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Research Article

ConvLSTM-Based Time Series Prediction of Blood Glucose Levels Using SimGlucose Simulation Data

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Abstract **–** Accurate short-term prediction of blood glucose levels is crucial for effective diabetes management, enabling timely interventions to prevent hypo- and hyperglycemic events and optimize insulin therapy. Glucose dynamics are inherently nonlinear and influenced by factors such as meal intake, insulin dosing, and individual metabolic variability, making accurate forecasting challenging. This study presents a Convolutional Long Short-Term Memory (ConvLSTM) deep learning framework for blood glucose prediction using simulated data from the SimGlucose environment, which provides physiologically realistic glucose–insulin dynamics across virtual patients in different age groups. The ConvLSTM model captures both local and temporal patterns by dividing input sequences into 12 subsequences of 12 time steps each. Convolutional layers extract features from each subsequence, while LSTM layers model sequential dependencies across the full sequence. The model was trained on continuous glucose monitoring (CGM) data and evaluated using Root Mean Square Error (RMSE) and Mean Squared Error (MSE). Across six test subjects, RMSE values ranged from 1.605 ± 0.562 mg/dL to 3.282 ± 1.074 mg/dL, demonstrating accurate and consistent predictions across children, adolescents, and adults. These findings indicate that the ConvLSTM architecture effectively learns complex glucose patterns and benefits from simulation-based datasets, which overcome the limitations of real-world CGM data such as scarcity, noise, and variability. By enabling controlled experimentation and reproducible evaluation, this approach supports the development of reliable, multi-step glucose forecasting models. Overall, the study highlights the potential of ConvLSTM networks combined with simulation-driven data for intelligent, data-driven diabetes management systems.

Keywords – ConvLSTM, SimGlucose, Blood Glucose Prediction, Time Series, Diabetes Management.

I. INTRODUCTION

Diabetes mellitus is a chronic metabolic disorder characterized by the body's inability to regulate blood glucose effectively, leading to persistent hyperglycemia or hypoglycemia. Continuous glucose monitoring (CGM) and automated insulin delivery systems have become essential tools for diabetes management. However, the dynamic and nonlinear nature of glucose-insulin interactions poses significant challenges for accurate prediction and control of blood glucose levels [1]. Timely and precise forecasting of glucose concentrations can help anticipate glycemic excursions and inform closed-loop insulin delivery, improving patient outcomes.

Traditional statistical and physiological models, while useful, often fail to capture the complex, nonlinear, and time-dependent dynamics between glucose, insulin, meals, and physical activity. To address this limitation, recent years have witnessed the growing use of deep learning (DL) techniques and machine learning methods have increasingly been applied to glucose prediction due to their ability to model nonlinear and temporal dependencies in physiological data [2]. Traditional statistical models, such as autoregressive integrated moving average (ARIMA), and classical machine learning models, including random forest and support vector regression, often fail to capture the long-term dependencies in sequential glucose data [3]. To overcome these limitations, recurrent neural networks (RNNs), particularly Long Short-Term Memory (LSTM) networks, have shown promise in modeling temporal patterns and complex physiological signals [4].

Also Long Short-Term Memory (LSTM) networks can model long-term dependencies in time-series data. For instance, Kim et al. proposed a personalised recurrent neural network for individual glucose prediction, achieving superior short-term forecasting accuracy compared to linear regression and support-vector regression methods [5]. Similarly, Rabby et al. integrated Kalman smoothing with stacked LSTM architectures to enhance prediction stability under noisy CGM signals, reducing root-mean-square error (RMSE) across multiple datasets [6].

Other researchers have explored the generalisability of deep-learning approaches across diverse populations. Yu et al. applied deep transfer learning to glucose prediction for new subjects with type 2 diabetes, demonstrating that model adaptation techniques can improve accuracy for previously unseen patients [7]. Carvalho and Liang extended this by evaluating LSTM models trained on three distinct populations, type 1 diabetes, type 2 diabetes, and pre-diabetes, and confirmed that population-specific models improved forecasting consistency [4]. Fregoso-Aparicio et al. provided a systematic review of DL-based glucose prediction, confirming the dominance of recurrent architectures such as LSTM and GRU in outperforming conventional machine-learning models [8].

