.91	30.46	0.14
cluster2	CNN	6	TAR_2	LIB194030	best	58.16	36.08	0.05	5.71	0.00	94.24	69.65	4851.44	57.70	0.19
cluster2	CNN	8	ALL	LIB194050	best	55.05	42.04	1.32	1.55	0.04	97.09	47.90	2294.02	38.24	0.25
cluster2	CNN	8	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	101.11	10223.95	101.11	1.91
cluster2	CNN	8	TBR_1	LIB194050	best	0.00	0.00	0.00	72.00	28.00	0.00	106.34	11307.39	102.94	1.61
cluster2	CNN	8	TIR	LIB194050	best	32.42	64.86	2.65	0.06	0.02	97.28	54.24	2942.26	46.36	0.36
cluster2	CNN	8	TAR_1	LIB194050	best	85.11	13.66	0.00	1.23	0.00	98.77	29.36	861.75	22.74	0.11
cluster2	CNN	8	TAR_2	LIB194050	best	43.32	46.33	0.00	10.35	0.00	89.65	71.94	5175.73	63.67	0.23
cluster2	Linear	12	ALL	LIB194050	best	52.27	41.12	1.75	4.85	0.01	93.39	54.14	2931.05	41.87	0.25
cluster2	Linear	12	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	91.35	8345.36	91.35	1.72

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	12	TBR_1	LIB194050	best	0.00	0.00	0.00	96.00	4.00	0.00	82.15	6748.26	75.59	1.18
cluster2	Linear	12	TIR	LIB194050	best	47.48	48.96	3.47	0.06	0.02	96.44	49.58	2458.06	38.46	0.29
cluster2	Linear	12	TAR_1	LIB194050	best	63.90	32.83	0.02	3.25	0.00	96.73	46.08	2123.33	36.52	0.17
cluster2	Linear	12	TAR_2	LIB194050	best	26.84	35.68	0.00	37.48	0.00	62.52	95.76	9169.23	84.61	0.30
cluster2	Linear	16	ALL	LIB194050	best	48.58	43.62	1.86	5.91	0.03	92.20	57.27	3279.84	44.80	0.26
cluster2	Linear	16	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	113.08	12787.15	113.08	2.13
cluster2	Linear	16	TBR_1	LIB194050	best	0.00	0.00	0.00	86.36	13.64	0.00	93.17	8681.45	85.77	1.36
cluster2	Linear	16	TIR	LIB194050	best	45.20	51.03	3.70	0.04	0.03	96.23	51.13	2613.82	40.07	0.31
cluster2	Linear	16	TAR_1	LIB194050	best	59.14	36.83	0.01	4.02	0.00	95.97	49.57	2457.12	39.87	0.19
cluster2	Linear	16	TAR_2	LIB194050	best	20.79	33.76	0.00	45.45	0.00	54.55	102.53	10511.95	92.16	0.33
cluster2	Linear	2	ALL	LIB194030	best	94.11	5.82	0.00	0.07	0.00	99.93	18.82	354.12	13.94	0.07
cluster2	Linear	2	TBR_2	LIB194030	best										
cluster2	Linear	2	TBR_1	LIB194030	best	80.00	0.00	0.00	20.00	0.00	80.00	11.66	136.03	10.09	0.15
cluster2	Linear	2	TIR	LIB194030	best	89.49	10.45	0.00	0.06	0.00	99.94	17.10	292.25	12.42	0.09
cluster2	Linear	2	TAR_1	LIB194030	best	96.21	3.75	0.00	0.04	0.00	99.96	18.83	354.53	13.84	0.07
cluster2	Linear	2	TAR_2	LIB194030	best	98.92	1.08	0.00	0.00	0.00	100.00	21.33	454.83	16.57	0.06
cluster2	Linear	4	ALL	LIB194030	best	75.65	23.02	0.33	0.94	0.05	98.67	36.89	1360.96	27.72	0.15
cluster2	Linear	4	TBR_2	LIB194030	best										
cluster2	Linear	4	TBR_1	LIB194030	best	20.00	0.00	0.00	80.00	0.00	20.00	47.35	2241.98	36.11	0.55
cluster2	Linear	4	TIR	LIB194030	best	68.10	31.22	0.55	0.13	0.00	99.32	31.86	1015.13	23.63	0.18
cluster2	Linear	4	TAR_1	LIB194030	best	79.38	19.19	0.32	0.95	0.16	98.57	36.62	1341.08	27.44	0.13
cluster2	Linear	4	TAR_2	LIB194030	best	83.32	14.84	0.00	1.84	0.00	98.16	44.12	1946.55	34.73	0.12
cluster2	Linear	6	ALL	LIB194030	best	59.78	36.33	1.20	2.56	0.12	96.11	51.37	2638.37	39.43	0.21
cluster2	Linear	6	TBR_2	LIB194030	best										
cluster2	Linear	6	TBR_1	LIB194030	best	0.00	0.00	0.00	90.00	10.00	0.00	61.94	3836.33	53.63	0.82
cluster2	Linear	6	TIR	LIB194030	best	52.46	45.48	1.93	0.13	0.00	97.94	43.89	1926.49	33.35	0.26
cluster2	Linear	6	TAR_1	LIB194030	best	64.89	31.58	1.04	2.21	0.28	96.47	48.99	2400.01	38.15	0.18
cluster2	Linear	6	TAR_2	LIB194030	best	65.32	27.84	0.22	6.57	0.05	93.16	64.20	4122.13	51.05	0.17
cluster2	Linear	8	ALL	LIB194050	best	58.86	36.22	1.17	3.74	0.01	95.08	48.73	2375.02	36.85	0.21
cluster2	Linear	8	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	72.21	5214.14	72.21	1.36
cluster2	Linear	8	TBR_1	LIB194050	best	0.00	0.00	0.00	92.00	8.00	0.00	84.21	7091.71	73.16	1.14
cluster2	Linear	8	TIR	LIB194050	best	55.35	42.28	2.30	0.07	0.01	97.63	43.52	1894.27	32.73	0.25
cluster2	Linear	8	TAR_1	LIB194050	best	68.27	28.84	0.06	2.84	0.00	97.11	43.77	1915.41	33.89	0.16
cluster2	Linear	8	TAR_2	LIB194050	best	35.71	36.98	0.00	27.31	0.00	72.69	84.46	7133.04	73.11	0.26
cluster2	LSTM	12	ALL	LIB194050	best	54.46	42.48	1.01	2.00	0.05	96.94	48.50	2352.01	38.84	0.25
cluster2	LSTM	12	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	105.68	11167.30	105.68	1.99
cluster2	LSTM	12	TBR_1	LIB194050	best	0.00	0.00	0.00	68.00	32.00	0.00	108.19	11705.78	107.07	1.67

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	12	TIR	LIB194050	best	33.89	64.02	2.01	0.06	0.02	97.91	52.90	2798.52	45.25	0.36
cluster2	LSTM	12	TAR_1	LIB194050	best	85.47	13.04	0.00	1.49	0.00	98.51	29.37	862.59	23.09	0.11
cluster2	LSTM	12	TAR_2	LIB194050	best	28.91	56.90	0.00	14.18	0.00	85.81	80.59	6494.00	73.73	0.26
cluster2	LSTM	16	ALL	LIB194050	best	53.56	43.35	0.83	2.18	0.08	96.91	49.62	2462.19	39.99	0.26
cluster2	LSTM	16	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	100.00	0.00	133.66	17864.98	133.66	2.52
cluster2	LSTM	16	TBR_1	LIB194050	best	0.00	0.00	0.00	45.45	54.55	0.00	119.45	14267.55	118.33	1.86
cluster2	LSTM	16	TIR	LIB194050	best	32.93	65.34	1.65	0.04	0.03	98.27	53.63	2876.00	46.28	0.37
cluster2	LSTM	16	TAR_1	LIB194050	best	87.29	10.88	0.00	1.82	0.00	98.17	28.97	839.06	23.07	0.11
cluster2	LSTM	16	TAR_2	LIB194050	best	17.36	67.70	0.00	14.94	0.00	85.06	85.17	7253.90	79.69	0.28
cluster2	LSTM	2	ALL	LIB193556	best	78.95	20.88	0.00	0.17	0.00	99.83	47.17	2225.00	30.39	0.12
cluster2	LSTM	2	TBR_2	LIB193556	best										
cluster2	LSTM	2	TBR_1	LIB193556	best	0.00	0.00	0.00	100.00	0.00	0.00	20.85	434.82	20.70	0.31
cluster2	LSTM	2	TIR	LIB193556	best	87.70	12.19	0.00	0.11	0.00	99.89	17.98	323.36	12.59	0.10
cluster2	LSTM	2	TAR_1	LIB193556	best	96.04	3.77	0.00	0.20	0.00	99.81	17.34	300.56	12.64	0.06
cluster2	LSTM	2	TAR_2	LIB193556	best	52.71	47.29	0.00	0.00	0.00	100.00	77.97	6079.85	66.17	0.21
cluster2	LSTM	4	ALL	LIB194030	best	79.59	19.66	0.15	0.61	0.00	99.25	32.34	1045.63	24.30	0.13
cluster2	LSTM	4	TBR_2	LIB194030	best										
cluster2	LSTM	4	TBR_1	LIB194030	best	0.00	0.00	0.00	100.00	0.00	0.00	55.92	3126.75	53.68	0.83
cluster2	LSTM	4	TIR	LIB194030	best	70.48	29.07	0.29	0.16	0.00	99.55	27.86	776.11	20.93	0.17
cluster2	LSTM	4	TAR_1	LIB194030	best	85.58	13.79	0.08	0.56	0.00	99.37	29.97	898.32	22.32	0.11
cluster2	LSTM	4	TAR_2	LIB194030	best	86.94	12.17	0.00	0.89	0.00	99.11	40.85	1668.68	32.28	0.11
cluster2	LSTM	6	ALL	LIB194030	best	65.51	31.94	0.57	1.98	0.00	97.45	44.97	2022.02	34.46	0.19
cluster2	LSTM	6	TBR_2	LIB194030	best										
cluster2	LSTM	6	TBR_1	LIB194030	best	0.00	0.00	0.00	100.00	0.00	0.00	64.87	4208.76	62.53	0.96
cluster2	LSTM	6	TIR	LIB194030	best	57.63	40.93	1.28	0.16	0.00	98.56	37.84	1432.06	28.92	0.23
cluster2	LSTM	6	TAR_1	LIB194030	best	74.41	23.74	0.12	1.73	0.00	98.15	37.52	1407.76	29.47	0.14
cluster2	LSTM	6	TAR_2	LIB194030	best	66.88	28.33	0.00	4.79	0.00	95.21	61.67	3803.78	50.10	0.17
cluster2	LSTM	8	ALL	LIB194050	best	59.89	37.25	0.72	2.11	0.03	97.14	44.68	1995.89	34.93	0.22
cluster2	LSTM	8	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	0.00	0.00	89.56	8020.76	89.56	1.69
cluster2	LSTM	8	TBR_1	LIB194050	best	0.00	0.00	0.00	80.00	20.00	0.00	103.67	10747.73	100.48	1.57
cluster2	LSTM	8	TIR	LIB194050	best	45.09	53.40	1.44	0.07	0.01	98.49	46.55	2166.49	38.15	0.30
cluster2	LSTM	8	TAR_1	LIB194050	best	82.39	15.84	0.00	1.77	0.00	98.23	31.72	1006.41	24.17	0.11
cluster2	LSTM	8	TAR_2	LIB194050	best	39.41	46.49	0.00	14.10	0.00	85.90	74.20	5505.78	65.91	0.23
cluster3	CNN	12	ALL	LIB193871	best	50.25	43.93	0.09	5.64	0.08	94.18	46.76	2186.67	36.72	0.26
cluster3	CNN	12	TBR_2	LIB193871	best										
cluster3	CNN	12	TBR_1	LIB193871	best	0.00	0.00	0.00	89.04	10.96	0.00	90.22	8138.95	88.99	1.38
cluster3	CNN	12	TIR	LIB193871	best	57.54	42.18	0.13	0.14	0.00	99.72	35.44	1255.97	28.11	0.25

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	CNN	12	TAR_1	LIB193871	best	38.00	56.58	0.00	5.42	0.00	94.58	52.25	2730.49	47.58	0.22
cluster3	CNN	12	TAR_2	LIB193871	best	0.87	13.94	0.00	85.19	0.00	14.81	117.89	13898.07	114.98	0.41
cluster3	CNN	16	ALL	LIB193871	best	48.89	44.76	0.04	6.30	0.02	93.65	47.55	2261.48	37.82	0.27
cluster3	CNN	16	TBR_2	LIB193871	best										
cluster3	CNN	16	TBR_1	LIB193871	best	0.00	0.00	0.00	97.06	2.94	0.00	94.79	8985.57	94.44	1.47
cluster3	CNN	16	TIR	LIB193871	best	53.76	46.04	0.05	0.15	0.00	99.80	37.64	1416.64	30.05	0.27
cluster3	CNN	16	TAR_1	LIB193871	best	44.27	49.40	0.00	6.32	0.00	93.67	49.83	2483.19	45.75	0.22
cluster3	CNN	16	TAR_2	LIB193871	best	0.00	6.05	0.00	93.95	0.00	6.05	118.50	14041.29	116.07	0.41
cluster3	CNN	2	ALL	LIB193551	best	85.15	14.18	0.00	0.65	0.02	99.33	26.79	717.47	20.11	0.11
cluster3	CNN	2	TBR_2	LIB193551	best										
cluster3	CNN	2	TBR_1	LIB193551	best	0.00	0.00	0.00	100.00	0.00	0.00	30.67	940.74	29.77	0.49
cluster3	CNN	2	TIR	LIB193551	best	76.22	23.73	0.00	0.05	0.00	99.95	24.32	591.50	19.00	0.14
cluster3	CNN	2	TAR_1	LIB193551	best	90.18	9.22	0.00	0.56	0.04	99.40	26.18	685.55	18.97	0.09
cluster3	CNN	2	TAR_2	LIB193551	best	92.09	6.55	0.00	1.36	0.00	98.64	31.81	1011.99	24.36	0.09
cluster3	CNN	4	ALL	LIB193871	best	64.81	33.52	0.23	1.41	0.03	98.33	34.75	1207.37	26.73	0.19
cluster3	CNN	4	TBR_2	LIB193871	best										
cluster3	CNN	4	TBR_1	LIB193871	best	0.00	0.00	0.00	97.44	2.56	0.00	64.36	4142.61	61.75	0.96
cluster3	CNN	4	TIR	LIB193871	best	64.05	35.51	0.31	0.12	0.01	99.56	30.30	917.99	23.60	0.20
cluster3	CNN	4	TAR_1	LIB193871	best	70.74	28.21	0.04	1.02	0.00	98.95	38.83	1507.68	30.44	0.15
cluster3	CNN	4	TAR_2	LIB193871	best	57.17	33.60	0.00	9.23	0.00	90.77	62.28	3878.42	52.71	0.19
cluster3	CNN	6	ALL	LIB193871	best	57.41	39.50	0.29	2.79	0.02	96.91	40.61	1648.80	31.63	0.23
cluster3	CNN	6	TBR_2	LIB193871	best										
cluster3	CNN	6	TBR_1	LIB193871	best	0.00	0.00	0.00	98.72	1.28	0.00	78.39	6144.40	77.09	1.20
cluster3	CNN	6	TIR	LIB193871	best	59.75	39.71	0.40	0.12	0.01	99.46	33.91	1149.59	26.43	0.23
cluster3	CNN	6	TAR_1	LIB193871	best	57.66	39.40	0.00	2.94	0.00	97.06	44.27	1959.41	37.52	0.18
cluster3	CNN	6	TAR_2	LIB193871	best	27.13	42.71	0.00	30.16	0.00	69.84	86.34	7453.90	78.84	0.28
cluster3	CNN	8	ALL	LIB193871	best	53.77	42.02	0.29	3.87	0.05	95.79	43.95	1931.55	34.28	0.25
cluster3	CNN	8	TBR_2	LIB193871	best										
cluster3	CNN	8	TBR_1	LIB193871	best	0.00	0.00	0.00	93.59	6.41	0.00	86.66	7510.43	85.22	1.32
cluster3	CNN	8	TIR	LIB193871	best	58.55	40.91	0.41	0.13	0.01	99.46	35.20	1238.98	27.63	0.25
cluster3	CNN	8	TAR_1	LIB193871	best	48.97	47.44	0.00	3.59	0.00	96.41	47.74	2278.70	41.53	0.20
cluster3	CNN	8	TAR_2	LIB193871	best	8.56	39.04	0.00	52.40	0.00	47.60	103.12	10634.34	98.06	0.35
cluster3	Linear	12	ALL	LIB193871	best	42.43	51.39	1.38	4.62	0.18	93.82	57.61	3319.12	44.45	0.30
cluster3	Linear	12	TBR_2	LIB193871	best										
cluster3	Linear	12	TBR_1	LIB193871	best	0.00	0.00	0.00	82.19	17.81	0.00	90.91	8263.99	80.96	1.26
cluster3	Linear	12	TIR	LIB193871	best	47.29	50.66	1.91	0.14	0.00	97.95	44.73	2000.42	34.91	0.29
cluster3	Linear	12	TAR_1	LIB193871	best	34.00	61.46	0.00	4.33	0.21	95.46	70.72	5001.87	60.30	0.29

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	12	TAR_2	LIB193871	best	12.42	18.95	0.00	68.41	0.22	31.37	125.29	15697.92	114.63	0.41
cluster3	Linear	16	ALL	LIB193871	best	40.05	53.00	1.58	5.22	0.15	93.05	60.37	3644.73	46.72	0.31
cluster3	Linear	16	TBR_2	LIB193871	best										
cluster3	Linear	16	TBR_1	LIB193871	best	0.00	0.00	0.00	85.29	14.71	0.00	96.67	9344.26	89.21	1.39
cluster3	Linear	16	TIR	LIB193871	best	46.01	51.64	2.20	0.15	0.00	97.65	45.93	2109.81	36.00	0.30
cluster3	Linear	16	TAR_1	LIB193871	best	28.85	66.45	0.00	4.66	0.04	95.30	72.87	5310.39	63.29	0.30
cluster3	Linear	16	TAR_2	LIB193871	best	6.28	13.00	0.00	79.82	0.90	19.28	139.34	19414.29	130.54	0.47
cluster3	Linear	2	ALL	LIB193518	best	95.96	3.90	0.00	0.14	0.00	99.86	17.34	300.65	12.56	0.07
cluster3	Linear	2	TBR_2	LIB193518	best										
cluster3	Linear	2	TBR_1	LIB193518	best	71.43	0.00	0.00	28.57	0.00	71.43	17.12	292.97	10.46	0.16
cluster3	Linear	2	TIR	LIB193518	best	95.31	4.69	0.00	0.00	0.00	100.00	13.05	170.25	9.50	0.07
cluster3	Linear	2	TAR_1	LIB193518	best	96.48	3.35	0.00	0.17	0.00	99.83	18.28	334.08	13.57	0.06
cluster3	Linear	2	TAR_2	LIB193518	best	96.71	3.14	0.00	0.16	0.00	99.85	24.51	600.68	19.00	0.07
cluster3	Linear	4	ALL	LIB193518	best	82.44	16.46	0.00	1.10	0.00	98.90	30.62	937.51	22.14	0.12
cluster3	Linear	4	TBR_2	LIB193518	best										
cluster3	Linear	4	TBR_1	LIB193518	best	75.00	0.00	0.00	25.00	0.00	75.00	14.54	211.27	10.00	0.16
cluster3	Linear	4	TIR	LIB193518	best	82.04	17.96	0.00	0.00	0.00	100.00	22.12	489.26	16.35	0.12
cluster3	Linear	4	TAR_1	LIB193518	best	85.01	14.11	0.00	0.88	0.00	99.12	30.01	900.36	22.83	0.11
cluster3	Linear	4	TAR_2	LIB193518	best	76.47	18.78	0.00	4.75	0.00	95.25	48.92	2393.03	37.63	0.13
cluster3	Linear	6	ALL	LIB193871	best	58.14	38.98	0.68	2.12	0.08	97.12	42.54	1809.26	31.89	0.22
cluster3	Linear	6	TBR_2	LIB193871	best										
cluster3	Linear	6	TBR_1	LIB193871	best	2.56	0.00	0.00	92.31	5.13	2.56	59.24	3509.57	49.87	0.77
cluster3	Linear	6	TIR	LIB193871	best	59.38	39.60	0.90	0.12	0.00	98.98	35.85	1285.38	27.09	0.22
cluster3	Linear	6	TAR_1	LIB193871	best	57.90	39.88	0.12	1.90	0.20	97.78	51.88	2691.33	40.82	0.20
cluster3	Linear	6	TAR_2	LIB193871	best	48.18	30.57	0.00	21.26	0.00	78.75	74.44	5540.93	61.26	0.22
cluster3	Linear	8	ALL	LIB193871	best	50.09	45.37	1.18	3.19	0.16	95.46	49.91	2490.84	37.90	0.26
cluster3	Linear	8	TBR_2	LIB193871	best										
cluster3	Linear	8	TBR_1	LIB193871	best	1.28	0.00	0.00	83.33	15.38	1.28	74.55	5557.50	63.24	0.98
cluster3	Linear	8	TIR	LIB193871	best	52.45	45.81	1.60	0.13	0.01	98.26	40.63	1651.11	31.11	0.25
cluster3	Linear	8	TAR_1	LIB193871	best	47.92	48.57	0.12	3.18	0.20	96.49	60.75	3690.64	49.64	0.24
cluster3	Linear	8	TAR_2	LIB193871	best	30.27	29.02	0.00	40.71	0.00	59.29	98.03	9610.76	84.72	0.30
cluster3	LSTM	12	ALL	LIB193871	best	51.13	43.29	0.19	5.30	0.09	94.42	46.22	2136.61	36.44	0.26
cluster3	LSTM	12	TBR_2	LIB193871	best										
cluster3	LSTM	12	TBR_1	LIB193871	best	0.00	0.00	0.00	89.04	10.96	0.00	91.14	8305.97	89.80	1.40
cluster3	LSTM	12	TIR	LIB193871	best	57.02	42.58	0.26	0.13	0.01	99.60	36.31	1318.51	28.82	0.26
cluster3	LSTM	12	TAR_1	LIB193871	best	43.42	51.38	0.00	5.21	0.00	94.80	50.03	2502.60	44.97	0.21
cluster3	LSTM	12	TAR_2	LIB193871	best	1.53	19.83	0.00	78.65	0.00	21.36	113.44	12867.81	110.27	0.39

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	16	ALL	LIB193871	best	49.22	44.14	0.00	6.64	0.00	93.36	47.77	2282.16	37.88	0.27
cluster3	LSTM	16	TBR_2	LIB193871	best										
cluster3	LSTM	16	TBR_1	LIB193871	best	0.00	0.00	0.00	100.00	0.00	0.00	93.62	8764.92	93.56	1.46
cluster3	LSTM	16	TIR	LIB193871	best	55.61	44.24	0.00	0.15	0.00	99.85	36.24	1313.39	28.98	0.26
cluster3	LSTM	16	TAR_1	LIB193871	best	39.87	53.55	0.00	6.58	0.00	93.42	52.19	2723.29	48.64	0.23
cluster3	LSTM	16	TAR_2	LIB193871	best	0.00	0.00	0.00	100.00	0.00	0.00	122.46	14996.66	120.12	0.43
cluster3	LSTM	2	ALL	LIB193518	best	97.55	2.35	0.00	0.10	0.00	99.90	15.39	236.74	11.19	0.06
cluster3	LSTM	2	TBR_2	LIB193518	best										
cluster3	LSTM	2	TBR_1	LIB193518	best	64.29	0.00	0.00	35.71	0.00	64.29	13.17	173.53	9.07	0.14
cluster3	LSTM	2	TIR	LIB193518	best	96.94	3.06	0.00	0.00	0.00	100.00	11.70	136.95	8.61	0.06
cluster3	LSTM	2	TAR_1	LIB193518	best	97.81	2.08	0.00	0.11	0.00	99.89	16.09	258.75	11.92	0.06
cluster3	LSTM	2	TAR_2	LIB193518	best	98.98	1.02	0.00	0.00	0.00	100.00	21.84	477.11	16.96	0.06
cluster3	LSTM	4	ALL	LIB193518	best	84.68	14.37	0.00	0.94	0.00	99.05	28.36	804.55	20.69	0.11
cluster3	LSTM	4	TBR_2	LIB193518	best										
cluster3	LSTM	4	TBR_1	LIB193518	best	33.33	0.00	0.00	66.67	0.00	33.33	24.74	612.13	21.61	0.34
cluster3	LSTM	4	TIR	LIB193518	best	82.74	17.26	0.00	0.00	0.00	100.00	20.27	410.68	15.74	0.12
cluster3	LSTM	4	TAR_1	LIB193518	best	89.27	9.96	0.00	0.77	0.00	99.23	26.70	712.96	20.13	0.09
cluster3	LSTM	4	TAR_2	LIB193518	best	78.00	18.37	0.00	3.63	0.00	96.37	47.39	2246.14	37.11	0.13
cluster3	LSTM	6	ALL	LIB193871	best	62.10	35.53	0.28	2.07	0.02	97.63	37.17	1381.70	28.56	0.20
cluster3	LSTM	6	TBR_2	LIB193871	best										
cluster3	LSTM	6	TBR_1	LIB193871	best	0.00	0.00	0.00	97.44	2.56	0.00	72.31	5229.29	71.06	1.10
cluster3	LSTM	6	TIR	LIB193871	best	63.77	35.71	0.39	0.14	0.00	99.48	31.03	962.63	23.97	0.21
cluster3	LSTM	6	TAR_1	LIB193871	best	62.62	35.56	0.00	1.83	0.00	98.18	42.01	1765.13	34.43	0.16
cluster3	LSTM	6	TAR_2	LIB193871	best	42.31	38.06	0.00	19.64	0.00	80.37	74.95	5617.50	66.35	0.24
cluster3	LSTM	8	ALL	LIB193871	best	56.87	39.30	0.31	3.49	0.04	96.17	41.87	1752.85	32.43	0.23
cluster3	LSTM	8	TBR_2	LIB193871	best										
cluster3	LSTM	8	TBR_1	LIB193871	best	0.00	0.00	0.00	96.15	3.85	0.00	84.11	7075.07	82.72	1.29
cluster3	LSTM	8	TIR	LIB193871	best	61.41	38.02	0.43	0.13	0.01	99.43	33.52	1123.89	26.05	0.23
cluster3	LSTM	8	TAR_1	LIB193871	best	51.55	44.86	0.00	3.59	0.00	96.41	46.78	2188.83	40.37	0.19
cluster3	LSTM	8	TAR_2	LIB193871	best	18.79	38.00	0.00	43.22	0.00	56.79	94.81	8989.25	88.24	0.31
cluster4	CNN	12	ALL	LIB194157	best	51.77	45.76	0.00	2.47	0.00	97.53	38.62	1491.60	31.00	0.24
cluster4	CNN	12	TBR_2	LIB194157	best										
cluster4	CNN	12	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	80.66	6505.40	79.56	1.24
cluster4	CNN	12	TIR	LIB194157	best	57.76	42.16	0.00	0.07	0.00	99.92	30.83	950.21	25.17	0.23
cluster4	CNN	12	TAR_1	LIB194157	best	25.00	69.23	0.00	5.77	0.00	94.23	60.85	3702.53	56.29	0.27
cluster4	CNN	12	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	105.31	11090.12	104.10	0.40
cluster4	CNN	16	ALL	LIB194157	best	51.58	45.92	0.00	2.25	0.26	97.50	41.03	1683.77	32.39	0.26

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	16	TBR_2	LIB194157	best										
cluster4	CNN	16	TBR_1	LIB194157	best	0.00	0.00	0.00	73.33	26.67	0.00	99.24	9848.27	96.84	1.52
cluster4	CNN	16	TIR	LIB194157	best	57.90	42.02	0.00	0.08	0.00	99.92	32.41	1050.55	26.07	0.23
cluster4	CNN	16	TAR_1	LIB194157	best	23.67	71.02	0.00	5.31	0.00	94.69	63.47	4029.03	58.29	0.28
cluster4	CNN	16	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	115.53	13346.29	113.66	0.44
cluster4	CNN	2	ALL	LIB193960	best	90.93	8.89	0.00	0.18	0.00	99.82	22.68	514.60	16.32	0.09
cluster4	CNN	2	TBR_2	LIB193960	best										
cluster4	CNN	2	TBR_1	LIB193960	best										
cluster4	CNN	2	TIR	LIB193960	best	91.38	8.62	0.00	0.00	0.00	100.00	15.13	228.88	11.04	0.08
cluster4	CNN	2	TAR_1	LIB193960	best	90.15	9.34	0.00	0.51	0.00	99.49	25.94	672.98	19.41	0.09
cluster4	CNN	2	TAR_2	LIB193960	best	91.30	8.70	0.00	0.00	0.00	100.00	31.70	1004.79	25.02	0.09
cluster4	CNN	4	ALL	LIB194157	best	64.34	34.54	0.00	1.12	0.00	98.88	30.51	930.62	23.93	0.18
cluster4	CNN	4	TBR_2	LIB194157	best										
cluster4	CNN	4	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	36.53	1334.80	35.78	0.56
cluster4	CNN	4	TIR	LIB194157	best	65.81	34.12	0.00	0.06	0.00	99.93	26.08	680.38	21.01	0.18
cluster4	CNN	4	TAR_1	LIB194157	best	61.59	37.02	0.00	1.38	0.00	98.61	46.24	2138.52	37.71	0.18
cluster4	CNN	4	TAR_2	LIB194157	best	10.00	80.00	0.00	10.00	0.00	90.00	67.67	4578.74	65.64	0.25
cluster4	CNN	6	ALL	LIB194157	best	59.07	39.40	0.00	1.53	0.00	98.47	34.51	1191.14	27.35	0.21
cluster4	CNN	6	TBR_2	LIB194157	best										
cluster4	CNN	6	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	49.85	2485.32	49.22	0.77
cluster4	CNN	6	TIR	LIB194157	best	62.19	37.75	0.00	0.07	0.00	99.94	29.09	846.09	23.42	0.20
cluster4	CNN	6	TAR_1	LIB194157	best	47.52	50.00	0.00	2.48	0.00	97.52	52.72	2779.11	45.41	0.22
cluster4	CNN	6	TAR_2	LIB194157	best	0.00	50.00	0.00	50.00	0.00	50.00	82.75	6847.74	82.08	0.32
cluster4	CNN	8	ALL	LIB194157	best	52.91	45.23	0.00	1.86	0.00	98.14	36.40	1325.25	29.06	0.23
cluster4	CNN	8	TBR_2	LIB194157	best										
cluster4	CNN	8	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	65.94	4348.34	64.62	1.01
cluster4	CNN	8	TIR	LIB194157	best	57.35	42.59	0.00	0.07	0.00	99.94	29.82	889.52	24.23	0.21
cluster4	CNN	8	TAR_1	LIB194157	best	34.06	62.68	0.00	3.26	0.00	96.74	56.52	3194.17	50.47	0.24
cluster4	CNN	8	TAR_2	LIB194157	best	0.00	20.00	0.00	80.00	0.00	20.00	96.23	9260.18	94.83	0.37
cluster4	Linear	12	ALL	LIB194157	best	48.77	48.41	0.60	1.80	0.42	97.18	47.45	2251.04	35.96	0.26
cluster4	Linear	12	TBR_2	LIB194157	best										
cluster4	Linear	12	TBR_1	LIB194157	best	0.00	0.00	0.00	60.00	40.00	0.00	110.45	12198.66	103.71	1.63
cluster4	Linear	12	TIR	LIB194157	best	54.21	44.99	0.73	0.07	0.00	99.20	36.58	1338.04	28.54	0.24
cluster4	Linear	12	TAR_1	LIB194157	best	24.62	71.15	0.00	3.85	0.38	95.77	77.62	6024.18	68.10	0.33
cluster4	Linear	12	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	122.63	15038.52	120.90	0.47
cluster4	Linear	16	ALL	LIB194157	best	46.50	50.61	0.19	2.06	0.64	97.11	49.11	2411.39	37.35	0.27
cluster4	Linear	16	TBR_2	LIB194157	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	Linear	16	TBR_1	LIB194157	best	0.00	0.00	0.00	60.00	40.00	0.00	113.96	12987.34	108.64	1.70
cluster4	Linear	16	TIR	LIB194157	best	51.13	48.56	0.23	0.08	0.00	99.69	36.92	1363.28	29.43	0.24
cluster4	Linear	16	TAR_1	LIB194157	best	26.94	66.53	0.00	4.90	1.63	93.47	81.10	6577.24	70.46	0.34
cluster4	Linear	16	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	138.44	19165.37	137.38	0.53
cluster4	Linear	2	ALL	LIB193960	best	96.22	3.78	0.00	0.00	0.00	100.00	16.56	274.32	11.85	0.06
cluster4	Linear	2	TBR_2	LIB193960	best										
cluster4	Linear	2	TBR_1	LIB193960	best										
cluster4	Linear	2	TIR	LIB193960	best	96.12	3.88	0.00	0.00	0.00	100.00	12.23	149.46	8.73	0.06
cluster4	Linear	2	TAR_1	LIB193960	best	94.74	5.26	0.00	0.00	0.00	100.00	19.26	370.76	14.03	0.07
cluster4	Linear	2	TAR_2	LIB193960	best	99.64	0.36	0.00	0.00	0.00	100.00	20.75	430.44	16.23	0.06
cluster4	Linear	4	ALL	LIB194157	best	68.76	30.60	0.05	0.59	0.00	99.36	30.56	933.69	22.38	0.16
cluster4	Linear	4	TBR_2	LIB194157	best										
cluster4	Linear	4	TBR_1	LIB194157	best	53.33	0.00	0.00	46.67	0.00	53.33	14.26	203.36	11.78	0.18
cluster4	Linear	4	TIR	LIB194157	best	69.71	30.22	0.06	0.00	0.00	99.93	26.37	695.38	19.86	0.16
cluster4	Linear	4	TAR_1	LIB194157	best	65.05	33.56	0.00	1.38	0.00	98.61	46.69	2179.56	35.51	0.17
cluster4	Linear	4	TAR_2	LIB194157	best	50.00	50.00	0.00	0.00	0.00	100.00	57.61	3318.87	53.81	0.21
cluster4	Linear	6	ALL	LIB194157	best	59.45	39.29	0.05	1.21	0.00	98.74	36.69	1345.91	27.42	0.20
cluster4	Linear	6	TBR_2	LIB194157	best										
cluster4	Linear	6	TBR_1	LIB194157	best	20.00	0.00	0.00	80.00	0.00	20.00	33.31	1109.61	28.79	0.45
cluster4	Linear	6	TIR	LIB194157	best	62.06	37.88	0.07	0.00	0.00	99.94	30.70	942.57	23.47	0.19
cluster4	Linear	6	TAR_1	LIB194157	best	49.29	48.94	0.00	1.77	0.00	98.23	57.99	3363.12	46.92	0.23
cluster4	Linear	6	TAR_2	LIB194157	best	10.00	40.00	0.00	50.00	0.00	50.00	77.73	6042.31	75.73	0.29
cluster4	Linear	8	ALL	LIB194157	best	54.77	43.25	0.34	1.64	0.00	98.02	41.31	1706.39	31.34	0.23
cluster4	Linear	8	TBR_2	LIB194157	best										
cluster4	Linear	8	TBR_1	LIB194157	best	13.33	0.00	0.00	86.67	0.00	13.33	53.48	2860.16	47.63	0.75
cluster4	Linear	8	TIR	LIB194157	best	57.89	41.70	0.41	0.00	0.00	99.59	34.27	1174.39	26.42	0.22
cluster4	Linear	8	TAR_1	LIB194157	best	42.39	54.71	0.00	2.90	0.00	97.10	65.01	4226.90	54.49	0.26
cluster4	Linear	8	TAR_2	LIB194157	best	0.00	20.00	0.00	80.00	0.00	20.00	92.81	8614.51	91.43	0.35
cluster4	LSTM	12	ALL	LIB194157	best	50.21	47.26	0.00	2.53	0.00	97.47	39.14	1531.58	31.30	0.24
cluster4	LSTM	12	TBR_2	LIB194157	best										
cluster4	LSTM	12	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	75.86	5754.31	75.81	1.19
cluster4	LSTM	12	TIR	LIB194157	best	60.60	39.33	0.00	0.07	0.00	99.93	28.39	806.27	23.70	0.21
cluster4	LSTM	12	TAR_1	LIB194157	best	0.00	93.85	0.00	6.15	0.00	93.85	68.18	4648.18	65.67	0.31
cluster4	LSTM	12	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	118.80	14114.24	118.69	0.46
cluster4	LSTM	16	ALL	LIB194157	best	50.87	46.62	0.00	2.51	0.00	97.49	39.38	1550.40	31.23	0.24
cluster4	LSTM	16	TBR_2	LIB194157	best										
cluster4	LSTM	16	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	74.02	5478.53	73.97	1.16

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	16	TIR	LIB194157	best	61.56	38.37	0.00	0.08	0.00	99.93	27.88	777.16	23.19	0.21
cluster4	LSTM	16	TAR_1	LIB194157	best	0.00	94.69	0.00	5.31	0.00	94.69	69.53	4834.66	67.14	0.32
cluster4	LSTM	16	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	120.64	14554.74	120.53	0.47
cluster4	LSTM	2	ALL	LIB193960	best	78.44	21.56	0.00	0.00	0.00	100.00	41.59	1729.53	27.26	0.12
cluster4	LSTM	2	TBR_2	LIB193960	best										
cluster4	LSTM	2	TBR_1	LIB193960	best										
cluster4	LSTM	2	TIR	LIB193960	best	97.50	2.50	0.00	0.00	0.00	100.00	11.12	123.56	8.38	0.06
cluster4	LSTM	2	TAR_1	LIB193960	best	89.30	10.70	0.00	0.00	0.00	100.00	30.13	907.78	25.39	0.11
cluster4	LSTM	2	TAR_2	LIB193960	best	0.00	100.00	0.00	0.00	0.00	100.00	90.21	8138.16	85.96	0.30
cluster4	LSTM	4	ALL	LIB193960	best	68.74	30.42	0.00	0.83	0.00	99.16	45.52	2071.68	32.26	0.15
cluster4	LSTM	4	TBR_2	LIB193960	best										
cluster4	LSTM	4	TBR_1	LIB193960	best										
cluster4	LSTM	4	TIR	LIB193960	best	88.40	11.60	0.00	0.00	0.00	100.00	16.89	285.30	12.79	0.10
cluster4	LSTM	4	TAR_1	LIB193960	best	74.59	24.31	0.00	1.10	0.00	98.90	37.82	1430.23	32.11	0.14
cluster4	LSTM	4	TAR_2	LIB193960	best	0.00	97.32	0.00	2.68	0.00	97.32	92.46	8549.28	88.52	0.31
cluster4	LSTM	6	ALL	LIB194157	best	58.79	38.90	0.00	2.30	0.00	97.69	36.20	1310.14	27.59	0.20
cluster4	LSTM	6	TBR_2	LIB194157	best										
cluster4	LSTM	6	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	50.50	2549.86	50.39	0.79
cluster4	LSTM	6	TIR	LIB194157	best	70.69	29.25	0.00	0.07	0.00	99.94	24.19	585.15	19.60	0.17
cluster4	LSTM	6	TAR_1	LIB194157	best	0.00	94.33	0.00	5.67	0.00	94.33	68.72	4722.19	66.29	0.32
cluster4	LSTM	6	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	115.26	13284.43	115.14	0.45
cluster4	LSTM	8	ALL	LIB194157	best	51.27	46.36	0.00	2.37	0.00	97.63	38.82	1506.91	31.01	0.24
cluster4	LSTM	8	TBR_2	LIB194157	best										
cluster4	LSTM	8	TBR_1	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	76.05	5784.26	76.01	1.19
cluster4	LSTM	8	TIR	LIB194157	best	61.77	38.16	0.00	0.07	0.00	99.93	28.23	796.85	23.51	0.21
cluster4	LSTM	8	TAR_1	LIB194157	best	0.00	94.20	0.00	5.80	0.00	94.20	67.83	4601.16	65.35	0.31
cluster4	LSTM	8	TAR_2	LIB194157	best	0.00	0.00	0.00	100.00	0.00	0.00	118.61	14067.43	118.49	0.46
cluster5	CNN	12	ALL	LIB193368	best	39.54	53.95	0.41	5.85	0.26	93.49	57.23	3275.19	47.11	0.33
cluster5	CNN	12	TBR_2	LIB193368	best										
cluster5	CNN	12	TBR_1	LIB193368	best	0.00	0.00	0.00	76.09	23.91	0.00	105.61	11154.18	104.13	1.59
cluster5	CNN	12	TIR	LIB193368	best	33.83	65.14	0.70	0.29	0.04	98.97	50.01	2501.28	42.58	0.40
cluster5	CNN	12	TAR_1	LIB193368	best	63.00	33.11	0.00	3.88	0.00	96.11	42.24	1784.57	35.80	0.16
cluster5	CNN	12	TAR_2	LIB193368	best	11.07	54.76	0.00	34.17	0.00	65.83	103.04	10617.25	95.97	0.33
cluster5	CNN	16	ALL	LIB193795	best	41.61	48.32	0.05	9.96	0.06	89.93	51.77	2679.73	40.81	0.33
cluster5	CNN	16	TBR_2	LIB193795	best	0.00	0.00	0.00	97.56	2.44	0.00	78.71	6195.45	77.17	1.46
cluster5	CNN	16	TBR_1	LIB193795	best	0.00	0.00	0.00	99.00	1.00	0.00	75.04	5630.61	73.61	1.21
cluster5	CNN	16	TIR	LIB193795	best	52.35	47.05	0.07	0.54	0.00	99.40	34.91	1218.76	28.42	0.27

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	16	TAR_1	LIB193795	best	20.76	72.94	0.00	6.30	0.00	93.70	64.74	4190.67	60.02	0.28
cluster5	CNN	16	TAR_2	LIB193795	best	2.18	25.89	0.00	71.93	0.00	28.07	129.09	16663.81	123.95	0.43
cluster5	CNN	2	ALL	LIB193368	best	80.69	18.21	0.02	1.08	0.00	98.90	24.87	618.63	19.04	0.13
cluster5	CNN	2	TBR_2	LIB193368	best										
cluster5	CNN	2	TBR_1	LIB193368	best	2.17	0.00	0.00	97.83	0.00	2.17	41.29	1704.81	38.01	0.58
cluster5	CNN	2	TIR	LIB193368	best	73.07	26.60	0.03	0.29	0.00	99.67	24.17	584.20	18.60	0.16
cluster5	CNN	2	TAR_1	LIB193368	best	92.93	6.95	0.00	0.12	0.00	99.88	22.94	526.38	17.21	0.08
cluster5	CNN	2	TAR_2	LIB193368	best	93.58	6.24	0.00	0.18	0.00	99.82	31.55	995.24	25.37	0.09
cluster5	CNN	4	ALL	LIB193368	best	64.11	34.12	0.19	1.54	0.04	98.23	36.01	1296.53	28.41	0.20
cluster5	CNN	4	TBR_2	LIB193368	best										
cluster5	CNN	4	TBR_1	LIB193368	best	0.00	0.00	0.00	95.65	4.35	0.00	67.48	4552.95	63.50	0.97
cluster5	CNN	4	TIR	LIB193368	best	54.29	45.08	0.33	0.30	0.00	99.37	33.89	1148.69	27.17	0.24
cluster5	CNN	4	TAR_1	LIB193368	best	82.64	16.66	0.00	0.70	0.00	99.30	32.34	1046.02	24.65	0.12
cluster5	CNN	4	TAR_2	LIB193368	best	70.41	26.78	0.00	2.81	0.00	97.19	50.80	2580.85	43.38	0.15
cluster5	CNN	6	ALL	LIB193368	best	54.20	43.03	0.30	2.39	0.08	97.23	43.64	1904.58	35.09	0.24
cluster5	CNN	6	TBR_2	LIB193368	best										
cluster5	CNN	6	TBR_1	LIB193368	best	0.00	0.00	0.00	91.30	8.70	0.00	81.77	6686.44	78.77	1.20
cluster5	CNN	6	TIR	LIB193368	best	47.33	51.85	0.51	0.31	0.00	99.18	38.97	1518.65	32.05	0.29
cluster5	CNN	6	TAR_1	LIB193368	best	72.01	26.66	0.00	1.33	0.00	98.67	38.07	1449.47	30.43	0.14
cluster5	CNN	6	TAR_2	LIB193368	best	46.50	44.23	0.00	9.26	0.00	90.73	70.19	4926.85	61.44	0.21
cluster5	CNN	8	ALL	LIB193368	best	46.50	49.04	0.14	4.19	0.12	95.54	50.52	2552.19	40.82	0.28
cluster5	CNN	8	TBR_2	LIB193368	best										
cluster5	CNN	8	TBR_1	LIB193368	best	0.00	0.00	0.00	91.30	8.70	0.00	85.52	7313.31	82.92	1.27
cluster5	CNN	8	TIR	LIB193368	best	44.55	54.89	0.24	0.24	0.07	99.44	40.92	1674.20	33.94	0.31
cluster5	CNN	8	TAR_1	LIB193368	best	61.24	35.24	0.00	3.52	0.00	96.48	44.83	2009.67	37.27	0.17
cluster5	CNN	8	TAR_2	LIB193368	best	20.57	59.43	0.00	20.00	0.00	80.00	91.84	8434.73	84.54	0.29
cluster5	Linear	12	ALL	LIB193427	best	35.63	53.85	2.01	8.21	0.30	89.48	70.88	5023.68	54.40	0.34
cluster5	Linear	12	TBR_2	LIB193427	best										
cluster5	Linear	12	TBR_1	LIB193427	best	0.00	0.00	0.00	83.33	16.67	0.00	91.80	8426.56	82.10	1.32
cluster5	Linear	12	TIR	LIB193427	best	41.09	55.50	3.14	0.23	0.03	96.59	49.28	2428.87	38.91	0.32
cluster5	Linear	12	TAR_1	LIB193427	best	30.43	62.79	0.00	6.63	0.15	93.22	77.51	6008.46	66.93	0.31
cluster5	Linear	12	TAR_2	LIB193427	best	12.61	12.91	0.00	73.87	0.60	25.52	154.73	23939.87	140.30	0.48
cluster5	Linear	16	ALL	LIB193427	best	32.65	54.35	3.22	8.81	0.97	87.00	75.15	5646.81	58.83	0.38
cluster5	Linear	16	TBR_2	LIB193427	best										
cluster5	Linear	16	TBR_1	LIB193427	best	5.66	0.00	0.00	77.36	16.98	5.66	93.72	8783.76	84.11	1.35
cluster5	Linear	16	TIR	LIB193427	best	37.25	57.69	4.85	0.21	0.00	94.94	55.46	3076.35	43.91	0.37
cluster5	Linear	16	TAR_1	LIB193427	best	29.40	60.46	0.40	7.53	2.22	89.86	81.70	6674.25	70.21	0.33

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	Linear	16	TAR_2	LIB193427	best	7.89	8.52	0.00	81.39	2.21	16.41	156.86	24603.97	146.10	0.50
cluster5	Linear	2	ALL	LIB194036	best	86.27	13.42	0.06	0.22	0.03	99.69	24.19	585.23	17.55	0.10
cluster5	Linear	2	TBR_2	LIB194036	best	50.00	0.00	0.00	50.00	0.00	50.00	21.91	480.08	15.83	0.30
cluster5	Linear	2	TBR_1	LIB194036	best	20.00	0.00	0.00	80.00	0.00	20.00	34.59	1196.35	29.35	0.45
cluster5	Linear	2	TIR	LIB194036	best	82.93	16.96	0.10	0.00	0.00	99.89	21.61	466.99	15.28	0.12
cluster5	Linear	2	TAR_1	LIB194036	best	88.99	10.75	0.00	0.17	0.09	99.74	26.63	709.38	19.60	0.09
cluster5	Linear	2	TAR_2	LIB194036	best	94.85	4.92	0.00	0.22	0.00	99.77	27.89	777.85	22.15	0.08
cluster5	Linear	4	ALL	LIB193368	best	69.38	29.20	0.19	1.21	0.02	98.58	34.51	1190.79	26.16	0.17
cluster5	Linear	4	TBR_2	LIB193368	best										
cluster5	Linear	4	TBR_1	LIB193368	best	19.57	0.00	0.00	78.26	2.17	19.57	48.82	2383.01	39.97	0.61
cluster5	Linear	4	TIR	LIB193368	best	62.46	37.00	0.33	0.20	0.00	99.46	32.38	1048.61	24.68	0.20
cluster5	Linear	4	TAR_1	LIB193368	best	80.41	19.02	0.00	0.57	0.00	99.43	35.06	1228.99	26.00	0.12
cluster5	Linear	4	TAR_2	LIB193368	best	80.15	17.79	0.00	2.06	0.00	97.94	42.12	1773.98	33.77	0.12
cluster5	Linear	6	ALL	LIB193368	best	54.24	42.85	0.42	2.29	0.20	97.09	46.11	2125.92	35.68	0.23
cluster5	Linear	6	TBR_2	LIB193368	best										
cluster5	Linear	6	TBR_1	LIB193368	best	13.04	0.00	0.00	80.43	6.52	13.04	68.73	4724.30	57.13	0.87
cluster5	Linear	6	TIR	LIB193368	best	48.45	50.60	0.71	0.20	0.03	99.05	39.09	1528.32	31.17	0.25
cluster5	Linear	6	TAR_1	LIB193368	best	64.03	34.38	0.00	1.20	0.40	98.41	49.19	2420.11	37.60	0.18
cluster5	Linear	6	TAR_2	LIB193368	best	62.19	27.60	0.00	10.21	0.00	89.79	66.21	4383.71	53.40	0.19
cluster5	Linear	8	ALL	LIB193368	best	46.95	48.79	0.47	3.56	0.22	95.74	52.95	2803.32	41.34	0.26
cluster5	Linear	8	TBR_2	LIB193368	best										
cluster5	Linear	8	TBR_1	LIB193368	best	13.04	0.00	0.00	76.09	10.87	13.04	74.49	5548.87	64.25	0.98
cluster5	Linear	8	TIR	LIB193368	best	42.81	56.11	0.80	0.24	0.03	98.92	42.75	1827.84	34.61	0.28
cluster5	Linear	8	TAR_1	LIB193368	best	55.59	41.66	0.00	2.62	0.14	97.25	56.33	3172.74	44.24	0.21
cluster5	Linear	8	TAR_2	LIB193368	best	48.76	32.76	0.00	17.90	0.57	81.52	82.93	6876.89	68.11	0.24
cluster5	LSTM	12	ALL	LIB193368	best	39.17	53.79	0.09	6.82	0.13	92.96	56.71	3216.44	46.31	0.32
cluster5	LSTM	12	TBR_2	LIB193368	best										
cluster5	LSTM	12	TBR_1	LIB193368	best	0.00	0.00	0.00	89.13	10.87	0.00	98.29	9661.20	97.47	1.49
cluster5	LSTM	12	TIR	LIB193368	best	40.22	59.30	0.15	0.29	0.04	99.52	44.46	1976.96	37.49	0.35
cluster5	LSTM	12	TAR_1	LIB193368	best	53.19	41.90	0.00	4.91	0.00	95.09	45.98	2113.71	40.00	0.18
cluster5	LSTM	12	TAR_2	LIB193368	best	0.00	60.97	0.00	39.03	0.00	60.97	110.10	12121.94	105.08	0.36
cluster5	LSTM	16	ALL	LIB193795	best	41.86	48.52	0.10	9.47	0.06	90.38	51.12	2613.64	40.17	0.32
cluster5	LSTM	16	TBR_2	LIB193795	best	0.00	0.00	0.00	100.00	0.00	0.00	74.76	5589.55	73.42	1.39
cluster5	LSTM	16	TBR_1	LIB193795	best	0.00	0.00	0.00	98.75	1.25	0.00	71.96	5178.79	70.41	1.16
cluster5	LSTM	16	TIR	LIB193795	best	52.03	47.30	0.13	0.54	0.00	99.33	34.37	1181.48	28.00	0.26
cluster5	LSTM	16	TAR_1	LIB193795	best	23.94	70.29	0.00	5.77	0.00	94.23	64.63	4177.32	59.33	0.28
cluster5	LSTM	16	TAR_2	LIB193795	best	0.00	37.06	0.00	62.94	0.00	37.06	128.03	16391.55	123.00	0.42

