Sparse representation models of continuous glucose monitoring time-series

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***Abstract*— Continuous glucose monitoring (CGM) is essential towards effectively managing type 1 diabetes. Developing CGM time-series models may help identify clinically-meaningful signal components and rule-out noise providing new insights into treatment. As a step towards this goal, we propose to use sparse representation techniques with appropriately designed dictionaries to express CGM signals as a linear combination of a small set of knowledge-driven atoms. Results on a dataset of 25 patients diagnosed with type 1 diabetes indicate that the proposed framework is a viable solution for modeling CGM time-series reaching relative reconstruction error of 0.08 and suggest that this approach can be used to interpret the underlying CGM time-series in relation to clinical assessments.**

I. Introduction

Type 1 diabetes is a chronic condition related to the body's ability to produce insulin, an essential hormone to energy production. Patients suffering from this disease have to become actively involved in its management. Continuous glucose monitoring (CGM) systems can effectively provide real-time blood-glucose measures and warn individuals regarding dangerously high or low glucose levels [1]. While such systems have a great potential towards improving diabetes-related outcomes, the corresponding time-series might contain multiple sources of noise related to sensor limitations, needle drifts, and calibration issues. Thus, signal processing steps are needed to identify the meaningful signal components and appropriately interpret the underlying information. CGM time-series depict a characteristic structure over time, since the corresponding signal increases abruptly after food intake and slowly recovers. Taking this into account, we propose to use sparse representation methods with appropriately-designed signal-dependent dictionaries.

II. Methods and Results

Our data come from the publicly available DirecNet repository. The dataset contains 25 participants (8-19 years old) with type 1 diabetes wearing a continuous glucose monitor for 6-7 days [2]. Glucose values were sampled every 5 minutes resulting in 67,388 measurements.

Sparse decomposition models represent a signal using a small set of exemplar sub-signals, called "atoms", that are selected from a larger pool, called "dictionary". Dictionaries are designed from a set of parametric functions in a knowledge-driven way in order to simulate the expected structure of the CGM signal. For the current study, we used Bateman functions to represent the CGM signal fluctuations and straight lines to capture the overall glucose levels. Bateman functions are written as $\phi_1(t) = \left(e^{-b(st-t_0)} - e^{-a(st-t_0)}\right) u(t-t_0)$, $a < b$, where $u(t)$ is the step function centered at 0, $a \in \{.2, .4 \ldots, 2\}$ and $b \in \{.4, .8 \ldots, 2\}$ are parameters related to the steepness of recovery and onset of a CGM fluctuation, $s \in \{.6, .12 \ldots, .60\}$ is the time scale, and $t_0 \in \{0, 2, 4, \ldots, 120\}$ captures the time-shift of an atom within an analysis frame. We further included time-reversed atoms, i.e. $\phi_2 = \phi_1(120 - t)$, to capture multiple shapes of CGM fluctuations. The analysis window was empirically set to 120 samples (i.e. 10 hours) to account for enough context and variability within the original time-series, while the window shift was set to 40 samples. These resulted in a dictionary of 30,063 atoms. Signal decomposition was performed using the orthogonal matching pursuit (OMP) algorithm.

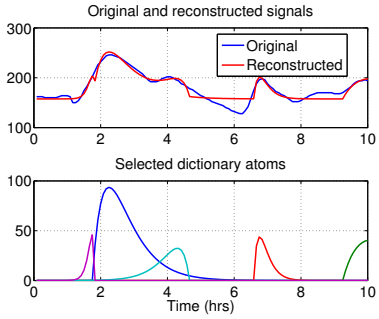

Fig. 1. Example of original and reconstructed continuous glucose monitoring (CGM) time-series and the selected Bateman atoms.

Results indicate a relative reconstruction error of 0.081. Visual inspection of the original and reconstructed signals (Fig. 1) suggests that the proposed model achieves reliable signal representation, while the selected atoms can be meaningfully interpreted according to the corresponding signal fluctuations. Future work will quantitatively evaluate this approach in relation to clinically-relevant outcomes.

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