A Glucose Prediction Model based on Variational Mode Decomposition and Least Squares Support Vector Regression

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Abstract. Online prediction of subcutaneous glucose concentration plays a critical role in glucose management for type 1 diabetes. In this work, a new method combining Variational Mode Decomposition (VMD) and Least Squares Support Vector Regression (LSSVR) is proposed with three main stages to improve the prediction accuracy. Firstly, the time series of blood glucose are decomposed into different frequency series by VMD method. Secondly, the LSSVR model is trained to predict each subsequence. Finally, the predicted sequences are reconstructed to obtain the overall glucose predictions. The experimental results demonstrate the effectiveness and accuracy of the proposed model for short term glucose prediction.

1. Introduction

Type 1 diabetes (T1D) is a disease characterized by the inability of the body to regulate blood glucose concentration[1, 2]. In recent years, with development of Continuous Glucose Monitoring system (CGMs), new opportunities for glycemic management appear by detecting the glucose values of subcutaneous interstitial fluid through continuous glucose sensors and providing blood glucose concentrations with predefined time intervals. In order to design an effective glucose regulations for T1D patients, a reliable and appropriate prediction model becomes necessary to obtain an accurate 30min short-term-ahead blood glucose concentration[3].

Consider of the nonlinear and non-stationary of blood glucose time series, the prediction accuracy and the computational efficiency of the prediction model has attracted more and more attention. In the literatures, various approaches have been proposed to predict blood glucose levels. Compared with physiological model, the data-driven model could neglect the prior knowledge of physiology and only applies time-series signals, from CGM, to predict short-term glucose concentration. Sparacino et al.[4] compared the predictive performance of a first-order polynomial model with a first-order autoregressive (AR) model, which obtained that the AR model with time-varying parameters shown more accurate prediction performance then general physiological model. Pérez et al.[5] used a feed-forward ANN model based on the CGM values, and Hamdi et al.[6] proposed the combination of SVR method and differential evolution algorithm to improve prediction performance. Recently, the decomposition method has been utilized in prediction models to analyze the time-series[7, 8]. The most commonly used signal decomposition methods include wavelet transform, Empirical Mode Decomposition (EMD) and Variational Mode Decomposition (VMD)[9-11]. In this paper, a designed VMD method is used to overcome the mode mixing problem of EMD, and the LSSVR algorithm is applied to learn from different mode component, and obtains 30min short-term-ahead predicted components. Then, superimposing the predicted components to obtain the obtain the overall glucose
predictions.

The rest of the paper is organized as follows: Section 2 introduces the general principle of VMD method, and Section 3 describes the LSSSVR algorithm. Section 4 proposes the VMD-LSSSVR prediction model and the parameter selection regulation. The simulation experiments and the discussion of results are introduced in Section 5 which includes a comparison with previous works to highlight the reliability of the proposed method. Finally, the conclusion is presented in Section 6.

2. Variational Mode Decomposition (VMD) methodology

VMD algorithm was proposed in the basis of EMD algorithm in 2014[12], which could avoid model mixing. It is a decomposition method commonly used for non-stationary signals. The purpose of VMD is to decompose the original signal into K band-limited modes $u_k$ (k=1, ..., K), and it assumes that each subseries is considered to compact around the center pulsation ($\omega_k$). The bandwidth of each subseries is estimated as following steps: The time series of blood glucose is decomposed by Hilbert transform, and $u_k$ is calculated to have the corresponding unilateral spectrum; The frequency spectrum of each mode $u_k(t)$ is modulated to the corresponding baseband, by mixing $e^{-j\omega_k t}$ to the respective estimated the center frequency ($\omega_k$); The bandwidth is estimated by calculating the squared $L^2$ norm of demodulated signal gradient. Subsequently, constrained variational problem could be described as follows:

$$\min_{\{u_k\},\{\omega_k\}} \left\{ \sum_k \left\| \frac{\partial}{\partial t} \left[ (\delta(t) + \frac{1}{\pi t}) * u_k(t) \right] e^{-j\omega_k t} \right\|_2^2 \right\}$$