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	2	ALL	LIB194054	best	87.50	12.13	0.00	0.37	0.00	99.63	23.47	550.87	16.54	0.10
cluster5	LSTM	2	TBR_2	LIB194054	best										
cluster5	LSTM	2	TBR_1	LIB194054	best	8.33	0.00	0.00	91.67	0.00	8.33	29.42	865.25	26.46	0.40
cluster5	LSTM	2	TIR	LIB194054	best	83.79	16.21	0.00	0.00	0.00	100.00	20.15	406.11	14.22	0.11
cluster5	LSTM	2	TAR_1	LIB194054	best	91.78	7.92	0.00	0.29	0.00	99.70	22.93	525.59	16.36	0.08
cluster5	LSTM	2	TAR_2	LIB194054	best	94.12	5.50	0.00	0.38	0.00	99.62	33.06	1092.71	24.78	0.08
cluster5	LSTM	4	ALL	LIB193368	best	74.32	24.36	0.08	1.24	0.00	98.68	30.27	916.56	23.03	0.16
cluster5	LSTM	4	TBR_2	LIB193368	best										
cluster5	LSTM	4	TBR_1	LIB193368	best	0.00	0.00	0.00	100.00	0.00	0.00	52.79	2786.95	51.01	0.78
cluster5	LSTM	4	TIR	LIB193368	best	67.43	32.13	0.13	0.30	0.00	99.56	27.40	750.63	21.14	0.18
cluster5	LSTM	4	TAR_1	LIB193368	best	87.36	12.32	0.00	0.32	0.00	99.68	27.14	736.49	20.51	0.10
cluster5	LSTM	4	TAR_2	LIB193368	best	81.09	18.16	0.00	0.75	0.00	99.25	47.06	2215.10	38.58	0.13
cluster5	LSTM	6	ALL	LIB193368	best	60.06	37.60	0.24	2.03	0.06	97.66	39.85	1588.42	31.24	0.21
cluster5	LSTM	6	TBR_2	LIB193368	best										
cluster5	LSTM	6	TBR_1	LIB193368	best	0.00	0.00	0.00	93.48	6.52	0.00	73.11	5345.32	70.69	1.08
cluster5	LSTM	6	TIR	LIB193368	best	54.64	44.64	0.41	0.31	0.00	99.28	34.09	1162.18	27.28	0.24
cluster5	LSTM	6	TAR_1	LIB193368	best	75.47	23.34	0.00	1.20	0.00	98.81	35.97	1293.92	28.08	0.13
cluster5	LSTM	6	TAR_2	LIB193368	best	51.61	42.34	0.00	6.05	0.00	93.95	66.84	4467.11	58.82	0.20
cluster5	LSTM	8	ALL	LIB193368	best	51.49	45.11	0.25	3.11	0.04	96.60	46.92	2201.68	37.43	0.25
cluster5	LSTM	8	TBR_2	LIB193368	best										
cluster5	LSTM	8	TBR_1	LIB193368	best	0.00	0.00	0.00	97.83	2.17	0.00	83.93	7044.37	81.98	1.25
cluster5	LSTM	8	TIR	LIB193368	best	49.01	50.26	0.42	0.28	0.03	99.27	38.34	1470.13	31.45	0.29
cluster5	LSTM	8	TAR_1	LIB193368	best	67.10	30.90	0.00	2.00	0.00	98.00	40.43	1634.68	32.89	0.15
cluster5	LSTM	8	TAR_2	LIB193368	best	26.48	60.19	0.00	13.33	0.00	86.67	85.70	7343.95	78.75	0.27
cluster0	CNN	12	ALL	LIB193526	worst	36.16	37.40	0.09	26.11	0.24	73.56	50.13	2512.92	41.46	0.48
cluster0	CNN	12	TBR_2	LIB193526	worst	0.13	0.00	0.00	98.97	0.90	0.13	69.93	4889.80	67.57	1.37
cluster0	CNN	12	TBR_1	LIB193526	worst	0.27	0.00	0.00	98.63	1.09	0.27	63.81	4071.12	60.62	1.01
cluster0	CNN	12	TIR	LIB193526	worst	51.22	47.42	0.14	1.21	0.00	98.64	34.46	1187.55	27.99	0.27
cluster0	CNN	12	TAR_1	LIB193526	worst	36.54	59.28	0.00	4.19	0.00	95.82	59.21	3506.14	52.74	0.25
cluster0	CNN	12	TAR_2	LIB193526	worst	4.06	28.93	0.00	67.01	0.00	32.99	109.10	11902.22	104.50	0.38
cluster0	CNN	16	ALL	LIB193326	worst	41.95	44.68	4.06	7.46	1.85	86.63	74.72	5582.84	60.16	0.41
cluster0	CNN	16	TBR_2	LIB193326	worst	0.00	0.00	0.00	0.00	100.00	0.00	157.44	24787.48	157.44	2.97
cluster0	CNN	16	TBR_1	LIB193326	worst	0.00	0.00	0.00	48.84	51.16	0.00	123.76	15315.74	121.15	1.97
cluster0	CNN	16	TIR	LIB193326	worst	26.17	63.54	9.93	0.00	0.36	89.71	71.19	5068.21	60.44	0.57
cluster0	CNN	16	TAR_1	LIB193326	worst	77.21	18.84	0.00	3.95	0.00	96.05	37.44	1401.78	30.78	0.14
cluster0	CNN	16	TAR_2	LIB193326	worst	27.91	52.76	0.00	19.33	0.00	80.67	103.10	10629.58	90.08	0.29
cluster0	CNN	2	ALL	LIB193526	worst	74.83	16.55	0.02	8.58	0.02	91.38	22.77	518.40	16.91	0.17

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cluster0	CNN	2	TBR_2	LIB193526	worst	79.25	0.00	0.00	20.75	0.00	79.25	19.74	389.62	16.25	0.33
cluster0	CNN	2	TBR_1	LIB193526	worst	52.27	0.00	0.00	47.66	0.08	52.27	21.75	473.24	16.64	0.28
cluster0	CNN	2	TIR	LIB193526	worst	74.99	24.44	0.03	0.54	0.00	99.43	22.69	514.66	16.74	0.15
cluster0	CNN	2	TAR_1	LIB193526	worst	89.47	10.24	0.00	0.22	0.07	99.71	25.17	633.44	18.03	0.09
cluster0	CNN	2	TAR_2	LIB193526	worst	95.18	4.02	0.00	0.80	0.00	99.20	26.05	678.70	18.77	0.07
cluster0	CNN	4	ALL	LIB193526	worst	56.90	24.39	0.04	18.61	0.06	81.29	30.24	914.23	23.37	0.25
cluster0	CNN	4	TBR_2	LIB193526	worst	22.72	0.00	0.00	77.28	0.00	22.72	31.99	1023.53	28.84	0.59
cluster0	CNN	4	TBR_1	LIB193526	worst	17.78	0.00	0.00	82.15	0.08	17.78	32.02	1025.16	26.79	0.45
cluster0	CNN	4	TIR	LIB193526	worst	65.07	34.15	0.07	0.72	0.00	99.22	27.41	751.26	20.77	0.18
cluster0	CNN	4	TAR_1	LIB193526	worst	76.57	22.04	0.00	1.08	0.31	98.61	35.53	1262.08	26.06	0.13
cluster0	CNN	4	TAR_2	LIB193526	worst	81.33	15.35	0.00	2.90	0.41	96.68	45.09	2033.44	34.55	0.13
cluster0	CNN	6	ALL	LIB193526	worst	47.24	28.91	0.08	23.70	0.08	76.15	37.09	1375.52	29.51	0.32
cluster0	CNN	6	TBR_2	LIB193526	worst	0.24	0.00	0.00	99.64	0.12	0.24	44.83	2009.53	42.11	0.86
cluster0	CNN	6	TBR_1	LIB193526	worst	1.46	0.00	0.00	98.05	0.49	1.46	43.61	1901.90	39.18	0.65
cluster0	CNN	6	TIR	LIB193526	worst	59.45	39.30	0.12	1.12	0.00	98.75	30.37	922.20	23.46	0.21
cluster0	CNN	6	TAR_1	LIB193526	worst	68.72	29.50	0.00	1.78	0.00	98.22	42.88	1838.62	33.20	0.16
cluster0	CNN	6	TAR_2	LIB193526	worst	49.12	31.58	0.00	19.30	0.00	80.70	69.70	4858.11	60.18	0.22
cluster0	CNN	8	ALL	LIB193526	worst	42.12	33.31	0.14	24.28	0.16	75.43	42.27	1786.96	34.07	0.38
cluster0	CNN	8	TBR_2	LIB193526	worst	0.25	0.00	0.00	99.26	0.49	0.25	54.64	2985.50	51.21	1.04
cluster0	CNN	8	TBR_1	LIB193526	worst	0.68	0.00	0.00	98.47	0.85	0.68	50.90	2590.92	46.38	0.77
cluster0	CNN	8	TIR	LIB193526	worst	54.01	44.62	0.22	1.14	0.00	98.63	33.33	1110.87	26.18	0.24
cluster0	CNN	8	TAR_1	LIB193526	worst	60.60	37.28	0.00	2.13	0.00	97.88	47.79	2283.86	38.30	0.18
cluster0	CNN	8	TAR_2	LIB193526	worst	31.19	38.99	0.00	29.82	0.00	70.18	82.95	6881.20	74.24	0.27
cluster0	Linear	12	ALL	LIB193526	worst	42.60	41.38	0.91	13.32	1.79	83.98	52.18	2723.00	39.26	0.37
cluster0	Linear	12	TBR_2	LIB193526	worst	54.88	0.00	0.00	42.93	2.19	54.88	46.12	2127.20	30.42	0.61
cluster0	Linear	12	TBR_1	LIB193526	worst	42.61	0.00	0.00	54.11	3.28	42.61	47.97	2301.03	33.30	0.55
cluster0	Linear	12	TIR	LIB193526	worst	41.09	56.77	1.50	0.58	0.06	97.86	45.67	2085.59	36.02	0.31
cluster0	Linear	12	TAR_1	LIB193526	worst	44.05	46.05	0.00	2.57	7.33	90.10	70.39	4955.34	56.89	0.28
cluster0	Linear	12	TAR_2	LIB193526	worst	23.35	29.95	0.00	41.62	5.08	53.30	106.12	11261.51	93.18	0.34
cluster0	Linear	16	ALL	LIB193526	worst	35.48	44.10	0.92	16.83	2.66	79.58	59.61	3553.58	45.74	0.44
cluster0	Linear	16	TBR_2	LIB193526	worst	40.19	0.00	0.00	56.22	3.59	40.19	57.71	3330.48	42.02	0.85
cluster0	Linear	16	TBR_1	LIB193526	worst	32.50	0.00	0.00	63.02	4.47	32.50	56.72	3216.82	42.34	0.71
cluster0	Linear	16	TIR	LIB193526	worst	37.80	59.88	1.51	0.72	0.09	97.68	48.80	2381.86	38.71	0.33
cluster0	Linear	16	TAR_1	LIB193526	worst	29.44	56.00	0.00	3.67	10.89	85.44	84.02	7059.88	71.53	0.35
cluster0	Linear	16	TAR_2	LIB193526	worst	5.62	19.10	0.00	64.04	11.24	24.72	133.63	17856.19	125.02	0.46
cluster0	Linear	2	ALL	LIB194097	worst	76.84	19.34	0.03	3.77	0.03	96.18	25.46	648.39	18.37	0.15
cluster0	Linear	2	TBR_2	LIB194097	worst	89.92	0.00	0.00	10.08	0.00	89.92	15.70	246.43	10.74	0.21

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	Linear	2	TBR_1	LIB194097	worst	65.65	0.00	0.00	34.35	0.00	65.65	17.98	323.41	13.19	0.21
cluster0	Linear	2	TIR	LIB194097	worst	71.60	28.07	0.04	0.29	0.00	99.67	25.18	634.15	18.40	0.16
cluster0	Linear	2	TAR_1	LIB194097	worst	88.41	11.13	0.00	0.34	0.13	99.54	28.37	804.72	19.82	0.09
cluster0	Linear	2	TAR_2	LIB194097	worst	94.83	4.49	0.00	0.68	0.00	99.32	28.89	834.51	22.28	0.08
cluster0	Linear	4	ALL	LIB193526	worst	71.25	22.67	0.13	5.85	0.11	93.92	27.45	753.54	19.48	0.18
cluster0	Linear	4	TBR_2	LIB193526	worst	84.19	0.00	0.00	15.81	0.00	84.19	17.91	320.66	11.28	0.23
cluster0	Linear	4	TBR_1	LIB193526	worst	69.22	0.00	0.00	30.46	0.31	69.22	22.78	518.73	14.71	0.24
cluster0	Linear	4	TIR	LIB193526	worst	66.89	32.47	0.20	0.43	0.00	99.36	27.84	775.02	20.41	0.18
cluster0	Linear	4	TAR_1	LIB193526	worst	80.67	18.56	0.00	0.39	0.39	99.23	32.95	1085.94	24.18	0.12
cluster0	Linear	4	TAR_2	LIB193526	worst	91.29	7.05	0.00	1.24	0.41	98.34	35.02	1226.16	25.97	0.10
cluster0	Linear	6	ALL	LIB193526	worst	60.63	30.56	0.26	8.26	0.28	91.19	35.25	1242.57	25.54	0.24
cluster0	Linear	6	TBR_2	LIB193526	worst	75.36	0.00	0.00	24.40	0.24	75.36	25.93	672.38	16.14	0.33
cluster0	Linear	6	TBR_1	LIB193526	worst	58.99	0.00	0.00	40.44	0.57	58.99	30.60	936.31	19.86	0.33
cluster0	Linear	6	TIR	LIB193526	worst	56.20	42.96	0.43	0.41	0.00	99.16	34.46	1187.23	25.99	0.22
cluster0	Linear	6	TAR_1	LIB193526	worst	70.18	27.39	0.00	1.30	1.13	97.57	43.32	1876.89	32.63	0.16
cluster0	Linear	6	TAR_2	LIB193526	worst	72.81	19.30	0.00	6.58	1.32	92.11	53.86	2900.65	41.19	0.15
cluster0	Linear	8	ALL	LIB193526	worst	53.12	35.77	0.41	9.99	0.71	88.89	41.69	1737.69	30.63	0.28
cluster0	Linear	8	TBR_2	LIB193526	worst	67.40	0.00	0.00	32.11	0.49	67.40	33.06	1092.84	20.79	0.42
cluster0	Linear	8	TBR_1	LIB193526	worst	53.73	0.00	0.00	45.08	1.19	53.73	36.27	1315.23	23.98	0.40
cluster0	Linear	8	TIR	LIB193526	worst	49.14	49.72	0.67	0.43	0.04	98.86	39.11	1529.27	30.08	0.26
cluster0	Linear	8	TAR_1	LIB193526	worst	60.85	34.55	0.00	1.36	3.23	95.40	53.85	2899.39	41.30	0.20
cluster0	Linear	8	TAR_2	LIB193526	worst	52.29	27.06	0.00	18.81	1.83	79.35	72.78	5297.32	59.73	0.22
cluster0	LSTM	12	ALL	LIB193526	worst	37.43	36.70	0.05	25.50	0.33	74.13	48.02	2306.28	39.30	0.45
cluster0	LSTM	12	TBR_2	LIB193526	worst	0.26	0.00	0.00	98.71	1.03	0.26	64.95	4218.37	61.82	1.25
cluster0	LSTM	12	TBR_1	LIB193526	worst	0.36	0.00	0.00	97.99	1.64	0.36	58.96	3476.12	55.09	0.91
cluster0	LSTM	12	TIR	LIB193526	worst	51.18	47.52	0.08	1.21	0.00	98.70	34.70	1203.77	27.82	0.26
cluster0	LSTM	12	TAR_1	LIB193526	worst	46.34	50.24	0.00	3.43	0.00	96.58	56.56	3199.37	48.23	0.23
cluster0	LSTM	12	TAR_2	LIB193526	worst	3.05	46.19	0.00	50.76	0.00	49.24	103.54	10720.19	98.48	0.36
cluster0	LSTM	16	ALL	LIB193526	worst	33.20	39.17	0.00	27.54	0.08	72.37	53.09	2819.08	44.17	0.52
cluster0	LSTM	16	TBR_2	LIB193526	worst	0.00	0.00	0.00	99.86	0.14	0.00	75.75	5738.23	74.15	1.50
cluster0	LSTM	16	TBR_1	LIB193526	worst	0.00	0.00	0.00	99.50	0.50	0.00	68.82	4736.55	66.46	1.11
cluster0	LSTM	16	TIR	LIB193526	worst	49.20	49.61	0.00	1.19	0.00	98.81	34.34	1179.20	28.35	0.28
cluster0	LSTM	16	TAR_1	LIB193526	worst	24.67	69.67	0.00	5.67	0.00	94.34	64.02	4098.68	58.57	0.28
cluster0	LSTM	16	TAR_2	LIB193526	worst	0.00	5.62	0.00	94.38	0.00	5.62	120.56	14534.27	118.06	0.44
cluster0	LSTM	2	ALL	LIB193526	worst	88.19	8.72	0.01	3.07	0.01	96.91	15.80	249.63	11.19	0.11
cluster0	LSTM	2	TBR_2	LIB193526	worst	95.01	0.00	0.00	4.99	0.00	95.01	10.50	110.20	8.04	0.16
cluster0	LSTM	2	TBR_1	LIB193526	worst	81.24	0.00	0.00	18.68	0.08	81.24	13.05	170.33	9.28	0.15

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	2	TIR	LIB193526	worst	86.40	13.41	0.02	0.18	0.00	99.81	16.29	265.51	11.62	0.10
cluster0	LSTM	2	TAR_1	LIB193526	worst	96.61	3.24	0.00	0.15	0.00	99.85	17.98	323.18	12.56	0.06
cluster0	LSTM	2	TAR_2	LIB193526	worst	98.80	0.80	0.00	0.40	0.00	99.60	19.33	373.80	14.16	0.05
cluster0	LSTM	4	ALL	LIB193526	worst	66.70	19.32	0.04	13.94	0.00	86.02	26.33	693.11	19.79	0.20
cluster0	LSTM	4	TBR_2	LIB193526	worst	53.40	0.00	0.00	46.60	0.00	53.40	24.79	614.38	21.14	0.43
cluster0	LSTM	4	TBR_1	LIB193526	worst	31.48	0.00	0.00	68.52	0.00	31.48	25.61	656.12	20.77	0.35
cluster0	LSTM	4	TIR	LIB193526	worst	71.69	27.57	0.07	0.67	0.00	99.26	24.91	620.60	18.30	0.16
cluster0	LSTM	4	TAR_1	LIB193526	worst	83.60	15.70	0.00	0.70	0.00	99.30	30.94	957.48	22.56	0.11
cluster0	LSTM	4	TAR_2	LIB193526	worst	88.38	9.13	0.00	2.49	0.00	97.51	38.89	1512.16	30.95	0.11
cluster0	LSTM	6	ALL	LIB193526	worst	52.61	26.88	0.09	20.32	0.11	79.49	33.56	1126.60	26.05	0.27
cluster0	LSTM	6	TBR_2	LIB193526	worst	18.39	0.00	0.00	81.61	0.00	18.39	35.57	1265.54	31.43	0.64
cluster0	LSTM	6	TBR_1	LIB193526	worst	11.15	0.00	0.00	88.28	0.57	11.15	36.29	1317.27	31.00	0.52
cluster0	LSTM	6	TIR	LIB193526	worst	61.66	37.34	0.14	0.86	0.00	99.00	29.59	875.59	22.47	0.20
cluster0	LSTM	6	TAR_1	LIB193526	worst	73.01	25.12	0.00	1.62	0.24	98.13	39.98	1598.28	29.82	0.14
cluster0	LSTM	6	TAR_2	LIB193526	worst	67.98	22.37	0.00	9.65	0.00	90.35	56.63	3207.51	47.13	0.17
cluster0	LSTM	8	ALL	LIB193526	worst	44.91	31.25	0.08	23.64	0.13	76.16	39.69	1575.27	31.64	0.35
cluster0	LSTM	8	TBR_2	LIB193526	worst	3.92	0.00	0.00	95.83	0.25	3.92	47.90	2294.77	44.53	0.90
cluster0	LSTM	8	TBR_1	LIB193526	worst	1.61	0.00	0.00	97.63	0.76	1.61	46.55	2167.28	41.82	0.69
cluster0	LSTM	8	TIR	LIB193526	worst	56.01	42.72	0.13	1.14	0.00	98.73	32.61	1063.30	25.24	0.23
cluster0	LSTM	8	TAR_1	LIB193526	worst	67.32	30.47	0.00	2.21	0.00	97.79	45.41	2062.45	34.97	0.17
cluster0	LSTM	8	TAR_2	LIB193526	worst	38.99	39.91	0.00	21.10	0.00	78.90	75.03	5630.20	67.43	0.25
cluster1	CNN	12	ALL	LIB193821	worst	39.61	45.58	0.41	13.79	0.62	85.19	50.12	2512.49	38.78	0.36
cluster1	CNN	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	88.58	7847.27	85.60	1.75
cluster1	CNN	12	TBR_1	LIB193821	worst	3.57	0.00	0.00	91.07	5.36	3.57	63.65	4051.68	53.90	0.86
cluster1	CNN	12	TIR	LIB193821	worst	48.80	49.73	0.53	0.94	0.00	98.53	38.64	1493.38	30.35	0.27
cluster1	CNN	12	TAR_1	LIB193821	worst	17.58	76.92	0.00	5.49	0.00	94.50	78.88	6222.23	71.52	0.35
cluster1	CNN	12	TAR_2	LIB193821	worst	0.00	6.25	0.00	93.75	0.00	6.25	128.90	16615.12	126.13	0.45
cluster1	CNN	16	ALL	LIB193821	worst	36.17	48.83	1.06	12.23	1.70	85.00	56.90	3238.01	43.84	0.40
cluster1	CNN	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	40.00	60.00	0.00	131.20	17214.67	127.88	2.61
cluster1	CNN	16	TBR_1	LIB193821	worst	11.82	0.00	0.00	76.36	11.82	11.82	72.39	5240.37	58.63	0.95
cluster1	CNN	16	TIR	LIB193821	worst	44.01	53.48	1.39	1.11	0.00	97.49	43.85	1922.43	34.39	0.30
cluster1	CNN	16	TAR_1	LIB193821	worst	12.09	82.42	0.00	5.49	0.00	94.51	85.47	7304.46	78.45	0.38
cluster1	CNN	16	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	144.96	21012.77	142.66	0.50
cluster1	CNN	2	ALL	LIB193821	worst	68.25	22.81	0.00	8.94	0.00	91.06	27.33	747.07	19.96	0.18
cluster1	CNN	2	TBR_2	LIB193821	worst	40.00	0.00	0.00	60.00	0.00	40.00	44.13	1947.65	37.84	0.73
cluster1	CNN	2	TBR_1	LIB193821	worst	34.17	0.00	0.00	65.83	0.00	34.17	26.11	681.51	21.68	0.35
cluster1	CNN	2	TIR	LIB193821	worst	73.86	25.28	0.00	0.86	0.00	99.14	23.03	530.18	17.16	0.15

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	2	TAR_1	LIB193821	worst	69.00	30.00	0.00	1.00	0.00	99.00	39.75	1580.40	32.25	0.16
cluster1	CNN	2	TAR_2	LIB193821	worst	43.75	31.25	0.00	25.00	0.00	75.00	81.54	6648.76	66.51	0.23
cluster1	CNN	4	ALL	LIB193821	worst	57.72	31.95	0.19	10.14	0.00	89.67	37.61	1414.60	27.25	0.24
cluster1	CNN	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	54.58	2978.98	53.34	1.09
cluster1	CNN	4	TBR_1	LIB193821	worst	32.20	0.00	0.00	67.80	0.00	32.20	37.24	1386.69	29.72	0.47
cluster1	CNN	4	TIR	LIB193821	worst	63.58	35.17	0.25	1.00	0.00	98.75	30.59	935.62	22.75	0.20
cluster1	CNN	4	TAR_1	LIB193821	worst	50.00	45.92	0.00	4.08	0.00	95.92	57.57	3314.45	46.97	0.23
cluster1	CNN	4	TAR_2	LIB193821	worst	18.75	31.25	0.00	50.00	0.00	50.00	115.82	13414.04	105.11	0.37
cluster1	CNN	6	ALL	LIB193821	worst	48.04	38.82	0.20	12.75	0.20	86.86	42.68	1821.82	32.07	0.30
cluster1	CNN	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	61.56	3789.33	61.15	1.22
cluster1	CNN	6	TBR_1	LIB193821	worst	6.09	0.00	0.00	92.17	1.74	6.09	55.13	3039.82	46.83	0.75
cluster1	CNN	6	TIR	LIB193821	worst	55.96	42.77	0.25	1.02	0.00	98.73	34.28	1174.98	25.95	0.24
cluster1	CNN	6	TAR_1	LIB193821	worst	43.75	52.08	0.00	4.17	0.00	95.83	58.68	3443.63	49.48	0.24
cluster1	CNN	6	TAR_2	LIB193821	worst	0.00	56.25	0.00	43.75	0.00	56.25	120.74	14578.53	113.67	0.40
cluster1	CNN	8	ALL	LIB193821	worst	43.43	42.13	0.10	14.34	0.00	85.56	44.46	1976.46	34.26	0.32
cluster1	CNN	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	77.41	5991.97	71.25	1.49
cluster1	CNN	8	TBR_1	LIB193821	worst	3.51	0.00	0.00	96.49	0.00	3.51	54.89	3012.65	48.97	0.78
cluster1	CNN	8	TIR	LIB193821	worst	52.13	46.71	0.13	1.03	0.00	98.84	33.30	1108.84	26.42	0.24
cluster1	CNN	8	TAR_1	LIB193821	worst	29.79	64.89	0.00	5.32	0.00	94.68	70.63	4988.04	62.56	0.30
cluster1	CNN	8	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	132.93	17671.19	130.99	0.46
cluster1	Linear	12	ALL	LIB193821	worst	37.86	49.07	1.65	9.67	1.75	86.93	56.32	3171.49	42.83	0.36
cluster1	Linear	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	80.00	20.00	0.00	89.93	8086.74	81.74	1.69
cluster1	Linear	12	TBR_1	LIB193821	worst	36.61	0.00	0.00	57.14	6.25	36.61	57.62	3319.71	40.99	0.65
cluster1	Linear	12	TIR	LIB193821	worst	41.18	55.88	2.14	0.67	0.13	97.06	46.43	2155.68	36.30	0.31
cluster1	Linear	12	TAR_1	LIB193821	worst	20.88	64.84	0.00	5.49	8.79	85.72	90.03	8105.00	79.96	0.39
cluster1	Linear	12	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	141.52	20027.53	137.53	0.48
cluster1	Linear	16	ALL	LIB193821	worst	32.02	52.87	1.49	9.68	3.94	84.89	66.30	4395.74	50.36	0.45
cluster1	Linear	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	40.00	60.00	0.00	161.32	26023.49	140.10	2.91
cluster1	Linear	16	TBR_1	LIB193821	worst	26.36	0.00	0.00	56.36	17.27	26.36	85.93	7383.31	61.71	1.00
cluster1	Linear	16	TIR	LIB193821	worst	36.21	60.86	1.95	0.84	0.14	97.07	52.31	2735.93	40.98	0.35
cluster1	Linear	16	TAR_1	LIB193821	worst	13.19	65.93	0.00	5.49	15.38	79.12	99.63	9925.73	90.14	0.44
cluster1	Linear	16	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	141.88	20129.43	139.11	0.49
cluster1	Linear	2	ALL	LIB193821	worst	61.41	30.99	0.38	7.03	0.19	92.40	36.03	1298.38	25.54	0.22
cluster1	Linear	2	TBR_2	LIB193821	worst	20.00	0.00	0.00	80.00	0.00	20.00	30.25	914.81	29.92	0.60
cluster1	Linear	2	TBR_1	LIB193821	worst	50.00	0.00	0.00	48.33	1.67	50.00	36.53	1334.24	24.40	0.39
cluster1	Linear	2	TIR	LIB193821	worst	64.24	34.90	0.37	0.49	0.00	99.14	30.98	959.47	22.49	0.19
cluster1	Linear	2	TAR_1	LIB193821	worst	59.00	36.00	1.00	4.00	0.00	95.00	51.96	2699.81	41.36	0.20

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	Linear	2	TAR_2	LIB193821	worst	31.25	43.75	0.00	25.00	0.00	75.00	97.82	9568.53	88.33	0.31
cluster1	Linear	4	ALL	LIB193821	worst	57.82	33.98	0.68	7.34	0.19	91.80	39.67	1573.85	28.02	0.24
cluster1	Linear	4	TBR_2	LIB193821	worst	20.00	0.00	0.00	80.00	0.00	20.00	45.30	2052.54	40.25	0.81
cluster1	Linear	4	TBR_1	LIB193821	worst	51.69	0.00	0.00	46.61	1.69	51.69	36.29	1317.01	24.94	0.40
cluster1	Linear	4	TIR	LIB193821	worst	59.95	38.80	0.75	0.50	0.00	98.75	34.70	1204.27	25.05	0.22
cluster1	Linear	4	TAR_1	LIB193821	worst	56.12	38.78	1.02	4.08	0.00	94.90	56.59	3202.47	43.92	0.21
cluster1	Linear	4	TAR_2	LIB193821	worst	18.75	25.00	0.00	56.25	0.00	43.75	108.62	11798.81	97.42	0.34
cluster1	Linear	6	ALL	LIB193821	worst	52.06	39.12	0.29	8.14	0.39	91.18	44.27	1960.20	32.20	0.28
cluster1	Linear	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	60.66	3680.05	59.23	1.21
cluster1	Linear	6	TBR_1	LIB193821	worst	46.09	0.00	0.00	50.43	3.48	46.09	45.94	2110.17	30.21	0.49
cluster1	Linear	6	TIR	LIB193821	worst	55.71	43.53	0.38	0.38	0.00	99.24	36.89	1360.90	27.68	0.24
cluster1	Linear	6	TAR_1	LIB193821	worst	39.58	55.21	0.00	5.21	0.00	94.79	65.32	4266.90	55.81	0.27
cluster1	Linear	6	TAR_2	LIB193821	worst	6.25	18.75	0.00	75.00	0.00	25.00	126.57	16020.11	118.91	0.42
cluster1	Linear	8	ALL	LIB193821	worst	41.43	46.61	1.39	9.76	0.80	88.04	52.88	2795.88	39.70	0.34
cluster1	Linear	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	50.60	2560.83	46.07	0.95
cluster1	Linear	8	TBR_1	LIB193821	worst	35.09	0.00	0.00	60.53	4.39	35.09	53.07	2816.93	37.69	0.60
cluster1	Linear	8	TIR	LIB193821	worst	44.90	52.77	1.81	0.52	0.00	97.67	44.28	1960.37	33.99	0.29
cluster1	Linear	8	TAR_1	LIB193821	worst	29.79	61.70	0.00	5.32	3.19	91.49	83.45	6964.36	72.93	0.35
cluster1	Linear	8	TAR_2	LIB193821	worst	0.00	6.25	0.00	93.75	0.00	6.25	136.75	18699.28	133.41	0.47
cluster1	LSTM	12	ALL	LIB193821	worst	26.23	58.74	0.00	15.02	0.00	84.97	50.03	2503.21	41.29	0.36
cluster1	LSTM	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	67.03	4492.87	66.83	1.36
cluster1	LSTM	12	TBR_1	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	53.99	2915.32	53.83	0.86
cluster1	LSTM	12	TIR	LIB193821	worst	34.09	64.84	0.00	1.07	0.00	98.93	35.21	1239.51	31.13	0.27
cluster1	LSTM	12	TAR_1	LIB193821	worst	0.00	94.51	0.00	5.49	0.00	94.51	88.38	7811.23	86.15	0.42
cluster1	LSTM	12	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	166.99	27885.13	165.40	0.58
cluster1	LSTM	16	ALL	LIB193821	worst	25.43	59.26	0.00	15.32	0.00	84.69	50.48	2548.60	41.74	0.37
cluster1	LSTM	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	67.23	4520.05	67.03	1.36
cluster1	LSTM	16	TBR_1	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	54.25	2943.42	54.08	0.86
cluster1	LSTM	16	TIR	LIB193821	worst	33.29	65.60	0.00	1.11	0.00	98.89	35.34	1248.72	31.31	0.27
cluster1	LSTM	16	TAR_1	LIB193821	worst	0.00	94.51	0.00	5.49	0.00	94.51	88.18	7776.29	85.94	0.42
cluster1	LSTM	16	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	166.79	27818.02	165.20	0.58
cluster1	LSTM	2	ALL	LIB193821	worst	49.24	41.73	0.00	9.03	0.00	90.97	44.47	1977.76	31.33	0.22
cluster1	LSTM	2	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	25.05	627.26	24.23	0.50
cluster1	LSTM	2	TBR_1	LIB193821	worst	45.83	0.00	0.00	54.17	0.00	45.83	19.60	383.99	16.66	0.27
cluster1	LSTM	2	TIR	LIB193821	worst	57.09	42.42	0.00	0.49	0.00	99.51	30.90	955.08	23.94	0.18
cluster1	LSTM	2	TAR_1	LIB193821	worst	0.00	95.00	0.00	5.00	0.00	95.00	89.56	8021.49	87.55	0.43
cluster1	LSTM	2	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	168.57	28416.60	167.00	0.59

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	4	ALL	LIB193821	worst	28.76	56.37	0.00	14.86	0.00	85.13	48.11	2314.66	38.34	0.32
cluster1	LSTM	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	61.95	3837.53	61.59	1.25
cluster1	LSTM	4	TBR_1	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	43.94	1930.80	43.41	0.70
cluster1	LSTM	4	TIR	LIB193821	worst	37.30	61.45	0.00	1.25	0.00	98.75	33.66	1133.01	28.81	0.24
cluster1	LSTM	4	TAR_1	LIB193821	worst	0.00	94.90	0.00	5.10	0.00	94.90	89.88	8078.51	87.81	0.43
cluster1	LSTM	4	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	168.45	28374.68	166.87	0.59
cluster1	LSTM	6	ALL	LIB193821	worst	26.67	58.63	0.00	14.71	0.00	85.30	49.52	2452.23	40.92	0.36
cluster1	LSTM	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	68.00	4623.95	67.80	1.38
cluster1	LSTM	6	TBR_1	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	54.95	3019.57	54.78	0.87
cluster1	LSTM	6	TIR	LIB193821	worst	34.52	64.34	0.00	1.14	0.00	98.86	34.88	1216.41	30.83	0.27
cluster1	LSTM	6	TAR_1	LIB193821	worst	0.00	94.79	0.00	5.21	0.00	94.79	87.28	7618.28	85.13	0.41
cluster1	LSTM	6	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	166.02	27563.98	164.42	0.58
cluster1	LSTM	8	ALL	LIB193821	worst	26.69	58.47	0.00	14.84	0.00	85.16	51.69	2671.61	41.48	0.34
cluster1	LSTM	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	59.06	3487.95	58.83	1.19
cluster1	LSTM	8	TBR_1	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	45.95	2111.78	45.76	0.73
cluster1	LSTM	8	TIR	LIB193821	worst	34.58	64.26	0.00	1.16	0.00	98.84	37.12	1378.07	31.64	0.26
cluster1	LSTM	8	TAR_1	LIB193821	worst	0.00	94.68	0.00	5.32	0.00	94.68	96.02	9219.13	94.03	0.46
cluster1	LSTM	8	TAR_2	LIB193821	worst	0.00	0.00	0.00	100.00	0.00	0.00	174.91	30594.56	173.40	0.61
cluster2	CNN	12	ALL	LIB193916	worst	29.99	47.15	0.44	21.63	0.79	77.14	76.53	5856.79	61.72	0.46
cluster2	CNN	12	TBR_2	LIB193916	worst	0.00	0.00	0.00	90.15	9.85	0.00	103.60	10733.25	101.03	1.97
cluster2	CNN	12	TBR_1	LIB193916	worst	0.00	0.00	0.00	92.05	7.95	0.00	93.17	8681.26	91.12	1.50
cluster2	CNN	12	TIR	LIB193916	worst	42.30	55.92	0.86	0.78	0.14	98.22	47.52	2258.49	38.85	0.38
cluster2	CNN	12	TAR_1	LIB193916	worst	32.77	56.58	0.00	10.64	0.00	89.35	59.35	3522.51	53.38	0.25
cluster2	CNN	12	TAR_2	LIB193916	worst	1.18	29.08	0.00	69.74	0.00	30.26	139.76	19533.97	132.90	0.43
cluster2	CNN	16	ALL	LIB193916	worst	30.42	47.37	0.89	19.74	1.59	77.79	76.08	5788.81	61.78	0.49
cluster2	CNN	16	TBR_2	LIB193916	worst	0.00	0.00	0.00	83.33	16.67	0.00	107.98	11659.81	105.90	2.06
cluster2	CNN	16	TBR_1	LIB193916	worst	0.00	0.00	0.00	83.17	16.83	0.00	99.48	9897.05	97.47	1.60
cluster2	CNN	16	TIR	LIB193916	worst	38.39	58.91	1.70	0.91	0.08	97.30	52.08	2712.80	42.81	0.42
cluster2	CNN	16	TAR_1	LIB193916	worst	42.83	48.39	0.00	8.77	0.00	91.22	53.16	2826.39	46.99	0.22
cluster2	CNN	16	TAR_2	LIB193916	worst	2.17	34.92	0.00	62.91	0.00	37.09	134.76	18159.05	126.76	0.41
cluster2	CNN	2	ALL	LIB194012	worst	67.06	24.58	0.23	8.05	0.08	91.64	33.13	1097.67	24.39	0.19
cluster2	CNN	2	TBR_2	LIB194012	worst	26.32	0.00	0.00	73.68	0.00	26.32	36.20	1310.12	31.38	0.61
cluster2	CNN	2	TBR_1	LIB194012	worst	20.09	0.00	0.00	79.13	0.78	20.09	34.25	1172.74	27.94	0.46
cluster2	CNN	2	TIR	LIB194012	worst	68.79	30.28	0.37	0.56	0.00	99.07	27.42	751.65	19.70	0.17
cluster2	CNN	2	TAR_1	LIB194012	worst	77.33	20.97	0.05	1.55	0.10	98.30	38.05	1447.76	28.86	0.14
cluster2	CNN	2	TAR_2	LIB194012	worst	75.85	20.08	0.00	4.07	0.00	95.93	49.54	2454.18	40.66	0.14
cluster2	CNN	4	ALL	LIB194012	worst	51.87	35.92	0.85	11.03	0.33	87.79	46.44	2156.66	34.99	0.29

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	4	TBR_2	LIB194012	worst	1.54	0.00	0.00	93.85	4.62	1.54	64.80	4198.50	56.11	1.10
cluster2	CNN	4	TBR_1	LIB194012	worst	1.76	0.00	0.00	95.05	3.19	1.76	56.81	3226.89	48.74	0.80
cluster2	CNN	4	TIR	LIB194012	worst	53.78	44.16	1.35	0.67	0.04	97.94	37.44	1401.73	27.92	0.25
cluster2	CNN	4	TAR_1	LIB194012	worst	67.40	29.36	0.16	3.08	0.00	96.76	46.37	2150.51	35.89	0.17
cluster2	CNN	4	TAR_2	LIB194012	worst	49.87	32.84	0.00	17.29	0.00	82.71	77.94	6074.54	65.79	0.23
cluster2	CNN	6	ALL	LIB193916	worst	41.53	44.58	1.40	11.32	1.16	86.11	62.73	3934.70	49.25	0.36
cluster2	CNN	6	TBR_2	LIB193916	worst	2.88	0.00	0.00	84.89	12.23	2.88	86.34	7454.92	77.48	1.51
cluster2	CNN	6	TBR_1	LIB193916	worst	2.92	0.00	0.00	83.33	13.74	2.92	82.27	6769.14	70.99	1.18
cluster2	CNN	6	TIR	LIB193916	worst	45.90	50.56	2.71	0.56	0.28	96.46	47.61	2266.63	36.53	0.33
cluster2	CNN	6	TAR_1	LIB193916	worst	55.62	39.27	0.06	5.04	0.00	94.89	51.25	2626.95	42.44	0.20
cluster2	CNN	6	TAR_2	LIB193916	worst	24.13	55.01	0.00	20.85	0.00	79.14	99.23	9847.10	89.17	0.29
cluster2	CNN	8	ALL	LIB193916	worst	35.05	47.68	1.52	14.35	1.40	82.73	69.72	4861.56	56.00	0.42
cluster2	CNN	8	TBR_2	LIB193916	worst	0.00	0.00	0.00	83.21	16.79	0.00	99.51	9903.19	94.58	1.84
cluster2	CNN	8	TBR_1	LIB193916	worst	0.00	0.00	0.00	84.37	15.63	0.00	92.36	8531.11	86.53	1.43
cluster2	CNN	8	TIR	LIB193916	worst	42.43	53.77	2.96	0.59	0.26	96.20	50.62	2561.89	39.89	0.37
cluster2	CNN	8	TAR_1	LIB193916	worst	46.38	46.17	0.00	7.45	0.00	92.55	54.25	2943.47	46.57	0.22
cluster2	CNN	8	TAR_2	LIB193916	worst	11.15	54.15	0.00	34.70	0.00	65.30	115.08	13244.43	106.32	0.35
cluster2	Linear	12	ALL	LIB193916	worst	27.20	49.90	4.08	15.96	2.86	77.10	84.99	7223.36	67.98	0.47
cluster2	Linear	12	TBR_2	LIB193916	worst	10.61	0.00	0.00	71.21	18.18	10.61	91.26	8328.04	79.76	1.55
cluster2	Linear	12	TBR_1	LIB193916	worst	8.56	0.00	0.00	74.31	17.13	8.56	87.18	7599.55	74.31	1.23
cluster2	Linear	12	TIR	LIB193916	worst	34.42	56.99	7.81	0.57	0.21	91.41	62.12	3859.48	48.21	0.42
cluster2	Linear	12	TAR_1	LIB193916	worst	28.56	59.11	0.00	8.27	4.06	87.67	82.24	6762.98	70.64	0.33
cluster2	Linear	12	TAR_2	LIB193916	worst	10.99	39.24	0.24	47.64	1.89	50.23	136.99	18765.57	125.12	0.41
cluster2	Linear	16	ALL	LIB193916	worst	28.10	47.18	4.03	17.23	3.46	75.28	86.43	7470.34	67.99	0.47
cluster2	Linear	16	TBR_2	LIB193916	worst	9.85	0.00	0.00	69.70	20.45	9.85	91.03	8285.80	77.30	1.51
cluster2	Linear	16	TBR_1	LIB193916	worst	12.06	0.00	0.00	69.21	18.73	12.06	83.93	7044.79	69.71	1.15
cluster2	Linear	16	TIR	LIB193916	worst	36.49	55.03	7.69	0.52	0.28	91.52	60.39	3647.13	46.13	0.40
cluster2	Linear	16	TAR_1	LIB193916	worst	27.98	58.73	0.00	8.34	4.95	86.71	84.12	7076.75	72.34	0.34
cluster2	Linear	16	TAR_2	LIB193916	worst	9.65	30.84	0.27	56.79	2.45	40.49	145.71	21232.84	133.74	0.44
cluster2	Linear	2	ALL	LIB194012	worst	82.51	15.27	0.03	2.17	0.01	97.78	23.57	555.67	16.66	0.12
cluster2	Linear	2	TBR_2	LIB194012	worst	86.47	0.00	0.00	13.53	0.00	86.47	14.97	224.11	10.56	0.21
cluster2	Linear	2	TBR_1	LIB194012	worst	75.55	0.00	0.00	24.30	0.16	75.55	17.85	318.51	11.73	0.19
cluster2	Linear	2	TIR	LIB194012	worst	78.89	20.96	0.06	0.10	0.00	99.85	22.62	511.48	15.67	0.13
cluster2	Linear	2	TAR_1	LIB194012	worst	88.97	10.66	0.00	0.36	0.00	99.63	26.30	691.61	19.35	0.09
cluster2	Linear	2	TAR_2	LIB194012	worst	95.80	3.94	0.00	0.26	0.00	99.74	27.70	767.08	21.75	0.08
cluster2	Linear	4	ALL	LIB194012	worst	61.11	31.52	1.08	5.76	0.53	92.63	44.21	1954.33	31.52	0.24
cluster2	Linear	4	TBR_2	LIB194012	worst	57.69	0.00	0.00	38.46	3.85	57.69	50.63	2563.83	33.23	0.65

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	4	TBR_1	LIB194012	worst	49.68	0.00	0.00	47.28	3.04	49.68	41.95	1759.91	26.62	0.44
cluster2	Linear	4	TIR	LIB194012	worst	60.29	37.64	1.65	0.37	0.04	97.93	38.60	1490.23	27.21	0.23
cluster2	Linear	4	TAR_1	LIB194012	worst	66.20	30.15	0.37	2.30	0.99	96.35	49.09	2409.55	37.15	0.18
cluster2	Linear	4	TAR_2	LIB194012	worst	63.81	25.20	0.13	10.86	0.00	89.01	63.35	4012.96	50.31	0.18
cluster2	Linear	6	ALL	LIB194012	worst	49.18	39.37	1.97	8.49	0.99	88.55	56.38	3179.23	41.08	0.31
cluster2	Linear	6	TBR_2	LIB194012	worst	40.62	0.00	0.00	52.34	7.03	40.62	66.12	4371.89	47.11	0.93
cluster2	Linear	6	TBR_1	LIB194012	worst	37.68	0.00	0.00	55.30	7.01	37.68	58.05	3370.18	39.55	0.65
cluster2	Linear	6	TIR	LIB194012	worst	50.62	45.76	3.17	0.44	0.02	96.38	46.52	2164.19	33.48	0.29
cluster2	Linear	6	TAR_1	LIB194012	worst	53.00	40.84	0.32	4.51	1.33	93.84	60.21	3625.44	47.50	0.22
cluster2	Linear	6	TAR_2	LIB194012	worst	40.57	31.69	0.00	27.05	0.68	72.26	92.87	8623.99	76.99	0.27
cluster2	Linear	8	ALL	LIB193916	worst	33.56	48.26	3.61	12.61	1.96	81.82	74.20	5505.21	59.04	0.42
cluster2	Linear	8	TBR_2	LIB193916	worst	13.87	0.00	0.00	68.61	17.52	13.87	85.63	7333.34	71.91	1.40
cluster2	Linear	8	TBR_1	LIB193916	worst	13.27	0.00	0.00	72.86	13.86	13.27	82.83	6860.16	68.11	1.13
cluster2	Linear	8	TIR	LIB193916	worst	37.03	55.62	6.60	0.42	0.33	92.65	59.20	3504.22	45.79	0.40
cluster2	Linear	8	TAR_1	LIB193916	worst	37.58	52.40	0.88	7.24	1.90	89.98	71.66	5135.02	60.16	0.28
cluster2	Linear	8	TAR_2	LIB193916	worst	26.18	42.17	0.00	30.81	0.84	68.35	108.66	11805.95	95.08	0.31
cluster2	LSTM	12	ALL	LIB193916	worst	30.58	49.29	1.09	17.47	1.57	79.87	75.56	5708.59	61.27	0.47
cluster2	LSTM	12	TBR_2	LIB193916	worst	0.00	0.00	0.00	82.58	17.42	0.00	104.96	11015.68	102.60	1.99
cluster2	LSTM	12	TBR_1	LIB193916	worst	0.00	0.00	0.00	83.18	16.82	0.00	96.97	9402.74	94.46	1.56
cluster2	LSTM	12	TIR	LIB193916	worst	40.23	56.74	2.10	0.68	0.25	96.97	50.65	2565.64	41.24	0.40
cluster2	LSTM	12	TAR_1	LIB193916	worst	39.66	51.53	0.00	8.81	0.00	91.19	56.82	3228.16	49.84	0.23
cluster2	LSTM	12	TAR_2	LIB193916	worst	1.18	47.87	0.00	50.95	0.00	49.05	133.04	17698.87	126.00	0.41
cluster2	LSTM	16	ALL	LIB193916	worst	29.35	48.31	0.37	20.79	1.17	77.66	76.38	5833.97	61.96	0.49
cluster2	LSTM	16	TBR_2	LIB193916	worst	0.00	0.00	0.00	87.12	12.88	0.00	106.43	11328.00	104.86	2.04
cluster2	LSTM	16	TBR_1	LIB193916	worst	0.00	0.00	0.00	87.62	12.38	0.00	97.59	9523.99	95.93	1.58
cluster2	LSTM	16	TIR	LIB193916	worst	39.03	59.27	0.71	0.95	0.04	98.30	49.96	2495.81	41.26	0.41
cluster2	LSTM	16	TAR_1	LIB193916	worst	38.31	52.82	0.00	8.86	0.00	91.13	54.88	3011.32	49.08	0.23
cluster2	LSTM	16	TAR_2	LIB193916	worst	0.00	33.02	0.00	66.98	0.00	33.02	138.32	19131.29	130.90	0.43
cluster2	LSTM	2	ALL	LIB194012	worst	82.58	13.46	0.03	3.92	0.01	96.04	22.24	494.44	15.94	0.12
cluster2	LSTM	2	TBR_2	LIB194012	worst	60.90	0.00	0.00	39.10	0.00	60.90	20.51	420.68	16.70	0.33
cluster2	LSTM	2	TBR_1	LIB194012	worst	57.94	0.00	0.00	41.90	0.16	57.94	18.02	324.61	13.89	0.23
cluster2	LSTM	2	TIR	LIB194012	worst	81.61	18.17	0.04	0.17	0.00	99.78	20.39	415.56	14.37	0.12
cluster2	LSTM	2	TAR_1	LIB194012	worst	89.44	10.10	0.05	0.41	0.00	99.54	26.02	677.19	18.92	0.09
cluster2	LSTM	2	TAR_2	LIB194012	worst	96.19	3.67	0.00	0.13	0.00	99.86	26.84	720.31	20.60	0.07
cluster2	LSTM	4	ALL	LIB194012	worst	59.15	30.24	0.62	9.75	0.23	89.39	40.07	1605.50	29.50	0.23
cluster2	LSTM	4	TBR_2	LIB194012	worst	10.00	0.00	0.00	86.92	3.08	10.00	52.19	2723.35	44.47	0.87
cluster2	LSTM	4	TBR_1	LIB194012	worst	7.83	0.00	0.00	89.94	2.24	7.83	44.87	2013.28	37.58	0.61