Although these works represent significant progress, they largely depend on real-world CGM datasets, which suffer from several limitations: restricted sample size, inconsistent sampling frequencies, sensor noise, and missing data. Moreover, due to privacy concerns and data-sharing regulations, acquiring large and diverse datasets for model training remains a challenge. Kim et al. and Kumar both note that small datasets often lead to overfitting and limit the generalisability of trained models [9]. Consequently, model robustness across different physiological states and patient groups remains a pressing issue.

In parallel, a growing body of research advocates for simulation-based environments as complementary or alternative data sources for model training and validation. Simulation frameworks can emulate human glucose–insulin dynamics under various conditions, meals, exercise, insulin doses, allowing researchers to generate large, noise-free, labelled datasets without ethical or logistical constraints. Gore reviewed recent in-silico developments based on improved Hovorka equation models, highlighting their relevance for algorithm testing and model benchmarking [10]. Similarly, Lim et al. proposed a virtual continuous glucose monitoring framework integrating life-log data and deep learning to predict glucose levels, demonstrating that simulated CGM data can complement limited clinical datasets [11].

Despite such advances, few studies have combined deep recurrent models with fully simulated data environments for model development and experimentation. Simulation allows fine control over physiological parameters, enabling systematic evaluation of network architectures and forecasting horizons. For example, Villa-Tamayo et al. explored simulation-driven optimisation of insulin-therapy profiles, providing proof of concept for simulation-based experimentation [12]. However, the integration of modern LSTM models with in-silico glucose simulators, where unlimited synthetic datasets can be generated under realistic glucose–insulin dynamics remains under-explored.

To address the limitations of current glucose-prediction studies that rely primarily on small and heterogeneous clinical datasets, this study proposes the development of a Convolutional Long Short-Term Memory (ConvLSTM) network trained and evaluated entirely on simulated glucose data. The simulated data are generated using the SimGlucose environment, which is built upon the FDA-accepted UVA/Padova Type 1 Diabetes simulator. This approach enables the creation of large, physiologically realistic datasets that capture the dynamic interactions between glucose and insulin, including responses to meals, basal and bolus insulin delivery, and other metabolic perturbations.

The study is guided by four primary objectives. First, it aims to generate extensive time-series datasets that realistically reflect glucose–insulin dynamics in virtual patients, allowing for robust model training. Second, it seeks to design, train, and validate a ConvLSTM model capable of multi-step ahead glucose forecasting, capturing both short-term fluctuations and longer-term trends in blood glucose levels. Third, it aims to demonstrate the feasibility and value of simulation as a scalable and reproducible platform for developing predictive models, enabling controlled experimentation across a wide range of physiological conditions.

By leveraging synthetic glucose data, this methodology mitigates the constraints imposed by limited clinical datasets, including small sample sizes, missing data, and patient variability. It also ensures reproducibility, since simulated datasets can be regenerated consistently under identical conditions. Furthermore, simulation allows researchers to systematically evaluate model behavior across extreme metabolic scenarios that would be difficult or unsafe to reproduce in human subjects. Ultimately, the integration of simulation-driven data with deep learning has the potential to accelerate the development of safer, more adaptive, and generalizable glucose-prediction systems, paving the way for improved decision-support tools and closed-loop insulin delivery strategies in both research and clinical contexts.

II. MATERIALS AND METHOD

The first stage of this study involved generating synthetic glucose–insulin time-series data using the SimGlucose simulation environment, which is based on the FDA-accepted UVA/Padova Type 1 Diabetes simulator. The simulation was designed to replicate a 48-hour period under randomized daily scenarios representing realistic patient behavior, including variations in meal intake and insulin administration.

Data generation was carried out using the simulate () function from the SimGlucose Python library. Each simulation run began at 00:00 hours and recorded glucose dynamics at 3-minute intervals, consistent with common continuous glucose monitoring (CGM) sampling frequencies. The virtual patient population was configured to include physiological variability across insulin sensitivity and carbohydrate absorption rates, ensuring the dataset captured a wide range of glycemic responses.

