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Research Article

Stacked GRU-Based Glucose Prediction in Type 1 Diabetes

Ömer Atılım Koca[1*], Ali Türköz[2], Volkan Kılıç[3]

[1*] İzmir Katip Çelebi University, Graduate School of Natural And Applied Sciences, Software Engineering Graduate Program, İzmir, Turkey, (ORCID: 0009-0007-7286-6785), atilim.koca@bakircay.edu.tr

[2] İsmail Rahmi Karadavut Primary School, İzmir, Turkey, (ORCID: 0000-0002-3650-1435), saibturkoz@hotmail.com

[3] İzmir Katip Çelebi University, Faculty of Engineering and Architecture, Department of Electrical and Electronics, İzmir, Turkey, (ORCID: 0000-0002-3164-1981), volkan.kilic@ikcu.edu.tr

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Abstract

Recent advances in diabetes technology, especially continuous glucose monitoring (CGM) systems, provide reliable sources of glucose data. These data have accelerated advanced glucose prediction models for diabetics with technological advances in artificial intelligence and data-driven techniques. However, despite these advancements, accurately predicting glucose levels still is a challenge as the models struggle to learn contextual patterns in complex sequential data. In this paper, we propose a novel multilayer GRU-based model, including a convolutional layer for feature extraction from sequences of glucose values under the encoder-decoder framework. The open-access D1NAMO dataset was used to train and test the proposed multi-layer GRU-based model. The proposed model achieved a Root Mean Square Error of 9.88 mg/dL, Mean Absolute Error of 6.46 mg/dL, Coefficient of Determination of 0.92, and Mean Absolute Percentage Error of %4.83 for 30-min glucose prediction. Furthermore, the Parkes Error Grid was used as a clinical benchmark to assess the robustness of the prediction model. The proposed model demonstrates superior performance compared to state-of-the-art glucose prediction models.

Keywords: Artificial Intelligence, Deep Learning, Glucose Prediction, Gated Recurrent Unit.

Tip 1 Diyabette Çok Katmanlı GRU Tabanlı Glikoz Tahmini

Abstract

Diyabet teknolojisindeki son gelişmeler, özellikle de sürekli glikoz izleme (CGM) sistemleri, güvenilir glikoz veri kaynakları sağlamaktadır. Bu veriler, yapay zeka ve veri odaklı tekniklerdeki teknolojik ilerlemelerle diyabet hastaları için gelişmiş glikoz tahmin modellerini hızlandırmıştır. Ancak, bu gelişmelere rağmen, modeller karmaşık sıralı verilerdeki bağlamsal örüntüleri öğrenmekte zorlandığından, glikoz seviyelerini doğru bir şekilde tahmin etmek hala bir zorluktur. Bu makalede, kodlayıcı-kod çözücü çerçevesi altında glikoz değerleri dizilerinden özellik çıkarımı için bir konvolüsyonel katman içeren yeni bir çok katmanlı GRU tabanlı model öneriyoruz. Önerilen çok katmanlı GRU tabanlı modeli eğitmek ve test etmek için açık erişimli D1NAMO veri seti kullanılmıştır. Önerilen model, 30 dakikalık glikoz tahmini için 9,88 mg/dL Ortalama Karekök Hatası, 6,46 mg/dL Ortalama Mutlak Hata, 0,92 Belirleme Katsayısı ve %4,83 Ortalama Mutlak Yüzde Hatası elde etmiştir. Ayrıca, tahmin modelinin sağlamlığını değerlendirmek için klinik bir ölçüt olarak Parkes Hata Izgarası kullanılmıştır. Önerilen model, son teknoloji glikoz tahmin modellerine kıyasla üstün performans göstermektedir.

Anahtar Kelimeler: Yapay Zeka, Derin Öğrenme, Kan Şekeri Tahmini, Kapılı Tekrarlayan Hücre.