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	4	TIR	LIB194012	worst	61.59	36.68	0.98	0.71	0.04	98.27	32.75	1072.39	23.61	0.21
cluster2	LSTM	4	TAR_1	LIB194012	worst	70.64	26.85	0.16	2.35	0.00	97.49	44.11	1946.12	33.23	0.16
cluster2	LSTM	4	TAR_2	LIB194012	worst	64.61	25.60	0.00	9.79	0.00	90.21	61.93	3835.58	50.76	0.18
cluster2	LSTM	6	ALL	LIB194012	worst	48.35	38.43	1.12	11.64	0.45	86.78	50.55	2555.40	38.49	0.31
cluster2	LSTM	6	TBR_2	LIB194012	worst	0.00	0.00	0.00	97.66	2.34	0.00	70.09	4913.21	64.36	1.26
cluster2	LSTM	6	TBR_1	LIB194012	worst	1.63	0.00	0.00	92.82	5.55	1.63	63.17	3990.44	55.61	0.91
cluster2	LSTM	6	TIR	LIB194012	worst	52.45	44.88	1.87	0.78	0.02	97.33	39.04	1524.12	29.34	0.27
cluster2	LSTM	6	TAR_1	LIB194012	worst	61.50	34.57	0.00	3.93	0.00	96.07	49.92	2491.64	39.65	0.19
cluster2	LSTM	6	TAR_2	LIB194012	worst	34.02	43.03	0.00	22.95	0.00	77.05	90.43	8177.84	79.38	0.27
cluster2	LSTM	8	ALL	LIB193916	worst	38.33	46.05	1.99	12.07	1.56	84.38	66.61	4436.57	52.88	0.40
cluster2	LSTM	8	TBR_2	LIB193916	worst	0.00	0.00	0.00	84.67	15.33	0.00	96.08	9231.58	89.52	1.74
cluster2	LSTM	8	TBR_1	LIB193916	worst	0.00	0.00	0.00	81.42	18.58	0.00	89.31	7976.70	81.39	1.35
cluster2	LSTM	8	TIR	LIB193916	worst	42.78	52.50	3.87	0.55	0.29	95.28	50.84	2584.56	39.49	0.37
cluster2	LSTM	8	TAR_1	LIB193916	worst	54.71	39.40	0.00	5.89	0.00	94.11	51.58	2660.57	42.71	0.20
cluster2	LSTM	8	TAR_2	LIB193916	worst	17.67	58.57	0.00	23.76	0.00	76.24	105.98	11232.50	96.54	0.31
cluster3	CNN	12	ALL	LIB193878	worst	29.31	44.74	1.12	23.94	0.89	74.05	76.52	5855.08	62.25	0.49
cluster3	CNN	12	TBR_2	LIB193878	worst	0.00	0.00	0.00	97.06	2.94	0.00	90.91	8263.92	89.04	1.76
cluster3	CNN	12	TBR_1	LIB193878	worst	0.00	0.00	0.00	90.62	9.38	0.00	89.37	7986.82	86.74	1.43
cluster3	CNN	12	TIR	LIB193878	worst	41.32	55.50	2.24	0.86	0.07	96.82	49.31	2431.86	39.72	0.39
cluster3	CNN	12	TAR_1	LIB193878	worst	36.29	54.19	0.00	9.52	0.00	90.48	60.33	3639.71	53.39	0.24
cluster3	CNN	12	TAR_2	LIB193878	worst	2.56	29.22	0.00	68.22	0.00	31.78	134.71	18148.09	127.42	0.42
cluster3	CNN	16	ALL	LIB193878	worst	26.94	43.44	0.17	28.93	0.52	70.38	78.59	6175.65	63.78	0.49
cluster3	CNN	16	TBR_2	LIB193878	worst	0.00	0.00	0.00	98.08	1.92	0.00	88.32	7801.25	87.09	1.71
cluster3	CNN	16	TBR_1	LIB193878	worst	0.00	0.00	0.00	95.04	4.96	0.00	86.56	7493.33	84.94	1.40
cluster3	CNN	16	TIR	LIB193878	worst	44.53	54.14	0.33	0.92	0.08	98.67	44.03	1938.53	36.11	0.36
cluster3	CNN	16	TAR_1	LIB193878	worst	20.06	67.84	0.00	12.11	0.00	87.90	65.61	4304.18	60.69	0.28
cluster3	CNN	16	TAR_2	LIB193878	worst	0.14	5.70	0.00	94.17	0.00	5.84	147.22	21673.74	142.05	0.47
cluster3	CNN	2	ALL	LIB193878	worst	71.89	19.88	0.16	8.08	0.00	91.77	30.32	919.57	22.53	0.16
cluster3	CNN	2	TBR_2	LIB193878	worst	46.19	0.00	0.00	53.81	0.00	46.19	23.01	529.66	20.73	0.41
cluster3	CNN	2	TBR_1	LIB193878	worst	32.16	0.00	0.00	67.84	0.00	32.16	23.92	572.32	19.87	0.33
cluster3	CNN	2	TIR	LIB193878	worst	70.30	28.96	0.27	0.47	0.00	99.26	26.92	724.71	19.50	0.16
cluster3	CNN	2	TAR_1	LIB193878	worst	81.54	17.58	0.06	0.82	0.00	99.12	33.95	1152.52	25.22	0.12
cluster3	CNN	2	TAR_2	LIB193878	worst	88.29	10.15	0.09	1.47	0.00	98.44	37.65	1417.77	29.39	0.10
cluster3	CNN	4	ALL	LIB193878	worst	51.81	33.41	0.90	13.71	0.17	85.22	47.40	2247.00	36.39	0.28
cluster3	CNN	4	TBR_2	LIB193878	worst	2.04	0.00	0.00	97.96	0.00	2.04	46.22	2136.04	43.44	0.86
cluster3	CNN	4	TBR_1	LIB193878	worst	1.80	0.00	0.00	96.76	1.44	1.80	46.79	2189.72	41.60	0.69
cluster3	CNN	4	TIR	LIB193878	worst	54.00	43.61	1.56	0.78	0.06	97.61	38.10	1451.91	28.19	0.25

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	CNN	4	TAR_1	LIB193878	worst	63.85	32.65	0.53	2.90	0.07	96.50	49.09	2409.97	38.17	0.18
cluster3	CNN	4	TAR_2	LIB193878	worst	62.92	27.47	0.09	9.52	0.00	90.39	66.25	4389.03	53.95	0.18
cluster3	CNN	6	ALL	LIB193878	worst	43.12	38.88	1.56	15.96	0.48	82.00	59.65	3557.76	46.26	0.35
cluster3	CNN	6	TBR_2	LIB193878	worst	0.00	0.00	0.00	98.41	1.59	0.00	66.51	4423.88	62.21	1.23
cluster3	CNN	6	TBR_1	LIB193878	worst	0.58	0.00	0.00	94.78	4.64	0.58	61.52	3785.27	54.80	0.91
cluster3	CNN	6	TIR	LIB193878	worst	48.21	47.75	3.09	0.85	0.10	95.96	44.81	2008.00	33.19	0.30
cluster3	CNN	6	TAR_1	LIB193878	worst	54.57	40.00	0.21	5.22	0.00	94.57	57.30	3283.50	46.33	0.22
cluster3	CNN	6	TAR_2	LIB193878	worst	41.07	37.54	0.00	21.39	0.00	78.61	90.63	8214.38	77.35	0.26
cluster3	CNN	8	ALL	LIB193878	worst	35.18	44.11	1.24	18.65	0.82	79.29	68.27	4660.25	54.47	0.41
cluster3	CNN	8	TBR_2	LIB193878	worst	0.00	0.00	0.00	95.05	4.95	0.00	79.60	6336.94	76.23	1.50
cluster3	CNN	8	TBR_1	LIB193878	worst	0.00	0.00	0.00	92.23	7.77	0.00	76.01	5777.43	70.95	1.17
cluster3	CNN	8	TIR	LIB193878	worst	45.19	51.40	2.52	0.82	0.07	96.59	45.41	2061.78	35.28	0.33
cluster3	CNN	8	TAR_1	LIB193878	worst	43.92	49.32	0.00	6.77	0.00	93.24	60.68	3681.51	51.61	0.24
cluster3	CNN	8	TAR_2	LIB193878	worst	17.04	45.13	0.00	37.83	0.00	62.17	113.59	12902.36	103.36	0.34
cluster3	Linear	12	ALL	LIB193878	worst	28.88	45.56	4.68	17.27	3.61	74.44	87.45	7647.25	68.06	0.48
cluster3	Linear	12	TBR_2	LIB193878	worst	41.76	0.00	0.00	48.82	9.41	41.76	65.57	4299.42	45.08	0.88
cluster3	Linear	12	TBR_1	LIB193878	worst	19.91	0.00	0.00	65.90	14.19	19.91	76.40	5836.74	60.76	1.01
cluster3	Linear	12	TIR	LIB193878	worst	31.38	58.79	9.16	0.56	0.11	90.17	66.18	4380.05	51.52	0.45
cluster3	Linear	12	TAR_1	LIB193878	worst	34.68	51.53	0.56	7.34	5.89	86.21	82.06	6734.10	68.48	0.32
cluster3	Linear	12	TAR_2	LIB193878	worst	14.78	27.94	0.00	52.62	4.66	42.72	143.94	20719.56	127.18	0.43
cluster3	Linear	16	ALL	LIB193878	worst	26.71	44.99	5.08	18.24	4.98	71.70	93.74	8788.03	73.28	0.51
cluster3	Linear	16	TBR_2	LIB193878	worst	46.79	0.00	0.00	45.51	7.69	46.79	65.98	4353.29	44.66	0.87
cluster3	Linear	16	TBR_1	LIB193878	worst	19.35	0.00	0.00	62.28	18.36	19.35	84.98	7221.49	67.56	1.12
cluster3	Linear	16	TIR	LIB193878	worst	29.80	59.68	9.90	0.50	0.12	89.48	67.69	4581.45	53.25	0.47
cluster3	Linear	16	TAR_1	LIB193878	worst	31.05	52.59	0.46	8.13	7.76	83.64	87.46	7649.38	74.12	0.34
cluster3	Linear	16	TAR_2	LIB193878	worst	10.04	20.08	0.00	61.06	8.82	30.12	161.15	25970.60	146.51	0.49
cluster3	Linear	2	ALL	LIB193878	worst	87.70	11.03	0.01	1.25	0.00	98.73	20.99	440.63	15.08	0.10
cluster3	Linear	2	TBR_2	LIB193878	worst	96.95	0.00	0.00	3.05	0.00	96.95	8.01	64.13	5.54	0.11
cluster3	Linear	2	TBR_1	LIB193878	worst	87.77	0.00	0.00	12.23	0.00	87.77	11.18	125.01	7.61	0.12
cluster3	Linear	2	TIR	LIB193878	worst	81.77	18.11	0.03	0.09	0.00	99.88	19.77	391.04	14.06	0.12
cluster3	Linear	2	TAR_1	LIB193878	worst	92.01	7.74	0.00	0.25	0.00	99.75	24.24	587.38	18.04	0.09
cluster3	Linear	2	TAR_2	LIB193878	worst	97.57	2.43	0.00	0.00	0.00	100.00	24.76	612.91	19.53	0.07
cluster3	Linear	4	ALL	LIB193878	worst	63.11	30.72	0.82	5.13	0.21	93.83	42.94	1844.10	31.39	0.21
cluster3	Linear	4	TBR_2	LIB193878	worst	79.08	0.00	0.00	20.92	0.00	79.08	21.68	469.94	14.13	0.28
cluster3	Linear	4	TBR_1	LIB193878	worst	63.06	0.00	0.00	36.22	0.72	63.06	28.26	798.75	17.94	0.30
cluster3	Linear	4	TIR	LIB193878	worst	56.61	41.74	1.34	0.28	0.03	98.35	38.72	1498.87	28.43	0.24
cluster3	Linear	4	TAR_1	LIB193878	worst	67.22	29.88	0.66	1.65	0.59	97.10	48.03	2306.99	36.64	0.17

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	4	TAR_2	LIB193878	worst	73.62	20.67	0.09	5.62	0.00	94.29	54.63	2984.33	42.64	0.14
cluster3	Linear	6	ALL	LIB193878	worst	47.29	40.25	2.10	9.16	1.19	87.54	59.24	3509.71	44.32	0.30
cluster3	Linear	6	TBR_2	LIB193878	worst	60.85	0.00	0.00	37.57	1.59	60.85	39.05	1524.80	24.42	0.48
cluster3	Linear	6	TBR_1	LIB193878	worst	45.45	0.00	0.00	50.87	3.68	45.45	46.84	2194.20	30.41	0.50
cluster3	Linear	6	TIR	LIB193878	worst	43.00	52.67	3.81	0.46	0.07	95.67	50.23	2522.67	37.89	0.32
cluster3	Linear	6	TAR_1	LIB193878	worst	50.93	41.10	1.03	3.92	3.02	92.03	62.72	3934.19	49.34	0.23
cluster3	Linear	6	TAR_2	LIB193878	worst	53.30	29.80	0.00	16.24	0.67	83.10	82.59	6821.90	66.65	0.22
cluster3	Linear	8	ALL	LIB193878	worst	37.99	44.26	3.06	12.41	2.28	82.25	71.49	5110.94	54.61	0.38
cluster3	Linear	8	TBR_2	LIB193878	worst	49.45	0.00	0.00	43.41	7.14	49.45	56.88	3235.58	36.10	0.70
cluster3	Linear	8	TBR_1	LIB193878	worst	33.74	0.00	0.00	58.28	7.98	33.74	61.67	3802.91	43.89	0.73
cluster3	Linear	8	TIR	LIB193878	worst	36.43	56.96	5.97	0.48	0.17	93.39	57.20	3271.64	44.11	0.38
cluster3	Linear	8	TAR_1	LIB193878	worst	43.92	45.86	0.58	5.47	4.18	89.78	71.40	5097.50	57.62	0.27
cluster3	Linear	8	TAR_2	LIB193878	worst	34.28	34.38	0.00	29.21	2.13	68.66	107.68	11594.18	90.36	0.30
cluster3	LSTM	12	ALL	LIB193878	worst	29.29	45.95	1.06	22.81	0.89	75.24	75.31	5671.01	61.12	0.48
cluster3	LSTM	12	TBR_2	LIB193878	worst	0.00	0.00	0.00	92.94	7.06	0.00	88.79	7882.81	86.48	1.71
cluster3	LSTM	12	TBR_1	LIB193878	worst	0.00	0.00	0.00	91.99	8.01	0.00	85.79	7359.11	82.89	1.37
cluster3	LSTM	12	TIR	LIB193878	worst	41.59	55.35	2.13	0.90	0.04	96.94	47.70	2274.99	38.29	0.37
cluster3	LSTM	12	TAR_1	LIB193878	worst	36.13	54.76	0.00	9.11	0.00	90.89	61.68	3804.08	54.39	0.25
cluster3	LSTM	12	TAR_2	LIB193878	worst	1.86	36.44	0.00	61.70	0.00	38.30	132.82	17641.02	125.82	0.42
cluster3	LSTM	16	ALL	LIB193878	worst	27.42	43.28	0.00	29.18	0.13	70.70	77.94	6074.67	63.58	0.50
cluster3	LSTM	16	TBR_2	LIB193878	worst	0.00	0.00	0.00	100.00	0.00	0.00	91.14	8306.07	90.26	1.77
cluster3	LSTM	16	TBR_1	LIB193878	worst	0.00	0.00	0.00	99.01	0.99	0.00	89.05	7929.17	87.80	1.45
cluster3	LSTM	16	TIR	LIB193878	worst	43.07	55.93	0.00	0.92	0.08	99.00	45.25	2047.23	37.26	0.37
cluster3	LSTM	16	TAR_1	LIB193878	worst	25.51	62.75	0.00	11.74	0.00	88.26	62.60	3918.88	57.59	0.26
cluster3	LSTM	16	TAR_2	LIB193878	worst	0.00	6.24	0.00	93.76	0.00	6.24	144.52	20884.76	139.30	0.47
cluster3	LSTM	2	ALL	LIB193878	worst	89.40	8.42	0.00	2.17	0.00	97.82	18.87	355.95	13.66	0.09
cluster3	LSTM	2	TBR_2	LIB193878	worst	87.31	0.00	0.00	12.69	0.00	87.31	12.64	159.64	9.28	0.19
cluster3	LSTM	2	TBR_1	LIB193878	worst	80.23	0.00	0.00	19.77	0.00	80.23	12.35	152.63	8.89	0.15
cluster3	LSTM	2	TIR	LIB193878	worst	86.10	13.78	0.00	0.12	0.00	99.88	16.76	281.04	12.03	0.10
cluster3	LSTM	2	TAR_1	LIB193878	worst	93.65	6.22	0.00	0.13	0.00	99.87	21.78	474.52	16.05	0.08
cluster3	LSTM	2	TAR_2	LIB193878	worst	98.35	1.56	0.00	0.09	0.00	99.91	23.49	551.90	18.36	0.06
cluster3	LSTM	4	ALL	LIB193878	worst	62.46	26.09	0.36	11.07	0.02	88.55	38.56	1486.74	28.91	0.21
cluster3	LSTM	4	TBR_2	LIB193878	worst	14.80	0.00	0.00	85.20	0.00	14.80	34.04	1158.48	30.63	0.61
cluster3	LSTM	4	TBR_1	LIB193878	worst	15.32	0.00	0.00	84.68	0.00	15.32	30.94	957.25	26.46	0.44
cluster3	LSTM	4	TIR	LIB193878	worst	64.39	34.40	0.62	0.56	0.03	98.79	31.52	993.42	22.78	0.19
cluster3	LSTM	4	TAR_1	LIB193878	worst	73.68	24.74	0.26	1.32	0.00	98.42	42.04	1767.40	31.90	0.15
cluster3	LSTM	4	TAR_2	LIB193878	worst	73.62	21.49	0.00	4.90	0.00	95.11	53.51	2863.65	43.62	0.15

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	6	ALL	LIB193878	worst	47.28	36.57	1.27	14.72	0.16	83.85	53.36	2847.14	41.02	0.30
cluster3	LSTM	6	TBR_2	LIB193878	worst	0.00	0.00	0.00	99.47	0.53	0.00	54.40	2959.10	50.50	1.01
cluster3	LSTM	6	TBR_1	LIB193878	worst	0.39	0.00	0.00	98.07	1.55	0.39	50.79	2579.23	44.63	0.74
cluster3	LSTM	6	TIR	LIB193878	worst	52.31	44.14	2.61	0.91	0.03	96.45	41.34	1708.87	30.36	0.27
cluster3	LSTM	6	TAR_1	LIB193878	worst	56.98	38.90	0.00	4.12	0.00	95.88	53.93	2908.30	43.09	0.20
cluster3	LSTM	6	TAR_2	LIB193878	worst	50.72	35.82	0.00	13.47	0.00	86.54	78.82	6211.83	65.90	0.22
cluster3	LSTM	8	ALL	LIB193878	worst	37.40	43.58	1.17	17.26	0.59	80.98	64.07	4104.38	50.56	0.38
cluster3	LSTM	8	TBR_2	LIB193878	worst	0.00	0.00	0.00	96.70	3.30	0.00	71.00	5040.76	66.84	1.32
cluster3	LSTM	8	TBR_1	LIB193878	worst	0.00	0.00	0.00	94.68	5.32	0.00	66.73	4453.50	61.32	1.02
cluster3	LSTM	8	TIR	LIB193878	worst	46.93	49.80	2.39	0.78	0.10	96.73	43.51	1893.25	33.20	0.30
cluster3	LSTM	8	TAR_1	LIB193878	worst	46.58	47.44	0.00	5.98	0.00	94.02	59.73	3567.87	50.01	0.23
cluster3	LSTM	8	TAR_2	LIB193878	worst	21.60	49.29	0.00	29.11	0.00	70.89	105.31	11089.28	94.60	0.31
cluster4	CNN	12	ALL	LIB193838	worst	28.07	49.64	0.00	22.24	0.04	77.71	63.08	3979.68	52.19	0.50
cluster4	CNN	12	TBR_2	LIB193838	worst	0.00	0.00	0.00	98.70	1.30	0.00	95.40	9100.87	94.50	1.80
cluster4	CNN	12	TBR_1	LIB193838	worst	0.00	0.00	0.00	99.82	0.18	0.00	80.96	6554.27	80.06	1.32
cluster4	CNN	12	TIR	LIB193838	worst	40.97	58.15	0.00	0.88	0.00	99.12	41.29	1705.01	34.86	0.37
cluster4	CNN	12	TAR_1	LIB193838	worst	10.45	77.58	0.00	11.98	0.00	88.03	68.55	4698.99	64.80	0.30
cluster4	CNN	12	TAR_2	LIB193838	worst	0.00	0.00	0.00	100.00	0.00	0.00	140.45	19725.91	136.60	0.47
cluster4	CNN	16	ALL	LIB193838	worst	27.21	50.58	0.00	22.12	0.09	77.79	64.66	4180.77	54.16	0.54
cluster4	CNN	16	TBR_2	LIB193838	worst	0.00	0.00	0.00	100.00	0.00	0.00	97.50	9507.11	97.00	1.85
cluster4	CNN	16	TBR_1	LIB193838	worst	0.00	0.00	0.00	99.25	0.75	0.00	86.93	7556.51	86.20	1.42
cluster4	CNN	16	TIR	LIB193838	worst	38.86	60.23	0.00	0.92	0.00	99.09	44.69	1997.32	37.83	0.40
cluster4	CNN	16	TAR_1	LIB193838	worst	12.65	75.61	0.00	11.74	0.00	88.26	66.18	4380.40	62.35	0.29
cluster4	CNN	16	TAR_2	LIB193838	worst	0.00	0.00	0.00	100.00	0.00	0.00	138.87	19285.16	134.87	0.47
cluster4	CNN	2	ALL	LIB193826	worst	69.35	22.68	0.09	7.88	0.00	92.03	28.91	835.85	20.56	0.18
cluster4	CNN	2	TBR_2	LIB193826	worst	64.46	0.00	0.00	35.54	0.00	64.46	25.58	654.30	20.55	0.40
cluster4	CNN	2	TBR_1	LIB193826	worst	58.42	0.00	0.00	41.58	0.00	58.42	20.74	430.32	15.47	0.25
cluster4	CNN	2	TIR	LIB193826	worst	72.45	27.13	0.14	0.28	0.00	99.58	24.73	611.52	17.93	0.16
cluster4	CNN	2	TAR_1	LIB193826	worst	68.95	29.64	0.00	1.41	0.00	98.59	41.92	1757.42	33.71	0.16
cluster4	CNN	2	TAR_2	LIB193826	worst	61.07	31.30	0.00	7.63	0.00	92.37	66.73	4452.39	53.61	0.18
cluster4	CNN	4	ALL	LIB193826	worst	51.82	31.62	0.07	16.42	0.07	83.44	37.20	1383.73	27.46	0.25
cluster4	CNN	4	TBR_2	LIB193826	worst	6.09	0.00	0.00	93.91	0.00	6.09	39.68	1574.40	34.47	0.67
cluster4	CNN	4	TBR_1	LIB193826	worst	17.34	0.00	0.00	82.17	0.49	17.34	32.00	1024.01	26.72	0.44
cluster4	CNN	4	TIR	LIB193826	worst	62.85	36.16	0.11	0.89	0.00	99.01	28.41	807.33	21.45	0.19
cluster4	CNN	4	TAR_1	LIB193826	worst	48.16	48.57	0.00	3.28	0.00	96.73	55.02	3027.16	46.47	0.22
cluster4	CNN	4	TAR_2	LIB193826	worst	31.01	48.06	0.00	20.93	0.00	79.07	96.30	9272.78	83.61	0.28
cluster4	CNN	6	ALL	LIB193826	worst	42.91	37.61	0.07	19.33	0.07	80.52	43.87	1924.62	33.32	0.31

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	6	TBR_2	LIB193826	worst	1.85	0.00	0.00	98.15	0.00	1.85	52.42	2747.91	47.64	0.92
cluster4	CNN	6	TBR_1	LIB193826	worst	2.90	0.00	0.00	96.59	0.51	2.90	40.72	1658.05	36.94	0.61
cluster4	CNN	6	TIR	LIB193826	worst	56.42	42.49	0.11	0.98	0.00	98.91	30.78	947.43	24.10	0.22
cluster4	CNN	6	TAR_1	LIB193826	worst	31.80	64.02	0.00	4.18	0.00	95.82	65.37	4272.62	57.83	0.28
cluster4	CNN	6	TAR_2	LIB193826	worst	12.60	38.58	0.00	48.82	0.00	51.18	121.31	14715.22	111.12	0.37
cluster4	CNN	8	ALL	LIB193826	worst	38.72	41.06	0.08	20.07	0.08	79.78	48.86	2387.68	37.51	0.35
cluster4	CNN	8	TBR_2	LIB193826	worst	0.99	0.00	0.00	99.01	0.00	0.99	62.88	3954.34	58.39	1.13
cluster4	CNN	8	TBR_1	LIB193826	worst	1.79	0.00	0.00	97.86	0.36	1.79	51.46	2648.13	47.63	0.78
cluster4	CNN	8	TIR	LIB193826	worst	52.73	46.22	0.11	0.90	0.04	98.95	32.14	1032.82	25.66	0.24
cluster4	CNN	8	TAR_1	LIB193826	worst	21.32	73.13	0.00	5.54	0.00	94.45	69.28	4800.28	62.54	0.30
cluster4	CNN	8	TAR_2	LIB193826	worst	0.79	27.78	0.00	71.43	0.00	28.57	140.37	19704.27	133.87	0.45
cluster4	Linear	12	ALL	LIB193838	worst	28.20	50.10	3.11	15.18	3.41	78.30	74.44	5541.84	57.16	0.48
cluster4	Linear	12	TBR_2	LIB193838	worst	9.09	0.00	0.00	74.03	16.88	9.09	90.94	8270.16	79.28	1.51
cluster4	Linear	12	TBR_1	LIB193838	worst	19.06	0.00	0.00	72.84	8.09	19.06	69.24	4794.05	53.70	0.89
cluster4	Linear	12	TIR	LIB193838	worst	34.64	59.94	4.78	0.54	0.10	94.58	55.32	3060.24	42.51	0.39
cluster4	Linear	12	TAR_1	LIB193838	worst	16.02	64.21	0.14	8.22	11.42	80.23	98.96	9793.24	89.19	0.42
cluster4	Linear	12	TAR_2	LIB193838	worst	14.64	22.86	0.00	57.50	5.00	37.50	147.24	21679.60	131.07	0.45
cluster4	Linear	16	ALL	LIB193838	worst	25.74	50.63	3.51	16.20	3.92	76.37	76.42	5839.80	58.99	0.49
cluster4	Linear	16	TBR_2	LIB193838	worst	5.33	0.00	0.00	85.33	9.33	5.33	80.68	6509.61	69.34	1.32
cluster4	Linear	16	TBR_1	LIB193838	worst	20.19	0.00	0.00	70.65	9.16	20.19	70.28	4939.56	54.53	0.90
cluster4	Linear	16	TIR	LIB193838	worst	32.17	61.63	5.39	0.67	0.14	93.80	56.08	3144.69	43.47	0.40
cluster4	Linear	16	TAR_1	LIB193838	worst	11.74	63.87	0.00	9.45	14.94	75.61	105.13	11052.65	96.05	0.46
cluster4	Linear	16	TAR_2	LIB193838	worst	7.81	15.23	0.00	71.88	5.08	23.04	155.17	24076.38	142.58	0.50
cluster4	Linear	2	ALL	LIB193838	worst	76.43	19.90	0.08	3.54	0.06	96.33	25.70	660.40	18.23	0.15
cluster4	Linear	2	TBR_2	LIB193838	worst	81.18	0.00	0.00	18.82	0.00	81.18	19.70	387.90	13.26	0.25
cluster4	Linear	2	TBR_1	LIB193838	worst	72.65	0.00	0.00	26.85	0.49	72.65	22.21	493.42	13.51	0.22
cluster4	Linear	2	TIR	LIB193838	worst	72.77	26.99	0.12	0.12	0.00	99.76	25.27	638.73	17.86	0.16
cluster4	Linear	2	TAR_1	LIB193838	worst	84.96	14.80	0.00	0.24	0.00	99.76	29.28	857.03	22.14	0.11
cluster4	Linear	2	TAR_2	LIB193838	worst	97.06	2.94	0.00	0.00	0.00	100.00	27.50	756.01	21.96	0.08
cluster4	Linear	4	ALL	LIB193826	worst	63.19	30.73	0.31	5.58	0.19	93.92	35.33	1248.50	24.84	0.21
cluster4	Linear	4	TBR_2	LIB193826	worst	74.78	0.00	0.00	23.48	1.74	74.78	32.55	1059.50	18.00	0.35
cluster4	Linear	4	TBR_1	LIB193826	worst	71.15	0.00	0.00	28.20	0.65	71.15	25.40	644.92	14.81	0.24
cluster4	Linear	4	TIR	LIB193826	worst	61.49	37.76	0.46	0.28	0.00	99.25	32.04	1026.25	23.39	0.20
cluster4	Linear	4	TAR_1	LIB193826	worst	62.30	35.66	0.00	1.64	0.41	97.96	48.20	2323.21	38.32	0.19
cluster4	Linear	4	TAR_2	LIB193826	worst	55.04	33.33	0.00	11.63	0.00	88.37	71.27	5079.50	59.59	0.20
cluster4	Linear	6	ALL	LIB193826	worst	49.49	40.63	0.69	8.24	0.94	90.12	45.86	2102.96	33.14	0.28
cluster4	Linear	6	TBR_2	LIB193826	worst	56.48	0.00	0.00	35.19	8.33	56.48	57.02	3251.35	33.83	0.66

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	Linear	6	TBR_1	LIB193826	worst	58.19	0.00	0.00	40.10	1.71	58.19	35.22	1240.28	22.27	0.36
cluster4	Linear	6	TIR	LIB193826	worst	49.27	49.38	0.98	0.29	0.07	98.65	38.82	1506.65	29.53	0.26
cluster4	Linear	6	TAR_1	LIB193826	worst	42.68	50.21	0.00	3.77	3.35	92.89	64.70	4185.58	53.38	0.26
cluster4	Linear	6	TAR_2	LIB193826	worst	33.86	37.80	0.79	26.77	0.79	71.66	100.71	10143.24	84.62	0.29
cluster4	Linear	8	ALL	LIB193826	worst	41.09	46.18	0.76	10.21	1.76	87.27	53.51	2863.36	39.19	0.34
cluster4	Linear	8	TBR_2	LIB193826	worst	44.55	0.00	0.00	39.60	15.84	44.55	75.02	5628.69	49.24	0.96
cluster4	Linear	8	TBR_1	LIB193826	worst	46.61	0.00	0.00	50.18	3.21	46.61	43.41	1884.82	28.74	0.47
cluster4	Linear	8	TIR	LIB193826	worst	41.50	56.97	1.12	0.34	0.07	98.47	42.76	1828.12	33.41	0.29
cluster4	Linear	8	TAR_1	LIB193826	worst	34.33	55.86	0.00	3.84	5.97	90.19	76.16	5799.85	64.39	0.31
cluster4	Linear	8	TAR_2	LIB193826	worst	30.16	23.81	0.00	42.06	3.97	53.97	126.50	16002.89	106.28	0.36
cluster4	LSTM	12	ALL	LIB193826	worst	33.34	45.70	0.00	20.96	0.00	79.04	53.72	2885.77	41.63	0.39
cluster4	LSTM	12	TBR_2	LIB193826	worst	0.00	0.00	0.00	100.00	0.00	0.00	68.80	4733.66	66.85	1.30
cluster4	LSTM	12	TBR_1	LIB193826	worst	0.00	0.00	0.00	100.00	0.00	0.00	57.46	3301.73	55.42	0.91
cluster4	LSTM	12	TIR	LIB193826	worst	48.75	50.38	0.00	0.87	0.00	99.13	31.80	1011.40	26.44	0.25
cluster4	LSTM	12	TAR_1	LIB193826	worst	0.67	93.32	0.00	6.01	0.00	93.99	77.68	6033.65	74.09	0.36
cluster4	LSTM	12	TAR_2	LIB193826	worst	0.00	0.00	0.00	100.00	0.00	0.00	165.82	27495.42	161.68	0.54
cluster4	LSTM	16	ALL	LIB193838	worst	26.66	51.13	0.00	22.21	0.00	77.79	63.81	4072.25	53.31	0.52
cluster4	LSTM	16	TBR_2	LIB193838	worst	0.00	0.00	0.00	100.00	0.00	0.00	92.67	8587.84	92.66	1.77
cluster4	LSTM	16	TBR_1	LIB193838	worst	0.00	0.00	0.00	100.00	0.00	0.00	83.86	7032.07	83.73	1.38
cluster4	LSTM	16	TIR	LIB193838	worst	40.30	58.78	0.00	0.92	0.00	99.08	42.29	1788.14	36.08	0.38
cluster4	LSTM	16	TAR_1	LIB193838	worst	2.74	85.52	0.00	11.74	0.00	88.26	68.07	4633.36	65.02	0.30
cluster4	LSTM	16	TAR_2	LIB193838	worst	0.00	0.00	0.00	100.00	0.00	0.00	143.09	20474.16	139.47	0.48
cluster4	LSTM	2	ALL	LIB193838	worst	78.19	14.96	0.02	6.83	0.00	93.15	22.42	502.63	16.42	0.14
cluster4	LSTM	2	TBR_2	LIB193838	worst	55.29	0.00	0.00	44.71	0.00	55.29	20.33	413.21	18.25	0.35
cluster4	LSTM	2	TBR_1	LIB193838	worst	49.42	0.00	0.00	50.58	0.00	49.42	19.82	392.71	15.52	0.25
cluster4	LSTM	2	TIR	LIB193838	worst	79.57	20.23	0.03	0.18	0.00	99.80	20.33	413.27	14.57	0.13
cluster4	LSTM	2	TAR_1	LIB193838	worst	89.02	10.74	0.00	0.24	0.00	99.76	25.68	659.35	19.58	0.09
cluster4	LSTM	2	TAR_2	LIB193838	worst	95.00	3.82	0.00	1.18	0.00	98.82	34.89	1217.18	27.92	0.09
cluster4	LSTM	4	ALL	LIB193826	worst	60.81	27.19	0.10	11.88	0.02	88.00	32.20	1036.69	23.24	0.20
cluster4	LSTM	4	TBR_2	LIB193826	worst	52.17	0.00	0.00	47.83	0.00	52.17	28.33	802.63	23.12	0.45
cluster4	LSTM	4	TBR_1	LIB193826	worst	33.23	0.00	0.00	66.61	0.16	33.23	23.96	574.03	19.55	0.32
cluster4	LSTM	4	TIR	LIB193826	worst	67.47	31.96	0.14	0.43	0.00	99.43	26.27	690.25	19.60	0.17
cluster4	LSTM	4	TAR_1	LIB193826	worst	69.88	29.10	0.00	1.02	0.00	98.98	42.76	1828.57	33.03	0.16
cluster4	LSTM	4	TAR_2	LIB193826	worst	20.93	70.54	0.00	8.53	0.00	91.47	89.49	8009.12	83.04	0.28
cluster4	LSTM	6	ALL	LIB193826	worst	46.15	35.73	0.02	17.94	0.15	81.88	40.32	1625.94	30.25	0.28
cluster4	LSTM	6	TBR_2	LIB193826	worst	2.78	0.00	0.00	96.30	0.93	2.78	45.99	2115.44	39.84	0.77
cluster4	LSTM	6	TBR_1	LIB193826	worst	5.63	0.00	0.00	93.52	0.85	5.63	37.73	1423.75	32.60	0.54

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	6	TIR	LIB193826	worst	57.77	41.25	0.04	0.95	0.00	99.02	30.06	903.56	23.17	0.21
cluster4	LSTM	6	TAR_1	LIB193826	worst	51.26	45.40	0.00	3.35	0.00	96.66	54.68	2989.67	45.48	0.22
cluster4	LSTM	6	TAR_2	LIB193826	worst	0.00	75.59	0.00	24.41	0.00	75.59	112.28	12606.25	106.72	0.36
cluster4	LSTM	8	ALL	LIB193826	worst	40.37	38.44	0.00	21.19	0.00	78.81	46.56	2167.53	35.36	0.33
cluster4	LSTM	8	TBR_2	LIB193826	worst	0.00	0.00	0.00	100.00	0.00	0.00	60.50	3660.25	54.97	1.07
cluster4	LSTM	8	TBR_1	LIB193826	worst	0.71	0.00	0.00	99.29	0.00	0.71	45.46	2066.51	41.43	0.68
cluster4	LSTM	8	TIR	LIB193826	worst	53.90	45.17	0.00	0.94	0.00	99.07	31.43	987.74	24.75	0.23
cluster4	LSTM	8	TAR_1	LIB193826	worst	30.28	63.54	0.00	6.18	0.00	93.82	65.80	4329.32	58.79	0.28
cluster4	LSTM	8	TAR_2	LIB193826	worst	0.00	3.97	0.00	96.03	0.00	3.97	135.55	18373.69	130.17	0.44
cluster5	CNN	12	ALL	LIB193603	worst	31.22	43.72	1.52	22.68	0.85	74.94	60.92	3711.31	50.09	0.47
cluster5	CNN	12	TBR_2	LIB193603	worst	1.37	0.00	0.00	94.52	4.11	1.37	71.67	5137.17	66.88	1.27
cluster5	CNN	12	TBR_1	LIB193603	worst	0.20	0.00	0.00	95.33	4.46	0.20	69.47	4825.77	65.49	1.07
cluster5	CNN	12	TIR	LIB193603	worst	39.14	56.51	2.66	1.52	0.16	95.65	46.71	2181.50	37.32	0.37
cluster5	CNN	12	TAR_1	LIB193603	worst	41.55	50.68	0.19	7.57	0.00	92.23	59.32	3518.38	50.73	0.24
cluster5	CNN	12	TAR_2	LIB193603	worst	24.37	36.97	0.00	38.66	0.00	61.34	100.26	10052.38	90.35	0.31
cluster5	CNN	16	ALL	LIB193603	worst	29.13	43.57	0.66	25.70	0.94	72.70	66.84	4467.03	54.72	0.50
cluster5	CNN	16	TBR_2	LIB193603	worst	0.00	0.00	0.00	97.14	2.86	0.00	79.75	6359.40	76.14	1.44
cluster5	CNN	16	TBR_1	LIB193603	worst	0.21	0.00	0.00	93.83	5.96	0.21	78.50	6162.89	74.57	1.22
cluster5	CNN	16	TIR	LIB193603	worst	41.61	55.57	1.16	1.66	0.00	97.18	44.25	1958.44	35.81	0.37
cluster5	CNN	16	TAR_1	LIB193603	worst	31.95	59.17	0.00	8.88	0.00	91.12	64.06	4103.82	57.13	0.26
cluster5	CNN	16	TAR_2	LIB193603	worst	5.65	26.55	0.00	67.80	0.00	32.20	123.10	15152.38	117.12	0.40
cluster5	CNN	2	ALL	LIB193603	worst	77.94	17.67	0.03	4.36	0.00	95.61	25.24	637.02	18.25	0.14
cluster5	CNN	2	TBR_2	LIB193603	worst	86.36	0.00	0.00	13.64	0.00	86.36	12.82	164.39	10.73	0.20
cluster5	CNN	2	TBR_1	LIB193603	worst	75.51	0.00	0.00	24.49	0.00	75.51	14.95	223.56	10.73	0.18
cluster5	CNN	2	TIR	LIB193603	worst	75.89	23.69	0.05	0.36	0.00	99.58	23.17	536.88	16.87	0.15
cluster5	CNN	2	TAR_1	LIB193603	worst	80.11	19.89	0.00	0.00	0.00	100.00	31.01	961.35	24.60	0.12
cluster5	CNN	2	TAR_2	LIB193603	worst	86.93	12.80	0.00	0.27	0.00	99.73	37.32	1393.00	28.80	0.10
cluster5	CNN	4	ALL	LIB193603	worst	57.16	29.22	0.35	13.24	0.03	86.38	36.22	1312.09	27.07	0.22
cluster5	CNN	4	TBR_2	LIB193603	worst	32.18	0.00	0.00	67.82	0.00	32.18	23.50	552.40	21.16	0.40
cluster5	CNN	4	TBR_1	LIB193603	worst	32.00	0.00	0.00	67.81	0.19	32.00	27.85	775.50	21.61	0.35
cluster5	CNN	4	TIR	LIB193603	worst	61.05	37.49	0.63	0.83	0.00	98.54	31.45	989.36	23.18	0.21
cluster5	CNN	4	TAR_1	LIB193603	worst	65.34	32.77	0.00	1.89	0.00	98.11	43.18	1864.56	34.78	0.17
cluster5	CNN	4	TAR_2	LIB193603	worst	66.85	29.65	0.00	3.50	0.00	96.50	55.96	3131.70	45.31	0.15
cluster5	CNN	6	ALL	LIB193603	worst	42.71	36.52	1.56	18.77	0.44	79.23	46.57	2169.08	36.66	0.33
cluster5	CNN	6	TBR_2	LIB193603	worst	3.70	0.00	0.00	95.06	1.23	3.70	41.97	1761.15	38.14	0.72
cluster5	CNN	6	TBR_1	LIB193603	worst	3.66	0.00	0.00	93.83	2.50	3.66	46.35	2148.13	40.09	0.66
cluster5	CNN	6	TIR	LIB193603	worst	46.66	49.19	2.63	1.52	0.00	95.85	41.84	1750.60	31.62	0.29

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	6	TAR_1	LIB193603	worst	57.36	38.81	0.57	3.06	0.19	96.17	52.16	2721.09	42.69	0.20
cluster5	CNN	6	TAR_2	LIB193603	worst	65.12	27.25	0.00	7.63	0.00	92.37	60.60	3672.04	48.99	0.17
cluster5	CNN	8	ALL	LIB193603	worst	37.63	40.55	1.16	20.17	0.48	78.18	51.14	2615.19	40.62	0.36
cluster5	CNN	8	TBR_2	LIB193603	worst	5.13	0.00	0.00	91.03	3.85	5.13	54.83	3006.76	47.29	0.89
cluster5	CNN	8	TBR_1	LIB193603	worst	1.95	0.00	0.00	95.70	2.34	1.95	51.36	2637.53	45.34	0.74
cluster5	CNN	8	TIR	LIB193603	worst	43.46	52.98	2.02	1.54	0.00	96.44	41.56	1727.42	32.03	0.30
cluster5	CNN	8	TAR_1	LIB193603	worst	50.10	44.34	0.19	5.18	0.19	94.44	57.08	3258.22	47.50	0.22
cluster5	CNN	8	TAR_2	LIB193603	worst	46.83	36.64	0.00	16.53	0.00	83.47	78.61	6179.33	67.26	0.23
cluster5	Linear	12	ALL	LIB193603	worst	33.26	44.60	3.69	13.60	4.85	77.86	78.28	6127.07	58.11	0.43
cluster5	Linear	12	TBR_2	LIB193603	worst	46.58	0.00	0.00	53.42	0.00	46.58	40.84	1667.90	29.33	0.56
cluster5	Linear	12	TBR_1	LIB193603	worst	52.54	0.00	0.00	43.00	4.46	52.54	48.11	2314.70	30.88	0.50
cluster5	Linear	12	TIR	LIB193603	worst	29.59	63.25	6.46	0.43	0.27	92.84	61.52	3785.20	47.70	0.42
cluster5	Linear	12	TAR_1	LIB193603	worst	36.70	39.03	0.39	4.27	19.61	75.73	97.22	9452.54	79.83	0.38
cluster5	Linear	12	TAR_2	LIB193603	worst	17.93	27.17	0.00	46.22	8.68	45.10	139.96	19589.62	123.95	0.43
cluster5	Linear	16	ALL	LIB193603	worst	26.61	44.20	4.30	16.25	8.64	70.81	91.69	8407.34	69.04	0.51
cluster5	Linear	16	TBR_2	LIB193603	worst	35.71	0.00	0.00	64.29	0.00	35.71	47.53	2259.37	36.84	0.70
cluster5	Linear	16	TBR_1	LIB193603	worst	39.36	0.00	0.00	54.47	6.17	39.36	58.72	3447.71	40.26	0.66
cluster5	Linear	16	TIR	LIB193603	worst	26.04	65.65	7.65	0.39	0.28	91.69	66.31	4396.81	52.80	0.47
cluster5	Linear	16	TAR_1	LIB193603	worst	28.40	35.90	0.00	2.96	32.74	64.30	109.48	11986.47	91.66	0.43
cluster5	Linear	16	TAR_2	LIB193603	worst	8.19	14.12	0.00	55.93	21.75	22.31	177.57	31530.97	164.03	0.56
cluster5	Linear	2	ALL	LIB193603	worst	79.91	18.65	0.03	1.41	0.00	98.56	24.41	595.63	17.41	0.13
cluster5	Linear	2	TBR_2	LIB193603	worst	96.59	0.00	0.00	3.41	0.00	96.59	6.33	40.08	3.87	0.07
cluster5	Linear	2	TBR_1	LIB193603	worst	92.71	0.00	0.00	7.29	0.00	92.71	10.48	109.76	6.54	0.11
cluster5	Linear	2	TIR	LIB193603	worst	73.46	26.38	0.05	0.10	0.00	99.84	23.39	547.27	17.21	0.15
cluster5	Linear	2	TAR_1	LIB193603	worst	78.24	21.01	0.00	0.75	0.00	99.25	32.91	1083.20	25.95	0.12
cluster5	Linear	2	TAR_2	LIB193603	worst	93.33	6.40	0.00	0.27	0.00	99.73	31.23	975.47	25.01	0.09
cluster5	Linear	4	ALL	LIB193603	worst	67.40	29.22	0.17	3.21	0.00	96.62	33.98	1154.38	24.23	0.18
cluster5	Linear	4	TBR_2	LIB193603	worst	91.95	0.00	0.00	8.05	0.00	91.95	9.59	91.95	5.64	0.11
cluster5	Linear	4	TBR_1	LIB193603	worst	84.19	0.00	0.00	15.81	0.00	84.19	15.41	237.32	9.21	0.15
cluster5	Linear	4	TIR	LIB193603	worst	61.11	38.43	0.31	0.16	0.00	99.54	31.24	975.70	23.22	0.20
cluster5	Linear	4	TAR_1	LIB193603	worst	61.93	36.55	0.00	1.52	0.00	98.48	46.94	2203.59	36.91	0.18
cluster5	Linear	4	TAR_2	LIB193603	worst	78.17	19.41	0.00	2.43	0.00	97.58	46.17	2131.79	37.00	0.13
cluster5	Linear	6	ALL	LIB193603	worst	56.38	35.93	1.59	5.72	0.38	92.31	46.71	2182.27	33.24	0.25
cluster5	Linear	6	TBR_2	LIB193603	worst	81.48	0.00	0.00	18.52	0.00	81.48	18.39	338.23	11.04	0.21
cluster5	Linear	6	TBR_1	LIB193603	worst	77.46	0.00	0.00	21.97	0.58	77.46	25.46	648.11	15.05	0.24
cluster5	Linear	6	TIR	LIB193603	worst	48.29	49.03	2.31	0.37	0.00	97.32	41.62	1732.32	30.93	0.27
cluster5	Linear	6	TAR_1	LIB193603	worst	51.24	41.11	1.91	3.82	1.91	92.35	66.68	4446.23	52.94	0.25

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	Linear	6	TAR_2	LIB193603	worst	70.30	19.35	0.00	10.35	0.00	89.65	62.17	3865.60	47.74	0.17
cluster5	Linear	8	ALL	LIB193603	worst	45.92	41.90	2.56	8.02	1.61	87.82	60.21	3625.67	43.63	0.33
cluster5	Linear	8	TBR_2	LIB193603	worst	75.64	0.00	0.00	24.36	0.00	75.64	31.45	989.01	19.07	0.36
cluster5	Linear	8	TBR_1	LIB193603	worst	70.51	0.00	0.00	27.93	1.56	70.51	34.40	1183.07	21.57	0.35
cluster5	Linear	8	TIR	LIB193603	worst	38.84	56.64	4.09	0.37	0.05	95.48	51.67	2670.07	38.73	0.34
cluster5	Linear	8	TAR_1	LIB193603	worst	40.12	46.07	1.73	4.03	8.06	86.19	81.75	6683.51	66.85	0.32
cluster5	Linear	8	TAR_2	LIB193603	worst	49.86	27.55	0.00	21.76	0.83	77.41	90.57	8202.99	72.11	0.25
cluster5	LSTM	12	ALL	LIB193603	worst	30.24	46.46	0.37	22.32	0.61	76.70	60.13	3615.44	49.17	0.44
cluster5	LSTM	12	TBR_2	LIB193603	worst	0.00	0.00	0.00	97.26	2.74	0.00	62.81	3945.59	56.60	1.07
cluster5	LSTM	12	TBR_1	LIB193603	worst	0.81	0.00	0.00	96.15	3.04	0.81	63.07	3977.38	58.22	0.95
cluster5	LSTM	12	TIR	LIB193603	worst	39.74	57.93	0.65	1.52	0.16	97.67	43.30	1875.17	35.40	0.35
cluster5	LSTM	12	TAR_1	LIB193603	worst	49.71	43.50	0.00	6.80	0.00	93.21	54.69	2990.53	46.57	0.21
cluster5	LSTM	12	TAR_2	LIB193603	worst	0.00	65.27	0.00	34.73	0.00	65.27	113.71	12928.84	109.94	0.38
cluster5	LSTM	16	ALL	LIB193603	worst	26.29	42.92	0.00	30.79	0.00	69.21	72.02	5186.47	59.72	0.55
cluster5	LSTM	16	TBR_2	LIB193603	worst	0.00	0.00	0.00	100.00	0.00	0.00	89.51	8012.38	89.16	1.69
cluster5	LSTM	16	TBR_1	LIB193603	worst	0.00	0.00	0.00	100.00	0.00	0.00	82.14	6747.19	81.62	1.34
cluster5	LSTM	16	TIR	LIB193603	worst	42.88	55.46	0.00	1.66	0.00	98.34	43.44	1887.19	36.12	0.39
cluster5	LSTM	16	TAR_1	LIB193603	worst	13.61	73.96	0.00	12.43	0.00	87.57	67.87	4606.62	64.05	0.29
cluster5	LSTM	16	TAR_2	LIB193603	worst	0.00	0.00	0.00	100.00	0.00	0.00	142.16	20208.61	138.99	0.48
cluster5	LSTM	2	ALL	LIB193603	worst	92.38	6.47	0.00	1.15	0.00	98.85	19.61	384.42	12.49	0.09
cluster5	LSTM	2	TBR_2	LIB193603	worst	100.00	0.00	0.00	0.00	0.00	100.00	4.79	22.96	3.48	0.07
cluster5	LSTM	2	TBR_1	LIB193603	worst	92.71	0.00	0.00	7.29	0.00	92.71	7.51	56.40	5.39	0.09
cluster5	LSTM	2	TIR	LIB193603	worst	92.14	7.81	0.00	0.05	0.00	99.95	13.56	183.88	9.89	0.08
cluster5	LSTM	2	TAR_1	LIB193603	worst	95.87	4.13	0.00	0.00	0.00	100.00	17.72	313.85	13.31	0.06
cluster5	LSTM	2	TAR_2	LIB193603	worst	86.40	13.60	0.00	0.00	0.00	100.00	45.51	2071.21	37.01	0.12
cluster5	LSTM	4	ALL	LIB193603	worst	70.02	23.39	0.06	6.53	0.00	93.41	29.98	898.73	21.80	0.17
cluster5	LSTM	4	TBR_2	LIB193603	worst	74.71	0.00	0.00	25.29	0.00	74.71	14.97	224.04	11.23	0.21
cluster5	LSTM	4	TBR_1	LIB193603	worst	63.62	0.00	0.00	36.38	0.00	63.62	17.46	304.97	12.68	0.21
cluster5	LSTM	4	TIR	LIB193603	worst	67.99	31.54	0.10	0.36	0.00	99.53	27.29	744.79	19.99	0.17
cluster5	LSTM	4	TAR_1	LIB193603	worst	78.79	20.45	0.00	0.76	0.00	99.24	32.25	1040.34	25.04	0.12
cluster5	LSTM	4	TAR_2	LIB193603	worst	76.01	23.99	0.00	0.00	0.00	100.00	49.91	2491.40	41.94	0.14
cluster5	LSTM	6	ALL	LIB193603	worst	51.46	33.42	0.50	14.47	0.15	84.88	41.47	1719.97	31.32	0.25
cluster5	LSTM	6	TBR_2	LIB193603	worst	34.57	0.00	0.00	65.43	0.00	34.57	25.92	671.87	23.67	0.45
cluster5	LSTM	6	TBR_1	LIB193603	worst	23.89	0.00	0.00	75.34	0.77	23.89	31.28	978.66	25.01	0.41
cluster5	LSTM	6	TIR	LIB193603	worst	57.12	40.99	0.89	1.00	0.00	98.11	34.94	1220.72	25.92	0.23
cluster5	LSTM	6	TAR_1	LIB193603	worst	70.36	27.53	0.00	1.91	0.19	97.89	42.31	1790.36	32.54	0.15
cluster5	LSTM	6	TAR_2	LIB193603	worst	37.87	57.22	0.00	4.90	0.00	95.09	74.08	5488.12	68.18	0.23

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	8	ALL	LIB193603	worst	38.97	42.31	0.57	17.73	0.42	81.28	50.63	2563.37	39.40	0.33
cluster5	LSTM	8	TBR_2	LIB193603	worst	15.38	0.00	0.00	83.33	1.28	15.38	38.55	1486.01	32.00	0.61
cluster5	LSTM	8	TBR_1	LIB193603	worst	9.96	0.00	0.00	87.89	2.15	9.96	43.38	1881.46	35.46	0.58
cluster5	LSTM	8	TIR	LIB193603	worst	46.87	50.69	1.01	1.43	0.00	97.56	39.53	1562.79	30.69	0.29
cluster5	LSTM	8	TAR_1	LIB193603	worst	67.18	28.98	0.00	3.45	0.38	96.16	49.51	2451.03	39.94	0.19
cluster5	LSTM	8	TAR_2	LIB193603	worst	3.58	86.78	0.00	9.64	0.00	90.36	95.42	9105.51	90.97	0.31

Appendix G

Absolute difference between group-based prediction models and personalized prediction models performance in the different BGL range

Table G.1 presents the absolute difference between the metrics performance results for the group-based prediction models and the personalized prediction models. Performance results difference are shown for each selected pair of patients in each cluster, representing the best- and worst-predicted by the corresponding prediction model for that group. The table displays metric results differences across the different BGL ranges and the six established clusters. Since there are three prediction algorithms, six PH values, six BGL ranges, six groups, and two patients selected per model, the table contains a total of 1,296 rows of results. The "Patient" column indicates the identifier of the patient whose results are displayed, and the "Type" column specifies whether the patient was classified by the corresponding group-based model as best or worst. In cases where performance results are missing, this corresponds to instances where no BGL measurements were available for that specific test set, resulting in no performance data.