s.t. $\sum_k u_k = f$

where $\delta(t)$ is the Fermi-Dirac distribution, $\{u_k\} = \{u_1, ..., u_K\}$, $\sum_k = \sum_{k=1}^K \{\omega_k\} = \{\omega_1, ..., \omega_K\}$, and $\omega_k$ are the center frequency of each mode of $u_k$. In order to obtain the optimal solution, the augmented Lagrange equation is introduced as:

$$L(\{u_k\},\{\omega_k\},\lambda) = \alpha \sum_k \left\| \frac{\partial}{\partial t} \left[ (\delta(t) + \frac{1}{\pi t}) * u_k(t) \right] e^{-j\omega_k t} \right\|_2^2 + \|f(t) - \sum_k u_k(t)\|_2^2 + \langle \lambda(t), f(t) - \sum_k u_k(t) \rangle$$

where $\alpha$ is the quadratic penalty factor and $\lambda(t)$ is the Lagrangian multiplier. Iteratively optimize Lagrange equation of Equation (2) by alternate direction method of multipliers (ADMM). The solutions are expressed as:

$$\hat{\omega}_k^{n+1} = \frac{\hat{\omega}_k^n - \sum_k \hat{u}_k^n \hat{\lambda}(\omega) + \frac{\lambda(\omega)}{2}}{1 + 2\alpha(\omega - \omega_k)^2}$$

$$\hat{u}_k^{n+1} = \frac{\int_0^\infty \omega \hat{u}_k(\omega)^2 d\omega}{\int_0^\infty \hat{u}_k(\omega)^2 d\omega}$$

where $n$ is the number of iterations, $\hat{f}(\omega)$, $\hat{\omega}_k^{n+1}$, $\hat{u}_k(\omega)$, and $\hat{\lambda}(\omega)$ stand for the Fourier transform of $f(t), u_k^{n+1}(t), u(t)$ and $\lambda(t)$.

3. Least Squares Support Vector Regression (LSSVR)

The Support Vector Regression (SVR) is one of the regression algorithms in machine learning based on statistical learning theory. LSSVR is an improved algorithm of SVR, which replaces inequality constraints into equality constraints. Then, the quadratic programming problem in SVR could be converted into linear equations. Therefore, the LSSVR algorithm could reduce computational complexity and increase computational speed.

The training dataset of the LSSVR is $T = \{(x_i, y_i) | i = 1, 2, 3, ..., l\}$, where $x_i$ is the input data $x_i \in \mathbb{R}^n$, and $y_i$ is the output data $y_i \in \mathbb{R}^n$. The optimal decision function can be identified by the high-dimensional feature space. The regression function adopted by LSSVR can be described as follows
\[ y = \omega^T \Psi(x) + b \]  

(5)

where \( \Psi(x) \) is the nonlinear mapping function, \( \omega \) represents the weight coefficient vector, and \( b \) stands for bias. The objective function is as follows:

\[
\begin{align*}
\min Z(\omega,e) &= \frac{1}{2} \omega^T \omega + \frac{\gamma}{2} \sum_{i=1}^{T} e_i^2 \\
\text{s.t. } y_i &= \omega^T \Psi(x_i) + b + e_i
\end{align*}
\]

(6)

where \( e_i \) represents the error and \( \gamma \) donates the penalty coefficient. The optimization problem in Eq. (6) can be translated into linear equations by means of the Lagrange which solved be based on Karush-Kuhn-Tucher (KKT) conditions. Subsequently, in this study, Gaussian Radial Basis Function (RBF) is chosen as the kernel function of LSSVR, and the expression of the RBF kernel function is as follow:

\[ K(x,x_i) = \exp \left\{ -\frac{||x-x_i||^2}{2\sigma^2} \right\} \]

(7)

where \( \sigma^2 \) is kernel parameter. Therefore, the function of LSSVR can be obtained as follows:

\[ y = \sum_{i=1}^{T} \lambda_i K(x,x_i) = \sum_{i=1}^{T} \lambda_i \exp \left\{ -\frac{||x-x_i||^2}{2\sigma^2} \right\} \]

(8)

For the parameters \( \gamma \) and \( \sigma^2 \), the trial-and-error method is considered and applied to obtain the optimal parameters which has the basic guideline as follows: Firstly, randomly initializes the parameters, and observes the prediction accuracy. Then, fixes one parameter, and changes the other until the prediction accuracy becomes a constant level. Finally, gets the other parameter in the same steps.