[*] Corresponding Author: atilim.koca@bakircay.edu.tr

1. Introduction

Effective management of blood glucose levels is critical to reducing the impact of diabetes, as inadequate control can lead to serious long-term complications, including hypertension and stroke (Mercan et al., 2020; Mercan & Kılıç, 2020). To prevent these complications, continuous glucose monitoring (CGM) systems have emerged in recent years (Kılıç et al., 2022; Palaz et al., 2021). CGM systems primarily act as alarms and offer benefits such as the prevention of potentially dangerous hypoglycemia or hyperglycemia and the optimization of insulin dose requirements. However, a limitation of these systems is that they only generate alerts when glucose levels deviate from the target range. This means that the body may be exposed to high or low glucose levels for a period of time until the necessary action is taken to address the situation (Kılıç, 2021; Strollo et al., 2021). The development of AI-based models has improved the proactive management of diabetes through glucose prediction. Machine learning (ML) and deep learning (DL) architectures, which are sub-branches of artificial intelligence, are prominent in the development of glucose prediction models. ML algorithms are capable of producing results with limited computational resources and relatively small datasets. On the other hand, DL architectures require training on high-performance computing systems and larger datasets (Çaylı et al., 2021; Doğan et al., 2022). The training process of both ML and DL architectures involves the extraction of discriminative features from the dataset. In ML, this feature extraction process is typically performed manually, whereas in DL the features are extracted automatically (Akosman et al., 2021; Şen et al., 2022).

Due to their capacity to learn complex representations directly from the data, DL architectures require longer training times and larger datasets compared to ML approaches. This is because DL architectures can capture complex patterns and dependencies in the data, resulting in higher accuracy. The longer training process allows DL architectures to iteratively refine their internal representations, leading to improved performance. Furthermore, DL architectures exhibit enhanced robustness to noise and variation in the input data. The robust behavior exhibited by DL architectures can be attributed to their hierarchical nature. DL architectures are designed with multiple layers to enhance their capability to capture and represent complex patterns and dependencies within the data (Çaylı et al., 2023; Kılıç et al., 2014). McShinsky et al. investigated the impact of different algorithms on the prediction process (McShinsky & Marshall, 2020). Kalman filter, ML algorithms, and DL algorithms were among the algorithms evaluated in the study, which found that the Lasso algorithm outperformed other algorithms for 30-minute glucose prediction (Saiti et al., 2020). Saiti et al. investigated three ensembles combining ARX and SVR models with meta-algorithms (linear meta-regressor, bagging, boosting) for glucose prediction. The results showed better predictive accuracy in all ensembles compared to standalone ARX and SVR models. This highlights the efficacy of ensembles in improving glucose prediction accuracy. Alfian et al. found that an XGBoost model achieved the highest accuracy among the models tested, indicating its potential for glucose prediction (Alfian et al., 2020). Wang et al. used a LightGBM model and Bayesian to optimize its parameters. Their experiments showed that the optimized LightGBM model outperformed both the XGBoost and CatBoost models (Wang & Wang, 2020). Song et al. used a combination of Empirical Mode Decomposition and Long-Short Term Memory (LSTM) network for glucose prediction. The proposed model effectively handled rapid changes in glucose trends and outperformed a standalone LSTM model (Song et al., 2019). Zhu et al. proposed an extended recurrent neural network (RNN) model for short-term glucose prediction with a 30 PH. This model effectively captured long-term dependencies within the glucose data, resulting in improved prediction accuracy (Zhu et al., 2020).

Different from previous work, our research aims to capture meaningful patterns in sequential data and use these patterns to make accurate predictions. Here, we propose a prediction model that includes a convolutional layer-based encoder and a multi-layer GRU-based decoder. The encoder extracts important patterns and features from sequential data, while the decoder is used to build a robust prediction model based on these extracted features.

The rest of this paper is structured as follows: Section 2 provides comprehensive details on DL-based models, including their underlying principles and methods. The dataset and comparison with state-of-the-art approaches are presented in Section 3. Finally, Section 4 concludes the paper with a brief summary.

2. Methods

2.1. Recurrent Neural Network

RNNs are a type of artificial neural network model that is specifically designed for processing sequential data, such as time series data. Unlike traditional feedforward neural networks, RNNs have the ability to capture temporal dependencies and make use of information from previous steps to influence the computations in subsequent steps (Saeed et al., 2022). In this way, a temporal correlation between inputs can be established, and past knowledge can influence the decisions of the network. This ability allows feedback between layers, giving RNNs a memory-like property. Despite this advantage, RNNs are challenged by vanishing or exploding gradients. This problem occurs because of the need to backpropagate gradients over long sequences, resulting in a gradual shrinkage of gradient values layer by layer until they eventually disappear after a few steps (Hossain et al., 2019). Several variants of RNNs have been developed to address vanishing or exploding gradients, including LSTM and GRU (Çaylı et al., 2022). These variants have special gating mechanisms that facilitate information flow control and mitigate the problem of vanishing gradients.