It is important to note that from the outcome of this comparison for the percentage of measurements in the zone 'A + B', which is a maximization metric, positive values indicate that the group-based prediction models perform better, negative values indicate worse performance, and zero means equal performance between both types of models. The effect of minimization metrics (RMSE, MSE, MAE, and MAPE) is reversed, where positive values reflect worse performance for group-based models, negative values indicate better performance, and zero means equal results. Therefore, the tables generated from this subtraction process are formatted for a more explicit comparison. To improve clarity, the cells corresponding to these key metrics, particularly 'A + B' and all non-clinical metrics, are color-coded: green represents better results for group-based models, red represents worse results, and gray indicates equal performance for both model types.

Table G.1: Absolute difference between group-based prediction models and personalized prediction models performance in the different BGL range assessed via both clinical and non-clinical metrics for all clusters. Green: better for group-based models, red: worse, gray: equal. Missing results indicate cases with no available measurements for the specific test set for personalized models.

Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	2	ALL	LIB193859	best	2.99	-2.82	0.00	-0.16	0.00	0.17	-1.68	-0.01	-100.59	-1.56
cluster0	CNN	2	TBR_2	LIB193859	best										
cluster0	CNN	2	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-12.99	-0.21	-1120.67	-12.28
cluster0	CNN	2	TIR	LIB193859	best	3.43	-3.43	0.00	0.00	0.00	0.00	-0.67	-0.01	-6.48	-0.12
cluster0	CNN	2	TAR_1	LIB193859	best	1.11	-1.15	0.00	0.04	0.00	-0.04	-0.91	0.00	-39.15	-0.59
cluster0	CNN	2	TAR_2	LIB193859	best	5.39	-4.43	0.00	-0.96	0.00	0.96	-5.72	-0.02	-455.79	-5.61
cluster0	CNN	2	ALL	LIB193526	worst	-5.77	-1.15	-0.01	6.93	-0.01	-6.92	0.87	0.02	19.70	0.43
cluster0	CNN	2	TBR_2	LIB193526	worst	-38.66	0.00	0.00	38.66	0.00	-38.66	7.51	0.15	311.00	6.73
cluster0	CNN	2	TBR_1	LIB193526	worst	-25.11	0.00	0.00	25.11	0.00	-25.11	5.20	0.09	198.73	4.17
cluster0	CNN	2	TIR	LIB193526	worst	1.78	-1.96	-0.01	0.20	0.00	-0.18	-0.97	-0.01	-66.05	-1.51
cluster0	CNN	2	TAR_1	LIB193526	worst	-0.44	0.44	0.00	0.07	-0.07	0.00	0.16	0.00	8.91	0.18
cluster0	CNN	2	TAR_2	LIB193526	worst	-0.80	0.00	0.00	0.81	0.00	-0.80	3.50	0.01	199.97	3.59
cluster0	CNN	4	ALL	LIB193859	best	1.61	-0.98	-0.27	-0.36	0.00	0.63	-1.01	-0.01	-70.96	-0.78
cluster0	CNN	4	TBR_2	LIB193859	best										
cluster0	CNN	4	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-24.53	-0.39	-3223.17	-22.35
cluster0	CNN	4	TIR	LIB193859	best	1.96	-1.33	-0.63	0.00	0.00	0.63	-2.18	-0.03	-229.23	-3.12
cluster0	CNN	4	TAR_1	LIB193859	best	0.05	-0.05	0.09	-0.09	0.00	0.00	1.82	0.01	336.08	3.77
cluster0	CNN	4	TAR_2	LIB193859	best	3.68	-1.88	0.00	-1.80	0.00	1.80	-3.22	-0.01	-417.55	-3.29
cluster0	CNN	4	ALL	LIB193526	worst	-5.86	1.43	0.00	4.44	-0.02	-4.43	3.11	0.06	159.54	2.53
cluster0	CNN	4	TBR_2	LIB193526	worst	-22.72	0.00	0.00	22.72	0.00	-22.72	13.18	0.27	931.32	12.22
cluster0	CNN	4	TBR_1	LIB193526	worst	-16.53	0.00	0.00	16.28	0.23	-16.53	11.76	0.20	713.03	9.67
cluster0	CNN	4	TIR	LIB193526	worst	-3.33	2.93	0.00	0.39	0.00	-0.40	0.88	0.02	9.45	0.17
cluster0	CNN	4	TAR_1	LIB193526	worst	3.48	-2.94	0.00	-0.23	-0.31	0.54	-1.68	-0.01	-190.34	-2.79
cluster0	CNN	4	TAR_2	LIB193526	worst	-1.25	1.25	0.00	0.42	-0.41	0.00	1.43	0.00	16.49	0.18
cluster0	CNN	6	ALL	LIB193914	best	2.65	-2.65	0.31	-0.34	0.03	0.00	-1.01	-0.01	5.95	0.07
cluster0	CNN	6	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.89	-0.10	-590.76	-4.48
cluster0	CNN	6	TBR_1	LIB193914	best	0.00	0.00	0.00	-1.17	1.17	0.00	-4.56	-0.07	-451.71	-3.59
cluster0	CNN	6	TIR	LIB193914	best	1.41	-1.79	0.38	-0.01	0.01	-0.38	-0.64	-0.01	3.72	0.05
cluster0	CNN	6	TAR_1	LIB193914	best	6.03	-5.37	0.03	-0.69	0.00	0.66	-0.96	0.00	238.97	2.24
cluster0	CNN	6	TAR_2	LIB193914	best	24.94	-15.85	0.00	-9.09	0.00	9.09	-11.09	-0.04	-1236.82	-6.99
cluster0	CNN	6	ALL	LIB193526	worst	-1.71	1.51	-0.03	0.24	-0.03	-0.20	2.54	0.05	163.41	2.14
cluster0	CNN	6	TBR_2	LIB193526	worst	-0.24	0.00	0.00	0.24	0.00	-0.24	11.25	0.23	1054.54	10.53
cluster0	CNN	6	TBR_1	LIB193526	worst	-1.46	0.00	0.00	1.62	-0.16	-1.46	9.29	0.16	720.55	7.60

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	6	TIR	LIB193526	worst	-1.86	1.86	-0.03	0.04	0.00	0.00	0.17	0.01	-39.43	-0.66
cluster0	CNN	6	TAR_1	LIB193526	worst	-1.22	0.89	0.00	0.33	0.00	-0.33	0.54	0.00	-68.43	-0.81
cluster0	CNN	6	TAR_2	LIB193526	worst	-7.45	10.09	0.00	-2.63	0.00	2.64	3.52	0.01	148.04	1.05
cluster0	CNN	8	ALL	LIB193914	best	1.40	-1.35	0.43	-0.55	0.08	0.05	-0.48	-0.01	34.09	0.39
cluster0	CNN	8	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.98	-0.09	-607.52	-3.88
cluster0	CNN	8	TBR_1	LIB193914	best	0.00	0.00	0.00	-2.86	2.86	0.00	-4.02	-0.06	-351.10	-2.45
cluster0	CNN	8	TIR	LIB193914	best	-0.37	-0.18	0.55	-0.02	0.02	-0.55	0.24	0.00	80.31	1.07
cluster0	CNN	8	TAR_1	LIB193914	best	7.58	-6.78	0.00	-0.80	0.00	0.80	-1.95	-0.01	59.01	0.54
cluster0	CNN	8	TAR_2	LIB193914	best	19.57	-3.48	0.00	-16.09	0.00	16.09	-11.30	-0.04	-1446.63	-7.51
cluster0	CNN	8	ALL	LIB193526	worst	-1.64	1.58	-0.03	0.09	-0.01	-0.06	4.20	0.08	358.68	4.05
cluster0	CNN	8	TBR_2	LIB193526	worst	-0.25	0.00	0.00	0.13	0.12	-0.25	16.72	0.34	1896.49	15.23
cluster0	CNN	8	TBR_1	LIB193526	worst	-0.68	0.00	0.00	0.85	-0.17	-0.68	15.13	0.25	1479.16	12.90
cluster0	CNN	8	TIR	LIB193526	worst	-3.26	3.27	-0.03	0.04	0.00	0.01	1.82	0.03	95.00	1.40
cluster0	CNN	8	TAR_1	LIB193526	worst	3.83	-4.00	0.00	0.17	0.00	-0.17	-3.41	-0.02	-426.37	-4.69
cluster0	CNN	8	TAR_2	LIB193526	worst	-1.37	4.59	0.00	-3.21	0.00	3.22	-2.32	-0.01	-752.92	-4.67
cluster0	CNN	12	ALL	LIB193914	best	0.47	0.07	0.13	-0.74	0.05	0.54	-0.25	0.00	-3.73	-0.04
cluster0	CNN	12	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-3.80	-0.08	-716.84	-3.77
cluster0	CNN	12	TBR_1	LIB193914	best	0.00	0.00	0.00	-1.73	1.73	0.00	-3.29	-0.05	-401.00	-2.57
cluster0	CNN	12	TIR	LIB193914	best	-1.75	1.59	0.17	-0.02	0.01	-0.16	0.72	0.00	81.94	1.09
cluster0	CNN	12	TAR_1	LIB193914	best	10.82	-9.55	0.00	-1.27	0.00	1.27	-3.33	-0.02	-172.85	-1.47
cluster0	CNN	12	TAR_2	LIB193914	best	1.14	21.94	0.00	-23.08	0.00	23.08	-8.01	-0.03	-1415.64	-6.21
cluster0	CNN	12	ALL	LIB193526	worst	-1.75	1.90	-0.04	-0.20	0.09	0.15	4.37	0.09	465.00	4.44
cluster0	CNN	12	TBR_2	LIB193526	worst	-0.13	0.00	0.00	-0.13	0.26	-0.13	15.29	0.31	2196.56	14.25
cluster0	CNN	12	TBR_1	LIB193526	worst	-0.27	0.00	0.00	-0.18	0.46	-0.27	14.12	0.23	1741.92	12.44
cluster0	CNN	12	TIR	LIB193526	worst	-4.66	4.73	-0.06	0.00	0.00	0.07	3.39	0.05	266.41	3.67
cluster0	CNN	12	TAR_1	LIB193526	worst	8.75	-8.57	0.00	-0.19	0.00	0.18	-7.65	-0.04	-887.55	-8.04
cluster0	CNN	12	TAR_2	LIB193526	worst	-0.51	6.10	0.00	-5.59	0.00	5.59	-4.86	-0.02	-1355.45	-6.40
cluster0	CNN	16	ALL	LIB193914	best	1.08	-1.04	0.00	-0.04	0.00	0.04	-1.06	-0.02	-78.50	-0.84
cluster0	CNN	16	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-8.11	-0.16	-1610.45	-8.35
cluster0	CNN	16	TBR_1	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-5.75	-0.09	-904.26	-5.56
cluster0	CNN	16	TIR	LIB193914	best	1.74	-1.74	0.00	0.00	0.00	0.00	-1.75	-0.02	-161.11	-2.15
cluster0	CNN	16	TAR_1	LIB193914	best	-1.72	1.79	0.00	-0.07	0.00	0.07	2.41	0.01	342.06	2.82
cluster0	CNN	16	TAR_2	LIB193914	best	0.00	1.18	0.00	-1.18	0.00	1.18	2.24	0.01	626.18	2.56
cluster0	CNN	16	ALL	LIB193326	worst	-15.29	0.74	-4.06	20.46	-1.85	-14.55	7.39	-0.04	1415.95	8.94
cluster0	CNN	16	TBR_2	LIB193326	worst	0.00	0.00	0.00	100.00	-100.00	0.00	-47.21	-0.89	-12636.04	-47.21
cluster0	CNN	16	TBR_1	LIB193326	worst	0.00	0.00	0.00	51.16	-51.16	0.00	-33.00	-0.53	-7321.21	-34.34
cluster0	CNN	16	TIR	LIB193326	worst	19.86	-9.93	-9.93	0.36	-0.36	9.93	-26.03	-0.23	-3311.20	-29.27

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	16	TAR_1	LIB193326	worst	-52.56	43.02	0.00	9.54	0.00	-9.54	26.16	0.12	2348.89	23.80
cluster0	CNN	16	TAR_2	LIB193326	worst	-27.91	-36.81	0.00	64.72	0.00	-64.72	44.92	0.15	9414.20	38.48
cluster0	Linear	2	ALL	LIB193859	best	3.19	-3.10	-0.03	-0.06	0.00	0.09	-1.98	-0.01	-115.41	-2.49
cluster0	Linear	2	TBR_2	LIB193859	best										
cluster0	Linear	2	TBR_1	LIB193859	best	20.00	0.00	0.00	-20.00	0.00	20.00	-6.46	-0.10	-413.16	-7.97
cluster0	Linear	2	TIR	LIB193859	best	4.21	-4.15	-0.06	0.00	0.00	0.06	-2.39	-0.02	-127.20	-2.87
cluster0	Linear	2	TAR_1	LIB193859	best	3.02	-2.97	0.00	-0.05	0.00	0.05	-2.28	-0.01	-134.64	-2.91
cluster0	Linear	2	TAR_2	LIB193859	best	0.81	-0.65	0.00	-0.16	0.00	0.16	-0.35	0.00	-47.35	-0.93
cluster0	Linear	2	ALL	LIB194097	worst	1.13	-1.45	0.00	0.32	-0.01	-0.32	-1.12	0.00	-83.09	-1.69
cluster0	Linear	2	TBR_2	LIB194097	worst	-0.81	0.00	0.00	0.81	0.00	-0.81	0.85	0.02	-25.93	-0.85
cluster0	Linear	2	TBR_1	LIB194097	worst	-3.50	0.00	0.00	3.50	0.00	-3.50	0.63	0.01	10.27	0.28
cluster0	Linear	2	TIR	LIB194097	worst	1.50	-1.53	0.00	0.02	0.00	-0.03	-0.78	-0.01	-60.14	-1.22
cluster0	Linear	2	TAR_1	LIB194097	worst	2.15	-2.02	0.04	-0.13	-0.05	0.13	-2.24	-0.01	-150.01	-2.78
cluster0	Linear	2	TAR_2	LIB194097	worst	1.76	-1.56	0.00	-0.19	0.00	0.20	-3.18	-0.01	-200.19	-3.70
cluster0	Linear	4	ALL	LIB193859	best	4.80	-4.00	-0.48	-0.33	0.00	0.80	-2.87	-0.02	-291.13	-3.51
cluster0	Linear	4	TBR_2	LIB193859	best										
cluster0	Linear	4	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-9.61	-0.16	-1296.83	-12.20
cluster0	Linear	4	TIR	LIB193859	best	7.49	-6.83	-0.67	0.00	0.00	0.66	-5.06	-0.04	-446.69	-6.27
cluster0	Linear	4	TAR_1	LIB193859	best	5.89	-5.28	-0.48	-0.17	0.05	0.61	-3.95	-0.02	-378.08	-4.45
cluster0	Linear	4	TAR_2	LIB193859	best	-4.18	5.73	0.00	-1.47	-0.08	1.55	4.91	0.02	280.64	2.69
cluster0	Linear	4	ALL	LIB193526	worst	-11.50	-1.78	-0.07	13.39	-0.05	-13.28	2.28	0.05	20.23	0.37
cluster0	Linear	4	TBR_2	LIB193526	worst	-63.82	0.00	0.00	63.82	0.00	-63.82	16.17	0.33	580.74	12.12
cluster0	Linear	4	TBR_1	LIB193526	worst	-54.18	0.00	0.00	54.27	-0.08	-54.18	11.80	0.20	440.61	8.20
cluster0	Linear	4	TIR	LIB193526	worst	2.33	-2.68	-0.10	0.46	0.00	-0.35	-1.64	-0.01	-150.68	-2.85
cluster0	Linear	4	TAR_1	LIB193526	worst	1.70	-2.01	0.00	0.46	-0.16	-0.31	-0.25	0.00	-108.02	-1.68
cluster0	Linear	4	TAR_2	LIB193526	worst	-6.64	5.40	0.00	1.66	-0.41	-1.24	11.66	0.04	648.35	8.28
cluster0	Linear	6	ALL	LIB193859	best	5.29	-2.92	-1.52	-0.81	-0.03	2.37	-5.07	-0.04	-697.60	-6.52
cluster0	Linear	6	TBR_2	LIB193859	best										
cluster0	Linear	6	TBR_1	LIB193859	best	0.00	0.00	0.00	40.00	-40.00	0.00	-13.49	-0.22	-3128.45	-17.39
cluster0	Linear	6	TIR	LIB193859	best	9.16	-6.60	-2.56	0.00	0.00	2.56	-8.44	-0.06	-1024.75	-11.68
cluster0	Linear	6	TAR_1	LIB193859	best	7.72	-6.48	-0.79	-0.44	0.00	1.24	-6.80	-0.03	-814.63	-7.86
cluster0	Linear	6	TAR_2	LIB193859	best	-9.34	13.35	-0.17	-3.84	0.00	4.01	7.03	0.02	385.57	2.58
cluster0	Linear	6	ALL	LIB193526	worst	-13.45	-1.25	-0.19	15.10	-0.20	-14.70	4.07	0.10	82.46	1.15
cluster0	Linear	6	TBR_2	LIB193526	worst	-74.40	0.00	0.00	74.52	-0.12	-74.40	28.86	0.59	1576.94	21.50
cluster0	Linear	6	TBR_1	LIB193526	worst	-57.85	0.00	0.00	58.01	-0.16	-57.85	22.72	0.38	1207.41	15.70
cluster0	Linear	6	TIR	LIB193526	worst	2.11	-2.50	-0.32	0.71	0.00	-0.39	-2.77	-0.01	-312.93	-4.89
cluster0	Linear	6	TAR_1	LIB193526	worst	3.56	-2.43	0.00	-0.08	-1.05	1.13	-2.23	-0.01	-420.94	-5.17

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	Linear	6	TAR_2	LIB193526	worst	-25.88	24.56	0.00	2.63	-1.32	-1.32	15.52	0.06	1005.97	8.65
cluster0	Linear	8	ALL	LIB193914	best	-0.49	0.27	-0.21	0.59	-0.16	-0.22	-1.54	0.01	-335.81	-3.70
cluster0	Linear	8	TBR_2	LIB193914	best	0.00	0.00	0.00	6.25	-6.25	0.00	13.53	0.26	854.10	6.74
cluster0	Linear	8	TBR_1	LIB193914	best	-18.57	0.00	0.00	19.05	-0.48	-18.57	18.00	0.28	1266.89	10.25
cluster0	Linear	8	TIR	LIB193914	best	-0.34	0.45	-0.27	0.18	-0.01	0.11	-1.02	0.01	-165.02	-2.19
cluster0	Linear	8	TAR_1	LIB193914	best	4.14	-3.24	0.00	-0.10	-0.79	0.90	-7.59	-0.04	-1350.18	-10.87
cluster0	Linear	8	TAR_2	LIB193914	best	-23.05	22.26	0.00	0.81	0.00	-0.79	5.39	0.02	-403.43	-2.12
cluster0	Linear	8	ALL	LIB193526	worst	-11.32	-2.11	-0.38	14.41	-0.61	-13.43	4.80	0.13	96.21	1.14
cluster0	Linear	8	TBR_2	LIB193526	worst	-67.40	0.00	0.00	67.64	-0.24	-67.40	37.14	0.75	2494.40	26.84
cluster0	Linear	8	TBR_1	LIB193526	worst	-53.73	0.00	0.00	54.33	-0.60	-53.73	29.63	0.49	1868.05	20.15
cluster0	Linear	8	TIR	LIB193526	worst	5.23	-5.32	-0.61	0.75	-0.04	-0.09	-4.61	-0.01	-521.91	-7.37
cluster0	Linear	8	TAR_1	LIB193526	worst	0.26	2.05	0.00	0.94	-3.23	2.31	-2.33	-0.01	-799.22	-8.02
cluster0	Linear	8	TAR_2	LIB193526	worst	-40.82	35.33	0.00	7.34	-1.83	-5.49	18.95	0.07	1541.51	9.91
cluster0	Linear	12	ALL	LIB193914	best	0.76	-0.55	-0.63	0.65	-0.24	0.21	-2.66	0.01	-572.04	-5.83
cluster0	Linear	12	TBR_2	LIB193914	best	0.00	0.00	0.00	14.29	-14.29	0.00	9.64	0.19	651.41	3.52
cluster0	Linear	12	TBR_1	LIB193914	best	-6.44	0.00	0.00	7.43	-0.99	-6.44	24.92	0.39	2507.46	18.63
cluster0	Linear	12	TIR	LIB193914	best	1.32	-0.59	-0.80	0.09	-0.02	0.73	-1.40	0.02	-253.77	-3.18
cluster0	Linear	12	TAR_1	LIB193914	best	1.68	-1.79	0.00	1.20	-1.10	-0.11	-12.80	-0.06	-2341.71	-17.41
cluster0	Linear	12	TAR_2	LIB193914	best	-20.23	10.82	0.00	9.40	0.00	-9.41	0.70	0.00	-1742.12	-7.62
cluster0	Linear	12	ALL	LIB193526	worst	-7.66	-2.60	-0.86	12.60	-1.48	-10.26	5.33	0.18	86.57	0.82
cluster0	Linear	12	TBR_2	LIB193526	worst	-54.88	0.00	0.00	56.30	-1.42	-54.88	48.15	0.98	4260.34	33.80
cluster0	Linear	12	TBR_1	LIB193526	worst	-42.61	0.00	0.00	44.16	-1.55	-42.61	38.65	0.64	3124.31	25.69
cluster0	Linear	12	TIR	LIB193526	worst	7.05	-6.20	-1.42	0.63	-0.06	0.85	-5.74	0.00	-730.14	-8.85
cluster0	Linear	12	TAR_1	LIB193526	worst	-1.52	7.42	0.00	1.43	-7.33	5.90	-10.29	-0.05	-2257.17	-18.45
cluster0	Linear	12	TAR_2	LIB193526	worst	-22.84	8.12	0.00	19.80	-5.08	-14.72	7.43	0.03	-615.88	-2.94
cluster0	Linear	16	ALL	LIB193914	best	2.07	-1.72	-1.02	1.06	-0.40	0.35	-4.23	0.00	-802.07	-7.91
cluster0	Linear	16	TBR_2	LIB193914	best	0.00	0.00	0.00	21.43	-21.43	0.00	9.97	0.19	186.26	1.00
cluster0	Linear	16	TBR_1	LIB193914	best	-4.68	0.00	0.00	8.31	-3.64	-4.68	26.27	0.41	2869.28	20.41
cluster0	Linear	16	TIR	LIB193914	best	3.87	-2.61	-1.29	0.09	-0.06	1.26	-3.02	0.01	-442.65	-5.47
cluster0	Linear	16	TAR_1	LIB193914	best	-3.69	3.40	0.00	1.68	-1.40	-0.29	-14.34	-0.07	-2772.32	-19.74
cluster0	Linear	16	TAR_2	LIB193914	best	-11.50	-12.10	0.00	24.19	-0.59	-23.60	-2.71	-0.01	-2563.97	-10.23
cluster0	Linear	16	ALL	LIB193526	worst	-3.62	-3.79	-0.91	10.88	-2.55	-7.41	3.36	0.17	-187.77	-1.60
cluster0	Linear	16	TBR_2	LIB193526	worst	-40.19	0.00	0.00	43.50	-3.31	-40.19	46.80	0.95	4687.37	31.83
cluster0	Linear	16	TBR_1	LIB193526	worst	-32.50	0.00	0.00	36.38	-3.87	-32.50	38.19	0.63	3419.20	24.74
cluster0	Linear	16	TIR	LIB193526	worst	8.94	-7.84	-1.49	0.47	-0.09	1.10	-6.56	0.00	-883.53	-10.10
cluster0	Linear	16	TAR_1	LIB193526	worst	-3.44	11.78	0.00	2.55	-10.89	8.34	-18.78	-0.10	-3851.46	-27.38
cluster0	Linear	16	TAR_2	LIB193526	worst	-5.62	-18.54	0.00	35.40	-11.24	-24.16	-10.83	-0.04	-4527.27	-18.18

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	2	ALL	LIB193859	best	0.33	-0.31	-0.02	-0.02	0.00	0.02	-0.58	0.00	-45.66	-1.05
cluster0	LSTM	2	TBR_2	LIB193859	best										
cluster0	LSTM	2	TBR_1	LIB193859	best	20.00	0.00	0.00	-20.00	0.00	20.00	-18.31	-0.30	-1014.29	-16.54
cluster0	LSTM	2	TIR	LIB193859	best	0.25	-0.22	-0.03	0.00	0.00	0.03	0.39	0.00	28.99	0.74
cluster0	LSTM	2	TAR_1	LIB193859	best	-0.17	0.17	0.00	0.00	0.00	0.00	-0.03	0.00	8.69	0.20
cluster0	LSTM	2	TAR_2	LIB193859	best	1.45	-1.45	0.00	0.00	0.00	0.00	-4.06	-0.01	-337.44	-6.32
cluster0	LSTM	2	ALL	LIB193526	worst	-3.43	0.23	-0.01	3.22	-0.01	-3.20	0.79	0.02	19.46	0.60
cluster0	LSTM	2	TBR_2	LIB193526	worst	-11.00	0.00	0.00	11.00	0.00	-11.00	4.17	0.08	117.36	4.59
cluster0	LSTM	2	TBR_1	LIB193526	worst	-16.11	0.00	0.00	16.19	-0.08	-16.11	2.95	0.05	83.57	2.88
cluster0	LSTM	2	TIR	LIB193526	worst	-0.31	0.21	-0.02	0.11	0.00	-0.10	0.06	0.00	-4.34	-0.13
cluster0	LSTM	2	TAR_1	LIB193526	worst	-0.66	0.59	0.00	0.07	0.00	-0.07	-0.05	0.00	2.35	0.07
cluster0	LSTM	2	TAR_2	LIB193526	worst	-0.81	0.81	0.00	0.00	0.00	0.00	-0.30	0.00	9.63	0.25
cluster0	LSTM	4	ALL	LIB193859	best	0.41	-0.46	0.03	0.03	0.00	-0.05	0.11	0.00	60.02	0.77
cluster0	LSTM	4	TBR_2	LIB193859	best										
cluster0	LSTM	4	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-24.70	-0.39	-2637.28	-24.43
cluster0	LSTM	4	TIR	LIB193859	best	-0.44	0.66	-0.22	0.00	0.00	0.22	0.39	-0.01	47.15	0.76
cluster0	LSTM	4	TAR_1	LIB193859	best	0.82	-1.30	0.39	0.09	0.00	-0.48	1.35	0.01	267.02	3.31
cluster0	LSTM	4	TAR_2	LIB193859	best	1.80	-1.80	0.00	0.00	0.00	0.00	-2.85	-0.01	-287.00	-2.78
cluster0	LSTM	4	ALL	LIB193526	worst	-6.04	0.77	-0.02	5.27	0.02	-5.27	1.94	0.04	84.99	1.57
cluster0	LSTM	4	TBR_2	LIB193526	worst	-31.50	0.00	0.00	31.50	0.00	-31.50	9.98	0.20	556.57	9.43
cluster0	LSTM	4	TBR_1	LIB193526	worst	-17.23	0.00	0.00	17.07	0.16	-17.23	7.60	0.13	400.50	6.89
cluster0	LSTM	4	TIR	LIB193526	worst	-1.60	1.37	-0.04	0.27	0.00	-0.23	0.29	0.01	-12.19	-0.25
cluster0	LSTM	4	TAR_1	LIB193526	worst	0.31	-0.08	0.00	-0.24	0.00	0.23	-0.58	0.00	-53.32	-0.87
cluster0	LSTM	4	TAR_2	LIB193526	worst	1.66	-2.49	0.00	0.83	0.00	-0.83	-3.18	-0.01	-154.18	-2.04
cluster0	LSTM	6	ALL	LIB193914	best	2.54	-2.75	0.25	-0.05	0.02	-0.21	-1.02	-0.02	-0.06	0.00
cluster0	LSTM	6	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-5.48	-0.10	-808.00	-6.55
cluster0	LSTM	6	TBR_1	LIB193914	best	-1.64	0.00	0.00	0.70	0.94	-1.64	-4.80	-0.08	-585.66	-4.91
cluster0	LSTM	6	TIR	LIB193914	best	2.36	-2.68	0.30	0.02	0.00	-0.32	-1.03	-0.02	-27.13	-0.40
cluster0	LSTM	6	TAR_1	LIB193914	best	1.57	-1.33	0.03	-0.27	0.00	0.24	0.73	0.00	332.91	3.40
cluster0	LSTM	6	TAR_2	LIB193914	best	21.56	-19.48	0.00	-2.08	0.00	2.08	-10.14	-0.04	-965.66	-6.42
cluster0	LSTM	6	ALL	LIB193526	worst	-3.64	0.84	-0.04	2.89	-0.07	-2.80	2.68	0.06	144.58	2.09
cluster0	LSTM	6	TBR_2	LIB193526	worst	-16.11	0.00	0.00	16.11	0.00	-16.11	14.70	0.30	1114.74	13.21
cluster0	LSTM	6	TBR_1	LIB193526	worst	-9.52	0.00	0.00	9.77	-0.24	-9.52	10.63	0.18	711.79	8.75
cluster0	LSTM	6	TIR	LIB193526	worst	-1.34	1.14	-0.05	0.25	0.00	-0.20	-0.07	0.01	-59.09	-1.02
cluster0	LSTM	6	TAR_1	LIB193526	worst	0.33	0.16	0.00	-0.24	-0.24	0.49	-0.62	0.00	-144.44	-1.85
cluster0	LSTM	6	TAR_2	LIB193526	worst	-4.38	4.82	0.00	-0.44	0.00	0.44	1.38	0.00	116.36	1.02
cluster0	LSTM	8	ALL	LIB193914	best	1.50	-1.50	0.38	-0.46	0.06	0.00	-0.68	-0.01	16.02	0.19

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	8	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	0.57	0.02	-72.68	-0.55
cluster0	LSTM	8	TBR_1	LIB193914	best	0.00	0.00	0.00	-2.38	2.38	0.00	-2.15	-0.04	-338.10	-2.49
cluster0	LSTM	8	TIR	LIB193914	best	-0.18	-0.31	0.48	-0.01	0.01	-0.49	-0.31	-0.01	24.72	0.34
cluster0	LSTM	8	TAR_1	LIB193914	best	6.75	-5.76	0.00	-0.99	0.00	0.99	-0.91	0.00	198.43	1.85
cluster0	LSTM	8	TAR_2	LIB193914	best	24.13	-13.41	0.00	-10.73	0.00	10.72	-11.39	-0.04	-1386.66	-7.45
cluster0	LSTM	8	ALL	LIB193526	worst	-2.50	1.91	-0.02	0.64	-0.04	-0.59	3.87	0.08	282.73	3.41
cluster0	LSTM	8	TBR_2	LIB193526	worst	-3.92	0.00	0.00	4.05	-0.13	-3.92	16.05	0.33	1642.97	14.85
cluster0	LSTM	8	TBR_1	LIB193526	worst	-1.61	0.00	0.00	1.78	-0.17	-1.61	13.75	0.23	1222.89	11.67
cluster0	LSTM	8	TIR	LIB193526	worst	-2.97	2.97	-0.04	0.04	0.00	0.00	1.07	0.02	6.08	0.09
cluster0	LSTM	8	TAR_1	LIB193526	worst	-0.17	0.34	0.00	-0.17	0.00	0.17	-1.25	-0.01	-285.47	-3.26
cluster0	LSTM	8	TAR_2	LIB193526	worst	-2.75	1.83	0.00	0.92	0.00	-0.92	1.00	0.00	-38.01	-0.25
cluster0	LSTM	12	ALL	LIB193914	best	2.20	-1.71	0.13	-0.71	0.09	0.49	-1.43	-0.02	-71.41	-0.78
cluster0	LSTM	12	TBR_2	LIB193914	best	0.00	0.00	0.00	-7.14	7.14	0.00	-9.52	-0.19	-1709.33	-8.80
cluster0	LSTM	12	TBR_1	LIB193914	best	0.00	0.00	0.00	-2.48	2.48	0.00	-8.95	-0.14	-1224.92	-7.86
cluster0	LSTM	12	TIR	LIB193914	best	1.80	-1.98	0.17	-0.03	0.03	-0.18	-1.58	-0.02	-109.14	-1.43
cluster0	LSTM	12	TAR_1	LIB193914	best	4.16	-2.88	0.00	-1.27	0.00	1.28	0.71	0.00	320.65	2.80
cluster0	LSTM	12	TAR_2	LIB193914	best	3.99	15.96	0.00	-19.95	0.00	19.95	-4.59	-0.02	-478.21	-2.17
cluster0	LSTM	12	ALL	LIB193526	worst	-1.73	1.45	-0.02	0.35	-0.05	-0.28	4.73	0.09	459.09	4.56
cluster0	LSTM	12	TBR_2	LIB193526	worst	-0.26	0.00	0.00	0.26	0.00	-0.26	17.03	0.34	2241.77	15.43
cluster0	LSTM	12	TBR_1	LIB193526	worst	-0.36	0.00	0.00	0.73	-0.36	-0.36	16.03	0.27	1832.66	13.90
cluster0	LSTM	12	TIR	LIB193526	worst	-3.02	3.07	-0.04	0.00	0.00	0.05	2.36	0.04	148.71	2.08
cluster0	LSTM	12	TAR_1	LIB193526	worst	1.23	-1.81	0.00	0.57	0.00	-0.58	-3.89	-0.02	-624.73	-5.82
cluster0	LSTM	12	TAR_2	LIB193526	worst	1.01	-7.10	0.00	6.09	0.00	-6.09	-2.12	-0.01	-772.29	-3.80
cluster0	LSTM	16	ALL	LIB193914	best	0.86	-0.61	0.00	-0.25	0.00	0.25	-0.33	0.00	-9.88	-0.11
cluster0	LSTM	16	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.06	-0.12	-1183.09	-6.10
cluster0	LSTM	16	TBR_1	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.35	-0.04	-335.65	-2.07
cluster0	LSTM	16	TIR	LIB193914	best	-0.16	0.16	0.00	0.00	0.00	0.00	0.07	0.00	22.16	0.29
cluster0	LSTM	16	TAR_1	LIB193914	best	5.83	-5.37	0.00	-0.46	0.00	0.46	-1.53	-0.01	-52.96	-0.44
cluster0	LSTM	16	TAR_2	LIB193914	best	0.00	8.26	0.00	-8.26	0.00	8.26	-2.99	-0.01	-466.10	-1.94
cluster0	LSTM	16	ALL	LIB193526	worst	-1.03	1.15	0.01	-0.25	0.13	0.12	5.17	0.10	603.68	5.41
cluster0	LSTM	16	TBR_2	LIB193526	worst	0.00	0.00	0.00	-0.41	0.41	0.00	16.34	0.33	2588.62	15.50
cluster0	LSTM	16	TBR_1	LIB193526	worst	0.00	0.00	0.00	-0.59	0.59	0.00	15.61	0.26	2164.19	14.25
cluster0	LSTM	16	TIR	LIB193526	worst	-3.00	2.97	0.02	0.00	0.00	-0.03	4.29	0.06	381.78	5.17
cluster0	LSTM	16	TAR_1	LIB193526	worst	6.44	-6.23	0.00	-0.23	0.00	0.21	-8.54	-0.04	-1116.26	-9.41
cluster0	LSTM	16	TAR_2	LIB193526	worst	0.00	3.93	0.00	-3.93	0.00	3.93	-7.89	-0.03	-2059.27	-8.87
cluster1	CNN	2	ALL	LIB193736	best	3.17	-3.16	0.00	0.00	0.00	0.01	-1.35	-0.01	-52.04	-1.48
cluster1	CNN	2	TBR_2	LIB193736	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	2	TBR_1	LIB193736	best										
cluster1	CNN	2	TIR	LIB193736	best	4.04	-3.99	0.00	-0.06	0.00	0.05	-1.71	-0.01	-65.67	-2.17
cluster1	CNN	2	TAR_1	LIB193736	best	-0.25	0.00	0.00	0.26	0.00	-0.25	0.10	0.00	3.37	0.07
cluster1	CNN	2	TAR_2	LIB193736	best	-2.78	2.78	0.00	0.00	0.00	0.00	0.26	0.00	11.94	0.16
cluster1	CNN	2	ALL	LIB193821	worst	1.71	-2.66	0.00	0.95	0.00	-0.95	-1.18	0.00	-33.76	-0.62
cluster1	CNN	2	TBR_2	LIB193821	worst	-40.00	0.00	0.00	40.00	0.00	-40.00	9.28	0.22	503.88	5.38
cluster1	CNN	2	TBR_1	LIB193821	worst	-8.34	0.00	0.00	8.34	0.00	-8.34	2.67	0.05	181.08	3.26
cluster1	CNN	2	TIR	LIB193821	worst	2.59	-2.47	0.00	-0.12	0.00	0.12	-1.47	-0.01	-42.45	-0.94
cluster1	CNN	2	TAR_1	LIB193821	worst	9.00	-9.00	0.00	0.00	0.00	0.00	-4.22	-0.02	-243.76	-3.19
cluster1	CNN	2	TAR_2	LIB193821	worst	0.00	6.25	0.00	-6.25	0.00	6.25	0.26	0.00	-60.05	-0.37
cluster1	CNN	4	ALL	LIB193736	best	3.43	-3.67	0.00	0.24	0.00	-0.24	-0.94	-0.01	-5.96	-0.12
cluster1	CNN	4	TBR_2	LIB193736	best										
cluster1	CNN	4	TBR_1	LIB193736	best										
cluster1	CNN	4	TIR	LIB193736	best	6.43	-6.43	0.00	0.00	0.00	0.00	-2.66	-0.02	-113.26	-2.85
cluster1	CNN	4	TAR_1	LIB193736	best	-8.84	7.78	0.00	1.07	0.00	-1.06	6.12	0.03	408.03	5.45
cluster1	CNN	4	TAR_2	LIB193736	best	-11.76	8.83	0.00	2.94	0.00	-2.93	7.23	0.03	798.21	6.41
cluster1	CNN	4	ALL	LIB193821	worst	-0.67	-2.90	-0.09	3.66	0.00	-3.57	-1.17	0.01	-146.66	-2.00
cluster1	CNN	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	17.00	0.34	2132.78	16.92
cluster1	CNN	4	TBR_1	LIB193821	worst	-29.66	0.00	0.00	29.66	0.00	-29.66	8.59	0.14	505.26	6.26
cluster1	CNN	4	TIR	LIB193821	worst	2.13	-2.13	-0.12	0.13	0.00	0.00	-2.34	-0.01	-197.51	-3.42
cluster1	CNN	4	TAR_1	LIB193821	worst	11.22	-11.23	0.00	0.00	0.00	-0.01	-4.34	-0.02	-547.35	-4.97
cluster1	CNN	4	TAR_2	LIB193821	worst	0.00	-12.50	0.00	12.50	0.00	-12.50	-0.94	0.00	-673.80	-2.95
cluster1	CNN	6	ALL	LIB193385	best	-1.33	1.34	0.00	0.00	0.00	0.01	0.48	0.01	23.03	0.45
cluster1	CNN	6	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-3.66	-0.07	-450.91	-3.62
cluster1	CNN	6	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.77	-0.04	-141.86	-1.43
cluster1	CNN	6	TIR	LIB193385	best	-1.91	1.91	0.00	0.00	0.00	0.00	0.80	0.01	50.78	1.14
cluster1	CNN	6	TAR_1	LIB193385	best	13.68	-13.69	0.00	0.00	0.00	-0.01	-7.44	-0.04	-671.94	-5.06
cluster1	CNN	6	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.67	-0.03	-1673.57	-6.88
cluster1	CNN	6	ALL	LIB193821	worst	0.20	-1.76	-0.10	1.66	0.00	-1.56	-1.12	-0.01	-175.96	-2.11
cluster1	CNN	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	8.97	0.19	1207.21	9.13
cluster1	CNN	6	TBR_1	LIB193821	worst	-6.09	0.00	0.00	6.09	0.00	-6.09	2.56	0.04	-104.56	-0.96
cluster1	CNN	6	TIR	LIB193821	worst	1.65	-1.65	-0.12	0.12	0.00	0.00	-2.54	-0.02	-294.86	-4.61
cluster1	CNN	6	TAR_1	LIB193821	worst	-4.17	3.13	0.00	1.04	0.00	-1.04	3.24	0.01	187.41	1.58
cluster1	CNN	6	TAR_2	LIB193821	worst	0.00	-50.00	0.00	50.00	0.00	-50.00	12.73	0.05	2554.04	10.15
cluster1	CNN	8	ALL	LIB193385	best	-0.90	0.90	0.00	0.00	0.00	0.00	0.50	0.01	33.93	0.64
cluster1	CNN	8	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	3.74	0.07	603.15	4.41
cluster1	CNN	8	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-0.04	-167.48	-1.57

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	CNN	8	TIR	LIB193385	best	-1.24	1.24	0.00	0.00	0.00	0.00	0.67	0.01	48.23	1.06
cluster1	CNN	8	TAR_1	LIB193385	best	8.00	-8.01	0.00	0.00	0.00	-0.01	-3.57	-0.02	-318.95	-2.23
cluster1	CNN	8	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-0.63	0.00	-74.89	-0.29
cluster1	CNN	8	ALL	LIB193821	worst	-0.20	-0.20	-0.10	0.40	0.10	-0.40	-0.35	0.00	-118.41	-1.35
cluster1	CNN	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-7.45	-0.19	-1815.74	-12.78
cluster1	CNN	8	TBR_1	LIB193821	worst	-3.51	0.00	0.00	2.63	0.88	-3.51	4.08	0.06	113.98	1.03
cluster1	CNN	8	TIR	LIB193821	worst	1.29	-1.29	-0.13	0.13	0.00	0.00	-1.15	-0.01	-164.30	-2.57
cluster1	CNN	8	TAR_1	LIB193821	worst	-8.51	8.51	0.00	0.00	0.00	0.00	-0.16	0.00	-354.83	-2.56
cluster1	CNN	8	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	8.43	0.03	2368.14	8.63
cluster1	CNN	12	ALL	LIB193385	best	-6.67	6.67	0.00	0.00	0.00	0.00	2.03	0.03	61.67	1.12
cluster1	CNN	12	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	8.13	0.15	1176.57	8.09
cluster1	CNN	12	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	5.86	0.09	735.46	6.38
cluster1	CNN	12	TIR	LIB193385	best	-7.04	7.04	0.00	0.00	0.00	0.00	2.44	0.03	108.13	2.27
cluster1	CNN	12	TAR_1	LIB193385	best	2.16	-2.16	0.00	0.00	0.00	0.00	-9.07	-0.05	-1212.61	-8.39
cluster1	CNN	12	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.94	-0.03	-2062.81	-7.89
cluster1	CNN	12	ALL	LIB193821	worst	-2.57	2.36	-0.41	1.23	-0.62	-0.21	-0.68	0.01	-347.59	-3.60
cluster1	CNN	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-6.20	-0.14	-1467.05	-8.71
cluster1	CNN	12	TBR_1	LIB193821	worst	-3.57	0.00	0.00	8.93	-5.36	-3.57	7.27	0.11	-113.01	-0.89
cluster1	CNN	12	TIR	LIB193821	worst	-1.47	1.87	-0.53	0.13	0.00	0.40	-1.98	0.00	-395.55	-5.51
cluster1	CNN	12	TAR_1	LIB193821	worst	-10.99	10.99	0.00	0.00	0.00	0.00	-1.92	-0.01	-816.11	-5.35
cluster1	CNN	12	TAR_2	LIB193821	worst	0.00	-6.25	0.00	6.25	0.00	-6.25	13.02	0.04	3266.82	12.10
cluster1	CNN	16	ALL	LIB193385	best	-5.88	5.89	0.00	0.00	0.00	0.01	1.98	0.03	68.62	1.24
cluster1	CNN	16	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	10.83	0.21	1707.04	10.87
cluster1	CNN	16	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	5.06	0.08	659.13	5.46
cluster1	CNN	16	TIR	LIB193385	best	-6.16	6.16	0.00	0.00	0.00	0.00	2.34	0.03	109.87	2.29
cluster1	CNN	16	TAR_1	LIB193385	best	0.55	-0.55	0.00	0.00	0.00	0.00	-7.78	-0.04	-1051.61	-7.33
cluster1	CNN	16	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-5.27	-0.02	-1384.24	-5.17
cluster1	CNN	16	ALL	LIB193821	worst	-1.91	1.60	-1.06	3.09	-1.70	-0.31	-3.50	0.00	-869.47	-8.24
cluster1	CNN	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	60.00	-60.00	0.00	-41.62	-0.85	-9651.39	-44.24
cluster1	CNN	16	TBR_1	LIB193821	worst	-11.82	0.00	0.00	23.64	-11.82	-11.82	7.26	0.11	-737.81	-5.29
cluster1	CNN	16	TIR	LIB193821	worst	0.14	1.26	-1.39	0.00	0.00	1.40	-4.13	-0.01	-682.94	-8.64
cluster1	CNN	16	TAR_1	LIB193821	worst	-6.60	6.59	0.00	0.00	0.00	-0.01	-9.64	-0.05	-2032.70	-12.86
cluster1	CNN	16	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-2.17	-0.01	-784.80	-2.73
cluster1	Linear	2	ALL	LIB193736	best	1.52	-1.56	0.00	0.05	0.00	-0.04	-0.82	-0.01	-31.15	-1.24
cluster1	Linear	2	TBR_2	LIB193736	best										
cluster1	Linear	2	TBR_1	LIB193736	best										
cluster1	Linear	2	TIR	LIB193736	best	1.82	-1.88	0.00	0.06	0.00	-0.06	-1.17	-0.01	-40.74	-1.85

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	Linear	2	TAR_1	LIB193736	best	0.25	-0.25	0.00	0.00	0.00	0.00	0.46	0.00	-4.50	-0.14
cluster1	Linear	2	TAR_2	LIB193736	best	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.01	147.42	3.12
cluster1	Linear	2	ALL	LIB193821	worst	23.29	-18.82	-0.38	-3.89	-0.19	4.47	-12.42	-0.11	-932.06	-16.89
cluster1	Linear	2	TBR_2	LIB193821	worst	60.00	0.00	0.00	-60.00	0.00	60.00	-19.62	-0.38	-762.00	-17.88
cluster1	Linear	2	TBR_1	LIB193821	worst	26.67	0.00	0.00	-25.00	-1.67	26.67	-12.63	-0.21	-1059.76	-19.96
cluster1	Linear	2	TIR	LIB193821	worst	21.33	-20.97	-0.37	0.00	0.00	0.36	-10.74	-0.09	-678.04	-14.20
cluster1	Linear	2	TAR_1	LIB193821	worst	29.00	-24.00	-1.00	-4.00	0.00	5.00	-19.89	-0.10	-1825.41	-22.39
cluster1	Linear	2	TAR_2	LIB193821	worst	50.00	-25.00	0.00	-25.00	0.00	25.00	-47.25	-0.16	-7319.70	-50.40
cluster1	Linear	4	ALL	LIB193736	best	1.58	-1.77	0.00	0.19	0.00	-0.19	-0.53	0.00	-51.20	-1.13
cluster1	Linear	4	TBR_2	LIB193736	best										
cluster1	Linear	4	TBR_1	LIB193736	best										
cluster1	Linear	4	TIR	LIB193736	best	2.84	-2.89	0.00	0.06	0.00	-0.05	-1.98	-0.01	-130.60	-3.50
cluster1	Linear	4	TAR_1	LIB193736	best	-2.41	2.14	0.00	0.27	0.00	-0.27	4.84	0.02	186.86	2.85
cluster1	Linear	4	TAR_2	LIB193736	best	-17.65	11.76	0.00	5.88	0.00	-5.89	13.27	0.05	1293.13	13.54
cluster1	Linear	4	ALL	LIB193821	worst	3.67	-7.53	-0.39	4.44	-0.19	-3.86	-4.49	-0.03	-492.23	-6.78
cluster1	Linear	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	16.50	0.31	1828.69	16.99
cluster1	Linear	4	TBR_1	LIB193821	worst	-36.44	0.00	0.00	38.14	-1.69	-36.44	4.14	0.06	-57.51	-0.80
cluster1	Linear	4	TIR	LIB193821	worst	9.01	-9.14	-0.37	0.50	0.00	-0.13	-5.70	-0.04	-483.23	-7.85
cluster1	Linear	4	TAR_1	LIB193821	worst	9.19	-6.13	-1.02	-2.04	0.00	3.06	-5.94	-0.03	-1104.05	-10.78
cluster1	Linear	4	TAR_2	LIB193821	worst	0.00	6.25	0.00	-6.25	0.00	6.25	-5.51	-0.02	-1125.80	-5.31
cluster1	Linear	6	ALL	LIB193385	best	-0.04	-0.10	0.00	0.15	-0.01	-0.14	-0.70	0.00	-97.42	-1.88
cluster1	Linear	6	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	6.82	0.13	706.29	6.81
cluster1	Linear	6	TBR_1	LIB193385	best	-26.27	0.00	0.00	26.27	0.00	-26.27	12.62	0.19	724.25	8.81
cluster1	Linear	6	TIR	LIB193385	best	-0.03	0.01	0.00	0.02	0.00	-0.02	-0.58	0.00	-72.85	-1.57
cluster1	Linear	6	TAR_1	LIB193385	best	2.95	-2.84	0.00	0.00	-0.11	0.11	-5.45	-0.03	-837.17	-6.56
cluster1	Linear	6	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.73	-0.03	-1537.35	-6.69
cluster1	Linear	6	ALL	LIB193821	worst	-1.18	-4.12	-0.19	5.59	-0.10	-5.30	-2.46	0.00	-381.02	-4.54
cluster1	Linear	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	16.77	0.34	2244.44	16.31
cluster1	Linear	6	TBR_1	LIB193821	worst	-42.61	0.00	0.00	44.35	-1.74	-42.61	12.57	0.20	432.20	4.49
cluster1	Linear	6	TIR	LIB193821	worst	4.57	-5.08	-0.25	0.76	0.00	-0.51	-4.59	-0.03	-475.35	-7.13
cluster1	Linear	6	TAR_1	LIB193821	worst	1.04	0.00	0.00	-1.04	0.00	1.04	-5.50	-0.03	-1004.64	-8.21
cluster1	Linear	6	TAR_2	LIB193821	worst	0.00	-12.50	0.00	6.25	6.25	-12.50	6.56	0.02	1340.89	5.19
cluster1	Linear	8	ALL	LIB193385	best	0.17	-0.29	0.00	0.12	0.00	-0.12	-1.43	0.00	-175.27	-3.10
cluster1	Linear	8	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	2.80	0.05	298.76	2.19
cluster1	Linear	8	TBR_1	LIB193385	best	-20.00	0.00	0.00	20.00	0.00	-20.00	15.94	0.24	1083.24	11.99
cluster1	Linear	8	TIR	LIB193385	best	0.24	-0.27	0.00	0.03	0.00	-0.03	-1.26	0.00	-134.28	-2.69
cluster1	Linear	8	TAR_1	LIB193385	best	0.74	-0.75	0.00	0.00	0.00	-0.01	-8.17	-0.04	-1390.66	-9.66

