Poster Abstract: Predicting Blood Glucose Dynamics with Multi-time-series Deep Learning

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ABSTRACT

Predicting blood glucose dynamics is vital for people to take preventive measures in time against health risks. Previous efforts adopt handcrafted features and design prediction models for each person, which result in low accuracy due to ineffective feature representation and the limited training data. This work proposes MT-LSTM, a multi-time-series deep LSTM model for accurate and efficient blood glucose concentration prediction. MT-LSTM automatically learns feature representations and temporal dependencies of blood glucose dynamics by jointly sharing data among multiple users and utilizes an individual learning layer for personalized prediction. Evaluations on 112 users demonstrate that MT-LSTM significant outperform conventional predictive regression models.

CCS CONCEPTS

• **Computing methodologies → Machine learning**;

KEYWORDS

Multi-time-series analysis, Blood glucose inference

1 INTRODUCTION

Short-term prediction of blood glucose concentration is crucial for personal health. Awareness of future hyper- and hypo-glycemia events allows people to avoid various physiological complications or even death by taking timely counter-measures.

Researchers have proposed various blood glucose concentration prediction models. The process of glucose metabolism can be

mathematically formulated with physiological models [1]. Duke [2] analyzes the blood glucose dynamics and leverages Lasso and Ridge regression to predict short-term blood glucose concentration. However, these models have the following drawbacks. *(i)* The features are manually selected, which may fail to effectively model the blood glucose concentration. *(ii)* Previous models often ignores the temporal dependencies among a sequence of successive blood glucose measurements. *(iii)* Existing works either assume sufficient training data for each individual to build personal models or only learn a generic model without considering the personal difference.

In this work, we devise MT-LSTM, a multi-time-series deep LSTM-based model for accurate and effective short-term blood glucose prediction. It takes the current readings of continuous glucose monitoring (CGM) devices and external factors (meal, drug, insulin intake, physical activity and sleep quality) as inputs and outputs the personalized glucose concentration in the next hour. MT-LSTM adopts a representation learning scheme to automatically generate effective features driven by the true blood glucose measurements. Moreover, a multi-time-series structure learning model is used to learn the complex physiological-temporal dependencies among blood glucose concentration and external factors. Rather than directly learning from the limited data of each individual, MT-LSTM jointly shares and learns blood glucose measurements from different users to make full use of the data. To account for user-specific characteristics, MT-LSTM also utilizes an individual learning layer for personalized prediction. MT-LSTM is built upon our previous work of blood glucose level inference [3, 4], which focuses on the *current* and *discrete* blood glucose level classification using external factors without CGM as input. In contract, MT-LSTM tackles a different and more difficult problem of blood glucose concentration prediction. Evaluations on 112 users show that MT-LSTM achieves considerably lower prediction errors than conventional models. It also offers an opportunity to predict abnormal blood glucose events (*i.e.*, high/low level) to alarm users in advance, which helps in blood glucose control.

2 APPROACH

Fig. 1 shows the architecture of MT-LSTM. It consists three components: 1) feature representation learning, 2) multi-time-series structure learning and 3) individual model learning.
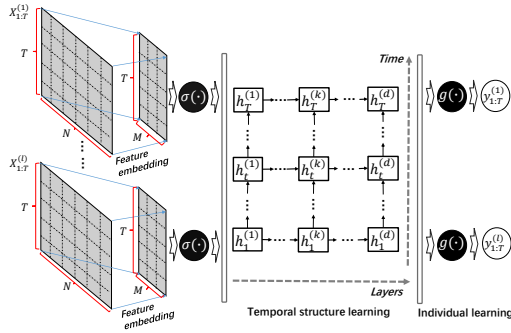
Figure 1: MT-LSTM architecture.