2.2. Long-Short Term Memory

The LSTM model represents a distinct variant of artificial neural networks that have demonstrated remarkable efficacy in the field of time series data analysis. LSTM networks are characterized by their ability to detect and model complex long-term dependencies

within sequential data (Van Geffen et al., 2020). Fundamentally, an LSTM network functions as an interconnected collection of cells, where each cell contains a special "memory cell" and three different "gates". These gates actively regulate the input, output, and memory operations of the LSTM, thereby facilitating its ability to effectively process and retain relevant information. The key feature of LSTMs is their ability to retain important information over long sequences by mitigation of the vanishing gradient problem. The memory cells allow LSTMs to accumulate information over time while selectively updating and preserving relevant context. This ability allows LSTMs to capture complex patterns and dependencies in sequential data better than traditional RNNs.

2.3. Gated Recurrent Unit

The GRU is a type of RNN that offers a more simplified and efficient alternative to LSTM networks (Cho et al., 2014). In particular, GRU incorporates a distinctive architectural design in which the forget and input gates are merged into a single updating gate (Chen, 2016). The GRU network structure differs from the LSTM network structure by incorporating two gate structures, namely the update gate and the reset gate (Uslu et al., 2022). The update gate determines the degree to which information from the previous time step is integrated into the current time step, allowing the network to selectively retain or discard relevant information. On the other hand, the reset gate controls the extent to which information from the previous time step is disregarded, enabling the network to reset its internal state and adapt to new input (Aydın et al., 2022; Li et al., 2021). The primary advantage of GRUs is their ability to effectively capture and utilize important contextual information while reducing the computational burden associated with memory cells (Keskin et al., 2021).

2.4. Attention Layer

The attention layer is a component in neural network architectures that allows the network to selectively focus on specific parts of the input data. The primary purpose of attention layers in neural networks is to facilitate the identification and highlighting of significant features within datasets characterized by temporal sequences. These attention layers play a crucial role in breaking down larger and more complex tasks into smaller, more manageable attentional domains (Niu et al., 2021). Attention mechanisms allow networks to actively focus on the most informative and relevant aspects of the data while ignoring extraneous details, enabling more efficient processing of complex data structures.

2.5. Convolution Layer

The convolutional layer is a fundamental building block of neural networks, specifically designed to extract meaningful and discernible features from input data. This layer identifies emerging patterns at different locations and features within the learned filters applied to the input data and generates feature maps that encapsulate these high-level features as output.
The convolutional layer in a neural network applies a filter matrix, often called a kernel, to the input data for converting sequential data into a numerical representation. This involves shifting the kernel over the input data and calculating the dot product between the kernel and the corresponding region of the input data (Shi et al., 2015). This iterative process produces an output value for each region of the filter matrix superimposed on the input data. Different filter matrices are used to capture different features of interest.

2.6. Proposed Prediction Model

This subsection presents the proposed model for glucose prediction using a convolutional layer-based encoder and a two-layer GRU architecture-based decoder with input variables generated using a sliding window approach. The sliding window approach divides the sequential glucose data into smaller subsequences, each representing a fixed time window length. Moving the window gradually through the sequential data encapsulates the temporal information within the window generating new input variables at each time step. These input variables include previous glucose levels, which are then used as input to the encoder. The convolution layer-based encoder generates feature maps for the decoder capturing dependencies in past glucose levels. The GRU architecture includes gating mechanisms that selectively maintain and update relevant information at each time step, facilitating efficient dissemination of information throughout the network. The two-layer configuration increases the representational capacity of the model, enabling understanding of complex relationships and more accurate glucose predictions (Fetiler et al., 2021). The proposed model uses the feature maps generated by the encoder as input to the first GRU layer. This layer plays a critical role in extracting temporal features from the input sequences, which are then passed to the second GRU layer. These features are further improved by the second GRU layer to produce the final predictions. The latent states of the second layer are then used as input to a fully connected output layer responsible for generating the 30 PH glucose prediction. The proposed approach aims to achieve improved accuracy in predicting glucose levels within the desired PH using the multilayer GRU-based encoder-decoder framework.