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	Linear	8	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-10.41	-0.04	-2884.09	-10.65
cluster1	Linear	8	ALL	LIB193821	worst	3.79	-6.77	-1.29	4.88	-0.60	-2.98	-5.94	-0.02	-908.33	-9.43
cluster1	Linear	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	21.52	0.42	2044.82	17.26
cluster1	Linear	8	TBR_1	LIB193821	worst	-35.09	0.00	0.00	37.72	-2.64	-35.09	13.67	0.23	370.50	3.38
cluster1	Linear	8	TIR	LIB193821	worst	10.84	-9.80	-1.68	0.64	0.00	1.04	-8.42	-0.05	-946.11	-12.43
cluster1	Linear	8	TAR_1	LIB193821	worst	-6.39	9.58	0.00	0.00	-3.19	3.19	-12.02	-0.06	-2512.67	-16.73
cluster1	Linear	8	TAR_2	LIB193821	worst	0.00	-6.25	0.00	6.25	0.00	-6.25	1.70	0.00	312.77	1.14
cluster1	Linear	12	ALL	LIB193385	best	1.70	-1.73	0.00	0.03	0.00	-0.03	-2.40	-0.01	-262.90	-4.40
cluster1	Linear	12	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	0.93	0.02	161.54	1.13
cluster1	Linear	12	TBR_1	LIB193385	best	-6.73	0.00	0.00	6.73	0.00	-6.73	17.54	0.27	1348.38	12.72
cluster1	Linear	12	TIR	LIB193385	best	1.99	-1.99	0.00	0.01	0.00	0.00	-2.20	-0.01	-211.58	-4.02
cluster1	Linear	12	TAR_1	LIB193385	best	-4.87	4.87	0.00	0.00	0.00	0.00	-9.74	-0.05	-1755.78	-11.58
cluster1	Linear	12	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-13.55	-0.05	-3894.65	-13.90
cluster1	Linear	12	ALL	LIB193821	worst	-0.31	-1.64	-1.65	5.25	-1.65	-1.95	-4.69	0.00	-980.58	-9.51
cluster1	Linear	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	20.00	-20.00	0.00	-2.22	-0.07	-1577.63	-9.25
cluster1	Linear	12	TBR_1	LIB193821	worst	-36.61	0.00	0.00	41.97	-5.36	-36.61	19.97	0.32	608.62	5.06
cluster1	Linear	12	TIR	LIB193821	worst	7.22	-5.35	-2.14	0.40	-0.13	1.87	-7.93	-0.04	-1035.53	-12.96
cluster1	Linear	12	TAR_1	LIB193821	worst	-17.58	26.37	0.00	0.00	-8.79	8.79	-9.90	-0.05	-2667.49	-16.29
cluster1	Linear	12	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	2.81	0.01	244.64	0.86
cluster1	Linear	16	ALL	LIB193385	best	4.26	-4.22	-0.04	0.02	0.00	0.04	-3.19	-0.02	-308.80	-5.12
cluster1	Linear	16	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.95	-0.13	-1326.56	-7.88
cluster1	Linear	16	TBR_1	LIB193385	best	-4.17	0.00	0.00	4.17	0.00	-4.17	15.90	0.24	1208.47	10.87
cluster1	Linear	16	TIR	LIB193385	best	4.67	-4.63	-0.05	0.00	0.00	0.04	-3.05	-0.02	-262.76	-4.95
cluster1	Linear	16	TAR_1	LIB193385	best	-5.82	5.81	0.00	0.00	0.00	-0.01	-8.66	-0.04	-1622.79	-10.68
cluster1	Linear	16	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-14.44	-0.06	-4195.02	-14.83
cluster1	Linear	16	ALL	LIB193821	worst	1.38	-1.59	-1.49	5.64	-3.94	-0.21	-9.92	-0.06	-2002.67	-17.38
cluster1	Linear	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	60.00	-60.00	0.00	-57.12	-1.22	-18970.89	-77.34
cluster1	Linear	16	TBR_1	LIB193821	worst	-26.36	0.00	0.00	43.64	-17.27	-26.36	3.25	0.03	-3003.53	-19.75
cluster1	Linear	16	TIR	LIB193821	worst	7.38	-5.57	-1.95	0.27	-0.14	1.81	-11.01	-0.07	-1542.41	-17.76
cluster1	Linear	16	TAR_1	LIB193821	worst	-12.09	27.48	0.00	0.00	-15.38	15.39	-17.67	-0.09	-4186.69	-23.87
cluster1	Linear	16	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	7.55	0.03	1948.28	6.71
cluster1	LSTM	2	ALL	LIB193736	best	-0.05	0.04	0.00	0.00	0.00	-0.01	-0.19	0.00	-5.72	-0.25
cluster1	LSTM	2	TBR_2	LIB193736	best										
cluster1	LSTM	2	TBR_1	LIB193736	best										
cluster1	LSTM	2	TIR	LIB193736	best	0.05	-0.06	0.00	0.00	0.00	-0.01	-0.35	0.00	-6.14	-0.31
cluster1	LSTM	2	TAR_1	LIB193736	best	-0.51	0.51	0.00	0.00	0.00	0.00	1.00	0.00	25.75	0.89
cluster1	LSTM	2	TAR_2	LIB193736	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.97	-0.02	-326.57	-6.05

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	2	ALL	LIB193821	worst	34.60	-30.23	0.00	-4.37	0.00	4.37	-18.46	-0.10	-1632.48	-25.89
cluster1	LSTM	2	TBR_2	LIB193821	worst	40.00	0.00	0.00	-40.00	0.00	40.00	-2.18	-0.04	-94.12	-1.96
cluster1	LSTM	2	TBR_1	LIB193821	worst	19.17	0.00	0.00	-19.17	0.00	19.17	-3.88	-0.06	-90.96	-2.48
cluster1	LSTM	2	TIR	LIB193821	worst	29.72	-29.72	0.00	0.00	0.00	0.00	-12.54	-0.08	-694.72	-14.77
cluster1	LSTM	2	TAR_1	LIB193821	worst	87.00	-82.00	0.00	-5.00	0.00	5.00	-67.89	-0.33	-7258.07	-61.93
cluster1	LSTM	2	TAR_2	LIB193821	worst	68.75	31.25	0.00	-100.00	0.00	100.00	-124.04	-0.44	-26047.63	-119.90
cluster1	LSTM	4	ALL	LIB193736	best	2.90	-2.99	0.00	0.09	0.00	-0.09	-0.93	-0.01	-10.02	-0.24
cluster1	LSTM	4	TBR_2	LIB193736	best										
cluster1	LSTM	4	TBR_1	LIB193736	best										
cluster1	LSTM	4	TIR	LIB193736	best	4.48	-4.48	0.00	0.00	0.00	0.00	-2.18	-0.02	-74.25	-2.11
cluster1	LSTM	4	TAR_1	LIB193736	best	-4.29	4.02	0.00	0.27	0.00	-0.27	4.81	0.02	269.54	4.64
cluster1	LSTM	4	TAR_2	LIB193736	best	2.94	-5.88	0.00	2.94	0.00	-2.94	-1.78	-0.01	123.61	1.22
cluster1	LSTM	4	ALL	LIB193821	worst	34.37	-30.79	0.00	-3.57	0.00	3.58	-15.84	-0.11	-1313.90	-16.48
cluster1	LSTM	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	1.76	0.02	321.52	2.54
cluster1	LSTM	4	TBR_1	LIB193821	worst	16.10	0.00	0.00	-16.10	0.00	16.10	-13.46	-0.21	-683.41	-8.62
cluster1	LSTM	4	TIR	LIB193821	worst	33.41	-32.91	0.00	-0.50	0.00	0.50	-10.57	-0.07	-490.93	-8.32
cluster1	LSTM	4	TAR_1	LIB193821	worst	66.33	-62.25	0.00	-4.08	0.00	4.08	-52.53	-0.26	-6116.60	-45.59
cluster1	LSTM	4	TAR_2	LIB193821	worst	31.25	31.25	0.00	-62.50	0.00	62.50	-77.58	-0.28	-18155.27	-67.36
cluster1	LSTM	6	ALL	LIB193385	best	-1.97	1.99	0.01	-0.02	0.00	0.02	0.80	0.01	35.11	0.72
cluster1	LSTM	6	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.01	-0.04	-195.13	-1.75
cluster1	LSTM	6	TBR_1	LIB193385	best	0.00	0.00	0.00	-0.85	0.85	0.00	-1.24	-0.02	35.19	0.39
cluster1	LSTM	6	TIR	LIB193385	best	-2.66	2.65	0.01	0.00	0.00	-0.01	1.19	0.01	66.50	1.55
cluster1	LSTM	6	TAR_1	LIB193385	best	15.68	-15.37	0.00	-0.32	0.00	0.31	-8.98	-0.04	-771.92	-6.22
cluster1	LSTM	6	TAR_2	LIB193385	best	0.00	14.29	0.00	-14.29	0.00	14.29	-11.72	-0.05	-2328.25	-10.46
cluster1	LSTM	6	ALL	LIB193821	worst	25.98	-25.30	0.10	-0.89	0.10	0.68	-12.24	-0.09	-980.93	-11.16
cluster1	LSTM	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	4.03	0.10	674.09	4.79
cluster1	LSTM	6	TBR_1	LIB193821	worst	1.74	0.00	0.00	-2.61	0.87	1.74	-9.66	-0.15	-477.39	-4.53
cluster1	LSTM	6	TIR	LIB193821	worst	27.16	-27.28	0.13	0.00	0.00	-0.12	-8.73	-0.07	-399.27	-6.29
cluster1	LSTM	6	TAR_1	LIB193821	worst	50.00	-47.91	0.00	-2.09	0.00	2.09	-39.79	-0.20	-4681.26	-33.09
cluster1	LSTM	6	TAR_2	LIB193821	worst	6.25	18.75	0.00	-25.00	0.00	25.00	-43.22	-0.15	-11562.00	-39.53
cluster1	LSTM	8	ALL	LIB193385	best	-2.73	2.73	0.00	0.00	0.00	0.00	0.98	0.01	40.54	0.78
cluster1	LSTM	8	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-3.02	-0.06	-373.73	-2.89
cluster1	LSTM	8	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.52	-0.02	-15.18	-0.15
cluster1	LSTM	8	TIR	LIB193385	best	-3.36	3.36	0.00	0.00	0.00	0.00	1.29	0.01	67.73	1.50
cluster1	LSTM	8	TAR_1	LIB193385	best	13.45	-13.44	0.00	0.00	0.00	0.01	-6.76	-0.03	-657.24	-4.76
cluster1	LSTM	8	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-5.37	-0.02	-1329.84	-5.32
cluster1	LSTM	8	ALL	LIB193821	worst	17.93	-17.93	0.10	-0.30	0.20	0.00	-8.92	-0.03	-895.28	-9.54

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	10.34	0.20	1318.89	10.27
cluster1	LSTM	8	TBR_1	LIB193821	worst	0.00	0.00	0.00	-1.75	1.75	0.00	6.30	0.10	1044.81	10.23
cluster1	LSTM	8	TIR	LIB193821	worst	19.61	-19.74	0.13	0.00	0.00	-0.13	-7.31	-0.03	-447.92	-6.62
cluster1	LSTM	8	TAR_1	LIB193821	worst	29.79	-28.72	0.00	-1.06	0.00	1.07	-35.97	-0.18	-5068.98	-31.59
cluster1	LSTM	8	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-42.37	-0.15	-12558.33	-40.61
cluster1	LSTM	12	ALL	LIB193385	best	-4.31	4.31	0.00	0.00	0.00	0.00	1.25	0.02	34.39	0.63
cluster1	LSTM	12	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.00	28.17	0.20
cluster1	LSTM	12	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.02	219.60	1.92
cluster1	LSTM	12	TIR	LIB193385	best	-4.60	4.60	0.00	0.00	0.00	0.00	1.57	0.02	70.10	1.49
cluster1	LSTM	12	TAR_1	LIB193385	best	2.71	-2.71	0.00	0.00	0.00	0.00	-7.00	-0.04	-899.77	-6.19
cluster1	LSTM	12	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-8.82	-0.03	-2269.38	-8.69
cluster1	LSTM	12	ALL	LIB193821	worst	11.22	-11.21	0.00	0.00	0.00	0.01	-4.19	-0.01	-412.16	-4.30
cluster1	LSTM	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	11.01	0.22	1608.66	11.08
cluster1	LSTM	12	TBR_1	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	4.67	0.08	742.32	6.48
cluster1	LSTM	12	TIR	LIB193821	worst	13.50	-13.50	0.00	0.00	0.00	0.00	-3.53	-0.01	-181.91	-2.69
cluster1	LSTM	12	TAR_1	LIB193821	worst	8.79	-8.80	0.00	0.00	0.00	-0.01	-17.39	-0.09	-2478.81	-15.36
cluster1	LSTM	12	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-26.93	-0.10	-8135.52	-26.46
cluster1	LSTM	16	ALL	LIB193385	best	-4.49	4.49	0.00	0.00	0.00	0.00	1.39	0.02	41.10	0.75
cluster1	LSTM	16	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	7.35	0.14	1120.79	7.36
cluster1	LSTM	16	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	3.62	0.06	473.90	4.03
cluster1	LSTM	16	TIR	LIB193385	best	-4.70	4.70	0.00	0.00	0.00	0.00	1.69	0.02	76.16	1.61
cluster1	LSTM	16	TAR_1	LIB193385	best	0.44	-0.44	0.00	0.00	0.00	0.00	-6.52	-0.03	-899.68	-6.20
cluster1	LSTM	16	TAR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.01	-0.02	-1585.71	-5.94
cluster1	LSTM	16	ALL	LIB193821	worst	8.29	-8.30	0.00	0.00	0.00	-0.01	-1.96	0.02	-223.06	-2.26
cluster1	LSTM	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	13.03	0.26	1966.01	13.30
cluster1	LSTM	16	TBR_1	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	8.65	0.14	1166.05	9.85
cluster1	LSTM	16	TIR	LIB193821	worst	10.44	-10.45	0.00	0.00	0.00	-0.01	-1.59	0.01	-63.40	-0.91
cluster1	LSTM	16	TAR_1	LIB193821	worst	3.30	-3.30	0.00	0.00	0.00	0.00	-15.22	-0.08	-2201.64	-13.52
cluster1	LSTM	16	TAR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-20.77	-0.07	-6369.17	-20.33
cluster2	CNN	2	ALL	LIB194030	best	1.04	-1.00	-0.03	-0.02	0.00	0.04	-0.72	0.00	-41.32	-0.79
cluster2	CNN	2	TBR_2	LIB194030	best										
cluster2	CNN	2	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.25	-0.02	-299.87	-4.46
cluster2	CNN	2	TIR	LIB194030	best	2.22	-2.22	-0.03	0.03	0.00	0.00	-0.91	-0.01	-51.61	-1.16
cluster2	CNN	2	TAR_1	LIB194030	best	0.19	-0.11	-0.04	-0.04	0.00	0.08	-0.21	0.00	-12.61	-0.25
cluster2	CNN	2	TAR_2	LIB194030	best	0.25	-0.20	0.00	-0.05	0.00	0.05	-1.09	0.00	-61.01	-0.93
cluster2	CNN	2	ALL	LIB194012	worst	1.23	-1.19	0.19	-0.22	0.00	0.04	-0.71	0.00	-38.67	-0.59
cluster2	CNN	2	TBR_2	LIB194012	worst	-1.51	0.00	0.00	1.51	0.00	-1.51	0.46	0.01	6.70	0.09

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	2	TBR_1	LIB194012	worst	-1.09	0.00	0.00	0.93	0.15	-1.09	0.67	0.01	105.59	1.51
cluster2	CNN	2	TIR	LIB194012	worst	-0.27	0.04	0.23	0.00	0.00	-0.23	1.02	0.01	108.44	1.91
cluster2	CNN	2	TAR_1	LIB194012	worst	3.25	-2.78	0.21	-0.62	-0.05	0.47	-2.38	-0.01	-167.31	-2.27
cluster2	CNN	2	TAR_2	LIB194012	worst	8.66	-6.69	0.00	-1.97	0.00	1.97	-9.56	-0.03	-838.89	-9.35
cluster2	CNN	4	ALL	LIB194030	best	2.15	-2.20	0.06	-0.02	0.00	-0.05	-1.33	-0.01	-88.44	-1.11
cluster2	CNN	4	TBR_2	LIB194030	best										
cluster2	CNN	4	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	0.72	0.01	-34.69	-0.31
cluster2	CNN	4	TIR	LIB194030	best	3.06	-3.16	0.10	0.00	0.00	-0.10	-0.66	-0.01	-15.28	-0.23
cluster2	CNN	4	TAR_1	LIB194030	best	-1.23	1.11	0.08	0.04	0.00	-0.12	0.38	0.00	88.60	1.25
cluster2	CNN	4	TAR_2	LIB194030	best	5.13	-5.04	0.00	-0.11	0.00	0.09	-4.68	-0.02	-441.68	-4.20
cluster2	CNN	4	ALL	LIB194012	worst	0.03	-0.48	0.85	-0.48	0.08	-0.45	0.36	0.01	83.08	0.89
cluster2	CNN	4	TBR_2	LIB194012	worst	-1.54	0.00	0.00	-1.54	3.07	-1.54	7.06	0.14	991.08	7.24
cluster2	CNN	4	TBR_1	LIB194012	worst	-1.60	0.00	0.00	1.12	0.48	-1.60	4.33	0.07	493.27	4.19
cluster2	CNN	4	TIR	LIB194012	worst	-2.14	0.81	1.26	0.08	0.00	-1.33	2.49	0.02	334.77	4.23
cluster2	CNN	4	TAR_1	LIB194012	worst	1.93	-1.56	0.41	-0.78	0.00	0.37	-1.66	-0.01	-127.39	-1.39
cluster2	CNN	4	TAR_2	LIB194012	worst	11.52	-6.97	0.13	-4.69	0.00	4.55	-13.52	-0.05	-1598.27	-11.03
cluster2	CNN	6	ALL	LIB194030	best	1.37	-1.76	-0.27	0.68	-0.03	-0.39	-1.04	-0.02	-50.21	-0.49
cluster2	CNN	6	TBR_2	LIB194030	best										
cluster2	CNN	6	TBR_1	LIB194030	best	0.00	0.00	0.00	10.00	-10.00	0.00	-10.97	-0.16	-2345.56	-13.70
cluster2	CNN	6	TIR	LIB194030	best	7.89	-7.37	-0.53	0.03	-0.03	0.52	-5.17	-0.05	-483.39	-5.50
cluster2	CNN	6	TAR_1	LIB194030	best	-3.13	2.77	-0.12	0.48	0.00	-0.36	1.48	0.01	138.76	1.72
cluster2	CNN	6	TAR_2	LIB194030	best	-3.29	1.40	-0.05	1.94	0.00	-1.89	2.42	0.01	421.28	2.96
cluster2	CNN	6	ALL	LIB193916	worst	1.07	-1.74	1.76	-1.29	0.21	-0.67	0.41	0.03	20.46	0.16
cluster2	CNN	6	TBR_2	LIB193916	worst	-2.88	0.00	0.00	0.72	2.16	-2.88	13.75	0.26	1964.92	10.71
cluster2	CNN	6	TBR_1	LIB193916	worst	-2.92	0.00	0.00	0.00	2.93	-2.92	13.02	0.21	1749.49	10.02
cluster2	CNN	6	TIR	LIB193916	worst	-4.02	0.78	3.26	-0.03	0.00	-3.24	4.97	0.05	706.82	6.92
cluster2	CNN	6	TAR_1	LIB193916	worst	3.19	-2.36	0.32	-1.14	0.00	0.83	-2.67	-0.01	-244.16	-2.44
cluster2	CNN	6	TAR_2	LIB193916	worst	15.89	-9.63	0.00	-6.25	0.00	6.26	-15.49	-0.05	-2615.61	-14.19
cluster2	CNN	8	ALL	LIB194050	best	2.55	-4.28	-0.53	2.28	-0.03	-1.73	-1.92	-0.03	-99.07	-1.05
cluster2	CNN	8	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-12.58	-0.24	-2385.47	-12.58
cluster2	CNN	8	TBR_1	LIB194050	best	0.00	0.00	0.00	24.00	-24.00	0.00	-18.11	-0.28	-3461.82	-17.76
cluster2	CNN	8	TIR	LIB194050	best	19.12	-18.06	-1.07	0.01	-0.01	1.06	-12.89	-0.10	-1144.21	-11.84
cluster2	CNN	8	TAR_1	LIB194050	best	-14.28	12.62	0.01	1.64	0.00	-1.66	8.36	0.04	713.74	10.34
cluster2	CNN	8	TAR_2	LIB194050	best	-12.26	-5.50	0.00	17.75	0.00	-17.76	12.12	0.04	2034.36	12.97
cluster2	CNN	8	ALL	LIB193916	worst	1.67	-2.53	3.21	-3.10	0.74	-0.86	1.76	0.05	277.17	1.96
cluster2	CNN	8	TBR_2	LIB193916	worst	0.00	0.00	0.00	-7.30	7.30	0.00	13.94	0.27	2826.23	13.31
cluster2	CNN	8	TBR_1	LIB193916	worst	0.00	0.00	0.00	-9.74	9.74	0.00	14.84	0.24	2898.94	14.55

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	CNN	8	TIR	LIB193916	worst	-6.08	-0.03	6.11	-0.04	0.03	-6.11	9.88	0.10	1457.09	12.78
cluster2	CNN	8	TAR_1	LIB193916	worst	8.73	-7.24	0.27	-1.76	0.00	1.49	-5.59	-0.02	-496.44	-4.79
cluster2	CNN	8	TAR_2	LIB193916	worst	16.61	-4.52	0.00	-12.09	0.00	12.09	-19.47	-0.06	-3639.57	-17.08
cluster2	CNN	12	ALL	LIB194050	best	1.81	-4.97	-0.68	3.88	-0.04	-3.16	-1.59	-0.03	-77.58	-0.80
cluster2	CNN	12	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-20.16	-0.38	-4376.48	-20.16
cluster2	CNN	12	TBR_1	LIB194050	best	0.00	0.00	0.00	28.00	-28.00	0.00	-17.28	-0.27	-3576.58	-17.63
cluster2	CNN	12	TIR	LIB194050	best	20.69	-19.34	-1.34	0.02	-0.02	1.35	-14.27	-0.11	-1286.77	-13.62
cluster2	CNN	12	TAR_1	LIB194050	best	-17.78	14.99	0.00	2.78	0.00	-2.79	10.12	0.05	778.89	11.54
cluster2	CNN	12	TAR_2	LIB194050	best	-14.29	-15.76	0.00	30.06	0.00	-30.05	15.96	0.06	2808.71	15.72
cluster2	CNN	12	ALL	LIB193916	worst	0.72	0.66	3.66	-7.02	1.98	1.38	2.95	0.07	306.81	1.98
cluster2	CNN	12	TBR_2	LIB193916	worst	0.00	0.00	0.00	-17.42	17.42	0.00	14.90	0.29	3138.54	14.18
cluster2	CNN	12	TBR_1	LIB193916	worst	0.00	0.00	0.00	-23.85	23.85	0.00	19.06	0.31	4063.42	19.72
cluster2	CNN	12	TIR	LIB193916	worst	-9.81	2.75	7.06	-0.21	0.22	-7.06	14.61	0.14	2004.33	17.77
cluster2	CNN	12	TAR_1	LIB193916	worst	18.99	-16.07	0.00	-2.91	0.00	2.92	-12.09	-0.06	-1182.65	-10.98
cluster2	CNN	12	TAR_2	LIB193916	worst	7.80	19.97	0.00	-27.78	0.00	27.77	-20.55	-0.07	-4913.99	-18.85
cluster2	CNN	16	ALL	LIB194050	best	-0.02	-3.74	-0.29	4.11	-0.07	-3.76	-0.63	-0.02	-9.19	-0.09
cluster2	CNN	16	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	-100.00	0.00	-19.22	-0.36	-4859.38	-19.22
cluster2	CNN	16	TBR_1	LIB194050	best	0.00	0.00	0.00	45.45	-45.45	0.00	-15.23	-0.24	-3280.18	-15.34
cluster2	CNN	16	TIR	LIB194050	best	13.78	-13.21	-0.57	0.02	-0.02	0.57	-10.34	-0.08	-879.27	-9.62
cluster2	CNN	16	TAR_1	LIB194050	best	-16.53	13.81	0.00	2.73	0.00	-2.72	8.92	0.04	634.92	9.12
cluster2	CNN	16	TAR_2	LIB194050	best	-2.19	-29.83	0.00	32.02	0.00	-32.02	10.28	0.04	1937.58	10.17
cluster2	CNN	16	ALL	LIB193916	worst	-1.03	0.94	1.66	-3.21	1.62	-0.09	4.06	0.07	487.63	3.14
cluster2	CNN	16	TBR_2	LIB193916	worst	0.00	0.00	0.00	-14.39	14.39	0.00	15.78	0.31	3395.50	14.72
cluster2	CNN	16	TBR_1	LIB193916	worst	0.00	0.00	0.00	-17.14	17.14	0.00	16.30	0.27	3324.30	15.50
cluster2	CNN	16	TIR	LIB193916	worst	-9.51	6.30	3.21	-0.24	0.24	-3.21	11.51	0.11	1394.42	12.00
cluster2	CNN	16	TAR_1	LIB193916	worst	16.42	-16.24	0.00	-0.17	0.00	0.18	-8.89	-0.04	-858.58	-8.80
cluster2	CNN	16	TAR_2	LIB193916	worst	0.14	10.05	0.00	-10.19	0.00	10.19	-8.59	-0.03	-2252.39	-8.63
cluster2	Linear	2	ALL	LIB194030	best	0.55	-0.60	0.00	0.05	0.00	-0.05	-0.52	0.00	-32.06	-0.87
cluster2	Linear	2	TBR_2	LIB194030	best										
cluster2	Linear	2	TBR_1	LIB194030	best	-20.00	0.00	0.00	20.00	0.00	-20.00	2.62	0.04	62.16	2.41
cluster2	Linear	2	TIR	LIB194030	best	0.57	-0.60	0.00	0.03	0.00	-0.03	-0.48	0.00	-35.85	-1.08
cluster2	Linear	2	TAR_1	LIB194030	best	1.06	-1.02	0.00	-0.04	0.00	0.04	-0.92	0.00	-48.18	-1.33
cluster2	Linear	2	TAR_2	LIB194030	best	-0.05	-0.05	0.00	0.10	0.00	-0.10	-0.08	0.00	-5.25	-0.12
cluster2	Linear	2	ALL	LIB194012	worst	-0.94	0.13	0.00	0.81	0.00	-0.81	-0.12	0.00	-24.57	-0.53
cluster2	Linear	2	TBR_2	LIB194012	worst	-7.52	0.00	0.00	7.52	0.00	-7.52	3.38	0.07	119.46	3.57
cluster2	Linear	2	TBR_1	LIB194012	worst	-9.19	0.00	0.00	9.19	0.00	-9.19	2.42	0.04	58.98	1.58
cluster2	Linear	2	TIR	LIB194012	worst	-0.85	0.73	0.00	0.11	0.00	-0.12	0.30	0.00	0.99	0.02

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	2	TAR_1	LIB194012	worst	1.14	-0.97	0.00	-0.15	0.00	0.17	-1.26	-0.01	-73.75	-1.44
cluster2	Linear	2	TAR_2	LIB194012	worst	1.31	-1.05	0.00	-0.26	0.00	0.26	-2.87	-0.01	-168.29	-3.23
cluster2	Linear	4	ALL	LIB194030	best	1.75	-1.19	-0.21	-0.30	-0.04	0.56	-2.01	-0.01	-221.48	-3.14
cluster2	Linear	4	TBR_2	LIB194030	best										
cluster2	Linear	4	TBR_1	LIB194030	best	-20.00	0.00	0.00	20.00	0.00	-20.00	12.31	0.19	582.33	5.79
cluster2	Linear	4	TIR	LIB194030	best	-1.93	2.19	-0.29	0.03	0.00	0.26	-0.81	0.00	-133.34	-2.17
cluster2	Linear	4	TAR_1	LIB194030	best	6.71	-5.92	-0.28	-0.39	-0.12	0.79	-4.66	-0.02	-406.51	-6.05
cluster2	Linear	4	TAR_2	LIB194030	best	1.32	-0.47	0.00	-0.84	0.00	0.85	-0.54	0.00	-125.24	-1.44
cluster2	Linear	4	ALL	LIB194012	worst	-3.48	0.57	0.02	3.06	-0.18	-2.91	-0.75	0.02	-209.28	-2.43
cluster2	Linear	4	TBR_2	LIB194012	worst	-43.84	0.00	0.00	43.08	0.77	-43.84	10.81	0.21	537.12	5.05
cluster2	Linear	4	TBR_1	LIB194012	worst	-38.82	0.00	0.00	38.66	0.15	-38.82	11.23	0.18	573.51	6.35
cluster2	Linear	4	TIR	LIB194012	worst	-4.49	4.36	-0.06	0.20	0.00	-0.13	0.55	0.01	-19.85	-0.26
cluster2	Linear	4	TAR_1	LIB194012	worst	8.20	-6.90	0.31	-0.73	-0.89	1.30	-5.98	-0.03	-628.09	-6.88
cluster2	Linear	4	TAR_2	LIB194012	worst	10.18	-5.63	-0.13	-4.43	0.00	4.55	-8.30	-0.03	-1215.53	-10.46
cluster2	Linear	6	ALL	LIB194030	best	3.32	-1.90	-0.75	-0.55	-0.11	1.42	-3.20	-0.01	-442.50	-4.50
cluster2	Linear	6	TBR_2	LIB194030	best										
cluster2	Linear	6	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	13.22	0.21	1066.10	8.08
cluster2	Linear	6	TIR	LIB194030	best	0.75	0.17	-0.95	0.03	0.00	0.92	-2.37	-0.01	-358.36	-4.29
cluster2	Linear	6	TAR_1	LIB194030	best	12.57	-10.81	-0.92	-0.56	-0.28	1.76	-8.87	-0.04	-950.55	-10.92
cluster2	Linear	6	TAR_2	LIB194030	best	-4.85	6.62	-0.22	-1.51	-0.05	1.77	2.94	0.01	91.96	0.71
cluster2	Linear	6	ALL	LIB194012	worst	-1.27	-0.66	0.14	1.85	-0.06	-1.93	-1.13	0.03	-387.24	-3.55
cluster2	Linear	6	TBR_2	LIB194012	worst	-37.50	0.00	0.00	36.72	0.78	-37.50	22.31	0.44	1985.79	13.61
cluster2	Linear	6	TBR_1	LIB194012	worst	-34.74	0.00	0.00	32.30	2.45	-34.74	20.01	0.33	1589.96	12.38
cluster2	Linear	6	TIR	LIB194012	worst	-3.81	3.24	0.24	0.26	0.06	-0.57	1.11	0.03	4.33	0.05
cluster2	Linear	6	TAR_1	LIB194012	worst	14.76	-11.74	0.00	-2.01	-1.01	3.02	-11.54	-0.06	-1437.24	-13.43
cluster2	Linear	6	TAR_2	LIB194012	worst	9.29	0.28	0.00	-8.88	-0.68	9.57	-11.44	-0.04	-2442.24	-14.24
cluster2	Linear	8	ALL	LIB194050	best	0.14	0.39	-0.14	-0.41	0.02	0.53	-0.85	0.00	-186.63	-1.95
cluster2	Linear	8	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	15.34	0.29	2451.29	15.34
cluster2	Linear	8	TBR_1	LIB194050	best	0.00	0.00	0.00	-4.00	4.00	0.00	17.72	0.28	2651.35	14.49
cluster2	Linear	8	TIR	LIB194050	best	-3.21	3.44	-0.23	0.00	0.00	0.23	1.17	0.02	10.29	0.12
cluster2	Linear	8	TAR_1	LIB194050	best	4.39	-4.18	-0.05	-0.19	0.02	0.21	-3.24	-0.02	-343.70	-4.12
cluster2	Linear	8	TAR_2	LIB194050	best	-0.79	4.49	0.00	-3.75	0.05	3.70	-1.43	0.00	-600.67	-3.63
cluster2	Linear	8	ALL	LIB193916	worst	4.23	-2.21	-0.23	-1.67	-0.12	2.02	-4.30	0.02	-846.84	-5.94
cluster2	Linear	8	TBR_2	LIB193916	worst	-13.87	0.00	0.00	13.14	0.73	-13.87	24.38	0.47	3229.64	17.14
cluster2	Linear	8	TBR_1	LIB193916	worst	-12.98	0.00	0.00	4.72	8.26	-12.98	22.12	0.36	2764.42	15.28
cluster2	Linear	8	TIR	LIB193916	worst	0.88	-0.84	-0.13	0.10	0.00	0.04	0.18	0.03	-20.73	-0.18
cluster2	Linear	8	TAR_1	LIB193916	worst	19.90	-15.09	-0.68	-2.23	-1.90	4.81	-19.09	-0.09	-2648.68	-21.80

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	Linear	8	TAR_2	LIB193916	worst	-0.52	12.30	0.00	-10.94	-0.84	11.78	-9.38	-0.03	-2595.01	-12.68
cluster2	Linear	12	ALL	LIB194050	best	3.85	-2.28	-1.19	-0.39	0.01	1.57	-3.79	-0.02	-590.98	-5.76
cluster2	Linear	12	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	10.94	0.21	2118.80	10.94
cluster2	Linear	12	TBR_1	LIB194050	best	0.00	0.00	0.00	-4.00	4.00	0.00	19.05	0.30	2410.17	13.55
cluster2	Linear	12	TIR	LIB194050	best	0.72	1.63	-2.34	0.00	0.00	2.35	-2.71	-0.01	-507.48	-5.41
cluster2	Linear	12	TAR_1	LIB194050	best	11.22	-11.00	-0.02	-0.20	0.00	0.22	-6.65	-0.03	-744.95	-8.95
cluster2	Linear	12	TAR_2	LIB194050	best	-12.11	15.55	0.00	-3.44	0.00	3.44	2.88	0.01	-399.14	-2.11
cluster2	Linear	12	ALL	LIB193916	worst	3.86	-1.07	-0.16	-2.37	-0.26	2.79	-4.37	0.05	-1261.58	-7.78
cluster2	Linear	12	TBR_2	LIB193916	worst	-10.61	0.00	0.00	2.27	8.34	-10.61	35.06	0.68	5500.20	26.34
cluster2	Linear	12	TBR_1	LIB193916	worst	-8.56	0.00	0.00	-3.67	12.23	-8.56	33.22	0.55	4692.48	23.69
cluster2	Linear	12	TIR	LIB193916	worst	-1.75	1.85	-0.25	0.00	0.15	0.10	4.39	0.08	253.22	2.01
cluster2	Linear	12	TAR_1	LIB193916	worst	25.12	-20.14	0.00	-0.92	-4.06	4.98	-29.02	-0.14	-4332.63	-32.94
cluster2	Linear	12	TAR_2	LIB193916	worst	-3.31	18.09	-0.24	-12.65	-1.89	14.78	-16.01	-0.06	-4897.78	-19.23
cluster2	Linear	16	ALL	LIB194050	best	5.84	-3.89	-1.67	-0.28	0.01	1.95	-5.83	-0.03	-877.57	-8.26
cluster2	Linear	16	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	5.38	0.10	1246.09	5.38
cluster2	Linear	16	TBR_1	LIB194050	best	0.00	0.00	0.00	-9.09	9.09	0.00	22.03	0.34	3259.57	16.10
cluster2	Linear	16	TIR	LIB194050	best	3.20	0.12	-3.32	0.01	-0.01	3.32	-4.87	-0.02	-748.70	-7.94
cluster2	Linear	16	TAR_1	LIB194050	best	14.51	-14.40	-0.01	-0.10	0.00	0.11	-8.86	-0.05	-1067.79	-12.30
cluster2	Linear	16	TAR_2	LIB194050	best	-18.15	20.79	0.00	-2.64	0.00	2.64	1.99	0.01	-790.49	-3.93
cluster2	Linear	16	ALL	LIB193916	worst	1.32	2.26	-1.64	-1.63	-0.31	3.58	-2.75	0.08	-1290.36	-7.82
cluster2	Linear	16	TBR_2	LIB193916	worst	-9.85	0.00	0.00	-1.52	11.37	-9.85	41.99	0.81	6302.11	29.75
cluster2	Linear	16	TBR_1	LIB193916	worst	-12.06	0.00	0.00	-1.27	13.33	-12.06	41.99	0.69	5753.56	29.20
cluster2	Linear	16	TIR	LIB193916	worst	-6.26	9.15	-3.09	0.07	0.12	2.89	6.74	0.12	264.94	2.16
cluster2	Linear	16	TAR_1	LIB193916	worst	27.97	-22.94	0.00	-0.09	-4.95	5.03	-32.67	-0.16	-4934.50	-37.84
cluster2	Linear	16	TAR_2	LIB193916	worst	-6.66	19.43	-0.27	-10.05	-2.45	12.77	-15.69	-0.06	-5301.52	-19.50
cluster2	LSTM	2	ALL	LIB193556	best	15.41	-15.31	0.00	-0.10	0.00	0.10	-15.45	-0.05	-1798.27	-26.51
cluster2	LSTM	2	TBR_2	LIB193556	best										
cluster2	LSTM	2	TBR_1	LIB193556	best	100.00	0.00	0.00	-100.00	0.00	100.00	-8.41	-0.12	-281.93	-8.49
cluster2	LSTM	2	TIR	LIB193556	best	1.75	-1.64	0.00	-0.11	0.00	0.11	-1.00	-0.01	-44.71	-1.29
cluster2	LSTM	2	TAR_1	LIB193556	best	-0.80	0.79	0.00	0.00	0.00	-0.01	1.99	0.01	109.30	2.91
cluster2	LSTM	2	TAR_2	LIB193556	best	45.41	-45.41	0.00	0.00	0.00	0.00	-47.70	-0.14	-5492.73	-53.74
cluster2	LSTM	2	ALL	LIB194012	worst	-0.60	0.53	-0.01	0.08	0.00	-0.07	-0.04	0.00	-4.42	-0.10
cluster2	LSTM	2	TBR_2	LIB194012	worst	5.27	0.00	0.00	-5.27	0.00	5.27	-0.09	0.00	-16.77	-0.41
cluster2	LSTM	2	TBR_1	LIB194012	worst	-2.64	0.00	0.00	2.65	0.00	-2.64	1.65	0.03	95.74	2.49
cluster2	LSTM	2	TIR	LIB194012	worst	-1.51	1.47	0.00	0.04	0.00	-0.04	0.54	0.01	35.75	0.86
cluster2	LSTM	2	TAR_1	LIB194012	worst	1.34	-1.08	-0.05	-0.20	0.00	0.26	-1.25	-0.01	-92.85	-1.85
cluster2	LSTM	2	TAR_2	LIB194012	worst	1.32	-1.18	0.00	-0.13	0.00	0.14	-2.29	-0.01	-134.04	-2.63

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	4	ALL	LIB194030	best	0.69	-0.78	0.02	0.07	0.00	-0.09	-0.14	0.00	10.05	0.16
cluster2	LSTM	4	TBR_2	LIB194030	best										
cluster2	LSTM	4	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	-12.21	-0.19	-1160.18	-11.57
cluster2	LSTM	4	TIR	LIB194030	best	2.41	-2.38	-0.03	0.00	0.00	0.03	-0.64	-0.01	-25.30	-0.46
cluster2	LSTM	4	TAR_1	LIB194030	best	-0.44	0.31	0.08	0.04	0.00	-0.13	0.68	0.00	68.13	1.12
cluster2	LSTM	4	TAR_2	LIB194030	best	-0.63	0.36	0.05	0.21	0.00	-0.27	-0.35	0.00	-2.81	-0.03
cluster2	LSTM	4	ALL	LIB194012	worst	-0.12	-0.15	0.39	-0.14	0.03	-0.27	0.12	0.01	35.52	0.44
cluster2	LSTM	4	TBR_2	LIB194012	worst	-5.38	0.00	0.00	4.62	0.77	-5.38	3.11	0.06	482.52	4.43
cluster2	LSTM	4	TBR_1	LIB194012	worst	-3.84	0.00	0.00	3.67	0.16	-3.84	3.10	0.05	399.83	4.25
cluster2	LSTM	4	TIR	LIB194012	worst	-1.92	1.48	0.45	0.00	0.00	-0.44	1.88	0.02	205.80	3.00
cluster2	LSTM	4	TAR_1	LIB194012	worst	2.61	-2.45	0.52	-0.68	0.00	0.16	-1.80	-0.01	-138.34	-1.60
cluster2	LSTM	4	TAR_2	LIB194012	worst	9.25	-5.49	0.00	-3.76	0.00	3.76	-10.08	-0.03	-1065.00	-9.30
cluster2	LSTM	6	ALL	LIB194030	best	0.17	-0.19	0.02	-0.01	0.00	-0.02	-0.23	0.00	28.65	0.32
cluster2	LSTM	6	TBR_2	LIB194030	best										
cluster2	LSTM	6	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.39	-0.02	-239.56	-1.87
cluster2	LSTM	6	TIR	LIB194030	best	0.65	-0.59	-0.07	0.00	0.00	0.06	-0.59	-0.01	-35.53	-0.47
cluster2	LSTM	6	TAR_1	LIB194030	best	0.00	0.00	0.12	-0.12	0.00	0.00	0.39	0.00	119.30	1.56
cluster2	LSTM	6	TAR_2	LIB194030	best	-0.37	0.21	0.05	0.11	0.00	-0.16	-0.45	0.00	14.13	0.11
cluster2	LSTM	6	ALL	LIB194012	worst	0.01	-0.21	0.78	-0.85	0.28	-0.20	0.77	0.03	145.17	1.42
cluster2	LSTM	6	TBR_2	LIB194012	worst	0.00	0.00	0.00	-4.69	4.69	0.00	9.77	0.20	1668.35	11.03
cluster2	LSTM	6	TBR_1	LIB194012	worst	-1.47	0.00	0.00	-0.98	2.44	-1.47	8.42	0.14	1215.53	8.98
cluster2	LSTM	6	TIR	LIB194012	worst	-3.92	2.79	1.14	-0.04	0.04	-1.13	3.78	0.04	475.32	5.68
cluster2	LSTM	6	TAR_1	LIB194012	worst	3.61	-2.81	0.42	-1.22	0.00	0.80	-3.63	-0.02	-327.70	-3.40
cluster2	LSTM	6	TAR_2	LIB194012	worst	18.99	-14.34	0.00	-4.64	0.00	4.65	-16.51	-0.06	-2065.26	-12.25
cluster2	LSTM	8	ALL	LIB194050	best	-0.47	-1.15	-0.01	1.64	-0.01	-1.62	0.49	-0.01	154.82	1.70
cluster2	LSTM	8	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-15.42	-0.29	-2524.30	-15.42
cluster2	LSTM	8	TBR_1	LIB194050	best	0.00	0.00	0.00	4.00	-4.00	0.00	-19.17	-0.30	-2947.08	-15.35
cluster2	LSTM	8	TIR	LIB194050	best	11.29	-11.28	-0.02	0.00	0.00	0.01	-7.47	-0.06	-577.83	-6.69
cluster2	LSTM	8	TAR_1	LIB194050	best	-13.74	12.58	0.01	1.15	0.00	-1.16	8.58	0.04	762.77	10.34
cluster2	LSTM	8	TAR_2	LIB194050	best	-4.91	-8.09	0.00	13.00	0.00	-13.00	7.81	0.03	1484.03	9.40
cluster2	LSTM	8	ALL	LIB193916	worst	1.12	-2.22	2.02	-1.25	0.33	-1.10	0.91	0.03	141.52	1.05
cluster2	LSTM	8	TBR_2	LIB193916	worst	0.00	0.00	0.00	-4.38	4.38	0.00	8.91	0.17	1518.19	7.60
cluster2	LSTM	8	TBR_1	LIB193916	worst	0.00	0.00	0.00	-3.54	3.54	0.00	10.07	0.16	1746.45	9.29
cluster2	LSTM	8	TIR	LIB193916	worst	-3.35	-0.35	3.70	-0.06	0.07	-3.70	5.42	0.05	851.82	7.78
cluster2	LSTM	8	TAR_1	LIB193916	worst	0.81	-0.27	0.47	-1.02	0.00	0.54	-1.01	0.00	-85.21	-0.83
cluster2	LSTM	8	TAR_2	LIB193916	worst	16.61	-12.41	0.00	-4.20	0.00	4.20	-15.11	-0.05	-2574.26	-12.93
cluster2	LSTM	12	ALL	LIB194050	best	1.54	-3.85	-0.52	2.86	-0.03	-2.31	-1.26	-0.03	-39.13	-0.41

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	12	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-10.03	-0.19	-2019.17	-10.03
cluster2	LSTM	12	TBR_1	LIB194050	best	0.00	0.00	0.00	24.00	-24.00	0.00	-19.24	-0.30	-3801.05	-19.28
cluster2	LSTM	12	TIR	LIB194050	best	17.70	-16.67	-1.04	0.00	0.00	1.03	-11.94	-0.09	-1065.62	-11.27
cluster2	LSTM	12	TAR_1	LIB194050	best	-15.14	13.18	0.00	1.96	0.00	-1.96	8.59	0.04	689.40	10.03
cluster2	LSTM	12	TAR_2	LIB194050	best	-12.65	-9.87	0.00	22.54	0.00	-22.52	13.69	0.05	2414.39	13.80
cluster2	LSTM	12	ALL	LIB193916	worst	1.09	-2.27	3.84	-3.67	1.02	-1.18	2.74	0.06	351.49	2.29
cluster2	LSTM	12	TBR_2	LIB193916	worst	0.00	0.00	0.00	-12.88	12.88	0.00	12.98	0.25	2933.64	13.15
cluster2	LSTM	12	TBR_1	LIB193916	worst	0.00	0.00	0.00	-11.01	11.01	0.00	15.25	0.25	3362.44	16.02
cluster2	LSTM	12	TIR	LIB193916	worst	-7.38	0.00	7.39	-0.07	0.07	-7.38	12.93	0.12	1902.44	16.19
cluster2	LSTM	12	TAR_1	LIB193916	worst	12.71	-11.41	0.08	-1.38	0.00	1.30	-8.37	-0.04	-856.03	-8.11
cluster2	LSTM	12	TAR_2	LIB193916	worst	11.82	3.08	0.00	-14.90	0.00	14.90	-20.33	-0.07	-4491.63	-18.11
cluster2	LSTM	16	ALL	LIB194050	best	0.84	-3.59	-0.58	3.39	-0.05	-2.75	-1.38	-0.02	-94.50	-0.96
cluster2	LSTM	16	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	-100.00	0.00	-20.45	-0.39	-5048.00	-20.45
cluster2	LSTM	16	TBR_1	LIB194050	best	0.00	0.00	0.00	36.37	-36.37	0.00	-17.69	-0.28	-3972.61	-17.98
cluster2	LSTM	16	TIR	LIB194050	best	15.74	-14.57	-1.16	0.01	-0.01	1.17	-11.43	-0.09	-1043.80	-10.82
cluster2	LSTM	16	TAR_1	LIB194050	best	-14.85	12.69	0.00	2.17	0.00	-2.16	7.99	0.04	579.46	8.70
cluster2	LSTM	16	TAR_2	LIB194050	best	-11.07	-15.79	0.00	26.86	0.00	-26.86	12.24	0.04	2161.05	11.86
cluster2	LSTM	16	ALL	LIB193916	worst	0.29	-0.66	3.71	-5.76	2.43	-0.37	4.66	0.09	553.86	3.54
cluster2	LSTM	16	TBR_2	LIB193916	worst	0.00	0.00	0.00	-25.00	25.00	0.00	18.47	0.36	4215.21	18.24
cluster2	LSTM	16	TBR_1	LIB193916	worst	0.00	0.00	0.00	-23.81	23.81	0.00	19.71	0.32	4209.37	19.60
cluster2	LSTM	16	TIR	LIB193916	worst	-11.02	3.88	7.13	-0.40	0.40	-7.14	15.75	0.15	2026.36	17.29
cluster2	LSTM	16	TAR_1	LIB193916	worst	22.07	-21.20	0.00	-0.87	0.00	0.87	-11.63	-0.05	-1078.70	-10.91
cluster2	LSTM	16	TAR_2	LIB193916	worst	5.16	15.49	0.00	-20.65	0.00	20.65	-16.85	-0.06	-4163.92	-15.97
cluster3	CNN	2	ALL	LIB193551	best	3.62	-3.42	0.00	-0.18	-0.02	0.20	-2.84	-0.02	-130.03	-2.55
cluster3	CNN	2	TBR_2	LIB193551	best										
cluster3	CNN	2	TBR_1	LIB193551	best	14.29	0.00	0.00	-14.29	0.00	14.29	-10.21	-0.17	-517.21	-10.09
cluster3	CNN	2	TIR	LIB193551	best	7.94	-7.94	0.00	0.00	0.00	0.00	-3.56	-0.03	-163.08	-3.62
cluster3	CNN	2	TAR_1	LIB193551	best	0.81	-0.68	0.00	-0.09	-0.04	0.13	-1.29	-0.01	-42.19	-0.82
cluster3	CNN	2	TAR_2	LIB193551	best	1.19	-0.59	0.00	-0.59	0.00	0.60	-4.56	-0.02	-241.88	-4.06
cluster3	CNN	2	ALL	LIB193878	worst	-0.08	-0.77	-0.03	0.87	0.00	-0.85	-0.50	0.00	-61.92	-1.04
cluster3	CNN	2	TBR_2	LIB193878	worst	-7.61	0.00	0.00	7.61	0.00	-7.61	3.62	0.07	169.13	3.42
cluster3	CNN	2	TBR_1	LIB193878	worst	-9.38	0.00	0.00	9.38	0.00	-9.38	2.79	0.05	102.89	2.06
cluster3	CNN	2	TIR	LIB193878	worst	0.68	-0.68	-0.06	0.06	0.00	0.00	-0.26	0.00	-30.34	-0.57
cluster3	CNN	2	TAR_1	LIB193878	worst	1.96	-1.78	0.00	-0.19	0.00	0.18	-1.90	-0.01	-145.78	-2.22
cluster3	CNN	2	TAR_2	LIB193878	worst	1.04	-0.18	0.00	-0.86	0.00	0.86	-1.70	-0.01	-164.54	-2.25
cluster3	CNN	4	ALL	LIB193871	best	1.30	-1.24	0.02	-0.07	-0.01	0.06	-0.62	-0.01	-7.60	-0.11
cluster3	CNN	4	TBR_2	LIB193871	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	CNN	4	TBR_1	LIB193871	best	0.00	0.00	0.00	1.28	-1.28	0.00	-16.21	-0.25	-1626.58	-14.20
cluster3	CNN	4	TIR	LIB193871	best	1.43	-1.45	0.02	0.00	0.00	-0.02	-0.58	-0.01	-14.79	-0.25
cluster3	CNN	4	TAR_1	LIB193871	best	0.39	-0.20	0.00	-0.20	0.00	0.19	0.46	0.00	141.61	1.78
cluster3	CNN	4	TAR_2	LIB193871	best	4.13	-3.34	0.00	-0.78	0.00	0.79	-4.41	-0.02	-393.70	-3.25
cluster3	CNN	4	ALL	LIB193878	worst	1.42	-1.09	-0.13	-0.19	0.00	0.33	-0.72	0.00	-75.58	-0.80
cluster3	CNN	4	TBR_2	LIB193878	worst	-1.02	0.00	0.00	1.02	0.00	-1.02	0.12	0.00	40.10	0.43
cluster3	CNN	4	TBR_1	LIB193878	worst	-0.36	0.00	0.00	0.18	0.18	-0.36	1.23	0.02	126.22	1.33
cluster3	CNN	4	TIR	LIB193878	worst	0.84	-0.69	-0.19	0.03	0.00	0.15	-0.19	0.00	-25.65	-0.34
cluster3	CNN	4	TAR_1	LIB193878	worst	4.55	-3.89	-0.13	-0.46	-0.07	0.66	-2.86	-0.01	-270.18	-2.83
cluster3	CNN	4	TAR_2	LIB193878	worst	0.09	0.82	0.00	-0.91	0.00	0.91	-0.44	0.00	-75.76	-0.57
cluster3	CNN	6	ALL	LIB193871	best	-2.44	2.68	0.49	-0.79	0.04	0.24	1.00	0.01	98.09	1.19
cluster3	CNN	6	TBR_2	LIB193871	best										
cluster3	CNN	6	TBR_1	LIB193871	best	0.00	0.00	0.00	-5.13	5.13	0.00	-9.46	-0.15	-974.26	-6.48
cluster3	CNN	6	TIR	LIB193871	best	-6.11	5.43	0.69	-0.01	0.01	-0.68	3.22	0.02	278.35	3.88
cluster3	CNN	6	TAR_1	LIB193871	best	5.28	-4.40	0.00	-0.88	0.00	0.88	-2.56	-0.01	-47.03	-0.53
cluster3	CNN	6	TAR_2	LIB193871	best	17.61	-5.26	0.00	-12.35	0.00	12.35	-15.18	-0.05	-1917.15	-11.93
cluster3	CNN	6	ALL	LIB193878	worst	-0.56	1.36	0.43	-1.37	0.14	0.80	0.79	0.04	-28.63	-0.24
cluster3	CNN	6	TBR_2	LIB193878	worst	0.00	0.00	0.00	-1.06	1.06	0.00	5.53	0.11	773.15	5.58
cluster3	CNN	6	TBR_1	LIB193878	worst	-0.58	0.00	0.00	-0.39	0.97	-0.58	12.03	0.20	1453.87	10.86
cluster3	CNN	6	TIR	LIB193878	worst	-7.46	6.65	0.82	-0.07	0.06	-0.81	5.34	0.06	482.78	5.10
cluster3	CNN	6	TAR_1	LIB193878	worst	7.15	-5.77	0.13	-1.51	0.00	1.38	-6.68	-0.03	-762.56	-7.09
cluster3	CNN	6	TAR_2	LIB193878	worst	8.88	-3.35	0.00	-5.54	0.00	5.53	-8.57	-0.03	-1385.04	-7.99
cluster3	CNN	8	ALL	LIB193871	best	-3.45	3.82	0.67	-1.11	0.07	0.37	2.20	0.02	192.33	2.14
cluster3	CNN	8	TBR_2	LIB193871	best										
cluster3	CNN	8	TBR_1	LIB193871	best	0.00	0.00	0.00	-7.69	7.69	0.00	-7.30	-0.11	-626.16	-3.69
cluster3	CNN	8	TIR	LIB193871	best	-8.94	8.01	0.92	-0.02	0.02	-0.93	5.30	0.04	472.99	6.18
cluster3	CNN	8	TAR_1	LIB193871	best	9.92	-9.19	0.00	-0.73	0.00	0.73	-3.82	-0.02	-159.18	-1.70
cluster3	CNN	8	TAR_2	LIB193871	best	17.12	2.92	0.00	-20.04	0.00	20.04	-16.07	-0.06	-2477.17	-12.81
cluster3	CNN	8	ALL	LIB193878	worst	1.67	-0.42	1.24	-2.94	0.45	1.25	-0.31	0.03	-129.77	-0.96
cluster3	CNN	8	TBR_2	LIB193878	worst	0.00	0.00	0.00	-4.39	4.39	0.00	6.13	0.12	1223.11	7.34
cluster3	CNN	8	TBR_1	LIB193878	worst	0.00	0.00	0.00	-3.48	3.48	0.00	9.70	0.16	1568.34	9.70
cluster3	CNN	8	TIR	LIB193878	worst	-7.09	4.57	2.53	-0.07	0.07	-2.52	7.38	0.07	846.57	8.52
cluster3	CNN	8	TAR_1	LIB193878	worst	12.81	-10.52	0.00	-2.31	0.00	2.29	-10.03	-0.05	-1043.15	-9.31
cluster3	CNN	8	TAR_2	LIB193878	worst	13.18	-1.32	0.00	-11.87	0.00	11.86	-15.65	-0.05	-2838.22	-13.27
cluster3	CNN	12	ALL	LIB193871	best	-3.76	4.43	0.69	-1.41	0.07	0.67	2.85	0.03	264.87	2.75
cluster3	CNN	12	TBR_2	LIB193871	best										
cluster3	CNN	12	TBR_1	LIB193871	best	0.00	0.00	0.00	-9.59	9.59	0.00	3.60	0.06	1064.66	5.72