Feature Representation Learning. The input of feature representation learning is a feature matrix $X = \{X_{1:T}^{(j)}|j \in \{1, \ldots, l\}\} \in \mathbb{R}^{l \times N \times T}$, where $X_{1:T}^{(j)}$ is the time sequence of blood glucose features $X_{1:T}$ of user j, $X_{1:T}^{(j)} \in \mathbb{R}^{N \times T}$, and N denotes the dimension of the initial features. Feature representation learning squashes the high-dimensional feature matrix into a low-dimensional one, *i.e.*, $\tilde{X}_{1:T}^{(j)} = \sigma(W'_{N \times M} X_{1:T}^{(j)})$, where $M \ll N$, and $\sigma(\cdot)$ is chosen as a softmax transfer function scaling the sum of M feature values to one in a new space. The embedded features, automatically selected by the labels, preserve the essential parts and eliminate the noise, thus boosting the learning speed and generalization capability. In MT-LSTM, the dimensions of the initial and the embedded features (*i.e.*, N and M) are 54 and 3, respectively. The 54-dimensional features are extracted based on the physiological models of blood glucose concentration [1] and the external impacting factors [2]. We refer readers to [4] for the details of the initial features.

Multi-Time-Series Structure Learning. MT-LSTM uses the Long short-term memory (LSTM) network to encode the hidden temporal properties of blood glucose sequence. Compared with conventional time-series models such as HMM and CRF, the blocks $h_t^{(k)}$ in multi-hidden layers of LSTM are capable of capturing the complex dependencies among successive samples. However, the deep LSTM structure also requires more training data than HMM and CRF. To make full use of the limited training data, we adopt a multi-task framework to merge the data $\tilde{X}_{1:T}^{(j)}$ from different users for the parameters training, and eventually obtain the predicted blood glucose concentration sequence $\hat{X}_{1:T}^{(j)}$ for each user j.

Individual Model Learning. Although the process of glucose metabolism is generic, the dynamics of blood glucose concentration is individual-specific [2]. Thus it is important to personalize the prediction model for each user. However, the unified parameters in LSTM can hardly represent the individual blood glucose characteristics. To address this issue, we add an individual learning layer to train personalized output for each user. Specifically, given $\hat{X}_{1:T}^{(j)}$ of user j, we calculate $\hat{y}_{1:T}^{(j)}$ by transferring it into a personal space using $\hat{y}_{1:T}^{(j)} = g(W_M X_{1:T}^{(j)})$, where W_M is a personal matrix to store individual information, and $g(\cdot)$ is the ReLU activation function.

Loss Function and Model Training. A quadratic loss function is adopted to measure the error L between the inferred $\hat{y}_{1:T}^{(j)}$ and the

true values $y_{1:T}^{(j)}$. We use L_2 regularization to enhance the generalization performance of the deep model. The final loss function is calculated as $L = \sum_{j=1}^{l} ||y_{1:T}^{(j)} - \hat{y}_{1:T}^{(j)}||_2 + \lambda_1 ||W_{N \times M}||_2 + \lambda_2 ||W_M||_2$.

Hyperparameters are optimized via Bayesian Optimization. We deploy this deep learning framework with Tensorflow and select the Back Propagation Through Time (BPTT) to train our model.

3 PRELIMINARY EVALUATION

Dataset. We evaluate the performance of MT-LSTM using the same dataset in [4].

Performance. Table 1 shows the prediction accuracy assessed by RMSE. MT-LSTM outperforms both classic shallow regression models (Lasso regression and Ridge regression) and conventional deep model (LSTM), which validates the effectiveness of data sharing using multi-time-series structure learning. MT-LSTM also yields 16.67% lower errors with automatic feature learning (compared with manual feature selection, denoted by MT-LSTM$_m$).

Table 1: Performance comparison.

Model	Lasso	Ridge	LSTM	MT-LSTM$_m$	MT-LSTM
RMSE (mmol/L)	1.30	1.82	1.52	0.91	0.78

Case Study. One important application of blood glucose concentration prediction is to alarm potential high (>7.8 mmol/L) and low (<3.9 mmol/L) blood glucose levels in advance. Table 2 shows the accuracy for abnormal blood glucose level prediction.

Table 2: Prediction accuracy of blood glucose levels.

Blood Glucose Level	High	Normal	Low
Accuracy	85.14%	81.43%	93.46%

4 CONCLUSIONS

Predicting blood glucose concentration is advantageous for timely blood glucose control. In this work, we propose MT-LSTM, a deep learning framework that *(i)* automatically learns feature representation and *(ii)* models multiple blood glucose time-series from different users to efficiently learn from the limited training data and accurately predict blood glucose concentration for each user. Experiments on 112 users demonstrate MT-LSTM is superior than the conventional methodologies in prediction accuracy.

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