3. Experimental Evaluations

3.1. Dataset

In this paper, the open-access D1NAMO dataset is used to train and test the proposed model (Dubosson et al., 2018). This dataset includes a diverse array of physiological signals, including electrocardiogram (ECG), respiratory, and accelerometer data, as well as vital glucose measurements and precisely annotated food images. The dataset shown in Figure 1 was collected from a cohort of twenty healthy subjects and nine people diagnosed with type 1 diabetes in real-life settings through four days of observation. Data collection was performed using Zephyr BioHarness three wearable devices, ensuring the accuracy and reliability of the information collected.

The proposed approach described in Subsection 2.6 used glucose data from eight type 1 diabetics with patient numbers 001-008 contained in the D1NAMO dataset.

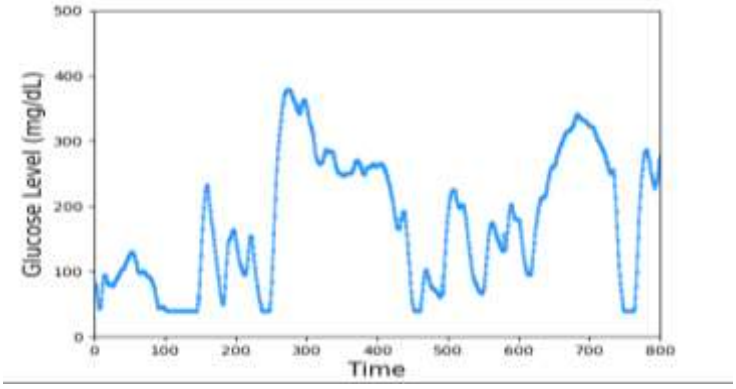

Figure 1. D1NAMO Dataset value distribution

3.2. Evaluation Metrics

The evaluation of the developed prediction model included incorporating four statistical metrics and one clinical metric. The statistical metrics used for evaluation included Root Mean Square Error (RMSE), Mean Absolute Error (MAE), Mean Absolute Percentage Error (MAPE), and Coefficient of Determination (R^2). In addition, the Parkes Error Grid (PEG) was used as the clinical metric for evaluation.

RMSE, MAE, and MAPE are statistical metrics commonly used to measure the discrepancy between predicted and actual values in a model. RMSE calculates the root mean square of the squared differences, emphasizing larger errors. MAE calculates the mean of the absolute differences, focusing on error sizes. MAPE measures the average percentage difference between predicted and actual values. R^2 is a statistical measure that quantifies the proportion of the total variance in the dependent variable that can be accounted for by the independent variables in a regression model. It serves as an indicator of the adequacy of the regression model to fit the observed data. The formulas for RMSE, MAE, MAPE, and R^2 can be expressed as follows:

$$\mathrm{RMSE} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2} \tag{1}$$

$$\mathrm{MAE} = \frac{1}{n}\sum_{i=1}^{n}|y_i - \hat{y}_i| \tag{2}$$

$$\mathrm{MAPE} = \frac{1}{n}\sum_{i=1}^{n}\left|\frac{y_i - \hat{y}_i}{y_i}\right| \times 100 \tag{3}$$

$$R^2 = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{n}(y_i - \bar{y})^2} \tag{4}$$

where n represents the total number of observations, i represents the index of each observation, y_i denotes the actual values, $\hat{y}_i$ represents the predicted values, and $\bar{y}$ represents the mean of the actual values.