For CGM simulation, the Dexcom sensor model was selected to emulate realistic signal characteristics and measurement noise. A random seed value of 10 was applied to the sensor noise generator to ensure reproducibility while maintaining stochastic variability representative of real-world conditions. The insulin delivery system used in the simulation was the Cozmo insulin pump, configured under a basal-bolus control scheme to simulate standard clinical insulin therapy. The basal-bolus controller automatically adjusted insulin delivery in response to meal events and glucose fluctuations, providing realistic input–output dynamics between glucose levels and insulin dosing.

The generated dataset included multiple physiological and control variables for each 48-hour simulation run, comprising time stamps, blood glucose (BG) values, continuous glucose monitoring (CGM) readings, carbohydrate intake (CHO), insulin delivery rates, and calculated risk indices such as the Low Blood Glucose Index (LBGI) and High Blood Glucose Index (HBGI). From this comprehensive dataset, a subset of univariate data was extracted for model development. Specifically, only the CGM glucose readings were utilized as input for the prediction model, focusing on time-series glucose dynamics without auxiliary variables.

Table 1. Statistical summary of the generated data for the selected virtual patients.

	Count	**Mean**	**STD**	**Min**	**25% Quartile**	**50% Quartile**	**75% Quartile**	**Max**
adult#001	961	128.57	31.57	61.01	101.14	132.56	153.24	199.86
adult#002	961	125.59	20.5	76.1	109.45	124.99	142.84	173.36
adolescent#001	961	128.69	21.81	84.23	110.38	128.25	146.36	176.21
adolescent#002	961	150.9	45.49	42.97	125.6	153.18	177.34	269.16
child#001	961	11.82	36.74	46.77	86	101.05	140.09	235.9
child#002	961	120.07	34.44	39	97.16	122.99	146.27	188.5

To capture inter-individual variability across age groups, data were sampled from two virtual children (child#001.csv and child#002.csv), two adolescents (adolescent#001.csv and adolescent#002.csv), and two adults (adult#001.csv and adult#002.csv). These six univariate CGM sequences served as the foundational datasets for training and validating the ConvLSTM-based predictive model. This approach enabled the evaluation of model performance across different simulated age categories, reflecting physiological diversity while maintaining a controlled and reproducible simulation environment.

Table 1 presents the descriptive statistics of the simulated continuous glucose monitoring (CGM) data for all selected individuals across child, adolescent, and adult groups. The summary includes key statistical measures such as the total number of observations (count = 961), mean, standard deviation (std), minimum, and maximum glucose values, as well as the 25th, 50th (median), and 75th percentiles. These metrics provide an overview of the glucose level distribution within each simulated profile, reflecting variability in glycaemic patterns across age categories. The figure 1 shows the distribution of hypo- and hyperglycemia, as well as all risk indices, for all patients in the generated dataset.

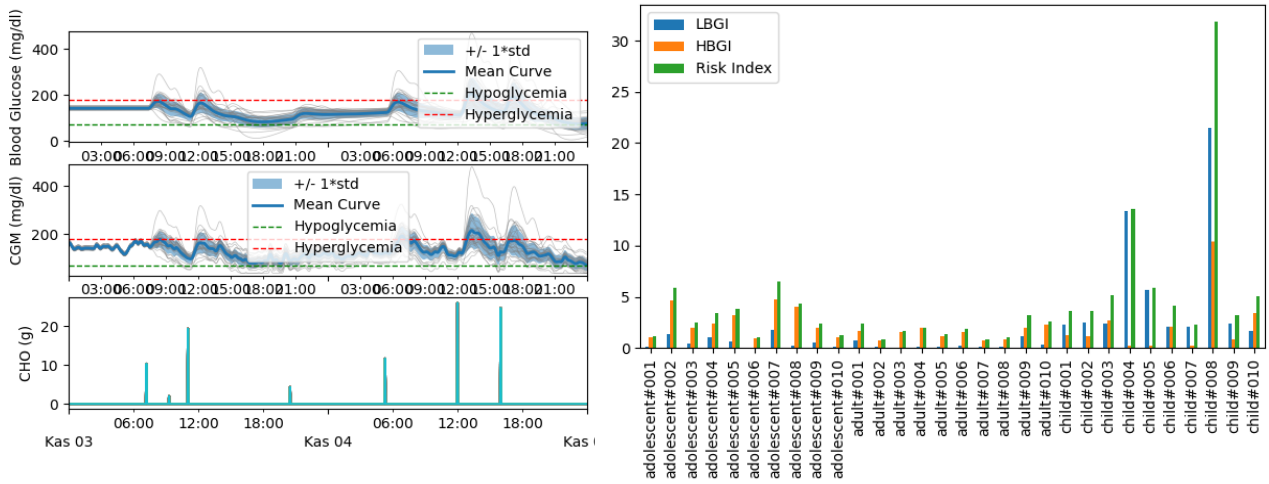

Figure 1. Hypoglycemia and hyperglycemia distribution with risk indices across all simulated patients