4. Overview of the VMD-LSSVR model

The structure of the proposed VMD-LSSVR prediction model is mainly composed of three stages, which could be described as follows:

Stage 1: The data preprocessing is adapted to reset the historical glucose data into 5-minutes sampling points. Then the glucose data are decomposed by the VMD-based decomposition model, and obtain a number of different subseries \{\( u_1, u_2, ..., u_K \)\}, and the training sets and test sets are constructed by subseries.

Stage 2: The forecasting components of subseries are trained by LSSVR algorithm. Then, updating the training sets by current glucose values to achieve online prediction.

Stage 3: The components of all modes are superimposed to obtain the overall glucose prediction.

5. Simulation Experiments and Results

In this section, the prediction method mentioned above were programmed in MATLAB 2019a to verify for online training and short-term glucose prediction. The experiments are based on the blood glucose time series from a silico subject in the FDA-approved UVa/Padova metabolic simulator. The entire dataset has a total of 863 points. The training samples and forecasting samples are made by using a sliding window with a capacity of 500 that moves one step per iteration. In the window, the first 494 blood glucose data are training samples, and the rest are forecasting samples. First of all, the training samples are decomposed into 7 separate sequences by VMD. Next, all subsequences are applied to predict the corresponding prediction values by LSSVR algorithm. Then, the predictions could be obtained from the combined 7 subsequences.

In order to assess the prediction performance of the VMD-LSSVR algorithm, Figure 1 presents a comparison between the actual blood glucose and the prediction results for a T1D patient for 30min prediction horizon (PH=30min). It can be seen that the proposed VMD-LSSVR method is remarkably accurate and could be potentially applied for time series prediction.
Figure 1. Prediction results of blood glucose for PH=30 min.

The Clarke error grid is shown in Figure 2. As shown, the proposed model has good fitting performance, and most points fall in ‘A’ area, which indicates that the accuracy of VMD-LSSVR model is high and within the acceptable range.

Figure 2. The Clarke error grid of blood glucose prediction for PH=30 min.

To demonstrate that the proposed method can effectively improve the prediction performance compared to another method, a comparable experiment is carried out in this paper. Figure 3 illustrates the comparison between the actual value and the predicted values by LSSVR and VMD-LSSVR. It is obvious that the proposed method VMD-LSSVR has better prediction performance, resulting in higher accuracy.
Figure 3. Blood glucose prediction of different algorithms for PH=30 min.

where $\hat{y}_i$ denotes the short-term glucose prediction, $y_i$ donates the test set, $i$ represents the sampling point, $N$ stands for the total number of blood glucose time series and $t$ denotes the number of training sets.

To characterize the prediction accuracy compared with actual CGM values, two metrics, Root Mean Square Error (RMSE) and Mean Absolute Percentage Error (MAPE), are used and calculated as following equations:

$$RMSE = \sqrt{\frac{1}{N-t}\sum_{i=t+1}^{N}(\hat{y}_i - y_i)^2}$$  \hspace{1cm} (9)

$$MAPE = \frac{1}{N}\sum_{i\in N}\left|\frac{y(i) - \hat{y}(i)}{y(i)}\right| \times 100\%$$  \hspace{1cm} (10)

The RMSE and MAPE for LSSVR and VMD-LSSVR are reported in Table 1. It is readily observed that the performance of the proposed prediction algorithm is superior than the conventional LSSVR algorithm.

Table 1. Prediction accuracy metrics of LSSVR and VMD-LSSVR.

| Model      | RMSE   | MAPE (%) |
|------------|--------|----------|
| LSSVR      | 15.9093| 5.5652   |
| VMD-LSSVR  | 8.9067 | 3.0537   |

6. Conclusion
In this paper, a new prediction algorithm, VMD-LSSVR, is developed for online prediction to make the optimum structure and accurate predictions. Through the VMD-based decomposition model, the nonlinear and nonstationary characteristics of blood glucose time-series are considered, and the 30min-ahead glucose concentration is obtained by summing all predictions of each subseries. Simulation results illustrates that the proposed method yielded better online prediction performance in terms of accuracy and stability than the conventional standard LSSVR.

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