Table 1 presents 30-minute glucose predictions from different 2-layer RNN-based architectures. It can be clearly seen that the stacked GRU-EnDe model without the attention layer achieves the lowest RMSE value. Increasing the number of layers in the models is positively correlated with predictive ability. However, the inclusion of the attention mechanism has the opposite effect on the overall performance. To further establish the reliability of these predictions, a PEG analysis was performed on patient 003, as shown in Figure 2. The PEG analysis performed on this patient demonstrates the agreement between the predictions generated by the proposed method and the actual observations, thus significantly enhancing its reliability and ensuring its safety. To enable a meaningful comparative analysis of the proposed model with prior research, we conducted a thorough review of experimental studies that have used the D1NAMO dataset. It was observed that only one study used the D1NAMO dataset and Table 2 provides an overview of this study. In particular, the proposed method outperformed the only study available for comparison. The RMSE obtained for a prediction horizon of 30 min was reported as 12.14 mg/dL. This relatively poor performance can be attributed to the limitations of traditional ML approaches in capturing the complex temporal features inherent in time series data. ML models often face challenges in capturing the dynamics and interdependencies present in complex datasets, leading to reduced prediction accuracy compared to DL-based prediction models.

Table 1. Statistical results for 30 PH glucose prediction with Stacked RNN-based models

	Methods	RMSE	MAE	MAPE	R^2
Without Attention	RNN	10.14	6.75	5.05	0.92
	LSTM	10.25	6.97	5.22	0.92
	GRU	10.30	7.04	5.27	0.92
	BRNN	10.17	6.79	5.07	0.92
	BiLSTM	10.28	7.00	5.25	0.92
	BiGRU	10.31	7.05	5.28	0.92
	RNN-EnDe	11.11	7.47	5.30	0.91
	LSTM-EnDe	11.13	7.53	5.37	0.91
	GRU-EnDe	10.98	7.37	5.31	0.91
With Attention	RNN	10.41	7.06	5.31	0.92
	LSTM	10.59	7.37	5.55	0.92
	GRU	10.47	7.28	5.47	0.92
	BRN	10.68	7.30	5.39	0.91
	BiLSTM	10.56	7.34	5.53	0.92
	BiGRU	10.38	7.19	5.40	0.92
	RNN-EnDe	11.03	7.52	5.36	0.91
	LSTM-EnDe	11.26	7.68	5.49	0.91
	GRU-EnDe	11.02	7.54	5.43	0.91

4. Conclusion

This paper presents a novel prediction model for glucose prediction using the Stacked GRU-based encoder-decoder model. The evaluations on the D1NAMO dataset show the remarkable accuracy and reliability of the proposed model for 30 PH glucose prediction. The proposed model shows promising results with an RMSE of 9.88 mg/dl, MAE of 6.46 mg/dl, R^2 value of 0.91, and MAPE of 4.83% for 30 min PH. These metrics show that the proposed model is superior to the compared studies for glucose prediction. In addition, the PEG of patient 003 shows that the glucose predictions obtained are within acceptable limits, demonstrating the robustness and reliability of the proposed method. In future work, the developed prediction model will be embedded in an Android application, allowing users to conveniently access and use the predictive capabilities of the model. This application enables users to make informed choices about their diet, physical activity, and overall health management.

Table 2. Comparison between proposed model and state-of-the-art for the glucose prediction

Methods	RMSE
AR, SVR [15]	12.14
Proposed Model	**9.88**

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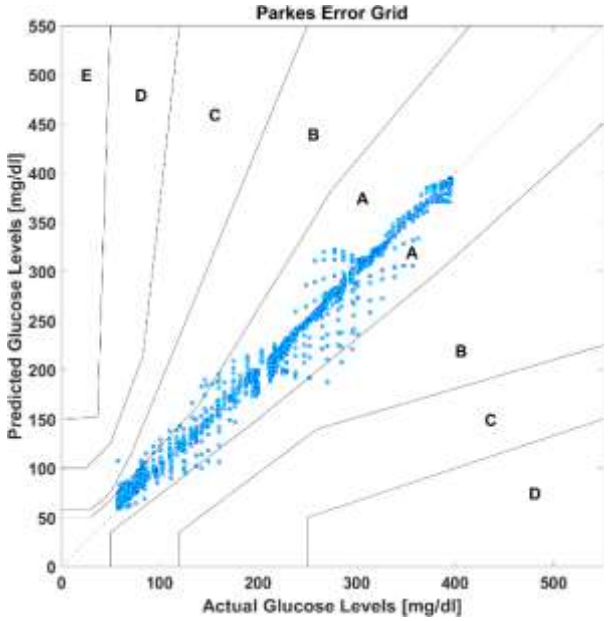

Figure 2. PEG of patient 003

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