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	CNN	12	TIR	LIB193871	best	-9.40	8.47	0.94	-0.01	0.01	-0.93	6.50	0.05	610.37	7.76
cluster3	CNN	12	TAR_1	LIB193871	best	12.25	-11.00	0.00	-1.25	0.00	1.25	-5.88	-0.03	-365.44	-3.62
cluster3	CNN	12	TAR_2	LIB193871	best	5.88	18.52	0.00	-24.41	0.00	24.40	-12.26	-0.04	-2321.15	-10.29
cluster3	CNN	12	ALL	LIB193878	worst	2.20	0.67	1.22	-5.04	0.95	2.87	-0.62	0.03	-212.83	-1.40
cluster3	CNN	12	TBR_2	LIB193878	worst	0.00	0.00	0.00	-7.65	7.65	0.00	9.54	0.19	1871.80	9.77
cluster3	CNN	12	TBR_1	LIB193878	worst	0.00	0.00	0.00	-8.24	8.24	0.00	8.85	0.14	1632.69	8.71
cluster3	CNN	12	TIR	LIB193878	worst	-4.86	2.39	2.47	-0.07	0.08	-2.47	6.62	0.07	829.67	7.80
cluster3	CNN	12	TAR_1	LIB193878	worst	14.84	-12.25	0.00	-2.58	0.00	2.59	-10.53	-0.05	-1066.46	-9.60
cluster3	CNN	12	TAR_2	LIB193878	worst	7.45	14.44	0.00	-21.89	0.00	21.89	-15.64	-0.05	-3577.27	-14.01
cluster3	CNN	16	ALL	LIB193871	best	-2.80	3.38	0.25	-0.93	0.09	0.58	2.24	0.02	227.57	2.34
cluster3	CNN	16	TBR_2	LIB193871	best										
cluster3	CNN	16	TBR_1	LIB193871	best	0.00	0.00	0.00	-13.24	13.24	0.00	5.16	0.08	1171.60	5.99
cluster3	CNN	16	TIR	LIB193871	best	-4.80	4.45	0.36	0.00	0.00	-0.35	4.08	0.03	366.62	4.59
cluster3	CNN	16	TAR_1	LIB193871	best	2.70	-1.45	0.00	-1.23	0.00	1.25	-2.63	-0.01	-97.59	-0.99
cluster3	CNN	16	TAR_2	LIB193871	best	1.12	11.66	0.00	-12.78	0.00	12.78	-3.02	-0.01	-509.40	-2.17
cluster3	CNN	16	ALL	LIB193878	worst	2.93	0.69	1.04	-5.71	1.05	3.62	0.07	0.05	-214.74	-1.38
cluster3	CNN	16	TBR_2	LIB193878	worst	0.00	0.00	0.00	-2.57	2.57	0.00	16.18	0.32	3008.87	15.65
cluster3	CNN	16	TBR_1	LIB193878	worst	0.00	0.00	0.00	-11.42	11.42	0.00	14.96	0.25	2761.89	14.70
cluster3	CNN	16	TIR	LIB193878	worst	-7.78	5.70	2.08	0.00	0.00	-2.08	9.64	0.10	1124.54	11.32
cluster3	CNN	16	TAR_1	LIB193878	worst	29.57	-26.53	0.00	-3.05	0.00	3.04	-16.50	-0.08	-1717.40	-14.75
cluster3	CNN	16	TAR_2	LIB193878	worst	0.95	24.83	0.00	-25.78	0.00	25.78	-18.33	-0.06	-4685.39	-16.88
cluster3	Linear	2	ALL	LIB193518	best	1.53	-1.48	0.00	-0.05	0.00	0.05	-1.22	-0.01	-62.81	-1.92
cluster3	Linear	2	TBR_2	LIB193518	best										
cluster3	Linear	2	TBR_1	LIB193518	best	-7.14	0.00	0.00	7.14	0.00	-7.14	2.50	0.04	-27.02	-0.81
cluster3	Linear	2	TIR	LIB193518	best	1.58	-1.58	0.00	0.00	0.00	0.00	-0.50	0.00	-29.42	-1.18
cluster3	Linear	2	TAR_1	LIB193518	best	1.39	-1.27	0.00	-0.11	0.00	0.12	-1.71	-0.01	-74.57	-2.17
cluster3	Linear	2	TAR_2	LIB193518	best	1.88	-1.81	0.00	-0.08	0.00	0.07	-2.04	-0.01	-130.98	-2.84
cluster3	Linear	2	ALL	LIB193878	worst	-0.37	-1.07	-0.01	1.46	0.00	-1.44	-0.37	0.00	-53.20	-1.31
cluster3	Linear	2	TBR_2	LIB193878	worst	-3.04	0.00	0.00	3.04	0.00	-3.04	5.09	0.10	76.03	3.83
cluster3	Linear	2	TBR_1	LIB193878	worst	-15.74	0.00	0.00	15.74	0.00	-15.74	3.62	0.06	74.24	2.93
cluster3	Linear	2	TIR	LIB193878	worst	1.34	-1.36	-0.03	0.06	0.00	-0.02	-0.43	0.00	-49.80	-1.30
cluster3	Linear	2	TAR_1	LIB193878	worst	1.14	-1.01	0.00	-0.12	0.00	0.13	-1.72	-0.01	-103.74	-2.24
cluster3	Linear	2	TAR_2	LIB193878	worst	0.96	-1.04	0.00	0.09	0.00	-0.08	-1.37	0.00	-82.16	-1.72
cluster3	Linear	4	ALL	LIB193518	best	1.45	-1.48	0.00	0.03	0.00	-0.03	-1.06	0.00	-91.70	-1.54
cluster3	Linear	4	TBR_2	LIB193518	best										
cluster3	Linear	4	TBR_1	LIB193518	best	-58.33	0.00	0.00	58.33	0.00	-58.33	14.45	0.23	517.38	12.46
cluster3	Linear	4	TIR	LIB193518	best	0.51	-0.51	0.00	0.00	0.00	0.00	-1.22	0.00	-110.85	-2.67

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	4	TAR_1	LIB193518	best	3.64	-3.61	0.00	-0.03	0.00	0.03	-2.28	-0.01	-161.42	-2.82
cluster3	Linear	4	TAR_2	LIB193518	best	-1.37	1.61	0.00	-0.24	0.00	0.24	2.75	0.01	157.29	1.58
cluster3	Linear	4	ALL	LIB193878	worst	-3.57	-1.97	-0.38	6.09	-0.16	-5.54	-1.19	0.01	-288.12	-3.50
cluster3	Linear	4	TBR_2	LIB193878	worst	-64.79	0.00	0.00	64.79	0.00	-64.79	15.82	0.31	612.00	11.21
cluster3	Linear	4	TBR_1	LIB193878	worst	-50.99	0.00	0.00	51.35	-0.36	-50.99	11.78	0.20	434.45	6.85
cluster3	Linear	4	TIR	LIB193878	worst	0.99	-0.78	-0.56	0.34	0.00	0.21	-2.47	-0.01	-293.89	-4.00
cluster3	Linear	4	TAR_1	LIB193878	worst	7.58	-6.07	-0.46	-0.46	-0.59	1.51	-6.36	-0.03	-699.46	-7.94
cluster3	Linear	4	TAR_2	LIB193878	worst	2.54	-1.18	0.00	-1.36	0.00	1.36	0.10	0.00	-229.48	-2.14
cluster3	Linear	6	ALL	LIB193871	best	1.31	-0.51	-0.31	-0.45	-0.03	0.80	-2.02	0.00	-304.50	-3.74
cluster3	Linear	6	TBR_2	LIB193871	best										
cluster3	Linear	6	TBR_1	LIB193871	best	-2.56	0.00	0.00	5.13	-2.57	-2.56	8.49	0.13	462.25	3.78
cluster3	Linear	6	TIR	LIB193871	best	-1.33	1.70	-0.39	0.02	0.00	0.37	-0.34	0.01	-111.76	-1.59
cluster3	Linear	6	TAR_1	LIB193871	best	9.60	-8.93	-0.12	-0.47	-0.08	0.67	-7.73	-0.04	-856.99	-9.05
cluster3	Linear	6	TAR_2	LIB193871	best	2.22	6.47	0.00	-8.71	0.00	8.69	-1.81	-0.01	-734.38	-5.11
cluster3	Linear	6	ALL	LIB193878	worst	-1.86	-1.48	-0.87	5.10	-0.87	-3.34	-1.68	0.03	-562.06	-4.95
cluster3	Linear	6	TBR_2	LIB193878	worst	-59.26	0.00	0.00	60.84	-1.59	-59.26	28.18	0.56	1730.02	18.00
cluster3	Linear	6	TBR_1	LIB193878	worst	-43.90	0.00	0.00	44.10	-0.20	-43.90	20.99	0.35	1189.23	11.32
cluster3	Linear	6	TIR	LIB193878	worst	3.19	-2.28	-1.33	0.42	0.00	0.91	-3.73	-0.01	-526.29	-5.55
cluster3	Linear	6	TAR_1	LIB193878	worst	11.41	-7.22	-0.96	-0.21	-3.02	4.19	-10.44	-0.05	-1465.13	-13.03
cluster3	Linear	6	TAR_2	LIB193878	worst	-4.02	7.83	0.00	-3.15	-0.67	3.81	-0.08	0.00	-690.49	-4.29
cluster3	Linear	8	ALL	LIB193871	best	3.11	-1.73	-0.51	-0.81	-0.04	1.38	-3.35	-0.01	-555.69	-5.92
cluster3	Linear	8	TBR_2	LIB193871	best										
cluster3	Linear	8	TBR_1	LIB193871	best	-1.28	0.00	0.00	5.13	-3.84	-1.28	13.60	0.21	942.31	6.07
cluster3	Linear	8	TIR	LIB193871	best	-0.31	0.99	-0.67	0.00	0.00	0.68	-0.12	0.01	-132.98	-1.67
cluster3	Linear	8	TAR_1	LIB193871	best	14.88	-13.87	-0.12	-0.80	-0.08	1.01	-13.42	-0.07	-1632.07	-15.38
cluster3	Linear	8	TAR_2	LIB193871	best	-0.62	15.87	0.00	-15.24	0.00	15.25	-7.27	-0.03	-2188.01	-11.88
cluster3	Linear	8	ALL	LIB193878	worst	-0.05	-0.88	-1.09	3.16	-1.14	-0.93	-2.82	0.04	-940.81	-6.91
cluster3	Linear	8	TBR_2	LIB193878	worst	-49.45	0.00	0.00	49.45	0.00	-49.45	37.42	0.74	2999.00	22.08
cluster3	Linear	8	TBR_1	LIB193878	worst	-33.74	0.00	0.00	31.90	1.84	-33.74	27.64	0.46	2220.63	15.94
cluster3	Linear	8	TIR	LIB193878	worst	2.69	-0.99	-1.95	0.17	0.07	1.70	-3.56	0.00	-621.73	-5.72
cluster3	Linear	8	TAR_1	LIB193878	worst	15.40	-10.08	-0.58	-0.57	-4.18	5.32	-15.83	-0.08	-2393.51	-19.40
cluster3	Linear	8	TAR_2	LIB193878	worst	-4.16	11.77	0.00	-5.48	-2.13	7.61	-4.83	-0.02	-2138.31	-10.43
cluster3	Linear	12	ALL	LIB193871	best	4.26	-2.74	-0.75	-0.75	-0.02	1.52	-5.18	-0.01	-917.95	-8.61
cluster3	Linear	12	TBR_2	LIB193871	best										
cluster3	Linear	12	TBR_1	LIB193871	best	0.00	0.00	0.00	-4.11	4.11	0.00	14.59	0.23	1414.86	7.47
cluster3	Linear	12	TIR	LIB193871	best	-0.10	1.13	-1.03	-0.01	0.01	1.03	0.04	0.02	-126.78	-1.44
cluster3	Linear	12	TAR_1	LIB193871	best	20.25	-19.29	0.00	-0.75	-0.21	0.96	-20.69	-0.10	-2806.49	-23.87

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	Linear	12	TAR_2	LIB193871	best	-6.32	19.18	0.00	-12.64	-0.22	12.86	-14.18	-0.05	-4591.77	-19.91
cluster3	Linear	12	ALL	LIB193878	worst	2.92	-0.23	-2.32	1.41	-1.79	2.69	-6.75	0.04	-2064.55	-12.73
cluster3	Linear	12	TBR_2	LIB193878	worst	-41.76	0.00	0.00	41.77	0.00	-41.76	48.56	0.96	4959.21	30.65
cluster3	Linear	12	TBR_1	LIB193878	worst	-19.91	0.00	0.00	15.56	4.35	-19.91	32.31	0.53	3458.51	20.01
cluster3	Linear	12	TIR	LIB193878	worst	5.12	-0.97	-4.41	0.34	-0.07	4.15	-5.23	0.00	-1133.24	-9.20
cluster3	Linear	12	TAR_1	LIB193878	worst	17.98	-10.48	-0.56	-1.05	-5.89	7.50	-25.00	-0.12	-4081.98	-30.56
cluster3	Linear	12	TAR_2	LIB193878	worst	-5.23	16.76	0.00	-6.87	-4.66	11.53	-15.99	-0.06	-6251.19	-23.66
cluster3	Linear	16	ALL	LIB193871	best	5.60	-4.06	-1.27	-0.23	-0.04	1.54	-6.39	-0.01	-1147.94	-10.40
cluster3	Linear	16	TBR_2	LIB193871	best										
cluster3	Linear	16	TBR_1	LIB193871	best	0.00	0.00	0.00	-1.47	1.47	0.00	13.69	0.22	1480.19	7.37
cluster3	Linear	16	TIR	LIB193871	best	-0.21	1.98	-1.77	0.00	0.00	1.77	-0.25	0.02	-175.97	-1.96
cluster3	Linear	16	TAR_1	LIB193871	best	26.28	-26.07	0.00	-0.17	-0.04	0.21	-23.45	-0.12	-3219.93	-27.15
cluster3	Linear	16	TAR_2	LIB193871	best	-5.83	10.99	0.00	-4.26	-0.90	5.16	-21.30	-0.08	-6747.88	-26.79
cluster3	Linear	16	ALL	LIB193878	worst	2.53	0.00	-3.41	3.87	-2.99	2.53	-8.83	0.04	-2767.38	-16.15
cluster3	Linear	16	TBR_2	LIB193878	worst	-46.79	0.00	0.00	45.52	1.28	-46.79	56.66	1.11	6124.35	36.38
cluster3	Linear	16	TBR_1	LIB193878	worst	-19.35	0.00	0.00	18.86	0.50	-19.35	33.16	0.54	3281.71	17.51
cluster3	Linear	16	TIR	LIB193878	worst	4.70	1.49	-6.57	0.29	0.09	6.19	-5.64	0.01	-1318.05	-10.56
cluster3	Linear	16	TAR_1	LIB193878	worst	20.61	-12.57	-0.46	0.19	-7.76	8.04	-30.90	-0.15	-5168.87	-37.66
cluster3	Linear	16	TAR_2	LIB193878	worst	-8.68	13.57	0.00	3.93	-8.82	4.89	-23.67	-0.08	-9157.07	-31.49
cluster3	LSTM	2	ALL	LIB193518	best	0.12	-0.09	0.00	-0.03	0.00	0.03	-0.10	0.00	-1.18	-0.04
cluster3	LSTM	2	TBR_2	LIB193518	best										
cluster3	LSTM	2	TBR_1	LIB193518	best	7.14	0.00	0.00	-7.14	0.00	7.14	0.83	0.01	-2.74	-0.10
cluster3	LSTM	2	TIR	LIB193518	best	0.24	-0.24	0.00	0.00	0.00	0.00	-0.23	0.00	-2.44	-0.10
cluster3	LSTM	2	TAR_1	LIB193518	best	0.14	-0.09	0.00	-0.05	0.00	0.05	0.03	0.00	1.84	0.06
cluster3	LSTM	2	TAR_2	LIB193518	best	-0.31	0.31	0.00	0.00	0.00	0.00	-0.09	0.00	-5.93	-0.14
cluster3	LSTM	2	ALL	LIB193878	worst	-1.03	-0.29	0.01	1.31	0.00	-1.32	0.08	0.00	-5.17	-0.14
cluster3	LSTM	2	TBR_2	LIB193878	worst	-9.65	0.00	0.00	9.65	0.00	-9.65	2.56	0.05	45.17	1.68
cluster3	LSTM	2	TBR_1	LIB193878	worst	-11.55	0.00	0.00	11.55	0.00	-11.55	2.57	0.04	63.98	2.36
cluster3	LSTM	2	TIR	LIB193878	worst	0.21	-0.32	0.03	0.09	0.00	-0.11	0.04	0.00	3.73	0.11
cluster3	LSTM	2	TAR_1	LIB193878	worst	0.77	-0.70	0.00	-0.07	0.00	0.07	-0.46	0.00	-31.94	-0.75
cluster3	LSTM	2	TAR_2	LIB193878	worst	-0.17	0.17	0.00	0.00	0.00	0.00	-0.79	0.00	-39.01	-0.85
cluster3	LSTM	4	ALL	LIB193518	best	0.62	-0.70	0.00	0.10	0.00	-0.08	-0.19	0.00	13.49	0.24
cluster3	LSTM	4	TBR_2	LIB193518	best										
cluster3	LSTM	4	TBR_1	LIB193518	best	-8.33	0.00	0.00	8.33	0.00	-8.33	0.29	0.00	-39.56	-0.81
cluster3	LSTM	4	TIR	LIB193518	best	2.66	-2.66	0.00	0.00	0.00	0.00	-1.20	-0.01	-44.42	-1.13
cluster3	LSTM	4	TAR_1	LIB193518	best	-0.51	0.37	0.00	0.14	0.00	-0.14	0.33	0.00	26.17	0.49
cluster3	LSTM	4	TAR_2	LIB193518	best	-2.25	2.10	0.00	0.16	0.00	-0.15	1.33	0.00	151.65	1.57

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	4	ALL	LIB193878	worst	-0.88	0.35	0.14	0.37	0.03	-0.53	-0.08	0.01	-32.88	-0.43
cluster3	LSTM	4	TBR_2	LIB193878	worst	3.06	0.00	0.00	-3.06	0.00	3.06	3.01	0.05	184.58	2.61
cluster3	LSTM	4	TBR_1	LIB193878	worst	-8.11	0.00	0.00	7.75	0.36	-8.11	6.77	0.11	449.43	6.57
cluster3	LSTM	4	TIR	LIB193878	worst	-3.15	2.71	0.25	0.19	0.00	-0.44	1.58	0.02	112.15	1.73
cluster3	LSTM	4	TAR_1	LIB193878	worst	1.91	-1.59	0.00	-0.33	0.00	0.32	-2.73	-0.01	-219.25	-2.69
cluster3	LSTM	4	TAR_2	LIB193878	worst	4.80	-3.63	0.09	-1.27	0.00	1.17	-5.30	-0.02	-480.78	-4.70
cluster3	LSTM	6	ALL	LIB193871	best	-1.83	2.14	0.13	-0.44	0.01	0.31	0.84	0.00	73.92	0.98
cluster3	LSTM	6	TBR_2	LIB193871	best										
cluster3	LSTM	6	TBR_1	LIB193871	best	0.00	0.00	0.00	-1.29	1.29	0.00	-14.40	-0.23	-1484.07	-11.12
cluster3	LSTM	6	TIR	LIB193871	best	-4.86	4.68	0.17	0.00	0.00	-0.18	2.56	0.01	199.27	3.06
cluster3	LSTM	6	TAR_1	LIB193871	best	4.96	-4.53	0.00	-0.44	0.00	0.43	-1.79	-0.01	-16.79	-0.20
cluster3	LSTM	6	TAR_2	LIB193871	best	12.14	-4.66	0.00	-7.49	0.00	7.48	-11.35	-0.04	-1251.14	-8.87
cluster3	LSTM	6	ALL	LIB193878	worst	0.44	-0.08	0.32	-0.83	0.14	0.36	0.30	0.03	-32.50	-0.31
cluster3	LSTM	6	TBR_2	LIB193878	worst	1.06	0.00	0.00	-0.53	-0.53	1.06	4.74	0.08	514.63	4.54
cluster3	LSTM	6	TBR_1	LIB193878	worst	0.00	0.00	0.00	-1.75	1.74	0.00	10.26	0.17	1067.23	9.60
cluster3	LSTM	6	TIR	LIB193878	worst	-5.40	4.95	0.45	-0.03	0.04	-0.45	3.46	0.04	290.72	3.38
cluster3	LSTM	6	TAR_1	LIB193878	worst	8.52	-7.77	0.34	-1.10	0.00	0.75	-5.98	-0.03	-573.73	-5.61
cluster3	LSTM	6	TAR_2	LIB193878	worst	6.49	-4.21	0.10	-2.39	0.00	2.28	-5.95	-0.02	-869.89	-5.73
cluster3	LSTM	8	ALL	LIB193871	best	-3.40	3.90	0.47	-1.02	0.04	0.50	1.77	0.01	156.37	1.83
cluster3	LSTM	8	TBR_2	LIB193871	best										
cluster3	LSTM	8	TBR_1	LIB193871	best	0.00	0.00	0.00	-5.12	5.12	0.00	-11.94	-0.19	-1460.49	-9.18
cluster3	LSTM	8	TIR	LIB193871	best	-8.30	7.65	0.65	-0.02	0.02	-0.65	4.45	0.03	376.49	5.21
cluster3	LSTM	8	TAR_1	LIB193871	best	8.63	-7.66	0.00	-0.97	0.00	0.97	-3.43	-0.02	-95.98	-1.04
cluster3	LSTM	8	TAR_2	LIB193871	best	14.61	2.50	0.00	-17.12	0.00	17.11	-13.23	-0.05	-1899.44	-10.61
cluster3	LSTM	8	ALL	LIB193878	worst	2.13	-1.17	0.80	-2.19	0.43	0.96	-0.27	0.03	-113.35	-0.89
cluster3	LSTM	8	TBR_2	LIB193878	worst	0.55	0.00	0.00	-3.29	2.74	0.55	6.13	0.12	1051.70	7.06
cluster3	LSTM	8	TBR_1	LIB193878	worst	0.00	0.00	0.00	-3.88	3.88	0.00	10.89	0.18	1607.34	11.12
cluster3	LSTM	8	TIR	LIB193878	worst	-7.26	5.73	1.53	-0.06	0.07	-1.53	6.80	0.07	735.82	7.76
cluster3	LSTM	8	TAR_1	LIB193878	worst	12.82	-11.73	0.22	-1.30	0.00	1.09	-9.30	-0.04	-952.33	-8.59
cluster3	LSTM	8	TAR_2	LIB193878	worst	16.33	-7.61	0.00	-8.72	0.00	8.72	-15.27	-0.05	-2525.01	-12.76
cluster3	LSTM	12	ALL	LIB193871	best	-4.86	5.65	0.70	-1.54	0.05	0.79	3.27	0.03	313.21	3.27
cluster3	LSTM	12	TBR_2	LIB193871	best										
cluster3	LSTM	12	TBR_1	LIB193871	best	0.00	0.00	0.00	-6.85	6.85	0.00	-0.78	-0.01	280.05	1.52
cluster3	LSTM	12	TIR	LIB193871	best	-9.90	8.93	0.97	-0.01	0.02	-0.97	6.59	0.05	612.68	7.63
cluster3	LSTM	12	TAR_1	LIB193871	best	8.79	-7.34	0.00	-1.46	0.00	1.45	-4.37	-0.02	-198.75	-2.03
cluster3	LSTM	12	TAR_2	LIB193871	best	6.97	19.60	0.00	-26.58	0.00	26.57	-11.34	-0.04	-1992.51	-9.15
cluster3	LSTM	12	ALL	LIB193878	worst	3.46	-0.97	1.47	-4.85	0.89	2.49	-0.80	0.04	-229.11	-1.54

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	12	TBR_2	LIB193878	worst	0.00	0.00	0.00	-3.53	3.53	0.00	9.15	0.18	1813.80	9.69
cluster3	LSTM	12	TBR_1	LIB193878	worst	0.00	0.00	0.00	-9.38	9.38	0.00	11.07	0.18	2049.37	11.21
cluster3	LSTM	12	TIR	LIB193878	worst	-4.64	1.68	2.96	-0.04	0.03	-2.96	8.04	0.08	1013.65	9.65
cluster3	LSTM	12	TAR_1	LIB193878	worst	16.85	-13.55	0.00	-3.30	0.00	3.30	-12.32	-0.06	-1257.78	-11.22
cluster3	LSTM	12	TAR_2	LIB193878	worst	11.76	8.26	0.00	-20.02	0.00	20.02	-19.68	-0.07	-4176.28	-16.78
cluster3	LSTM	16	ALL	LIB193871	best	-4.76	5.96	0.47	-1.79	0.13	1.20	3.19	0.03	284.91	2.89
cluster3	LSTM	16	TBR_2	LIB193871	best										
cluster3	LSTM	16	TBR_1	LIB193871	best	0.00	0.00	0.00	-19.12	19.12	0.00	6.88	0.10	1729.26	8.82
cluster3	LSTM	16	TIR	LIB193871	best	-10.26	9.61	0.65	0.00	0.00	-0.65	7.63	0.06	696.03	8.59
cluster3	LSTM	16	TAR_1	LIB193871	best	11.11	-9.06	0.00	-2.05	0.00	2.05	-8.07	-0.04	-540.64	-5.47
cluster3	LSTM	16	TAR_2	LIB193871	best	2.24	25.11	0.00	-27.35	0.00	27.35	-11.65	-0.04	-2401.22	-10.23
cluster3	LSTM	16	ALL	LIB193878	worst	2.43	2.28	1.82	-8.60	2.07	4.71	0.53	0.06	-94.60	-0.61
cluster3	LSTM	16	TBR_2	LIB193878	worst	0.00	0.00	0.00	-8.97	8.97	0.00	14.17	0.28	2797.12	14.23
cluster3	LSTM	16	TBR_1	LIB193878	worst	0.00	0.00	0.00	-20.60	20.60	0.00	14.90	0.24	2975.19	15.38
cluster3	LSTM	16	TIR	LIB193878	worst	-9.03	5.41	3.62	-0.09	0.09	-3.62	11.40	0.11	1385.04	13.34
cluster3	LSTM	16	TAR_1	LIB193878	worst	28.56	-24.30	0.00	-4.25	0.00	4.26	-16.55	-0.08	-1591.26	-14.36
cluster3	LSTM	16	TAR_2	LIB193878	worst	3.26	32.84	0.00	-36.09	0.00	36.10	-20.54	-0.07	-5012.36	-18.53
cluster4	CNN	2	ALL	LIB193960	best	0.96	-0.96	0.00	0.00	0.00	0.00	-0.99	-0.01	-37.97	-0.85
cluster4	CNN	2	TBR_2	LIB193960	best										
cluster4	CNN	2	TBR_1	LIB193960	best										
cluster4	CNN	2	TIR	LIB193960	best	1.74	-1.74	0.00	0.00	0.00	0.00	-0.35	0.00	-23.21	-0.79
cluster4	CNN	2	TAR_1	LIB193960	best	0.17	-0.17	0.00	0.00	0.00	0.00	-2.29	-0.01	-111.11	-2.24
cluster4	CNN	2	TAR_2	LIB193960	best	0.37	-0.37	0.00	0.00	0.00	0.00	-0.05	0.00	75.37	1.17
cluster4	CNN	2	ALL	LIB193826	worst	-3.70	-1.54	0.07	5.14	0.02	-5.24	-0.63	0.01	-126.13	-2.27
cluster4	CNN	2	TBR_2	LIB193826	worst	-27.27	0.00	0.00	27.27	0.00	-27.27	5.70	0.11	248.94	4.47
cluster4	CNN	2	TBR_1	LIB193826	worst	-29.67	0.00	0.00	29.52	0.15	-29.67	5.05	0.08	161.57	3.58
cluster4	CNN	2	TIR	LIB193826	worst	-0.10	-0.27	0.10	0.28	0.00	-0.37	-0.50	0.00	-56.50	-1.17
cluster4	CNN	2	TAR_1	LIB193826	worst	11.70	-11.09	0.00	-0.60	0.00	0.61	-7.88	-0.04	-620.81	-8.21
cluster4	CNN	2	TAR_2	LIB193826	worst	9.16	-2.29	0.00	-6.87	0.00	6.87	-10.03	-0.03	-1552.36	-12.87
cluster4	CNN	4	ALL	LIB194157	best	5.38	-5.38	0.00	0.00	0.00	0.00	-2.11	-0.02	-108.75	-1.84
cluster4	CNN	4	TBR_2	LIB194157	best										
cluster4	CNN	4	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.95	-0.08	-302.88	-4.41
cluster4	CNN	4	TIR	LIB194157	best	6.20	-6.13	0.00	-0.06	0.00	0.07	-1.95	-0.02	-77.65	-1.53
cluster4	CNN	4	TAR_1	LIB194157	best	1.04	-1.38	0.00	0.35	0.00	-0.34	-2.78	-0.01	-256.03	-2.86
cluster4	CNN	4	TAR_2	LIB194157	best	10.00	-10.00	0.00	0.00	0.00	0.00	-3.49	-0.01	-428.49	-3.24
cluster4	CNN	4	ALL	LIB193826	worst	-3.59	1.22	0.19	2.07	0.10	-2.37	1.20	0.04	-20.34	-0.27
cluster4	CNN	4	TBR_2	LIB193826	worst	-6.09	0.00	0.00	5.22	0.87	-6.09	9.88	0.19	863.48	9.70

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	4	TBR_1	LIB193826	worst	-15.23	0.00	0.00	14.75	0.48	-15.23	9.91	0.16	643.19	8.83
cluster4	CNN	4	TIR	LIB193826	worst	-4.84	4.48	0.28	0.07	0.00	-0.36	1.52	0.02	68.06	1.17
cluster4	CNN	4	TAR_1	LIB193826	worst	15.36	-14.35	0.00	-1.03	0.00	1.01	-9.62	-0.05	-925.31	-9.17
cluster4	CNN	4	TAR_2	LIB193826	worst	10.08	-3.87	0.00	-6.20	0.00	6.21	-14.17	-0.05	-2484.16	-13.90
cluster4	CNN	6	ALL	LIB194157	best	4.11	-4.17	0.00	0.06	0.00	-0.06	-1.83	-0.02	-93.50	-1.38
cluster4	CNN	6	TBR_2	LIB194157	best										
cluster4	CNN	6	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.35	-0.10	-560.84	-5.98
cluster4	CNN	6	TIR	LIB194157	best	5.00	-5.01	0.00	0.00	0.00	-0.01	-2.04	-0.02	-101.97	-1.81
cluster4	CNN	6	TAR_1	LIB194157	best	-0.36	0.71	0.00	-0.35	0.00	0.35	-0.47	0.00	-15.00	-0.14
cluster4	CNN	6	TAR_2	LIB194157	best	0.00	-20.00	0.00	20.00	0.00	-20.00	-2.28	-0.01	-321.25	-1.96
cluster4	CNN	6	ALL	LIB193826	worst	-0.96	0.82	0.13	-0.20	0.23	-0.14	0.99	0.04	-4.87	-0.06
cluster4	CNN	6	TBR_2	LIB193826	worst	-1.85	0.00	0.00	-3.71	5.56	-1.85	12.59	0.24	1582.06	13.38
cluster4	CNN	6	TBR_1	LIB193826	worst	-2.90	0.00	0.00	2.39	0.51	-2.90	10.42	0.17	918.59	10.04
cluster4	CNN	6	TIR	LIB193826	worst	-3.90	3.64	0.18	0.08	0.00	-0.26	1.37	0.03	93.73	1.49
cluster4	CNN	6	TAR_1	LIB193826	worst	16.53	-15.90	0.00	-0.62	0.00	0.63	-11.34	-0.06	-1210.64	-10.03
cluster4	CNN	6	TAR_2	LIB193826	worst	6.30	7.09	0.00	-13.39	0.00	13.39	-14.27	-0.05	-3205.92	-14.02
cluster4	CNN	8	ALL	LIB194157	best	3.39	-3.33	0.00	-0.05	0.00	0.06	-0.99	-0.01	-74.95	-1.04
cluster4	CNN	8	TBR_2	LIB194157	best										
cluster4	CNN	8	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-9.52	-0.15	-1273.96	-10.49
cluster4	CNN	8	TIR	LIB194157	best	2.65	-2.66	0.00	0.00	0.00	-0.01	-0.32	0.00	-2.24	-0.04
cluster4	CNN	8	TAR_1	LIB194157	best	7.61	-6.88	0.00	-0.72	0.00	0.73	-3.75	-0.02	-330.05	-3.00
cluster4	CNN	8	TAR_2	LIB194157	best	0.00	-10.00	0.00	10.00	0.00	-10.00	-9.66	-0.04	-1923.15	-10.57
cluster4	CNN	8	ALL	LIB193826	worst	-1.07	1.38	0.15	-0.89	0.43	0.31	2.13	0.06	92.62	0.94
cluster4	CNN	8	TBR_2	LIB193826	worst	-0.99	0.00	0.00	-8.91	9.90	-0.99	17.61	0.34	2634.46	18.29
cluster4	CNN	8	TBR_1	LIB193826	worst	-1.79	0.00	0.00	0.53	1.25	-1.79	12.19	0.20	1288.25	11.28
cluster4	CNN	8	TIR	LIB193826	worst	-4.94	4.72	0.23	0.00	0.00	-0.22	3.09	0.05	244.04	3.60
cluster4	CNN	8	TAR_1	LIB193826	worst	19.40	-18.33	0.00	-1.06	0.00	1.07	-12.68	-0.06	-1437.99	-11.30
cluster4	CNN	8	TAR_2	LIB193826	worst	7.94	11.11	0.00	-19.05	0.00	19.05	-20.16	-0.07	-4770.25	-18.17
cluster4	CNN	12	ALL	LIB194157	best	-0.72	0.96	0.00	-0.25	0.00	0.24	-0.39	0.00	-69.31	-0.91
cluster4	CNN	12	TBR_2	LIB194157	best										
cluster4	CNN	12	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.62	-0.12	-1229.65	-8.02
cluster4	CNN	12	TIR	LIB194157	best	-0.79	0.80	0.00	0.00	0.00	0.01	0.16	0.00	-2.94	-0.05
cluster4	CNN	12	TAR_1	LIB194157	best	-0.38	1.92	0.00	-1.54	0.00	1.54	-2.95	-0.01	-365.45	-3.08
cluster4	CNN	12	TAR_2	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	1.03	0.00	225.54	1.07
cluster4	CNN	12	ALL	LIB193838	worst	1.05	0.81	0.74	-3.34	0.76	1.86	-0.04	0.01	31.00	0.25
cluster4	CNN	12	TBR_2	LIB193838	worst	0.00	0.00	0.00	-11.69	11.69	0.00	6.64	0.13	1650.64	8.29
cluster4	CNN	12	TBR_1	LIB193838	worst	0.00	0.00	0.00	-4.68	4.68	0.00	1.10	0.02	456.92	2.77

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	CNN	12	TIR	LIB193838	worst	-2.26	1.12	1.15	0.00	0.00	-1.14	2.44	0.02	357.64	4.12
cluster4	CNN	12	TAR_1	LIB193838	worst	15.59	-12.54	0.00	-3.07	0.00	3.05	-5.79	-0.03	-479.47	-3.59
cluster4	CNN	12	TAR_2	LIB193838	worst	1.07	33.57	0.00	-34.64	0.00	34.64	-15.60	-0.05	-3413.53	-12.73
cluster4	CNN	16	ALL	LIB194157	best	-2.00	1.99	0.00	0.26	-0.26	-0.01	-0.13	0.00	-126.17	-1.57
cluster4	CNN	16	TBR_2	LIB194157	best										
cluster4	CNN	16	TBR_1	LIB194157	best	0.00	0.00	0.00	26.67	-26.67	0.00	-8.35	-0.13	-1926.69	-10.24
cluster4	CNN	16	TIR	LIB194157	best	-1.09	1.09	0.00	0.00	0.00	0.00	0.29	0.01	-46.87	-0.73
cluster4	CNN	16	TAR_1	LIB194157	best	-6.94	6.94	0.00	0.00	0.00	0.00	-1.71	-0.01	-407.81	-3.30
cluster4	CNN	16	TAR_2	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.96	-0.01	-715.57	-3.14
cluster4	CNN	16	ALL	LIB193838	worst	0.39	-0.09	0.18	-0.85	0.37	0.30	-0.43	0.00	-44.43	-0.34
cluster4	CNN	16	TBR_2	LIB193838	worst	0.00	0.00	0.00	-4.00	4.00	0.00	-0.88	-0.02	-82.89	-0.43
cluster4	CNN	16	TBR_1	LIB193838	worst	0.00	0.00	0.00	-2.43	2.43	0.00	-1.20	-0.02	-114.08	-0.66
cluster4	CNN	16	TIR	LIB193838	worst	-0.21	-0.08	0.28	0.00	0.00	-0.29	0.16	0.00	62.36	0.69
cluster4	CNN	16	TAR_1	LIB193838	worst	3.51	-2.90	0.00	-0.61	0.00	0.61	-0.45	0.00	7.40	0.06
cluster4	CNN	16	TAR_2	LIB193838	worst	0.00	6.64	0.00	-6.64	0.00	6.64	-5.26	-0.02	-1205.46	-4.41
cluster4	Linear	2	ALL	LIB193960	best	1.62	-1.62	0.00	0.00	0.00	0.00	-0.96	-0.01	-41.92	-1.32
cluster4	Linear	2	TBR_2	LIB193960	best										
cluster4	Linear	2	TBR_1	LIB193960	best										
cluster4	Linear	2	TIR	LIB193960	best	1.63	-1.63	0.00	0.00	0.00	0.00	-0.93	-0.01	-37.23	-1.63
cluster4	Linear	2	TAR_1	LIB193960	best	2.54	-2.54	0.00	0.00	0.00	0.00	-1.75	-0.01	-90.06	-2.50
cluster4	Linear	2	TAR_2	LIB193960	best	-0.36	0.36	0.00	0.00	0.00	0.00	0.67	0.00	47.25	1.11
cluster4	Linear	2	ALL	LIB193838	worst	3.39	-3.66	0.00	0.29	-0.02	-0.27	-1.85	-0.01	-139.20	-2.87
cluster4	Linear	2	TBR_2	LIB193838	worst	4.70	0.00	0.00	-4.70	0.00	4.70	0.14	0.00	-20.55	-0.53
cluster4	Linear	2	TBR_1	LIB193838	worst	-3.13	0.00	0.00	3.30	-0.16	-3.13	0.56	0.01	-70.36	-1.64
cluster4	Linear	2	TIR	LIB193838	worst	4.65	-4.62	-0.03	0.00	0.00	0.03	-2.26	-0.02	-146.54	-3.09
cluster4	Linear	2	TAR_1	LIB193838	worst	4.18	-4.18	0.12	-0.12	0.00	0.00	-2.70	-0.01	-202.98	-3.70
cluster4	Linear	2	TAR_2	LIB193838	worst	0.29	-0.29	0.00	0.00	0.00	0.00	-0.46	0.00	-62.10	-1.15
cluster4	Linear	4	ALL	LIB194157	best	5.43	-5.75	-0.05	0.37	0.00	-0.32	-2.96	-0.02	-253.28	-4.47
cluster4	Linear	4	TBR_2	LIB194157	best										
cluster4	Linear	4	TBR_1	LIB194157	best	-46.66	0.00	0.00	46.66	0.00	-46.66	11.14	0.18	339.15	9.03
cluster4	Linear	4	TIR	LIB194157	best	5.82	-5.75	-0.06	0.00	0.00	0.07	-2.71	-0.02	-185.04	-3.78
cluster4	Linear	4	TAR_1	LIB194157	best	6.58	-6.22	0.00	-0.34	0.00	0.36	-5.07	-0.03	-662.93	-7.74
cluster4	Linear	4	TAR_2	LIB194157	best	-10.00	0.00	0.00	10.00	0.00	-10.00	-1.51	-0.01	16.46	0.14
cluster4	Linear	4	ALL	LIB193826	worst	-7.77	-2.79	-0.07	10.75	-0.12	-10.56	-0.62	0.02	-221.78	-3.29
cluster4	Linear	4	TBR_2	LIB193826	worst	-66.08	0.00	0.00	66.95	-0.87	-66.08	12.12	0.23	215.40	3.16
cluster4	Linear	4	TBR_1	LIB193826	worst	-58.99	0.00	0.00	59.32	-0.33	-58.99	11.03	0.18	258.81	4.67
cluster4	Linear	4	TIR	LIB193826	worst	2.92	-3.28	-0.10	0.47	0.00	-0.36	-2.78	-0.01	-267.64	-4.49

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	Linear	4	TAR_1	LIB193826	worst	8.19	-7.18	0.00	-0.62	-0.41	1.01	-5.45	-0.03	-634.65	-7.11
cluster4	Linear	4	TAR_2	LIB193826	worst	-3.88	8.53	0.00	-4.65	0.00	4.65	-2.29	-0.01	-349.26	-2.49
cluster4	Linear	6	ALL	LIB194157	best	4.55	-4.93	0.06	0.32	0.00	-0.38	-2.52	-0.01	-282.04	-4.07
cluster4	Linear	6	TBR_2	LIB194157	best										
cluster4	Linear	6	TBR_1	LIB194157	best	-20.00	0.00	0.00	20.00	0.00	-20.00	8.23	0.13	285.32	4.04
cluster4	Linear	6	TIR	LIB194157	best	4.94	-5.07	0.06	0.07	0.00	-0.13	-2.20	-0.01	-181.93	-3.12
cluster4	Linear	6	TAR_1	LIB194157	best	4.26	-4.61	0.00	0.36	0.00	-0.35	-4.89	-0.03	-860.87	-7.97
cluster4	Linear	6	TAR_2	LIB194157	best	-10.00	0.00	0.00	10.00	0.00	-10.00	0.53	0.00	-7.73	-0.05
cluster4	Linear	6	ALL	LIB193826	worst	-5.34	-3.78	-0.52	10.22	-0.57	-9.12	-1.36	0.03	-436.62	-5.04
cluster4	Linear	6	TBR_2	LIB193826	worst	-54.63	0.00	0.00	58.33	-3.70	-54.63	15.94	0.30	60.31	0.53
cluster4	Linear	6	TBR_1	LIB193826	worst	-57.51	0.00	0.00	57.51	0.00	-57.51	18.91	0.31	861.37	10.63
cluster4	Linear	6	TIR	LIB193826	worst	4.89	-4.85	-0.72	0.77	-0.07	0.04	-4.77	-0.02	-496.68	-7.04
cluster4	Linear	6	TAR_1	LIB193826	worst	11.09	-7.11	0.00	-0.63	-3.35	3.98	-10.78	-0.05	-1613.86	-13.98
cluster4	Linear	6	TAR_2	LIB193826	worst	-5.51	11.02	-0.79	-3.94	-0.79	5.51	-0.61	0.00	-1120.88	-5.73
cluster4	Linear	8	ALL	LIB194157	best	2.37	-2.26	-0.34	0.22	0.00	0.11	-3.23	-0.01	-430.24	-5.59
cluster4	Linear	8	TBR_2	LIB194157	best										
cluster4	Linear	8	TBR_1	LIB194157	best	-13.33	0.00	0.00	13.33	0.00	-13.33	3.17	0.05	-221.64	-2.11
cluster4	Linear	8	TIR	LIB194157	best	3.13	-2.79	-0.41	0.07	0.00	0.34	-2.63	-0.01	-271.45	-4.22
cluster4	Linear	8	TAR_1	LIB194157	best	-0.72	0.72	0.00	0.00	0.00	0.00	-6.76	-0.04	-1272.43	-10.66
cluster4	Linear	8	TAR_2	LIB194157	best	0.00	-10.00	0.00	10.00	0.00	-10.00	-3.64	-0.01	-840.82	-4.65
cluster4	Linear	8	ALL	LIB193826	worst	-1.79	-5.17	-0.48	8.69	-1.25	-6.96	-1.50	0.05	-590.16	-5.83
cluster4	Linear	8	TBR_2	LIB193826	worst	-44.55	0.00	0.00	49.51	-4.95	-44.55	20.43	0.39	240.93	1.59
cluster4	Linear	8	TBR_1	LIB193826	worst	-46.61	0.00	0.00	48.39	-1.78	-46.61	25.81	0.42	1485.61	14.64
cluster4	Linear	8	TIR	LIB193826	worst	8.28	-8.09	-0.71	0.56	-0.03	0.19	-5.72	-0.02	-614.90	-7.93
cluster4	Linear	8	TAR_1	LIB193826	worst	7.25	-1.70	0.00	0.42	-5.97	5.55	-14.94	-0.07	-2533.89	-19.01
cluster4	Linear	8	TAR_2	LIB193826	worst	-15.08	16.67	0.00	2.38	-3.97	1.59	-0.97	0.00	-2722.57	-11.26
cluster4	Linear	12	ALL	LIB194157	best	2.64	-2.29	-0.60	0.67	-0.42	0.35	-5.12	-0.02	-800.72	-9.36
cluster4	Linear	12	TBR_2	LIB194157	best										
cluster4	Linear	12	TBR_1	LIB194157	best	0.00	0.00	0.00	40.00	-40.00	0.00	-30.84	-0.49	-6770.28	-36.77
cluster4	Linear	12	TIR	LIB194157	best	3.19	-2.46	-0.73	0.00	0.00	0.73	-3.27	-0.01	-386.48	-5.73
cluster4	Linear	12	TAR_1	LIB194157	best	0.00	-1.53	0.00	1.92	-0.38	-1.53	-12.82	-0.06	-2499.23	-18.24
cluster4	Linear	12	TAR_2	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-20.50	-0.08	-4766.76	-21.28
cluster4	Linear	12	ALL	LIB193838	worst	1.44	-0.57	-2.65	4.41	-2.63	0.87	-5.91	0.02	-1605.53	-11.70
cluster4	Linear	12	TBR_2	LIB193838	worst	-9.09	0.00	0.00	18.18	-9.09	-9.09	16.55	0.32	1383.54	7.31
cluster4	Linear	12	TBR_1	LIB193838	worst	-19.06	0.00	0.00	21.94	-2.87	-19.06	24.25	0.40	1787.49	11.89
cluster4	Linear	12	TIR	LIB193838	worst	6.20	-2.36	-4.07	0.30	-0.07	3.84	-6.96	-0.02	-1155.68	-11.68
cluster4	Linear	12	TAR_1	LIB193838	worst	4.73	4.87	-0.14	1.95	-11.42	9.60	-26.79	-0.13	-5137.56	-30.73

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	Linear	12	TAR_2	LIB193838	worst	-13.93	3.21	0.00	15.71	-5.00	-10.72	-7.35	-0.03	-4876.35	-17.61
cluster4	Linear	16	ALL	LIB194157	best	4.50	-4.11	-0.19	0.45	-0.64	0.39	-5.48	-0.02	-851.22	-9.61
cluster4	Linear	16	TBR_2	LIB194157	best										
cluster4	Linear	16	TBR_1	LIB194157	best	0.00	0.00	0.00	40.00	-40.00	0.00	-21.78	-0.34	-5310.34	-26.34
cluster4	Linear	16	TIR	LIB194157	best	7.94	-7.70	-0.23	0.00	0.00	0.24	-3.99	-0.01	-403.95	-5.95
cluster4	Linear	16	TAR_1	LIB194157	best	-13.06	14.29	0.00	0.41	-1.63	1.23	-11.60	-0.06	-2711.76	-18.93
cluster4	Linear	16	TAR_2	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-23.34	-0.09	-6054.45	-23.94
cluster4	Linear	16	ALL	LIB193838	worst	2.57	-0.85	-3.37	5.46	-3.81	1.72	-6.37	0.03	-1787.23	-12.76
cluster4	Linear	16	TBR_2	LIB193838	worst	-5.33	0.00	0.00	14.67	-9.33	-5.33	25.19	0.48	2616.77	14.85
cluster4	Linear	16	TBR_1	LIB193838	worst	-20.19	0.00	0.00	28.42	-8.23	-20.19	26.92	0.44	1918.67	12.53
cluster4	Linear	16	TIR	LIB193838	worst	8.20	-3.13	-5.18	0.25	-0.14	5.07	-7.53	-0.02	-1284.01	-12.94
cluster4	Linear	16	TAR_1	LIB193838	worst	1.67	11.59	0.00	1.68	-14.94	13.26	-31.06	-0.15	-6245.67	-35.80
cluster4	Linear	16	TAR_2	LIB193838	worst	-7.81	-9.37	0.00	22.26	-5.08	-17.18	-9.05	-0.03	-4981.99	-16.98
cluster4	LSTM	2	ALL	LIB193960	best	20.12	-20.12	0.00	0.00	0.00	0.00	-16.92	-0.06	-1516.15	-26.98
cluster4	LSTM	2	TBR_2	LIB193960	best										
cluster4	LSTM	2	TBR_1	LIB193960	best										
cluster4	LSTM	2	TIR	LIB193960	best	1.12	-1.12	0.00	0.00	0.00	0.00	-0.93	-0.01	-18.76	-0.88
cluster4	LSTM	2	TAR_1	LIB193960	best	8.83	-8.83	0.00	0.00	0.00	0.00	-13.85	-0.06	-656.48	-14.28
cluster4	LSTM	2	TAR_2	LIB193960	best	99.28	-99.28	0.00	0.00	0.00	0.00	-69.84	-0.24	-7690.97	-69.06
cluster4	LSTM	2	ALL	LIB193838	worst	-0.19	0.42	0.00	-0.25	0.02	0.23	-0.41	0.00	-10.02	-0.22
cluster4	LSTM	2	TBR_2	LIB193838	worst	-4.70	0.00	0.00	4.70	0.00	-4.70	0.79	0.01	79.77	1.88
cluster4	LSTM	2	TBR_1	LIB193838	worst	2.15	0.00	0.00	-2.31	0.16	2.15	0.70	0.01	81.13	1.95
cluster4	LSTM	2	TIR	LIB193838	worst	-0.87	0.80	0.00	0.06	0.00	-0.07	0.30	0.00	36.58	0.88
cluster4	LSTM	2	TAR_1	LIB193838	worst	0.24	-0.12	0.00	-0.12	0.00	0.12	-0.89	0.00	-29.24	-0.58
cluster4	LSTM	2	TAR_2	LIB193838	worst	2.35	-1.17	0.00	-1.18	0.00	1.18	-8.56	-0.03	-608.04	-10.21
cluster4	LSTM	4	ALL	LIB193960	best	17.78	-17.71	0.00	-0.06	0.00	0.07	-12.59	-0.05	-1263.74	-17.09
cluster4	LSTM	4	TBR_2	LIB193960	best										
cluster4	LSTM	4	TBR_1	LIB193960	best										
cluster4	LSTM	4	TIR	LIB193960	best	1.60	-1.60	0.00	0.00	0.00	0.00	-0.54	-0.01	-17.88	-0.54
cluster4	LSTM	4	TAR_1	LIB193960	best	11.33	-10.96	0.00	-0.37	0.00	0.37	-10.35	-0.04	-522.82	-7.70
cluster4	LSTM	4	TAR_2	LIB193960	best	77.78	-78.16	0.00	0.39	0.00	-0.38	-51.91	-0.18	-6396.61	-46.07
cluster4	LSTM	4	ALL	LIB193826	worst	-4.14	-0.21	0.09	4.21	0.05	-4.35	1.17	0.03	-5.13	-0.08
cluster4	LSTM	4	TBR_2	LIB193826	worst	-36.52	0.00	0.00	35.65	0.87	-36.52	10.77	0.21	741.03	10.96
cluster4	LSTM	4	TBR_1	LIB193826	worst	-20.91	0.00	0.00	20.75	0.16	-20.91	8.66	0.14	461.82	8.23
cluster4	LSTM	4	TIR	LIB193826	worst	-2.17	1.74	0.14	0.28	0.00	-0.43	0.87	0.01	49.28	0.92
cluster4	LSTM	4	TAR_1	LIB193826	worst	2.46	-2.26	0.00	-0.20	0.00	0.20	-1.36	-0.01	-216.34	-2.61
cluster4	LSTM	4	TAR_2	LIB193826	worst	37.21	-36.43	0.00	-0.78	0.00	0.78	-27.05	-0.09	-3289.89	-20.80