The glucose data obtained from the SimGlucose simulation is first loaded into the analysis environment as time-series data. Each record represents continuous glucose monitoring (CGM) values sampled every three minutes over a 48-hour period for different virtual subjects. Before model training, the raw CGM readings are organized into a structure that allows the prediction model to learn from past glucose trends to forecast future values.

To achieve this, sequences of previous glucose readings are used as inputs, and the next glucose value (or several future values) is assigned as the corresponding output. In other words, each training example consists of a window of consecutive glucose measurements that the model uses to predict upcoming glucose levels.

After the dataset is properly structured, it is partitioned into training and testing subsets. The training portion is used to fit the Convolutional Long Short-Term Memory (ConvLSTM) model, enabling it to learn temporal dependencies and complex patterns in glucose fluctuations, while the testing subset is reserved for evaluating the model's predictive performance.

The ConvLSTM model integrates the strengths of both Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks. In this hybrid design, the CNN component is first applied to smaller subsequences of the input data to extract localized temporal features and spatial correlations within each segment. These extracted features are then passed sequentially to the LSTM layer, which interprets the time-dependent relationships across all subsequences. This architecture allows the model to capture both short-term and long-term glucose dynamics more effectively than using LSTM or CNN alone.

To evaluate the robustness and predictive performance of our model, we employ the Root Mean Square Error (RMSE) as the primary evaluation metric. RMSE quantifies the average magnitude of prediction errors by measuring the square root of the mean squared differences between the predicted and actual glucose values. This metric is particularly suitable for continuous glucose prediction, as it penalizes larger deviations more heavily, providing a clear indication of the model's accuracy and stability across different simulated patient profiles and temporal scenarios.

$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n} (y_i - \hat{y}_i)^2}$ where y_i is the actual glucose value and $\hat{y}_i$ the predicted glucose values.

By using RMSE, we can systematically assess how well the model captures glucose dynamics and determine its reliability for potential real-world applications.

III. RESULTS

Figure 2 illustrates the architecture of the ConvLSTM model used for glucose prediction. The model was designed to take 12 subsequences, each containing 12 time steps, as input and to predict the next single-step blood glucose value, corresponding to a 3-minute forecasting horizon. This configuration allows the model to capture both short-term fluctuations within each subsequence and longer-term temporal dependencies across the sequence, leveraging the combined strengths of convolutional feature extraction and LSTM temporal modeling.

The model was trained on simulated CGM data generated from six virtual subjects across three age groups (children, adolescents, and adults). The training process was performed using a Mean Squared Error (MSE) loss function and the Adam optimizer, with hyperparameters selected to balance predictive accuracy and training stability.