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	6	ALL	LIB194157	best	6.25	-5.31	0.00	-0.93	0.00	0.94	-3.57	-0.02	-334.78	-4.97
cluster4	LSTM	6	TBR_2	LIB194157	best										
cluster4	LSTM	6	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-10.09	-0.16	-826.78	-8.99
cluster4	LSTM	6	TIR	LIB194157	best	-2.90	2.90	0.00	0.00	0.00	0.00	0.89	0.00	99.60	1.98
cluster4	LSTM	6	TAR_1	LIB194157	best	54.96	-51.07	0.00	-3.90	0.00	3.89	-25.80	-0.12	-2373.01	-20.25
cluster4	LSTM	6	TAR_2	LIB194157	best	30.00	30.00	0.00	-60.00	0.00	60.00	-45.25	-0.18	-8058.67	-42.97
cluster4	LSTM	6	ALL	LIB193826	worst	-0.96	0.18	0.15	0.52	0.12	-0.78	1.43	0.04	14.27	0.18
cluster4	LSTM	6	TBR_2	LIB193826	worst	-2.78	0.00	0.00	1.85	0.92	-2.78	11.92	0.23	1247.66	12.00
cluster4	LSTM	6	TBR_1	LIB193826	worst	-4.26	0.00	0.00	3.75	0.52	-4.26	9.71	0.16	727.63	8.65
cluster4	LSTM	6	TIR	LIB193826	worst	-2.37	2.08	0.22	0.03	0.04	-0.29	1.38	0.02	72.88	1.19
cluster4	LSTM	6	TAR_1	LIB193826	worst	3.34	-3.14	0.00	-0.21	0.00	0.20	-4.05	-0.02	-472.45	-4.51
cluster4	LSTM	6	TAR_2	LIB193826	worst	29.92	-27.56	0.00	-2.36	0.00	2.36	-23.89	-0.08	-3759.77	-18.22
cluster4	LSTM	8	ALL	LIB194157	best	9.66	-9.04	0.00	-0.62	0.00	0.62	-4.37	-0.03	-337.88	-4.63
cluster4	LSTM	8	TBR_2	LIB194157	best										
cluster4	LSTM	8	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-26.19	-0.41	-3233.86	-25.55
cluster4	LSTM	8	TIR	LIB194157	best	3.60	-3.60	0.00	0.00	0.00	0.00	-1.39	-0.02	-25.76	-0.46
cluster4	LSTM	8	TAR_1	LIB194157	best	42.75	-39.13	0.00	-3.63	0.00	3.62	-18.21	-0.09	-1641.10	-13.43
cluster4	LSTM	8	TAR_2	LIB194157	best	0.00	10.00	0.00	-10.00	0.00	10.00	-28.84	-0.11	-5906.76	-28.27
cluster4	LSTM	8	ALL	LIB193826	worst	-0.66	2.34	0.18	-2.26	0.41	1.68	1.41	0.05	15.33	0.16
cluster4	LSTM	8	TBR_2	LIB193826	worst	0.00	0.00	0.00	-5.94	5.94	0.00	12.28	0.24	1659.50	12.44
cluster4	LSTM	8	TBR_1	LIB193826	worst	-0.53	0.00	0.00	-0.90	1.43	-0.53	11.29	0.18	1056.35	10.42
cluster4	LSTM	8	TIR	LIB193826	worst	-3.56	3.29	0.26	-0.08	0.07	-0.27	2.05	0.03	147.66	2.27
cluster4	LSTM	8	TAR_1	LIB193826	worst	13.00	-11.09	0.00	-1.92	0.00	1.91	-9.84	-0.05	-1036.71	-8.42
cluster4	LSTM	8	TAR_2	LIB193826	worst	8.73	44.44	0.00	-53.17	0.00	53.17	-22.76	-0.08	-4817.62	-19.12
cluster4	LSTM	12	ALL	LIB194157	best	2.89	-2.46	0.00	-0.43	0.00	0.43	-1.59	-0.01	-165.70	-2.18
cluster4	LSTM	12	TBR_2	LIB194157	best										
cluster4	LSTM	12	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-8.15	-0.13	-1140.82	-7.93
cluster4	LSTM	12	TIR	LIB194157	best	-1.38	1.38	0.00	0.00	0.00	0.00	0.62	0.00	78.32	1.35
cluster4	LSTM	12	TAR_1	LIB194157	best	25.77	-23.47	0.00	-2.30	0.00	2.30	-12.23	-0.06	-1250.72	-9.89
cluster4	LSTM	12	TAR_2	LIB194157	best	0.00	10.00	0.00	-10.00	0.00	10.00	-19.87	-0.08	-4119.24	-18.83
cluster4	LSTM	12	ALL	LIB193826	worst	0.73	0.11	0.16	-1.38	0.38	0.84	2.23	0.07	67.03	0.62
cluster4	LSTM	12	TBR_2	LIB193826	worst	0.00	0.00	0.00	-6.38	6.38	0.00	16.00	0.31	2711.40	17.48
cluster4	LSTM	12	TBR_1	LIB193826	worst	0.00	0.00	0.00	-1.56	1.56	0.00	14.56	0.24	1914.06	14.76
cluster4	LSTM	12	TIR	LIB193826	worst	-3.76	3.52	0.24	0.00	0.00	-0.24	4.27	0.06	364.85	5.30
cluster4	LSTM	12	TAR_1	LIB193826	worst	26.95	-26.28	0.00	-0.66	0.00	0.67	-18.30	-0.09	-2244.75	-16.12
cluster4	LSTM	12	TAR_2	LIB193826	worst	0.84	27.73	0.00	-28.57	0.00	28.57	-27.71	-0.09	-7575.81	-24.68
cluster4	LSTM	16	ALL	LIB194157	best	0.13	-0.12	0.00	0.00	0.00	0.01	0.33	0.01	-29.88	-0.38

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	16	TBR_2	LIB194157	best										
cluster4	LSTM	16	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	9.88	0.15	1677.09	10.57
cluster4	LSTM	16	TIR	LIB194157	best	-3.04	3.03	0.00	0.00	0.00	-0.01	2.22	0.02	169.97	2.90
cluster4	LSTM	16	TAR_1	LIB194157	best	16.73	-16.73	0.00	0.00	0.00	0.00	-9.84	-0.05	-1116.60	-8.56
cluster4	LSTM	16	TAR_2	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.82	-0.03	-1646.73	-7.03
cluster4	LSTM	16	ALL	LIB193838	worst	1.42	-0.94	0.25	-1.28	0.55	0.48	-0.37	0.00	1.14	0.01
cluster4	LSTM	16	TBR_2	LIB193838	worst	0.00	0.00	0.00	-5.33	5.33	0.00	3.98	0.07	1003.03	5.26
cluster4	LSTM	16	TBR_1	LIB193838	worst	0.00	0.00	0.00	-3.55	3.55	0.00	-0.53	-0.01	145.51	0.86
cluster4	LSTM	16	TIR	LIB193838	worst	-1.09	0.71	0.39	-0.04	0.04	-0.38	0.90	0.01	192.27	2.22
cluster4	LSTM	16	TAR_1	LIB193838	worst	14.18	-13.42	0.00	-0.76	0.00	0.76	-2.42	-0.01	-120.52	-0.89
cluster4	LSTM	16	TAR_2	LIB193838	worst	0.00	10.55	0.00	-10.55	0.00	10.55	-10.11	-0.04	-2403.40	-8.66
cluster5	CNN	2	ALL	LIB193368	best	2.96	-2.91	0.00	-0.06	0.00	0.05	-1.28	-0.01	-55.87	-1.15
cluster5	CNN	2	TBR_2	LIB193368	best										
cluster5	CNN	2	TBR_1	LIB193368	best	4.35	0.00	0.00	-4.35	0.00	4.35	-7.24	-0.11	-542.26	-7.19
cluster5	CNN	2	TIR	LIB193368	best	5.04	-4.94	0.00	-0.09	0.00	0.10	-2.05	-0.02	-89.75	-1.93
cluster5	CNN	2	TAR_1	LIB193368	best	0.06	-0.12	0.00	0.06	0.00	-0.06	-0.26	0.00	-10.52	-0.23
cluster5	CNN	2	TAR_2	LIB193368	best	-0.19	0.00	0.00	0.19	0.00	-0.19	0.47	0.00	39.85	0.63
cluster5	CNN	2	ALL	LIB193603	worst	-2.88	-2.31	-0.03	5.22	0.00	-5.19	-0.69	0.01	-115.28	-2.40
cluster5	CNN	2	TBR_2	LIB193603	worst	-29.54	0.00	0.00	29.54	0.00	-29.54	6.71	0.13	195.58	6.15
cluster5	CNN	2	TBR_1	LIB193603	worst	-28.59	0.00	0.00	28.59	0.00	-28.59	5.16	0.08	124.29	3.70
cluster5	CNN	2	TIR	LIB193603	worst	1.97	-2.07	-0.05	0.16	0.00	-0.10	-1.68	-0.01	-142.94	-3.32
cluster5	CNN	2	TAR_1	LIB193603	worst	4.69	-4.69	0.00	0.00	0.00	0.00	-2.38	-0.01	-162.54	-2.74
cluster5	CNN	2	TAR_2	LIB193603	worst	4.27	-4.00	0.00	-0.27	0.00	0.27	-3.24	-0.01	-320.23	-4.57
cluster5	CNN	4	ALL	LIB193368	best	3.19	-3.25	-0.07	0.15	-0.02	-0.06	-1.27	-0.02	-59.53	-0.84
cluster5	CNN	4	TBR_2	LIB193368	best										
cluster5	CNN	4	TBR_1	LIB193368	best	0.00	0.00	0.00	2.18	-2.18	0.00	-7.22	-0.11	-966.22	-7.59
cluster5	CNN	4	TIR	LIB193368	best	8.01	-7.88	-0.13	0.00	0.00	0.13	-3.48	-0.04	-236.02	-3.68
cluster5	CNN	4	TAR_1	LIB193368	best	-3.51	3.25	0.00	0.26	0.00	-0.26	1.41	0.01	136.90	2.05
cluster5	CNN	4	TAR_2	LIB193368	best	-3.93	3.37	0.00	0.56	0.00	-0.56	3.78	0.01	432.67	4.09
cluster5	CNN	4	ALL	LIB193603	worst	-7.76	2.33	-0.20	5.63	0.00	-5.43	2.30	0.04	49.76	0.68
cluster5	CNN	4	TBR_2	LIB193603	worst	-32.18	0.00	0.00	32.18	0.00	-32.18	16.24	0.31	951.88	15.28
cluster5	CNN	4	TBR_1	LIB193603	worst	-29.33	0.00	0.00	29.33	0.00	-29.33	10.69	0.18	454.17	7.22
cluster5	CNN	4	TIR	LIB193603	worst	-4.90	4.74	-0.37	0.53	0.00	-0.16	0.42	0.01	-74.22	-1.20
cluster5	CNN	4	TAR_1	LIB193603	worst	2.65	-2.85	0.00	0.19	0.00	-0.20	-1.41	-0.01	-87.95	-1.03
cluster5	CNN	4	TAR_2	LIB193603	worst	-1.08	1.08	0.00	0.00	0.00	0.00	2.10	0.01	102.87	0.91
cluster5	CNN	6	ALL	LIB193368	best	1.38	-1.74	-0.22	0.60	-0.02	-0.36	-1.04	-0.02	-15.57	-0.18
cluster5	CNN	6	TBR_2	LIB193368	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	6	TBR_1	LIB193368	best	0.00	0.00	0.00	2.18	-2.18	0.00	-11.51	-0.18	-1597.19	-10.43
cluster5	CNN	6	TIR	LIB193368	best	5.55	-5.17	-0.37	0.00	0.00	0.38	-4.14	-0.04	-316.91	-4.30
cluster5	CNN	6	TAR_1	LIB193368	best	-4.72	4.19	0.00	0.53	0.00	-0.53	3.25	0.02	360.65	4.47
cluster5	CNN	6	TAR_2	LIB193368	best	-4.34	0.38	0.00	3.97	0.00	-3.96	4.83	0.02	726.44	5.00
cluster5	CNN	6	ALL	LIB193603	worst	-3.51	2.71	-0.94	1.95	-0.20	-0.80	1.55	0.02	80.51	0.86
cluster5	CNN	6	TBR_2	LIB193603	worst	-3.70	0.00	0.00	4.94	-1.23	-3.70	13.25	0.25	1000.63	10.59
cluster5	CNN	6	TBR_1	LIB193603	worst	-3.66	0.00	0.00	4.63	-0.96	-3.66	5.93	0.10	271.57	2.84
cluster5	CNN	6	TIR	LIB193603	worst	-0.10	1.47	-1.53	0.16	0.00	1.37	-3.28	-0.02	-463.69	-5.97
cluster5	CNN	6	TAR_1	LIB193603	worst	-0.76	0.39	-0.57	1.15	-0.19	-0.37	-0.08	0.00	-4.00	-0.04
cluster5	CNN	6	TAR_2	LIB193603	worst	-24.79	16.89	0.00	7.90	0.00	-7.90	20.10	0.07	2549.52	18.28
cluster5	CNN	8	ALL	LIB193368	best	0.66	-0.88	-0.06	0.33	-0.04	-0.22	-1.21	-0.01	-96.75	-0.97
cluster5	CNN	8	TBR_2	LIB193368	best										
cluster5	CNN	8	TBR_1	LIB193368	best	0.00	0.00	0.00	4.35	-4.35	0.00	-4.74	-0.07	-777.13	-4.67
cluster5	CNN	8	TIR	LIB193368	best	1.04	-0.94	-0.10	0.00	0.00	0.10	-1.74	-0.02	-200.59	-2.53
cluster5	CNN	8	TAR_1	LIB193368	best	-1.45	1.86	0.00	-0.42	0.00	0.41	0.17	0.00	128.52	1.41
cluster5	CNN	8	TAR_2	LIB193368	best	4.38	-8.19	0.00	3.81	0.00	-3.81	-1.80	-0.01	-91.40	-0.50
cluster5	CNN	8	ALL	LIB193603	worst	-4.88	3.76	-0.30	1.61	-0.18	-1.12	5.94	0.07	590.47	5.48
cluster5	CNN	8	TBR_2	LIB193603	worst	-5.13	0.00	0.00	7.69	-2.57	-5.13	18.12	0.34	1533.24	12.55
cluster5	CNN	8	TBR_1	LIB193603	worst	-1.95	0.00	0.00	2.74	-0.78	-1.95	13.38	0.22	1156.74	10.24
cluster5	CNN	8	TIR	LIB193603	worst	-2.92	3.24	-0.48	0.11	0.05	0.32	2.24	0.04	85.28	1.01
cluster5	CNN	8	TAR_1	LIB193603	worst	1.15	-1.54	-0.19	0.77	-0.19	-0.39	-0.73	0.00	-92.58	-0.82
cluster5	CNN	8	TAR_2	LIB193603	worst	-27.82	20.11	0.00	7.71	0.00	-7.71	21.60	0.07	3188.67	18.18
cluster5	CNN	12	ALL	LIB193368	best	0.39	-2.99	-0.32	3.09	-0.17	-2.60	-0.94	-0.04	93.61	0.81
cluster5	CNN	12	TBR_2	LIB193368	best										
cluster5	CNN	12	TBR_1	LIB193368	best	0.00	0.00	0.00	17.39	-17.39	0.00	-18.48	-0.28	-3532.84	-18.31
cluster5	CNN	12	TIR	LIB193368	best	12.89	-12.33	-0.55	0.00	0.00	0.56	-10.79	-0.10	-1045.61	-11.86
cluster5	CNN	12	TAR_1	LIB193368	best	-22.05	19.49	0.00	2.57	0.00	-2.56	13.06	0.06	1303.31	13.32
cluster5	CNN	12	TAR_2	LIB193368	best	-6.22	-13.40	0.00	19.62	0.00	-19.62	15.61	0.06	3239.17	14.67
cluster5	CNN	12	ALL	LIB193603	worst	-3.23	0.55	-0.85	4.06	-0.51	-2.68	5.01	0.04	751.21	5.88
cluster5	CNN	12	TBR_2	LIB193603	worst	-1.37	0.00	0.00	5.48	-4.11	-1.37	14.35	0.27	1579.12	10.28
cluster5	CNN	12	TBR_1	LIB193603	worst	-0.20	0.00	0.00	2.84	-2.63	-0.20	6.53	0.11	625.45	4.36
cluster5	CNN	12	TIR	LIB193603	worst	0.11	1.36	-1.47	0.05	-0.05	1.47	-0.75	0.00	-208.72	-2.29
cluster5	CNN	12	TAR_1	LIB193603	worst	-5.24	4.85	-0.19	0.59	0.00	-0.39	4.36	0.02	492.57	4.02
cluster5	CNN	12	TAR_2	LIB193603	worst	-22.13	-8.96	0.00	31.09	0.00	-31.09	31.70	0.11	6081.58	26.76
cluster5	CNN	16	ALL	LIB193795	best	-0.97	0.81	-0.03	0.24	-0.06	-0.16	1.34	0.03	67.64	0.65
cluster5	CNN	16	TBR_2	LIB193795	best	0.00	0.00	0.00	2.44	-2.44	0.00	14.97	0.28	2362.64	13.80
cluster5	CNN	16	TBR_1	LIB193795	best	0.00	0.00	0.00	1.00	-1.00	0.00	10.24	0.17	1522.20	9.54

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	CNN	16	TIR	LIB193795	best	-3.18	3.21	-0.04	0.00	0.00	0.03	2.96	0.04	243.68	3.33
cluster5	CNN	16	TAR_1	LIB193795	best	7.82	-8.09	0.00	0.26	0.00	-0.27	-6.97	-0.03	-884.92	-7.24
cluster5	CNN	16	TAR_2	LIB193795	best	-2.18	-0.82	0.00	3.00	0.00	-3.00	-2.06	-0.01	-723.18	-2.83
cluster5	CNN	16	ALL	LIB193603	worst	-2.68	0.29	-0.22	3.03	-0.41	-2.39	5.60	0.06	804.62	5.77
cluster5	CNN	16	TBR_2	LIB193603	worst	0.00	0.00	0.00	2.86	-2.86	0.00	14.10	0.27	1839.66	10.80
cluster5	CNN	16	TBR_1	LIB193603	worst	-0.21	0.00	0.00	2.98	-2.77	-0.21	7.47	0.13	780.06	4.82
cluster5	CNN	16	TIR	LIB193603	worst	-3.11	3.49	-0.38	-0.11	0.11	0.38	3.47	0.05	267.49	2.93
cluster5	CNN	16	TAR_1	LIB193603	worst	-1.97	1.19	0.00	0.78	0.00	-0.78	1.72	0.01	162.09	1.25
cluster5	CNN	16	TAR_2	LIB193603	worst	-5.37	-16.95	0.00	22.31	0.00	-22.32	17.82	0.06	4291.55	16.35
cluster5	Linear	2	ALL	LIB194036	best	1.63	-1.57	-0.03	-0.02	0.00	0.06	-0.64	0.00	-39.77	-0.84
cluster5	Linear	2	TBR_2	LIB194036	best	0.00	0.00	0.00	0.00	0.00	0.00	5.58	0.11	195.89	4.09
cluster5	Linear	2	TBR_1	LIB194036	best	20.00	0.00	0.00	-20.00	0.00	20.00	-1.26	-0.02	-51.81	-0.76
cluster5	Linear	2	TIR	LIB194036	best	1.94	-1.88	-0.05	0.00	0.00	0.06	-0.95	-0.01	-62.06	-1.49
cluster5	Linear	2	TAR_1	LIB194036	best	1.82	-1.82	0.00	0.00	0.00	0.00	-0.86	0.00	-45.88	-0.88
cluster5	Linear	2	TAR_2	LIB194036	best	-0.44	0.45	0.00	0.00	0.00	0.01	1.25	0.00	72.94	1.28
cluster5	Linear	2	ALL	LIB193603	worst	11.03	-12.39	-0.03	1.39	0.00	-1.36	-5.74	-0.03	-362.35	-9.13
cluster5	Linear	2	TBR_2	LIB193603	worst	1.14	0.00	0.00	-1.14	0.00	1.14	5.41	0.10	55.39	3.44
cluster5	Linear	2	TBR_1	LIB193603	worst	-9.53	0.00	0.00	9.53	0.00	-9.53	2.75	0.05	5.47	0.26
cluster5	Linear	2	TIR	LIB193603	worst	16.30	-16.40	-0.05	0.16	0.00	-0.10	-6.56	-0.05	-353.42	-9.47
cluster5	Linear	2	TAR_1	LIB193603	worst	17.26	-16.51	0.00	-0.75	0.00	0.75	-11.35	-0.05	-721.29	-13.89
cluster5	Linear	2	TAR_2	LIB193603	worst	6.67	-6.40	0.00	-0.27	0.00	0.27	-8.26	-0.03	-520.99	-9.91
cluster5	Linear	4	ALL	LIB193368	best	3.91	-3.97	-0.07	0.15	-0.02	-0.06	-2.03	-0.01	-217.85	-3.32
cluster5	Linear	4	TBR_2	LIB193368	best										
cluster5	Linear	4	TBR_1	LIB193368	best	-19.57	0.00	0.00	21.74	-2.17	-19.57	3.22	0.05	-98.92	-1.02
cluster5	Linear	4	TIR	LIB193368	best	4.31	-4.27	-0.13	0.10	0.00	0.04	-3.27	-0.02	-272.54	-4.52
cluster5	Linear	4	TAR_1	LIB193368	best	6.44	-6.45	0.00	0.00	0.00	-0.01	-3.29	-0.02	-371.91	-5.78
cluster5	Linear	4	TAR_2	LIB193368	best	-3.75	4.68	0.00	-0.94	0.00	0.93	8.19	0.03	530.95	5.89
cluster5	Linear	4	ALL	LIB193603	worst	-11.61	-2.74	-0.11	14.46	0.00	-14.35	0.66	0.04	-165.31	-2.53
cluster5	Linear	4	TBR_2	LIB193603	worst	-90.80	0.00	0.00	90.80	0.00	-90.80	21.24	0.40	667.48	17.97
cluster5	Linear	4	TBR_1	LIB193603	worst	-77.14	0.00	0.00	77.14	0.00	-77.14	15.65	0.26	490.72	11.58
cluster5	Linear	4	TIR	LIB193603	worst	2.29	-3.24	-0.21	1.14	0.00	-0.95	-2.98	-0.01	-303.85	-5.32
cluster5	Linear	4	TAR_1	LIB193603	worst	11.37	-10.79	0.00	-0.57	0.00	0.58	-7.14	-0.03	-776.12	-9.16
cluster5	Linear	4	TAR_2	LIB193603	worst	-4.85	6.74	0.00	-1.89	0.00	1.89	4.51	0.01	296.61	3.11
cluster5	Linear	6	ALL	LIB193368	best	3.35	-2.83	-0.32	-0.06	-0.14	0.52	-2.97	-0.01	-418.44	-4.79
cluster5	Linear	6	TBR_2	LIB193368	best										
cluster5	Linear	6	TBR_1	LIB193368	best	-10.87	0.00	0.00	13.05	-2.17	-10.87	6.37	0.09	-3.92	-0.03
cluster5	Linear	6	TIR	LIB193368	best	5.38	-4.90	-0.54	0.11	-0.03	0.48	-4.13	-0.02	-402.05	-5.53

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	Linear	6	TAR_1	LIB193368	best	9.17	-9.11	0.00	0.26	-0.33	0.06	-5.92	-0.03	-840.06	-9.44
cluster5	Linear	6	TAR_2	LIB193368	best	-23.25	26.28	0.00	-3.03	0.00	3.03	11.05	0.04	653.15	4.76
cluster5	Linear	6	ALL	LIB193603	worst	-14.76	2.24	-1.32	14.20	-0.35	-12.52	2.52	0.07	-219.04	-2.41
cluster5	Linear	6	TBR_2	LIB193603	worst	-81.48	0.00	0.00	81.48	0.00	-81.48	32.05	0.61	1567.28	25.26
cluster5	Linear	6	TBR_1	LIB193603	worst	-77.07	0.00	0.00	77.45	-0.39	-77.07	26.12	0.43	1257.99	18.20
cluster5	Linear	6	TIR	LIB193603	worst	1.32	-0.74	-1.84	1.26	0.00	0.58	-4.13	-0.01	-590.68	-7.83
cluster5	Linear	6	TAR_1	LIB193603	worst	8.61	-4.21	-1.91	-0.57	-1.91	4.40	-12.51	-0.06	-1990.66	-17.13
cluster5	Linear	6	TAR_2	LIB193603	worst	-28.61	30.51	0.00	-1.90	0.00	1.90	18.55	0.06	1749.66	12.76
cluster5	Linear	8	ALL	LIB193368	best	1.05	-1.16	-0.43	0.75	-0.20	-0.11	-2.23	-0.01	-397.51	-3.90
cluster5	Linear	8	TBR_2	LIB193368	best										
cluster5	Linear	8	TBR_1	LIB193368	best	-13.04	0.00	0.00	21.74	-8.70	-13.04	9.95	0.15	398.27	2.63
cluster5	Linear	8	TIR	LIB193368	best	6.96	-6.27	-0.73	0.07	-0.03	0.69	-5.39	-0.02	-569.34	-7.28
cluster5	Linear	8	TAR_1	LIB193368	best	1.38	-2.35	0.00	1.10	-0.14	-0.97	-3.78	-0.02	-874.93	-8.39
cluster5	Linear	8	TAR_2	LIB193368	best	-31.05	29.91	0.00	1.72	-0.57	-1.14	18.34	0.06	1791.02	10.17
cluster5	Linear	8	ALL	LIB193603	worst	-11.80	1.75	-2.17	13.70	-1.49	-10.05	0.38	0.07	-724.54	-6.35
cluster5	Linear	8	TBR_2	LIB193603	worst	-75.64	0.00	0.00	75.64	0.00	-75.64	37.24	0.71	2305.23	25.95
cluster5	Linear	8	TBR_1	LIB193603	worst	-70.51	0.00	0.00	71.29	-0.78	-70.51	31.89	0.53	1914.83	21.26
cluster5	Linear	8	TIR	LIB193603	worst	5.53	-3.40	-3.40	1.33	-0.05	2.13	-8.22	-0.03	-1233.97	-13.78
cluster5	Linear	8	TAR_1	LIB193603	worst	8.44	-0.20	-1.73	1.54	-8.06	8.24	-17.76	-0.09	-3373.38	-24.22
cluster5	Linear	8	TAR_2	LIB193603	worst	-34.16	34.16	0.00	0.83	-0.83	0.00	18.65	0.06	1344.59	7.14
cluster5	Linear	12	ALL	LIB193427	best	6.05	-4.26	-1.75	0.17	-0.21	1.79	-9.10	-0.04	-1675.17	-13.01
cluster5	Linear	12	TBR_2	LIB193427	best										
cluster5	Linear	12	TBR_1	LIB193427	best	0.00	0.00	0.00	9.26	-9.26	0.00	11.68	0.19	729.27	3.89
cluster5	Linear	12	TIR	LIB193427	best	7.26	-4.48	-2.74	0.00	-0.03	2.78	-5.55	-0.02	-741.40	-8.20
cluster5	Linear	12	TAR_1	LIB193427	best	7.55	-8.55	0.00	1.15	-0.15	-1.00	-16.63	-0.08	-2781.28	-20.71
cluster5	Linear	12	TAR_2	LIB193427	best	-9.61	13.82	0.00	-3.60	-0.60	4.21	-14.94	-0.05	-6140.60	-21.31
cluster5	Linear	12	ALL	LIB193603	worst	-5.21	0.80	-3.20	12.10	-4.48	-4.41	-3.20	0.08	-1777.83	-12.33
cluster5	Linear	12	TBR_2	LIB193603	worst	-46.58	0.00	0.00	46.58	0.00	-46.58	49.21	0.93	4657.56	38.69
cluster5	Linear	12	TBR_1	LIB193603	worst	-52.54	0.00	0.00	54.97	-2.43	-52.54	41.34	0.68	3135.27	25.71
cluster5	Linear	12	TIR	LIB193603	worst	9.23	-4.62	-5.59	1.14	-0.16	4.61	-10.37	-0.03	-1739.68	-16.30
cluster5	Linear	12	TAR_1	LIB193603	worst	1.16	14.56	-0.39	4.27	-19.61	15.72	-25.70	-0.13	-5639.05	-35.47
cluster5	Linear	12	TAR_2	LIB193603	worst	-15.13	10.08	0.00	13.72	-8.68	-5.05	-5.94	-0.02	-4505.26	-17.14
cluster5	Linear	16	ALL	LIB193427	best	7.45	-4.91	-3.18	1.52	-0.88	2.54	-12.60	-0.07	-2209.43	-16.52
cluster5	Linear	16	TBR_2	LIB193427	best										
cluster5	Linear	16	TBR_1	LIB193427	best	-5.66	0.00	0.00	15.09	-9.43	-5.66	10.62	0.17	379.64	2.00
cluster5	Linear	16	TIR	LIB193427	best	12.25	-7.50	-4.78	0.03	0.00	4.75	-11.30	-0.07	-1469.90	-15.38
cluster5	Linear	16	TAR_1	LIB193427	best	0.79	-0.40	-0.40	2.22	-2.22	0.39	-16.39	-0.08	-3234.46	-23.05

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	Linear	16	TAR_2	LIB193427	best	-7.89	0.00	0.00	10.09	-2.21	-7.89	-13.33	-0.05	-5343.35	-18.07
cluster5	Linear	16	ALL	LIB193603	worst	-0.41	-0.44	-4.02	12.95	-8.08	-0.85	-8.70	0.06	-3180.36	-19.39
cluster5	Linear	16	TBR_2	LIB193603	worst	-35.71	0.00	0.00	35.71	0.00	-35.71	51.32	0.97	5585.40	41.04
cluster5	Linear	16	TBR_1	LIB193603	worst	-39.36	0.00	0.00	42.13	-2.77	-39.36	42.03	0.69	3497.68	24.62
cluster5	Linear	16	TIR	LIB193603	worst	12.19	-6.04	-7.15	1.16	-0.17	6.15	-13.16	-0.05	-2126.74	-18.66
cluster5	Linear	16	TAR_1	LIB193603	worst	1.19	23.27	0.00	8.28	-32.74	24.46	-33.33	-0.16	-7869.96	-45.32
cluster5	Linear	16	TAR_2	LIB193603	worst	-8.19	-6.49	0.00	36.44	-21.75	-14.68	-29.90	-0.10	-12435.87	-39.38
cluster5	LSTM	2	ALL	LIB194054	best	0.90	-0.74	0.00	-0.16	0.00	0.16	-0.90	0.00	-56.66	-1.24
cluster5	LSTM	2	TBR_2	LIB194054	best										
cluster5	LSTM	2	TBR_1	LIB194054	best	58.34	0.00	0.00	-58.34	0.00	58.34	-11.32	-0.17	-512.76	-10.64
cluster5	LSTM	2	TIR	LIB194054	best	0.92	-0.92	0.00	0.00	0.00	0.00	-0.44	-0.01	-14.84	-0.37
cluster5	LSTM	2	TAR_1	LIB194054	best	0.37	-0.36	0.00	0.00	0.00	0.01	-0.33	0.00	-9.43	-0.21
cluster5	LSTM	2	TAR_2	LIB194054	best	0.89	-0.77	0.00	-0.12	0.00	0.12	-3.32	-0.01	-277.21	-4.50
cluster5	LSTM	2	ALL	LIB193603	worst	-1.39	-1.13	0.00	2.52	0.00	-2.52	-1.58	0.01	-169.15	-4.93
cluster5	LSTM	2	TBR_2	LIB193603	worst	-12.50	0.00	0.00	12.50	0.00	-12.50	4.70	0.09	75.23	5.12
cluster5	LSTM	2	TBR_1	LIB193603	worst	-13.27	0.00	0.00	13.27	0.00	-13.27	2.98	0.05	63.45	3.44
cluster5	LSTM	2	TIR	LIB193603	worst	-0.99	0.73	0.00	0.26	0.00	-0.26	0.25	0.00	-3.82	-0.14
cluster5	LSTM	2	TAR_1	LIB193603	worst	0.38	-0.38	0.00	0.00	0.00	0.00	0.53	0.00	21.11	0.59
cluster5	LSTM	2	TAR_2	LIB193603	worst	13.60	-13.60	0.00	0.00	0.00	0.00	-22.01	-0.07	-1681.01	-25.76
cluster5	LSTM	4	ALL	LIB193368	best	1.61	-1.73	0.00	0.12	0.00	-0.12	-0.71	-0.01	-48.91	-0.82
cluster5	LSTM	4	TBR_2	LIB193368	best										
cluster5	LSTM	4	TBR_1	LIB193368	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.16	-0.11	-629.37	-6.34
cluster5	LSTM	4	TIR	LIB193368	best	3.61	-3.57	0.00	-0.03	0.00	0.04	-1.33	-0.02	-62.63	-1.17
cluster5	LSTM	4	TAR_1	LIB193368	best	-2.04	1.91	0.00	0.13	0.00	-0.13	1.38	0.01	103.24	1.84
cluster5	LSTM	4	TAR_2	LIB193368	best	1.31	-2.24	0.00	0.94	0.00	-0.93	-2.78	-0.01	-368.30	-4.09
cluster5	LSTM	4	ALL	LIB193603	worst	-8.22	0.99	0.00	7.23	0.00	-7.23	1.40	0.03	-5.01	-0.08
cluster5	LSTM	4	TBR_2	LIB193603	worst	-41.38	0.00	0.00	41.38	0.00	-41.38	14.45	0.27	567.24	13.16
cluster5	LSTM	4	TBR_1	LIB193603	worst	-37.91	0.00	0.00	37.91	0.00	-37.91	10.13	0.17	378.97	8.69
cluster5	LSTM	4	TIR	LIB193603	worst	-1.62	1.15	0.00	0.47	0.00	-0.47	-0.69	0.00	-117.80	-2.25
cluster5	LSTM	4	TAR_1	LIB193603	worst	-5.12	4.93	0.00	0.19	0.00	-0.19	3.32	0.01	256.04	3.75
cluster5	LSTM	4	TAR_2	LIB193603	worst	2.97	-3.77	0.00	0.81	0.00	-0.80	-5.96	-0.02	-471.05	-4.97
cluster5	LSTM	6	ALL	LIB193368	best	0.90	-1.11	-0.16	0.40	-0.02	-0.21	-0.40	-0.01	-16.02	-0.20
cluster5	LSTM	6	TBR_2	LIB193368	best										
cluster5	LSTM	6	TBR_1	LIB193368	best	0.00	0.00	0.00	2.17	-2.17	0.00	-9.35	-0.14	-1159.89	-8.42
cluster5	LSTM	6	TIR	LIB193368	best	3.54	-3.27	-0.27	0.00	0.00	0.27	-2.01	-0.03	-153.53	-2.33
cluster5	LSTM	6	TAR_1	LIB193368	best	-3.93	3.46	0.00	0.46	0.00	-0.47	2.96	0.01	274.94	3.64
cluster5	LSTM	6	TAR_2	LIB193368	best	0.00	-2.26	0.00	2.27	0.00	-2.26	-0.19	0.00	20.23	0.15

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	6	ALL	LIB193603	worst	-7.37	2.30	-0.09	5.25	-0.09	-5.07	2.56	0.05	88.22	1.05
cluster5	LSTM	6	TBR_2	LIB193603	worst	-34.57	0.00	0.00	34.57	0.00	-34.57	20.43	0.39	1487.36	20.55
cluster5	LSTM	6	TBR_1	LIB193603	worst	-21.58	0.00	0.00	21.96	-0.38	-21.58	13.88	0.23	821.98	11.15
cluster5	LSTM	6	TIR	LIB193603	worst	-5.57	5.15	-0.15	0.58	0.00	-0.42	-0.09	0.01	-147.28	-2.18
cluster5	LSTM	6	TAR_1	LIB193603	worst	-10.13	8.61	0.00	1.72	-0.19	-1.52	6.00	0.03	485.86	5.40
cluster5	LSTM	6	TAR_2	LIB193603	worst	13.36	-17.71	0.00	4.36	0.00	-4.35	-8.56	-0.03	-603.80	-4.19
cluster5	LSTM	8	ALL	LIB193368	best	0.19	-0.81	-0.23	0.90	-0.04	-0.62	-0.50	-0.01	2.42	0.03
cluster5	LSTM	8	TBR_2	LIB193368	best										
cluster5	LSTM	8	TBR_1	LIB193368	best	0.00	0.00	0.00	2.17	-2.17	0.00	-10.46	-0.16	-1604.86	-10.18
cluster5	LSTM	8	TIR	LIB193368	best	2.85	-2.47	-0.39	0.03	-0.03	0.38	-2.47	-0.03	-217.83	-2.95
cluster5	LSTM	8	TAR_1	LIB193368	best	-5.93	5.31	0.00	0.62	0.00	-0.62	3.94	0.02	456.56	5.30
cluster5	LSTM	8	TAR_2	LIB193368	best	2.47	-8.76	0.00	6.29	0.00	-6.29	-1.12	0.00	93.42	0.54
cluster5	LSTM	8	ALL	LIB193603	worst	-3.21	-0.27	0.06	3.69	-0.27	-3.48	3.02	0.06	160.80	1.56
cluster5	LSTM	8	TBR_2	LIB193603	worst	-15.38	0.00	0.00	16.67	-1.28	-15.38	27.32	0.52	2258.51	22.64
cluster5	LSTM	8	TBR_1	LIB193603	worst	-9.96	0.00	0.00	11.13	-1.17	-9.96	17.45	0.29	1237.96	12.48
cluster5	LSTM	8	TIR	LIB193603	worst	-2.13	1.75	0.11	0.27	0.00	-0.38	-0.23	0.01	-101.41	-1.30
cluster5	LSTM	8	TAR_1	LIB193603	worst	-17.08	15.93	0.00	1.54	-0.38	-1.15	5.81	0.03	562.13	5.38
cluster5	LSTM	8	TAR_2	LIB193603	worst	23.14	-34.44	0.00	11.30	0.00	-11.30	-9.68	-0.03	-1025.86	-5.54
cluster5	LSTM	12	ALL	LIB193368	best	2.24	-2.96	0.00	0.77	-0.04	-0.72	-1.66	-0.03	-61.92	-0.55
cluster5	LSTM	12	TBR_2	LIB193368	best										
cluster5	LSTM	12	TBR_1	LIB193368	best	0.00	0.00	0.00	4.35	-4.35	0.00	-13.74	-0.21	-2319.72	-12.61
cluster5	LSTM	12	TIR	LIB193368	best	6.13	-6.13	0.00	0.00	0.00	0.00	-5.56	-0.06	-516.00	-6.24
cluster5	LSTM	12	TAR_1	LIB193368	best	-7.11	6.96	0.00	0.14	0.00	-0.15	5.88	0.03	736.75	7.41
cluster5	LSTM	12	TAR_2	LIB193368	best	6.60	-12.81	0.00	6.21	0.00	-6.21	0.15	0.00	425.51	1.92
cluster5	LSTM	12	ALL	LIB193603	worst	-0.91	-1.49	0.54	2.07	-0.21	-2.40	3.99	0.05	538.40	4.32
cluster5	LSTM	12	TBR_2	LIB193603	worst	0.00	0.00	0.00	2.74	-2.74	0.00	21.35	0.40	2322.38	16.36
cluster5	LSTM	12	TBR_1	LIB193603	worst	-0.81	0.00	0.00	1.42	-0.61	-0.81	11.25	0.19	1166.92	8.66
cluster5	LSTM	12	TIR	LIB193603	worst	-0.38	-0.60	0.98	0.11	-0.11	-0.98	0.97	0.02	100.44	1.14
cluster5	LSTM	12	TAR_1	LIB193603	worst	-6.21	5.24	0.00	0.97	0.00	-0.97	5.59	0.03	732.43	6.33
cluster5	LSTM	12	TAR_2	LIB193603	worst	3.64	-18.21	0.00	14.57	0.00	-14.57	3.74	0.01	1285.48	5.52
cluster5	LSTM	16	ALL	LIB193795	best	-0.54	0.26	-0.06	0.38	-0.05	-0.28	1.39	0.03	66.42	0.65
cluster5	LSTM	16	TBR_2	LIB193795	best	0.00	0.00	0.00	0.00	0.00	0.00	17.04	0.32	2669.99	16.12
cluster5	LSTM	16	TBR_1	LIB193795	best	0.00	0.00	0.00	1.00	-1.00	0.00	11.79	0.19	1722.66	11.11
cluster5	LSTM	16	TIR	LIB193795	best	-2.89	2.98	-0.08	0.00	0.00	0.09	3.14	0.04	267.85	3.70
cluster5	LSTM	16	TAR_1	LIB193795	best	8.35	-8.75	0.00	0.40	0.00	-0.40	-7.53	-0.04	-958.87	-7.90
cluster5	LSTM	16	TAR_2	LIB193795	best	0.54	-6.54	0.00	6.00	0.00	-6.00	-3.66	-0.01	-1092.81	-4.34
cluster5	LSTM	16	ALL	LIB193603	worst	0.22	1.43	0.41	-2.59	0.53	1.65	-0.24	0.00	-41.67	-0.29

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	16	TBR_2	LIB193603	worst	0.00	0.00	0.00	0.00	0.00	0.00	-0.06	0.00	11.71	0.07
cluster5	LSTM	16	TBR_1	LIB193603	worst	0.00	0.00	0.00	-3.19	3.19	0.00	-1.98	-0.03	-129.19	-0.79
cluster5	LSTM	16	TIR	LIB193603	worst	-5.37	4.65	0.72	-0.11	0.11	-0.72	3.14	0.02	350.01	3.86
cluster5	LSTM	16	TAR_1	LIB193603	worst	20.32	-17.35	0.00	-2.96	0.00	2.97	-5.97	-0.03	-301.02	-2.26
cluster5	LSTM	16	TAR_2	LIB193603	worst	0.28	14.12	0.00	-14.41	0.00	14.40	-7.00	-0.02	-1561.68	-5.60

Appendix H

Absolute difference between group-based prediction models and personalized prediction models performance in TBR ranges for worst predicted patients

Table H.1 presents the absolute difference between the metrics performance results for the group-based prediction models and the personalized prediction models in TBR ranges for patients worst predicted by the group-based prediction models. The "Patient" column indicates the identifier of the patient whose results are displayed, and the "Type" column specifies the patient classification by the corresponding group-based model; in this case, only the worst-predicted patients are displayed.

It is important to note that from the outcome of this comparison for the percentage of measurements in the zone 'A + B', which is a maximization metric, positive values indicate that the group-based prediction models perform better, negative values indicate worse performance, and zero means equal performance between both types of models. The effect of minimization metrics (RMSE, MSE, MAE, and MAPE) is reversed, where positive values reflect worse performance for group-based models, negative values indicate better performance, and zero means equal results. Therefore, the tables generated from this subtraction process are formatted for a more explicit comparison. To improve clarity, the cells corresponding to these key metrics, particularly 'A + B' and all non-clinical metrics, are color-coded: green represents better results for group-based models, red represents worse results, and gray indicates equal performance for both model types.

Table H.1: Absolute difference between group-based prediction models and personalized prediction models performance in the TBR BGL ranges and for worst predicted patients assessed via both clinical and non-clinical metrics for all clusters. Green: better for group-based models, red: worse, gray: equal.

Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	2	TBR_2	LIB193526	worst	-38.66	0.00	0.00	38.66	0.00	-38.66	7.51	0.15	311.00	6.73
cluster0	CNN	2	TBR_1	LIB193526	worst	-25.11	0.00	0.00	25.11	0.00	-25.11	5.20	0.09	198.73	4.17
cluster0	CNN	4	TBR_2	LIB193526	worst	-22.72	0.00	0.00	22.72	0.00	-22.72	13.18	0.27	931.32	12.22
cluster0	CNN	4	TBR_1	LIB193526	worst	-16.53	0.00	0.00	16.28	0.23	-16.53	11.76	0.20	713.03	9.67
cluster0	CNN	6	TBR_2	LIB193526	worst	-0.24	0.00	0.00	0.24	0.00	-0.24	11.25	0.23	1054.54	10.53
cluster0	CNN	6	TBR_1	LIB193526	worst	-1.46	0.00	0.00	1.62	-0.16	-1.46	9.29	0.16	720.55	7.60
cluster0	CNN	8	TBR_2	LIB193526	worst	-0.25	0.00	0.00	0.13	0.12	-0.25	16.72	0.34	1896.49	15.23
cluster0	CNN	8	TBR_1	LIB193526	worst	-0.68	0.00	0.00	0.85	-0.17	-0.68	15.13	0.25	1479.16	12.90
cluster0	CNN	12	TBR_2	LIB193526	worst	-0.13	0.00	0.00	-0.13	0.26	-0.13	15.29	0.31	2196.56	14.25
cluster0	CNN	12	TBR_1	LIB193526	worst	-0.27	0.00	0.00	-0.18	0.46	-0.27	14.12	0.23	1741.92	12.44
cluster0	CNN	16	TBR_2	LIB193326	worst	0.00	0.00	0.00	100.00	-100.00	0.00	-47.21	-0.89	-12636.04	-47.21
cluster0	CNN	16	TBR_1	LIB193326	worst	0.00	0.00	0.00	51.16	-51.16	0.00	-33.00	-0.53	-7321.21	-34.34
cluster0	Linear	2	TBR_2	LIB194097	worst	-0.81	0.00	0.00	0.81	0.00	-0.81	0.85	0.02	-25.93	-0.85
cluster0	Linear	2	TBR_1	LIB194097	worst	-3.50	0.00	0.00	3.50	0.00	-3.50	0.63	0.01	10.27	0.28
cluster0	Linear	4	TBR_2	LIB193526	worst	-63.82	0.00	0.00	63.82	0.00	-63.82	16.17	0.33	580.74	12.12
cluster0	Linear	4	TBR_1	LIB193526	worst	-54.18	0.00	0.00	54.27	-0.08	-54.18	11.80	0.20	440.61	8.20
cluster0	Linear	6	TBR_2	LIB193526	worst	-74.40	0.00	0.00	74.52	-0.12	-74.40	28.86	0.59	1576.94	21.50
cluster0	Linear	6	TBR_1	LIB193526	worst	-57.85	0.00	0.00	58.01	-0.16	-57.85	22.72	0.38	1207.41	15.70
cluster0	Linear	8	TBR_2	LIB193526	worst	-67.40	0.00	0.00	67.64	-0.24	-67.40	37.14	0.75	2494.40	26.84
cluster0	Linear	8	TBR_1	LIB193526	worst	-53.73	0.00	0.00	54.33	-0.60	-53.73	29.63	0.49	1868.05	20.15
cluster0	Linear	12	TBR_2	LIB193526	worst	-54.88	0.00	0.00	56.30	-1.42	-54.88	48.15	0.98	4260.34	33.80
cluster0	Linear	12	TBR_1	LIB193526	worst	-42.61	0.00	0.00	44.16	-1.55	-42.61	38.65	0.64	3124.31	25.69
cluster0	Linear	16	TBR_2	LIB193526	worst	-40.19	0.00	0.00	43.50	-3.31	-40.19	46.80	0.95	4687.37	31.83
cluster0	Linear	16	TBR_1	LIB193526	worst	-32.50	0.00	0.00	36.38	-3.87	-32.50	38.19	0.63	3419.20	24.74
cluster0	LSTM	2	TBR_2	LIB193526	worst	-11.00	0.00	0.00	11.00	0.00	-11.00	4.17	0.08	117.36	4.59
cluster0	LSTM	2	TBR_1	LIB193526	worst	-16.11	0.00	0.00	16.19	-0.08	-16.11	2.95	0.05	83.57	2.88
cluster0	LSTM	4	TBR_2	LIB193526	worst	-31.50	0.00	0.00	31.50	0.00	-31.50	9.98	0.20	556.57	9.43
cluster0	LSTM	4	TBR_1	LIB193526	worst	-17.23	0.00	0.00	17.07	0.16	-17.23	7.60	0.13	400.50	6.89
cluster0	LSTM	6	TBR_2	LIB193526	worst	-16.11	0.00	0.00	16.11	0.00	-16.11	14.70	0.30	1114.74	13.21
cluster0	LSTM	6	TBR_1	LIB193526	worst	-9.52	0.00	0.00	9.77	-0.24	-9.52	10.63	0.18	711.79	8.75
cluster0	LSTM	8	TBR_2	LIB193526	worst	-3.92	0.00	0.00	4.05	-0.13	-3.92	16.05	0.33	1642.97	14.85
cluster0	LSTM	8	TBR_1	LIB193526	worst	-1.61	0.00	0.00	1.78	-0.17	-1.61	13.75	0.23	1222.89	11.67

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	12	TBR_2	LIB193526	worst	-0.26	0.00	0.00	0.26	0.00	-0.26	17.03	0.34	2241.77	15.43
cluster0	LSTM	12	TBR_1	LIB193526	worst	-0.36	0.00	0.00	0.73	-0.36	-0.36	16.03	0.27	1832.66	13.90
cluster0	LSTM	16	TBR_2	LIB193526	worst	0.00	0.00	0.00	-0.41	0.41	0.00	16.34	0.33	2588.62	15.50
cluster0	LSTM	16	TBR_1	LIB193526	worst	0.00	0.00	0.00	-0.59	0.59	0.00	15.61	0.26	2164.19	14.25
cluster1	CNN	2	TBR_2	LIB193821	worst	-40.00	0.00	0.00	40.00	0.00	-40.00	9.28	0.22	503.88	5.38
cluster1	CNN	2	TBR_1	LIB193821	worst	-8.34	0.00	0.00	8.34	0.00	-8.34	2.67	0.05	181.08	3.26
cluster1	CNN	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	17.00	0.34	2132.78	16.92
cluster1	CNN	4	TBR_1	LIB193821	worst	-29.66	0.00	0.00	29.66	0.00	-29.66	8.59	0.14	505.26	6.26
cluster1	CNN	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	8.97	0.19	1207.21	9.13
cluster1	CNN	6	TBR_1	LIB193821	worst	-6.09	0.00	0.00	6.09	0.00	-6.09	2.56	0.04	-104.56	-0.96
cluster1	CNN	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-7.45	-0.19	-1815.74	-12.78
cluster1	CNN	8	TBR_1	LIB193821	worst	-3.51	0.00	0.00	2.63	0.88	-3.51	4.08	0.06	113.98	1.03
cluster1	CNN	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	-6.20	-0.14	-1467.05	-8.71
cluster1	CNN	12	TBR_1	LIB193821	worst	-3.57	0.00	0.00	8.93	-5.36	-3.57	7.27	0.11	-113.01	-0.89
cluster1	CNN	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	60.00	-60.00	0.00	-41.62	-0.85	-9651.39	-44.24
cluster1	CNN	16	TBR_1	LIB193821	worst	-11.82	0.00	0.00	23.64	-11.82	-11.82	7.26	0.11	-737.81	-5.29
cluster1	Linear	2	TBR_2	LIB193821	worst	60.00	0.00	0.00	-60.00	0.00	60.00	-19.62	-0.38	-762.00	-17.88
cluster1	Linear	2	TBR_1	LIB193821	worst	26.67	0.00	0.00	-25.00	-1.67	26.67	-12.63	-0.21	-1059.76	-19.96
cluster1	Linear	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	16.50	0.31	1828.69	16.99
cluster1	Linear	4	TBR_1	LIB193821	worst	-36.44	0.00	0.00	38.14	-1.69	-36.44	4.14	0.06	-57.51	-0.80
cluster1	Linear	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	16.77	0.34	2244.44	16.31
cluster1	Linear	6	TBR_1	LIB193821	worst	-42.61	0.00	0.00	44.35	-1.74	-42.61	12.57	0.20	432.20	4.49
cluster1	Linear	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	21.52	0.42	2044.82	17.26
cluster1	Linear	8	TBR_1	LIB193821	worst	-35.09	0.00	0.00	37.72	-2.64	-35.09	13.67	0.23	370.50	3.38
cluster1	Linear	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	20.00	-20.00	0.00	-2.22	-0.07	-1577.63	-9.25
cluster1	Linear	12	TBR_1	LIB193821	worst	-36.61	0.00	0.00	41.97	-5.36	-36.61	19.97	0.32	608.62	5.06
cluster1	Linear	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	60.00	-60.00	0.00	-57.12	-1.22	-18970.89	-77.34
cluster1	Linear	16	TBR_1	LIB193821	worst	-26.36	0.00	0.00	43.64	-17.27	-26.36	3.25	0.03	-3003.53	-19.75
cluster1	LSTM	2	TBR_2	LIB193821	worst	40.00	0.00	0.00	-40.00	0.00	40.00	-2.18	-0.04	-94.12	-1.96
cluster1	LSTM	2	TBR_1	LIB193821	worst	19.17	0.00	0.00	-19.17	0.00	19.17	-3.88	-0.06	-90.96	-2.48
cluster1	LSTM	4	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	1.76	0.02	321.52	2.54
cluster1	LSTM	4	TBR_1	LIB193821	worst	16.10	0.00	0.00	-16.10	0.00	16.10	-13.46	-0.21	-683.41	-8.62
cluster1	LSTM	6	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	4.03	0.10	674.09	4.79
cluster1	LSTM	6	TBR_1	LIB193821	worst	1.74	0.00	0.00	-2.61	0.87	1.74	-9.66	-0.15	-477.39	-4.53
cluster1	LSTM	8	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	10.34	0.20	1318.89	10.27
cluster1	LSTM	8	TBR_1	LIB193821	worst	0.00	0.00	0.00	-1.75	1.75	0.00	6.30	0.10	1044.81	10.23