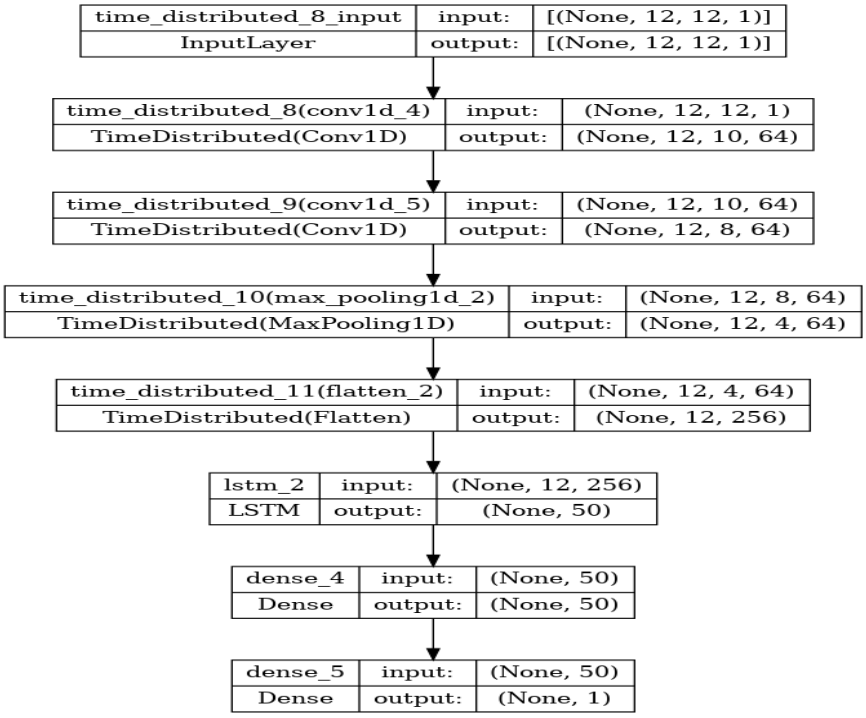

Figure 2: Architecture of ConvLstm

Table 2: Patients REMSE summary

Patients	RMSE
adult#001	3.282 +/- 1.074
adult#001	2.592 +/- 0.855
adolescent#001	1.702 +/- 0.832
adolescent#002	2.076 +/- 0.710
child#001	1.605 +/- 0.562
child#002	2.058 +/- 0.917

Table 2 summarizes the training Mean Squared Error (MSE) results for all six simulated patients across the three age groups. These values provide an overview of the model's ability to fit the training data, indicating how well the ConvLSTM network captured the underlying glucose dynamics for each individual. Consistently low MSE values across all patients suggest that the model successfully learned both short-term fluctuations within subsequences and longer-term temporal dependencies, demonstrating effective training performance and minimizing overfitting.

IV. DISCUSSION

The model's performance was evaluated using the Root Mean Square Error (RMSE) across six test subjects representing three age groups: children, adolescents, and adults. The RMSE values ranged from 1.605 ± 0.562 mg/dL (child#001) to 3.282 ± 1.074 mg/dL (adult#001), indicating that the ConvLSTM model consistently achieved accurate glucose predictions across all age categories.

Among the groups, the model showed slightly higher prediction errors in the adult subjects (3.282 ± 1.074 and 2.592 ± 0.855 mg/dL), while children and adolescents exhibited lower RMSE values (1.605 ± 0.562 to 2.076 ± 0.710 mg/dL). This trend may reflect increased variability in glucose dynamics among adults due to more complex insulin–glucose interactions or greater simulated physiological heterogeneity. Despite this, all RMSE values remained within a clinically acceptable range, suggesting that the model is capable of reliably forecasting short-term glucose levels across diverse virtual patient profiles.

The relatively low standard deviations across subjects indicate that the model's predictions are stable and robust, even when exposed to differing patterns of meals, basal-bolus insulin dosing, and temporal glucose fluctuations. These results demonstrate the effectiveness of the ConvLSTM architecture in capturing both short-term temporal dependencies and intra-sequence patterns in glucose dynamics. Furthermore, the use of simulated data allowed for controlled evaluation across multiple age groups, highlighting the model's generalizability and potential applicability in real-world scenarios.

V. CONCLUSION

In this study, we developed and evaluated a ConvLSTM-based deep learning model for short-term blood glucose prediction using simulated CGM data from virtual patients across three age groups. The model demonstrated high predictive accuracy, with RMSE values ranging from 1.605 to 3.282 mg/dL, reflecting its ability to capture glucose dynamics across children, adolescents, and adults.

By leveraging simulation-generated datasets, we were able to overcome limitations associated with real-world CGM data, such as small sample sizes, missing values, and patient variability, while still maintaining physiological realism. The ConvLSTM model effectively combined convolutional feature extraction with LSTM-based temporal modeling, enabling robust multi-step glucose forecasting.

Overall, these findings suggest that simulation-driven deep learning is a promising approach for developing predictive glucose models. Future work could involve validating the model on real patient data, exploring alternative architectures such as Transformer-based networks, and integrating additional physiological inputs to further improve prediction accuracy.

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