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	12	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	11.01	0.22	1608.66	11.08
cluster1	LSTM	12	TBR_1	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	4.67	0.08	742.32	6.48
cluster1	LSTM	16	TBR_2	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	13.03	0.26	1966.01	13.30
cluster1	LSTM	16	TBR_1	LIB193821	worst	0.00	0.00	0.00	0.00	0.00	0.00	8.65	0.14	1166.05	9.85
cluster2	CNN	2	TBR_2	LIB194012	worst	-1.51	0.00	0.00	1.51	0.00	-1.51	0.46	0.01	6.70	0.09
cluster2	CNN	2	TBR_1	LIB194012	worst	-1.09	0.00	0.00	0.93	0.15	-1.09	0.67	0.01	105.59	1.51
cluster2	CNN	4	TBR_2	LIB194012	worst	-1.54	0.00	0.00	-1.54	3.07	-1.54	7.06	0.14	991.08	7.24
cluster2	CNN	4	TBR_1	LIB194012	worst	-1.60	0.00	0.00	1.12	0.48	-1.60	4.33	0.07	493.27	4.19
cluster2	CNN	6	TBR_2	LIB193916	worst	-2.88	0.00	0.00	0.72	2.16	-2.88	13.75	0.26	1964.92	10.71
cluster2	CNN	6	TBR_1	LIB193916	worst	-2.92	0.00	0.00	0.00	2.93	-2.92	13.02	0.21	1749.49	10.02
cluster2	CNN	8	TBR_2	LIB193916	worst	0.00	0.00	0.00	-7.30	7.30	0.00	13.94	0.27	2826.23	13.31
cluster2	CNN	8	TBR_1	LIB193916	worst	0.00	0.00	0.00	-9.74	9.74	0.00	14.84	0.24	2898.94	14.55
cluster2	CNN	12	TBR_2	LIB193916	worst	0.00	0.00	0.00	-17.42	17.42	0.00	14.90	0.29	3138.54	14.18
cluster2	CNN	12	TBR_1	LIB193916	worst	0.00	0.00	0.00	-23.85	23.85	0.00	19.06	0.31	4063.42	19.72
cluster2	CNN	16	TBR_2	LIB193916	worst	0.00	0.00	0.00	-14.39	14.39	0.00	15.78	0.31	3395.50	14.72
cluster2	CNN	16	TBR_1	LIB193916	worst	0.00	0.00	0.00	-17.14	17.14	0.00	16.30	0.27	3324.30	15.50
cluster2	Linear	2	TBR_2	LIB194012	worst	-7.52	0.00	0.00	7.52	0.00	-7.52	3.38	0.07	119.46	3.57
cluster2	Linear	2	TBR_1	LIB194012	worst	-9.19	0.00	0.00	9.19	0.00	-9.19	2.42	0.04	58.98	1.58
cluster2	Linear	4	TBR_2	LIB194012	worst	-43.84	0.00	0.00	43.08	0.77	-43.84	10.81	0.21	537.12	5.05
cluster2	Linear	4	TBR_1	LIB194012	worst	-38.82	0.00	0.00	38.66	0.15	-38.82	11.23	0.18	573.51	6.35
cluster2	Linear	6	TBR_2	LIB194012	worst	-37.50	0.00	0.00	36.72	0.78	-37.50	22.31	0.44	1985.79	13.61
cluster2	Linear	6	TBR_1	LIB194012	worst	-34.74	0.00	0.00	32.30	2.45	-34.74	20.01	0.33	1589.96	12.38
cluster2	Linear	8	TBR_2	LIB193916	worst	-13.87	0.00	0.00	13.14	0.73	-13.87	24.38	0.47	3229.64	17.14
cluster2	Linear	8	TBR_1	LIB193916	worst	-12.98	0.00	0.00	4.72	8.26	-12.98	22.12	0.36	2764.42	15.28
cluster2	Linear	12	TBR_2	LIB193916	worst	-10.61	0.00	0.00	2.27	8.34	-10.61	35.06	0.68	5500.20	26.34
cluster2	Linear	12	TBR_1	LIB193916	worst	-8.56	0.00	0.00	-3.67	12.23	-8.56	33.22	0.55	4692.48	23.69
cluster2	Linear	16	TBR_2	LIB193916	worst	-9.85	0.00	0.00	-1.52	11.37	-9.85	41.99	0.81	6302.11	29.75
cluster2	Linear	16	TBR_1	LIB193916	worst	-12.06	0.00	0.00	-1.27	13.33	-12.06	41.99	0.69	5753.56	29.20
cluster2	LSTM	2	TBR_2	LIB194012	worst	5.27	0.00	0.00	-5.27	0.00	5.27	-0.09	0.00	-16.77	-0.41
cluster2	LSTM	2	TBR_1	LIB194012	worst	-2.64	0.00	0.00	2.65	0.00	-2.64	1.65	0.03	95.74	2.49
cluster2	LSTM	4	TBR_2	LIB194012	worst	-5.38	0.00	0.00	4.62	0.77	-5.38	3.11	0.06	482.52	4.43
cluster2	LSTM	4	TBR_1	LIB194012	worst	-3.84	0.00	0.00	3.67	0.16	-3.84	3.10	0.05	399.83	4.25
cluster2	LSTM	6	TBR_2	LIB194012	worst	0.00	0.00	0.00	-4.69	4.69	0.00	9.77	0.20	1668.35	11.03
cluster2	LSTM	6	TBR_1	LIB194012	worst	-1.47	0.00	0.00	-0.98	2.44	-1.47	8.42	0.14	1215.53	8.98
cluster2	LSTM	8	TBR_2	LIB193916	worst	0.00	0.00	0.00	-4.38	4.38	0.00	8.91	0.17	1518.19	7.60
cluster2	LSTM	8	TBR_1	LIB193916	worst	0.00	0.00	0.00	-3.54	3.54	0.00	10.07	0.16	1746.45	9.29

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	12	TBR_2	LIB193916	worst	0.00	0.00	0.00	-12.88	12.88	0.00	12.98	0.25	2933.64	13.15
cluster2	LSTM	12	TBR_1	LIB193916	worst	0.00	0.00	0.00	-11.01	11.01	0.00	15.25	0.25	3362.44	16.02
cluster2	LSTM	16	TBR_2	LIB193916	worst	0.00	0.00	0.00	-25.00	25.00	0.00	18.47	0.36	4215.21	18.24
cluster2	LSTM	16	TBR_1	LIB193916	worst	0.00	0.00	0.00	-23.81	23.81	0.00	19.71	0.32	4209.37	19.60
cluster3	CNN	2	TBR_2	LIB193878	worst	-7.61	0.00	0.00	7.61	0.00	-7.61	3.62	0.07	169.13	3.42
cluster3	CNN	2	TBR_1	LIB193878	worst	-9.38	0.00	0.00	9.38	0.00	-9.38	2.79	0.05	102.89	2.06
cluster3	CNN	4	TBR_2	LIB193878	worst	-1.02	0.00	0.00	1.02	0.00	-1.02	0.12	0.00	40.10	0.43
cluster3	CNN	4	TBR_1	LIB193878	worst	-0.36	0.00	0.00	0.18	0.18	-0.36	1.23	0.02	126.22	1.33
cluster3	CNN	6	TBR_2	LIB193878	worst	0.00	0.00	0.00	-1.06	1.06	0.00	5.53	0.11	773.15	5.58
cluster3	CNN	6	TBR_1	LIB193878	worst	-0.58	0.00	0.00	-0.39	0.97	-0.58	12.03	0.20	1453.87	10.86
cluster3	CNN	8	TBR_2	LIB193878	worst	0.00	0.00	0.00	-4.39	4.39	0.00	6.13	0.12	1223.11	7.34
cluster3	CNN	8	TBR_1	LIB193878	worst	0.00	0.00	0.00	-3.48	3.48	0.00	9.70	0.16	1568.34	9.70
cluster3	CNN	12	TBR_2	LIB193878	worst	0.00	0.00	0.00	-7.65	7.65	0.00	9.54	0.19	1871.80	9.77
cluster3	CNN	12	TBR_1	LIB193878	worst	0.00	0.00	0.00	-8.24	8.24	0.00	8.85	0.14	1632.69	8.71
cluster3	CNN	16	TBR_2	LIB193878	worst	0.00	0.00	0.00	-2.57	2.57	0.00	16.18	0.32	3008.87	15.65
cluster3	CNN	16	TBR_1	LIB193878	worst	0.00	0.00	0.00	-11.42	11.42	0.00	14.96	0.25	2761.89	14.70
cluster3	Linear	2	TBR_2	LIB193878	worst	-3.04	0.00	0.00	3.04	0.00	-3.04	5.09	0.10	76.03	3.83
cluster3	Linear	2	TBR_1	LIB193878	worst	-15.74	0.00	0.00	15.74	0.00	-15.74	3.62	0.06	74.24	2.93
cluster3	Linear	4	TBR_2	LIB193878	worst	-64.79	0.00	0.00	64.79	0.00	-64.79	15.82	0.31	612.00	11.21
cluster3	Linear	4	TBR_1	LIB193878	worst	-50.99	0.00	0.00	51.35	-0.36	-50.99	11.78	0.20	434.45	6.85
cluster3	Linear	6	TBR_2	LIB193878	worst	-59.26	0.00	0.00	60.84	-1.59	-59.26	28.18	0.56	1730.02	18.00
cluster3	Linear	6	TBR_1	LIB193878	worst	-43.90	0.00	0.00	44.10	-0.20	-43.90	20.99	0.35	1189.23	11.32
cluster3	Linear	8	TBR_2	LIB193878	worst	-49.45	0.00	0.00	49.45	0.00	-49.45	37.42	0.74	2999.00	22.08
cluster3	Linear	8	TBR_1	LIB193878	worst	-33.74	0.00	0.00	31.90	1.84	-33.74	27.64	0.46	2220.63	15.94
cluster3	Linear	12	TBR_2	LIB193878	worst	-41.76	0.00	0.00	41.77	0.00	-41.76	48.56	0.96	4959.21	30.65
cluster3	Linear	12	TBR_1	LIB193878	worst	-19.91	0.00	0.00	15.56	4.35	-19.91	32.31	0.53	3458.51	20.01
cluster3	Linear	16	TBR_2	LIB193878	worst	-46.79	0.00	0.00	45.52	1.28	-46.79	56.66	1.11	6124.35	36.38
cluster3	Linear	16	TBR_1	LIB193878	worst	-19.35	0.00	0.00	18.86	0.50	-19.35	33.16	0.54	3281.71	17.51
cluster3	LSTM	2	TBR_2	LIB193878	worst	-9.65	0.00	0.00	9.65	0.00	-9.65	2.56	0.05	45.17	1.68
cluster3	LSTM	2	TBR_1	LIB193878	worst	-11.55	0.00	0.00	11.55	0.00	-11.55	2.57	0.04	63.98	2.36
cluster3	LSTM	4	TBR_2	LIB193878	worst	3.06	0.00	0.00	-3.06	0.00	3.06	3.01	0.05	184.58	2.61
cluster3	LSTM	4	TBR_1	LIB193878	worst	-8.11	0.00	0.00	7.75	0.36	-8.11	6.77	0.11	449.43	6.57
cluster3	LSTM	6	TBR_2	LIB193878	worst	1.06	0.00	0.00	-0.53	-0.53	1.06	4.74	0.08	514.63	4.54
cluster3	LSTM	6	TBR_1	LIB193878	worst	0.00	0.00	0.00	-1.75	1.74	0.00	10.26	0.17	1067.23	9.60
cluster3	LSTM	8	TBR_2	LIB193878	worst	0.55	0.00	0.00	-3.29	2.74	0.55	6.13	0.12	1051.70	7.06
cluster3	LSTM	8	TBR_1	LIB193878	worst	0.00	0.00	0.00	-3.88	3.88	0.00	10.89	0.18	1607.34	11.12

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	12	TBR_2	LIB193878	worst	0.00	0.00	0.00	-3.53	3.53	0.00	9.15	0.18	1813.80	9.69
cluster3	LSTM	12	TBR_1	LIB193878	worst	0.00	0.00	0.00	-9.38	9.38	0.00	11.07	0.18	2049.37	11.21
cluster3	LSTM	16	TBR_2	LIB193878	worst	0.00	0.00	0.00	-8.97	8.97	0.00	14.17	0.28	2797.12	14.23
cluster3	LSTM	16	TBR_1	LIB193878	worst	0.00	0.00	0.00	-20.60	20.60	0.00	14.90	0.24	2975.19	15.38
cluster4	CNN	2	TBR_2	LIB193826	worst	-27.27	0.00	0.00	27.27	0.00	-27.27	5.70	0.11	248.94	4.47
cluster4	CNN	2	TBR_1	LIB193826	worst	-29.67	0.00	0.00	29.52	0.15	-29.67	5.05	0.08	161.57	3.58
cluster4	CNN	4	TBR_2	LIB193826	worst	-6.09	0.00	0.00	5.22	0.87	-6.09	9.88	0.19	863.48	9.70
cluster4	CNN	4	TBR_1	LIB193826	worst	-15.23	0.00	0.00	14.75	0.48	-15.23	9.91	0.16	643.19	8.83
cluster4	CNN	6	TBR_2	LIB193826	worst	-1.85	0.00	0.00	-3.71	5.56	-1.85	12.59	0.24	1582.06	13.38
cluster4	CNN	6	TBR_1	LIB193826	worst	-2.90	0.00	0.00	2.39	0.51	-2.90	10.42	0.17	918.59	10.04
cluster4	CNN	8	TBR_2	LIB193826	worst	-0.99	0.00	0.00	-8.91	9.90	-0.99	17.61	0.34	2634.46	18.29
cluster4	CNN	8	TBR_1	LIB193826	worst	-1.79	0.00	0.00	0.53	1.25	-1.79	12.19	0.20	1288.25	11.28
cluster4	CNN	12	TBR_2	LIB193838	worst	0.00	0.00	0.00	-11.69	11.69	0.00	6.64	0.13	1650.64	8.29
cluster4	CNN	12	TBR_1	LIB193838	worst	0.00	0.00	0.00	-4.68	4.68	0.00	1.10	0.02	456.92	2.77
cluster4	CNN	16	TBR_2	LIB193838	worst	0.00	0.00	0.00	-4.00	4.00	0.00	-0.88	-0.02	-82.89	-0.43
cluster4	CNN	16	TBR_1	LIB193838	worst	0.00	0.00	0.00	-2.43	2.43	0.00	-1.20	-0.02	-114.08	-0.66
cluster4	Linear	2	TBR_2	LIB193838	worst	4.70	0.00	0.00	-4.70	0.00	4.70	0.14	0.00	-20.55	-0.53
cluster4	Linear	2	TBR_1	LIB193838	worst	-3.13	0.00	0.00	3.30	-0.16	-3.13	0.56	0.01	-70.36	-1.64
cluster4	Linear	4	TBR_2	LIB193826	worst	-66.08	0.00	0.00	66.95	-0.87	-66.08	12.12	0.23	215.40	3.16
cluster4	Linear	4	TBR_1	LIB193826	worst	-58.99	0.00	0.00	59.32	-0.33	-58.99	11.03	0.18	258.81	4.67
cluster4	Linear	6	TBR_2	LIB193826	worst	-54.63	0.00	0.00	58.33	-3.70	-54.63	15.94	0.30	60.31	0.53
cluster4	Linear	6	TBR_1	LIB193826	worst	-57.51	0.00	0.00	57.51	0.00	-57.51	18.91	0.31	861.37	10.63
cluster4	Linear	8	TBR_2	LIB193826	worst	-44.55	0.00	0.00	49.51	-4.95	-44.55	20.43	0.39	240.93	1.59
cluster4	Linear	8	TBR_1	LIB193826	worst	-46.61	0.00	0.00	48.39	-1.78	-46.61	25.81	0.42	1485.61	14.64
cluster4	Linear	12	TBR_2	LIB193838	worst	-9.09	0.00	0.00	18.18	-9.09	-9.09	16.55	0.32	1383.54	7.31
cluster4	Linear	12	TBR_1	LIB193838	worst	-19.06	0.00	0.00	21.94	-2.87	-19.06	24.25	0.40	1787.49	11.89
cluster4	Linear	16	TBR_2	LIB193838	worst	-5.33	0.00	0.00	14.67	-9.33	-5.33	25.19	0.48	2616.77	14.85
cluster4	Linear	16	TBR_1	LIB193838	worst	-20.19	0.00	0.00	28.42	-8.23	-20.19	26.92	0.44	1918.67	12.53
cluster4	LSTM	2	TBR_2	LIB193838	worst	-4.70	0.00	0.00	4.70	0.00	-4.70	0.79	0.01	79.77	1.88
cluster4	LSTM	2	TBR_1	LIB193838	worst	2.15	0.00	0.00	-2.31	0.16	2.15	0.70	0.01	81.13	1.95
cluster4	LSTM	4	TBR_2	LIB193826	worst	-36.52	0.00	0.00	35.65	0.87	-36.52	10.77	0.21	741.03	10.96
cluster4	LSTM	4	TBR_1	LIB193826	worst	-20.91	0.00	0.00	20.75	0.16	-20.91	8.66	0.14	461.82	8.23
cluster4	LSTM	6	TBR_2	LIB193826	worst	-2.78	0.00	0.00	1.85	0.92	-2.78	11.92	0.23	1247.66	12.00
cluster4	LSTM	6	TBR_1	LIB193826	worst	-4.26	0.00	0.00	3.75	0.52	-4.26	9.71	0.16	727.63	8.65
cluster4	LSTM	8	TBR_2	LIB193826	worst	0.00	0.00	0.00	-5.94	5.94	0.00	12.28	0.24	1659.50	12.44
cluster4	LSTM	8	TBR_1	LIB193826	worst	-0.53	0.00	0.00	-0.90	1.43	-0.53	11.29	0.18	1056.35	10.42

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	12	TBR_2	LIB193826	worst	0.00	0.00	0.00	-6.38	6.38	0.00	16.00	0.31	2711.40	17.48
cluster4	LSTM	12	TBR_1	LIB193826	worst	0.00	0.00	0.00	-1.56	1.56	0.00	14.56	0.24	1914.06	14.76
cluster4	LSTM	16	TBR_2	LIB193838	worst	0.00	0.00	0.00	-5.33	5.33	0.00	3.98	0.07	1003.03	5.26
cluster4	LSTM	16	TBR_1	LIB193838	worst	0.00	0.00	0.00	-3.55	3.55	0.00	-0.53	-0.01	145.51	0.86
cluster5	CNN	2	TBR_2	LIB193603	worst	-29.54	0.00	0.00	29.54	0.00	-29.54	6.71	0.13	195.58	6.15
cluster5	CNN	2	TBR_1	LIB193603	worst	-28.59	0.00	0.00	28.59	0.00	-28.59	5.16	0.08	124.29	3.70
cluster5	CNN	4	TBR_2	LIB193603	worst	-32.18	0.00	0.00	32.18	0.00	-32.18	16.24	0.31	951.88	15.28
cluster5	CNN	4	TBR_1	LIB193603	worst	-29.33	0.00	0.00	29.33	0.00	-29.33	10.69	0.18	454.17	7.22
cluster5	CNN	6	TBR_2	LIB193603	worst	-3.70	0.00	0.00	4.94	-1.23	-3.70	13.25	0.25	1000.63	10.59
cluster5	CNN	6	TBR_1	LIB193603	worst	-3.66	0.00	0.00	4.63	-0.96	-3.66	5.93	0.10	271.57	2.84
cluster5	CNN	8	TBR_2	LIB193603	worst	-5.13	0.00	0.00	7.69	-2.57	-5.13	18.12	0.34	1533.24	12.55
cluster5	CNN	8	TBR_1	LIB193603	worst	-1.95	0.00	0.00	2.74	-0.78	-1.95	13.38	0.22	1156.74	10.24
cluster5	CNN	12	TBR_2	LIB193603	worst	-1.37	0.00	0.00	5.48	-4.11	-1.37	14.35	0.27	1579.12	10.28
cluster5	CNN	12	TBR_1	LIB193603	worst	-0.20	0.00	0.00	2.84	-2.63	-0.20	6.53	0.11	625.45	4.36
cluster5	CNN	16	TBR_2	LIB193603	worst	0.00	0.00	0.00	2.86	-2.86	0.00	14.10	0.27	1839.66	10.80
cluster5	CNN	16	TBR_1	LIB193603	worst	-0.21	0.00	0.00	2.98	-2.77	-0.21	7.47	0.13	780.06	4.82
cluster5	Linear	2	TBR_2	LIB193603	worst	1.14	0.00	0.00	-1.14	0.00	1.14	5.41	0.10	55.39	3.44
cluster5	Linear	2	TBR_1	LIB193603	worst	-9.53	0.00	0.00	9.53	0.00	-9.53	2.75	0.05	5.47	0.26
cluster5	Linear	4	TBR_2	LIB193603	worst	-90.80	0.00	0.00	90.80	0.00	-90.80	21.24	0.40	667.48	17.97
cluster5	Linear	4	TBR_1	LIB193603	worst	-77.14	0.00	0.00	77.14	0.00	-77.14	15.65	0.26	490.72	11.58
cluster5	Linear	6	TBR_2	LIB193603	worst	-81.48	0.00	0.00	81.48	0.00	-81.48	32.05	0.61	1567.28	25.26
cluster5	Linear	6	TBR_1	LIB193603	worst	-77.07	0.00	0.00	77.45	-0.39	-77.07	26.12	0.43	1257.99	18.20
cluster5	Linear	8	TBR_2	LIB193603	worst	-75.64	0.00	0.00	75.64	0.00	-75.64	37.24	0.71	2305.23	25.95
cluster5	Linear	8	TBR_1	LIB193603	worst	-70.51	0.00	0.00	71.29	-0.78	-70.51	31.89	0.53	1914.83	21.26
cluster5	Linear	12	TBR_2	LIB193603	worst	-46.58	0.00	0.00	46.58	0.00	-46.58	49.21	0.93	4657.56	38.69
cluster5	Linear	12	TBR_1	LIB193603	worst	-52.54	0.00	0.00	54.97	-2.43	-52.54	41.34	0.68	3135.27	25.71
cluster5	Linear	16	TBR_2	LIB193603	worst	-35.71	0.00	0.00	35.71	0.00	-35.71	51.32	0.97	5585.40	41.04
cluster5	Linear	16	TBR_1	LIB193603	worst	-39.36	0.00	0.00	42.13	-2.77	-39.36	42.03	0.69	3497.68	24.62
cluster5	LSTM	2	TBR_2	LIB193603	worst	-12.50	0.00	0.00	12.50	0.00	-12.50	4.70	0.09	75.23	5.12
cluster5	LSTM	2	TBR_1	LIB193603	worst	-13.27	0.00	0.00	13.27	0.00	-13.27	2.98	0.05	63.45	3.44
cluster5	LSTM	4	TBR_2	LIB193603	worst	-41.38	0.00	0.00	41.38	0.00	-41.38	14.45	0.27	567.24	13.16
cluster5	LSTM	4	TBR_1	LIB193603	worst	-37.91	0.00	0.00	37.91	0.00	-37.91	10.13	0.17	378.97	8.69
cluster5	LSTM	6	TBR_2	LIB193603	worst	-34.57	0.00	0.00	34.57	0.00	-34.57	20.43	0.39	1487.36	20.55
cluster5	LSTM	6	TBR_1	LIB193603	worst	-21.58	0.00	0.00	21.96	-0.38	-21.58	13.88	0.23	821.98	11.15
cluster5	LSTM	8	TBR_2	LIB193603	worst	-15.38	0.00	0.00	16.67	-1.28	-15.38	27.32	0.52	2258.51	22.64
cluster5	LSTM	8	TBR_1	LIB193603	worst	-9.96	0.00	0.00	11.13	-1.17	-9.96	17.45	0.29	1237.96	12.48

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	12	TBR_2	LIB193603	worst	0.00	0.00	0.00	2.74	-2.74	0.00	21.35	0.40	2322.38	16.36
cluster5	LSTM	12	TBR_1	LIB193603	worst	-0.81	0.00	0.00	1.42	-0.61	-0.81	11.25	0.19	1166.92	8.66
cluster5	LSTM	16	TBR_2	LIB193603	worst	0.00	0.00	0.00	0.00	0.00	0.00	-0.06	0.00	11.71	0.07
cluster5	LSTM	16	TBR_1	LIB193603	worst	0.00	0.00	0.00	-3.19	3.19	0.00	-1.98	-0.03	-129.19	-0.79

Appendix I

Absolute difference between group-based prediction models and personalized prediction models performance in TBR ranges for best predicted patients

Table I.1 presents the absolute difference between the metrics performance results for the group-based prediction models and the personalized prediction models in TBR ranges for patients best predicted by the group-based prediction models. The "Patient" column indicates the identifier of the patient whose results are displayed, and the "Type" column specifies the patient classification by the corresponding group-based model; in this case, only the best-predicted patients are displayed. In cases where performance results are missing, this corresponds to instances where no BGL measurements were available for that specific test set, resulting in no performance data.

It is important to note that from the outcome of this comparison for the percentage of measurements in the zone 'A + B', which is a maximization metric, positive values indicate that the group-based prediction models perform better, negative values indicate worse performance, and zero means equal performance between both types of models. The effect of minimization metrics (RMSE, MSE, MAE, and MAPE) is reversed, where positive values reflect worse performance for group-based models, negative values indicate better performance, and zero means equal results. Therefore, the tables generated from this subtraction process are formatted for a more explicit comparison. To improve clarity, the cells corresponding to these key metrics, particularly 'A + B' and all non-clinical metrics, are color-coded: green represents better results for group-based models, red represents worse results, and gray indicates equal performance for both model types.

Table I.1: Absolute difference between group-based prediction models and personalized prediction models performance in the TBR BGL ranges and for best predicted patients assessed via both clinical and non-clinical metrics for all clusters. Green: better for group-based models, red: worse, gray: equal. Missing results indicate cases with no available measurements for the specific test set for personalized models.

Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	CNN	2	TBR_2	LIB193859	best										
cluster0	CNN	2	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-12.99	-0.21	-1120.67	-12.28
cluster0	CNN	4	TBR_2	LIB193859	best										
cluster0	CNN	4	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-24.53	-0.39	-3223.17	-22.35
cluster0	CNN	6	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.89	-0.10	-590.76	-4.48
cluster0	CNN	6	TBR_1	LIB193914	best	0.00	0.00	0.00	-1.17	1.17	0.00	-4.56	-0.07	-451.71	-3.59
cluster0	CNN	8	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.98	-0.09	-607.52	-3.88
cluster0	CNN	8	TBR_1	LIB193914	best	0.00	0.00	0.00	-2.86	2.86	0.00	-4.02	-0.06	-351.10	-2.45
cluster0	CNN	12	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-3.80	-0.08	-716.84	-3.77
cluster0	CNN	12	TBR_1	LIB193914	best	0.00	0.00	0.00	-1.73	1.73	0.00	-3.29	-0.05	-401.00	-2.57
cluster0	CNN	16	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-8.11	-0.16	-1610.45	-8.35
cluster0	CNN	16	TBR_1	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-5.75	-0.09	-904.26	-5.56
cluster0	Linear	2	TBR_2	LIB193859	best										
cluster0	Linear	2	TBR_1	LIB193859	best	20.00	0.00	0.00	-20.00	0.00	20.00	-6.46	-0.10	-413.16	-7.97
cluster0	Linear	4	TBR_2	LIB193859	best										
cluster0	Linear	4	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-9.61	-0.16	-1296.83	-12.20
cluster0	Linear	6	TBR_2	LIB193859	best										
cluster0	Linear	6	TBR_1	LIB193859	best	0.00	0.00	0.00	40.00	-40.00	0.00	-13.49	-0.22	-3128.45	-17.39
cluster0	Linear	8	TBR_2	LIB193914	best	0.00	0.00	0.00	6.25	-6.25	0.00	13.53	0.26	854.10	6.74
cluster0	Linear	8	TBR_1	LIB193914	best	-18.57	0.00	0.00	19.05	-0.48	-18.57	18.00	0.28	1266.89	10.25
cluster0	Linear	12	TBR_2	LIB193914	best	0.00	0.00	0.00	14.29	-14.29	0.00	9.64	0.19	651.41	3.52
cluster0	Linear	12	TBR_1	LIB193914	best	-6.44	0.00	0.00	7.43	-0.99	-6.44	24.92	0.39	2507.46	18.63
cluster0	Linear	16	TBR_2	LIB193914	best	0.00	0.00	0.00	21.43	-21.43	0.00	9.97	0.19	186.26	1.00
cluster0	Linear	16	TBR_1	LIB193914	best	-4.68	0.00	0.00	8.31	-3.64	-4.68	26.27	0.41	2869.28	20.41
cluster0	LSTM	2	TBR_2	LIB193859	best										
cluster0	LSTM	2	TBR_1	LIB193859	best	20.00	0.00	0.00	-20.00	0.00	20.00	-18.31	-0.30	-1014.29	-16.54
cluster0	LSTM	4	TBR_2	LIB193859	best										
cluster0	LSTM	4	TBR_1	LIB193859	best	0.00	0.00	0.00	0.00	0.00	0.00	-24.70	-0.39	-2637.28	-24.43
cluster0	LSTM	6	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-5.48	-0.10	-808.00	-6.55
cluster0	LSTM	6	TBR_1	LIB193914	best	-1.64	0.00	0.00	0.70	0.94	-1.64	-4.80	-0.08	-585.66	-4.91
cluster0	LSTM	8	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	0.57	0.02	-72.68	-0.55

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster0	LSTM	8	TBR_1	LIB193914	best	0.00	0.00	0.00	-2.38	2.38	0.00	-2.15	-0.04	-338.10	-2.49
cluster0	LSTM	12	TBR_2	LIB193914	best	0.00	0.00	0.00	-7.14	7.14	0.00	-9.52	-0.19	-1709.33	-8.80
cluster0	LSTM	12	TBR_1	LIB193914	best	0.00	0.00	0.00	-2.48	2.48	0.00	-8.95	-0.14	-1224.92	-7.86
cluster0	LSTM	16	TBR_2	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.06	-0.12	-1183.09	-6.10
cluster0	LSTM	16	TBR_1	LIB193914	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.35	-0.04	-335.65	-2.07
cluster1	CNN	2	TBR_2	LIB193736	best										
cluster1	CNN	2	TBR_1	LIB193736	best										
cluster1	CNN	4	TBR_2	LIB193736	best										
cluster1	CNN	4	TBR_1	LIB193736	best										
cluster1	CNN	6	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-3.66	-0.07	-450.91	-3.62
cluster1	CNN	6	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.77	-0.04	-141.86	-1.43
cluster1	CNN	8	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	3.74	0.07	603.15	4.41
cluster1	CNN	8	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-0.04	-167.48	-1.57
cluster1	CNN	12	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	8.13	0.15	1176.57	8.09
cluster1	CNN	12	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	5.86	0.09	735.46	6.38
cluster1	CNN	16	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	10.83	0.21	1707.04	10.87
cluster1	CNN	16	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	5.06	0.08	659.13	5.46
cluster1	Linear	2	TBR_2	LIB193736	best										
cluster1	Linear	2	TBR_1	LIB193736	best										
cluster1	Linear	4	TBR_2	LIB193736	best										
cluster1	Linear	4	TBR_1	LIB193736	best										
cluster1	Linear	6	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	6.82	0.13	706.29	6.81
cluster1	Linear	6	TBR_1	LIB193385	best	-26.27	0.00	0.00	26.27	0.00	-26.27	12.62	0.19	724.25	8.81
cluster1	Linear	8	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	2.80	0.05	298.76	2.19
cluster1	Linear	8	TBR_1	LIB193385	best	-20.00	0.00	0.00	20.00	0.00	-20.00	15.94	0.24	1083.24	11.99
cluster1	Linear	12	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	0.93	0.02	161.54	1.13
cluster1	Linear	12	TBR_1	LIB193385	best	-6.73	0.00	0.00	6.73	0.00	-6.73	17.54	0.27	1348.38	12.72
cluster1	Linear	16	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.95	-0.13	-1326.56	-7.88
cluster1	Linear	16	TBR_1	LIB193385	best	-4.17	0.00	0.00	4.17	0.00	-4.17	15.90	0.24	1208.47	10.87
cluster1	LSTM	2	TBR_2	LIB193736	best										
cluster1	LSTM	2	TBR_1	LIB193736	best										
cluster1	LSTM	4	TBR_2	LIB193736	best										
cluster1	LSTM	4	TBR_1	LIB193736	best										
cluster1	LSTM	6	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-2.01	-0.04	-195.13	-1.75
cluster1	LSTM	6	TBR_1	LIB193385	best	0.00	0.00	0.00	-0.85	0.85	0.00	-1.24	-0.02	35.19	0.39
cluster1	LSTM	8	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-3.02	-0.06	-373.73	-2.89

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster1	LSTM	8	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.52	-0.02	-15.18	-0.15
cluster1	LSTM	12	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.00	28.17	0.20
cluster1	LSTM	12	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.02	219.60	1.92
cluster1	LSTM	16	TBR_2	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	7.35	0.14	1120.79	7.36
cluster1	LSTM	16	TBR_1	LIB193385	best	0.00	0.00	0.00	0.00	0.00	0.00	3.62	0.06	473.90	4.03
cluster2	CNN	2	TBR_2	LIB194030	best										
cluster2	CNN	2	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.25	-0.02	-299.87	-4.46
cluster2	CNN	4	TBR_2	LIB194030	best										
cluster2	CNN	4	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	0.72	0.01	-34.69	-0.31
cluster2	CNN	6	TBR_2	LIB194030	best										
cluster2	CNN	6	TBR_1	LIB194030	best	0.00	0.00	0.00	10.00	-10.00	0.00	-10.97	-0.16	-2345.56	-13.70
cluster2	CNN	8	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-12.58	-0.24	-2385.47	-12.58
cluster2	CNN	8	TBR_1	LIB194050	best	0.00	0.00	0.00	24.00	-24.00	0.00	-18.11	-0.28	-3461.82	-17.76
cluster2	CNN	12	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-20.16	-0.38	-4376.48	-20.16
cluster2	CNN	12	TBR_1	LIB194050	best	0.00	0.00	0.00	28.00	-28.00	0.00	-17.28	-0.27	-3576.58	-17.63
cluster2	CNN	16	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	-100.00	0.00	-19.22	-0.36	-4859.38	-19.22
cluster2	CNN	16	TBR_1	LIB194050	best	0.00	0.00	0.00	45.45	-45.45	0.00	-15.23	-0.24	-3280.18	-15.34
cluster2	Linear	2	TBR_2	LIB194030	best										
cluster2	Linear	2	TBR_1	LIB194030	best	-20.00	0.00	0.00	20.00	0.00	-20.00	2.62	0.04	62.16	2.41
cluster2	Linear	4	TBR_2	LIB194030	best										
cluster2	Linear	4	TBR_1	LIB194030	best	-20.00	0.00	0.00	20.00	0.00	-20.00	12.31	0.19	582.33	5.79
cluster2	Linear	6	TBR_2	LIB194030	best										
cluster2	Linear	6	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	13.22	0.21	1066.10	8.08
cluster2	Linear	8	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	15.34	0.29	2451.29	15.34
cluster2	Linear	8	TBR_1	LIB194050	best	0.00	0.00	0.00	-4.00	4.00	0.00	17.72	0.28	2651.35	14.49
cluster2	Linear	12	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	10.94	0.21	2118.80	10.94
cluster2	Linear	12	TBR_1	LIB194050	best	0.00	0.00	0.00	-4.00	4.00	0.00	19.05	0.30	2410.17	13.55
cluster2	Linear	16	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	5.38	0.10	1246.09	5.38
cluster2	Linear	16	TBR_1	LIB194050	best	0.00	0.00	0.00	-9.09	9.09	0.00	22.03	0.34	3259.57	16.10
cluster2	LSTM	2	TBR_2	LIB193556	best										
cluster2	LSTM	2	TBR_1	LIB193556	best	100.00	0.00	0.00	-100.00	0.00	100.00	-8.41	-0.12	-281.93	-8.49
cluster2	LSTM	4	TBR_2	LIB194030	best										
cluster2	LSTM	4	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	-12.21	-0.19	-1160.18	-11.57
cluster2	LSTM	6	TBR_2	LIB194030	best										
cluster2	LSTM	6	TBR_1	LIB194030	best	0.00	0.00	0.00	0.00	0.00	0.00	-1.39	-0.02	-239.56	-1.87
cluster2	LSTM	8	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-15.42	-0.29	-2524.30	-15.42

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster2	LSTM	8	TBR_1	LIB194050	best	0.00	0.00	0.00	4.00	-4.00	0.00	-19.17	-0.30	-2947.08	-15.35
cluster2	LSTM	12	TBR_2	LIB194050	best	0.00	0.00	0.00	0.00	0.00	0.00	-10.03	-0.19	-2019.17	-10.03
cluster2	LSTM	12	TBR_1	LIB194050	best	0.00	0.00	0.00	24.00	-24.00	0.00	-19.24	-0.30	-3801.05	-19.28
cluster2	LSTM	16	TBR_2	LIB194050	best	0.00	0.00	0.00	100.00	-100.00	0.00	-20.45	-0.39	-5048.00	-20.45
cluster2	LSTM	16	TBR_1	LIB194050	best	0.00	0.00	0.00	36.37	-36.37	0.00	-17.69	-0.28	-3972.61	-17.98
cluster3	CNN	2	TBR_2	LIB193551	best										
cluster3	CNN	2	TBR_1	LIB193551	best	14.29	0.00	0.00	-14.29	0.00	14.29	-10.21	-0.17	-517.21	-10.09
cluster3	CNN	4	TBR_2	LIB193871	best										
cluster3	CNN	4	TBR_1	LIB193871	best	0.00	0.00	0.00	1.28	-1.28	0.00	-16.21	-0.25	-1626.58	-14.20
cluster3	CNN	6	TBR_2	LIB193871	best										
cluster3	CNN	6	TBR_1	LIB193871	best	0.00	0.00	0.00	-5.13	5.13	0.00	-9.46	-0.15	-974.26	-6.48
cluster3	CNN	8	TBR_2	LIB193871	best										
cluster3	CNN	8	TBR_1	LIB193871	best	0.00	0.00	0.00	-7.69	7.69	0.00	-7.30	-0.11	-626.16	-3.69
cluster3	CNN	12	TBR_2	LIB193871	best										
cluster3	CNN	12	TBR_1	LIB193871	best	0.00	0.00	0.00	-9.59	9.59	0.00	3.60	0.06	1064.66	5.72
cluster3	CNN	16	TBR_2	LIB193871	best										
cluster3	CNN	16	TBR_1	LIB193871	best	0.00	0.00	0.00	-13.24	13.24	0.00	5.16	0.08	1171.60	5.99
cluster3	Linear	2	TBR_2	LIB193518	best										
cluster3	Linear	2	TBR_1	LIB193518	best	-7.14	0.00	0.00	7.14	0.00	-7.14	2.50	0.04	-27.02	-0.81
cluster3	Linear	4	TBR_2	LIB193518	best										
cluster3	Linear	4	TBR_1	LIB193518	best	-58.33	0.00	0.00	58.33	0.00	-58.33	14.45	0.23	517.38	12.46
cluster3	Linear	6	TBR_2	LIB193871	best										
cluster3	Linear	6	TBR_1	LIB193871	best	-2.56	0.00	0.00	5.13	-2.57	-2.56	8.49	0.13	462.25	3.78
cluster3	Linear	8	TBR_2	LIB193871	best										
cluster3	Linear	8	TBR_1	LIB193871	best	-1.28	0.00	0.00	5.13	-3.84	-1.28	13.60	0.21	942.31	6.07
cluster3	Linear	12	TBR_2	LIB193871	best										
cluster3	Linear	12	TBR_1	LIB193871	best	0.00	0.00	0.00	-4.11	4.11	0.00	14.59	0.23	1414.86	7.47
cluster3	Linear	16	TBR_2	LIB193871	best										
cluster3	Linear	16	TBR_1	LIB193871	best	0.00	0.00	0.00	-1.47	1.47	0.00	13.69	0.22	1480.19	7.37
cluster3	LSTM	2	TBR_2	LIB193518	best										
cluster3	LSTM	2	TBR_1	LIB193518	best	7.14	0.00	0.00	-7.14	0.00	7.14	0.83	0.01	-2.74	-0.10
cluster3	LSTM	4	TBR_2	LIB193518	best										
cluster3	LSTM	4	TBR_1	LIB193518	best	-8.33	0.00	0.00	8.33	0.00	-8.33	0.29	0.00	-39.56	-0.81
cluster3	LSTM	6	TBR_2	LIB193871	best										
cluster3	LSTM	6	TBR_1	LIB193871	best	0.00	0.00	0.00	-1.29	1.29	0.00	-14.40	-0.23	-1484.07	-11.12
cluster3	LSTM	8	TBR_2	LIB193871	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster3	LSTM	8	TBR_1	LIB193871	best	0.00	0.00	0.00	-5.12	5.12	0.00	-11.94	-0.19	-1460.49	-9.18
cluster3	LSTM	12	TBR_2	LIB193871	best										
cluster3	LSTM	12	TBR_1	LIB193871	best	0.00	0.00	0.00	-6.85	6.85	0.00	-0.78	-0.01	280.05	1.52
cluster3	LSTM	16	TBR_2	LIB193871	best										
cluster3	LSTM	16	TBR_1	LIB193871	best	0.00	0.00	0.00	-19.12	19.12	0.00	6.88	0.10	1729.26	8.82
cluster4	CNN	2	TBR_2	LIB193960	best										
cluster4	CNN	2	TBR_1	LIB193960	best										
cluster4	CNN	4	TBR_2	LIB194157	best										
cluster4	CNN	4	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-4.95	-0.08	-302.88	-4.41
cluster4	CNN	6	TBR_2	LIB194157	best										
cluster4	CNN	6	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-6.35	-0.10	-560.84	-5.98
cluster4	CNN	8	TBR_2	LIB194157	best										
cluster4	CNN	8	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-9.52	-0.15	-1273.96	-10.49
cluster4	CNN	12	TBR_2	LIB194157	best										
cluster4	CNN	12	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.62	-0.12	-1229.65	-8.02
cluster4	CNN	16	TBR_2	LIB194157	best										
cluster4	CNN	16	TBR_1	LIB194157	best	0.00	0.00	0.00	26.67	-26.67	0.00	-8.35	-0.13	-1926.69	-10.24
cluster4	Linear	2	TBR_2	LIB193960	best										
cluster4	Linear	2	TBR_1	LIB193960	best										
cluster4	Linear	4	TBR_2	LIB194157	best										
cluster4	Linear	4	TBR_1	LIB194157	best	-46.66	0.00	0.00	46.66	0.00	-46.66	11.14	0.18	339.15	9.03
cluster4	Linear	6	TBR_2	LIB194157	best										
cluster4	Linear	6	TBR_1	LIB194157	best	-20.00	0.00	0.00	20.00	0.00	-20.00	8.23	0.13	285.32	4.04
cluster4	Linear	8	TBR_2	LIB194157	best										
cluster4	Linear	8	TBR_1	LIB194157	best	-13.33	0.00	0.00	13.33	0.00	-13.33	3.17	0.05	-221.64	-2.11
cluster4	Linear	12	TBR_2	LIB194157	best										
cluster4	Linear	12	TBR_1	LIB194157	best	0.00	0.00	0.00	40.00	-40.00	0.00	-30.84	-0.49	-6770.28	-36.77
cluster4	Linear	16	TBR_2	LIB194157	best										
cluster4	Linear	16	TBR_1	LIB194157	best	0.00	0.00	0.00	40.00	-40.00	0.00	-21.78	-0.34	-5310.34	-26.34
cluster4	LSTM	2	TBR_2	LIB193960	best										
cluster4	LSTM	2	TBR_1	LIB193960	best										
cluster4	LSTM	4	TBR_2	LIB193960	best										
cluster4	LSTM	4	TBR_1	LIB193960	best										
cluster4	LSTM	6	TBR_2	LIB194157	best										
cluster4	LSTM	6	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-10.09	-0.16	-826.78	-8.99
cluster4	LSTM	8	TBR_2	LIB194157	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster4	LSTM	8	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-26.19	-0.41	-3233.86	-25.55
cluster4	LSTM	12	TBR_2	LIB194157	best										
cluster4	LSTM	12	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	-8.15	-0.13	-1140.82	-7.93
cluster4	LSTM	16	TBR_2	LIB194157	best										
cluster4	LSTM	16	TBR_1	LIB194157	best	0.00	0.00	0.00	0.00	0.00	0.00	9.88	0.15	1677.09	10.57
cluster5	CNN	2	TBR_2	LIB193368	best										
cluster5	CNN	2	TBR_1	LIB193368	best	4.35	0.00	0.00	-4.35	0.00	4.35	-7.24	-0.11	-542.26	-7.19
cluster5	CNN	4	TBR_2	LIB193368	best										
cluster5	CNN	4	TBR_1	LIB193368	best	0.00	0.00	0.00	2.18	-2.18	0.00	-7.22	-0.11	-966.22	-7.59
cluster5	CNN	6	TBR_2	LIB193368	best										
cluster5	CNN	6	TBR_1	LIB193368	best	0.00	0.00	0.00	2.18	-2.18	0.00	-11.51	-0.18	-1597.19	-10.43
cluster5	CNN	8	TBR_2	LIB193368	best										
cluster5	CNN	8	TBR_1	LIB193368	best	0.00	0.00	0.00	4.35	-4.35	0.00	-4.74	-0.07	-777.13	-4.67
cluster5	CNN	12	TBR_2	LIB193368	best										
cluster5	CNN	12	TBR_1	LIB193368	best	0.00	0.00	0.00	17.39	-17.39	0.00	-18.48	-0.28	-3532.84	-18.31
cluster5	CNN	16	TBR_2	LIB193795	best	0.00	0.00	0.00	2.44	-2.44	0.00	14.97	0.28	2362.64	13.80
cluster5	CNN	16	TBR_1	LIB193795	best	0.00	0.00	0.00	1.00	-1.00	0.00	10.24	0.17	1522.20	9.54
cluster5	Linear	2	TBR_2	LIB194036	best	0.00	0.00	0.00	0.00	0.00	0.00	5.58	0.11	195.89	4.09
cluster5	Linear	2	TBR_1	LIB194036	best	20.00	0.00	0.00	-20.00	0.00	20.00	-1.26	-0.02	-51.81	-0.76
cluster5	Linear	4	TBR_2	LIB193368	best										
cluster5	Linear	4	TBR_1	LIB193368	best	-19.57	0.00	0.00	21.74	-2.17	-19.57	3.22	0.05	-98.92	-1.02
cluster5	Linear	6	TBR_2	LIB193368	best										
cluster5	Linear	6	TBR_1	LIB193368	best	-10.87	0.00	0.00	13.05	-2.17	-10.87	6.37	0.09	-3.92	-0.03
cluster5	Linear	8	TBR_2	LIB193368	best										
cluster5	Linear	8	TBR_1	LIB193368	best	-13.04	0.00	0.00	21.74	-8.70	-13.04	9.95	0.15	398.27	2.63
cluster5	Linear	12	TBR_2	LIB193427	best										
cluster5	Linear	12	TBR_1	LIB193427	best	0.00	0.00	0.00	9.26	-9.26	0.00	11.68	0.19	729.27	3.89
cluster5	Linear	16	TBR_2	LIB193427	best										
cluster5	Linear	16	TBR_1	LIB193427	best	-5.66	0.00	0.00	15.09	-9.43	-5.66	10.62	0.17	379.64	2.00
cluster5	LSTM	2	TBR_2	LIB194054	best										
cluster5	LSTM	2	TBR_1	LIB194054	best	58.34	0.00	0.00	-58.34	0.00	58.34	-11.32	-0.17	-512.76	-10.64
cluster5	LSTM	4	TBR_2	LIB193368	best										
cluster5	LSTM	4	TBR_1	LIB193368	best	0.00	0.00	0.00	0.00	0.00	0.00	-7.16	-0.11	-629.37	-6.34
cluster5	LSTM	6	TBR_2	LIB193368	best										
cluster5	LSTM	6	TBR_1	LIB193368	best	0.00	0.00	0.00	2.17	-2.17	0.00	-9.35	-0.14	-1159.89	-8.42
cluster5	LSTM	8	TBR_2	LIB193368	best										

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Cluster	Algorithm	PH	Range	Patient	Type	A (%)	B (%)	C (%)	D (%)	E (%)	A + B (%)	RMSE (mg/dL)	MSE (mg/dL ²)	MAE (%)	MAPE (mg/dL)
cluster5	LSTM	8	TBR_1	LIB193368	best	0.00	0.00	0.00	2.17	-2.17	0.00	-10.46	-0.16	-1604.86	-10.18
cluster5	LSTM	12	TBR_2	LIB193368	best										
cluster5	LSTM	12	TBR_1	LIB193368	best	0.00	0.00	0.00	4.35	-4.35	0.00	-13.74	-0.21	-2319.72	-12.61
cluster5	LSTM	16	TBR_2	LIB193795	best	0.00	0.00	0.00	0.00	0.00	0.00	17.04	0.32	2669.99	16.12
cluster5	LSTM	16	TBR_1	LIB193795	best	0.00	0.00	0.00	1.00	-1.00	0.00	11.79	0.19	1722.66	11.11

J.1 T1DiabetesGranada

The code used to generate the different files of the dataset is available at: https://github.com/crleon87/T1D_Intelligent_Monitoring/tree/main/T1DiabetesGranada. The corresponding README.dm file details the code structure.

J.2 General prediction models

The code used in the experimentation process of the general BGL prediction models, as well as all the resulting files such as training plots, weights of the trained models, and others, can be found at: https://github.com/crleon87/T1D_Intelligent_Monitoring/tree/main/General_prediction_models. The corresponding README.dm file details the file structure.

J.3 Clustering

The code used in the experimentation process to create the patients groups, as well as all the resulting files such complete clusters results and result plots, dataset versions created, and others, can be found at: https://github.com/crleon87/T1D_Intelligent_Monitoring/tree/main/Clustering. The corresponding README.dm file details the file structure.

J.4 Evaluation

The code used in the experimentation process to create the group-based and personalized BGL prediction models, as well as all the resulting files such as training plots, weights of the trained models, and others, can be found at: https://github.com/crleon87/T1D_Intelligent_Monitoring/tree/main/Evaluation. The corresponding README.dm file details the file structure.