X-Calibration

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Machine Learning for Healthcare

Learning Insulin-Glucose Dynamics in the Wild

Andrew C. Miller

ACMILLER@APPLE.COM

Apple Seattle, WA, USA

Nicholas J. Foti

NICHOLAS_FOTI@APPLE.COM

Apple Seattle, WA, USA

Emily Fox Emily_fox@apple.com

Apple Seattle W

Seattle, WA, USA

Summary

- new model of carbs-insulin-glucose dynamics for type 1 diabetes
- fully learned models like LSTM yield implausible predictions
- this work combines mechanistic knowledge and prob. models
- glucose levels are noisy measurement of latent state, which evolves wrt a diff eq.

Data Collected

- two T1D participants using a continuous glucose monitor (CGM) and an insulin pump
- instantaneous continuous blood glucose measurements
- other measurements using Apple Healthkit: estimated carb ingestion + active energy burned.

Cohort + Validation

- management of T1D highly personalized.
- here, study two individuals
- data: 150 days, train/valid on 120 days, test prediction on 30 days
- one sample every 5 min., each participant has over 40k points recorded

Data Example

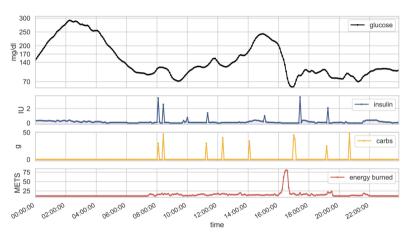


Figure 1: Data for a single day: blood glucose as measured by CGM, insulin delivered by pump, user carbohydrate log, and energy use captured every five minutes by HealthKit.

Existing Methods

- prob. models:
 - can predict glucose change from carbs, insulin
 - unstable for long term predictions (why?)
- physiological models
 - predict over long periods in controlled settings
 - UVA/Padova simulator: interaction of glucose, insulin, and orally ingested carbohydrates (Dalla Man et al., 2014)
 - not robust to noise and missing data, doesn't account for fluctuations in insulin sensitivity, meal absorption

Model

$$\begin{aligned} & \boldsymbol{z}_0 \sim \mathcal{N}(\boldsymbol{\mu}_0, \boldsymbol{\Sigma}_0) & \text{initial latent state} & & (1) \\ & \boldsymbol{z}_t \sim A \boldsymbol{z}_{t-1} + B \boldsymbol{a}_t + Q^{1/2} \boldsymbol{\epsilon}_t, \ \boldsymbol{\epsilon}_t \sim \mathcal{N}(\mathbf{0}, I) & \text{latent temporal dynamics} & (2) \\ & \boldsymbol{d}_t = \text{NN}_{\phi}(\boldsymbol{z}_t) & \text{dynamic simulator params.} & (3) \\ & \boldsymbol{x}_t = \text{UVA-step}(\boldsymbol{x}_{t-1}, \boldsymbol{d}_t, \boldsymbol{u}_t, \boldsymbol{s}, \boldsymbol{\Delta}_t) & \text{T1D simulator} & (4) \\ & \boldsymbol{y}_t \sim \mathcal{N}(\text{CGM}(\boldsymbol{x}_t, \boldsymbol{s}), \sigma^2) & \text{CGM observation} & (5) \end{aligned}$$

where $\mathbf{z}_t \in \mathbb{R}^D$, $\mathbf{d}_t \in \mathbb{R}^K$, $\mathbf{x}_t \in \mathbb{R}^{13}$, $\mathbf{u}_t \in \mathbb{R}^J$, and $\mathbf{s} \in \mathbb{R}^J$. The dimensionality of the latent space D can be tuned. The physiological state \mathbf{x}_t size is fixed by the simulator definition. The simulator parameters chosen to be dynamic, K, and static, J, is a hyperparameter setting, which we fix for this work and describe in Appendix A.

Diff Eq

$$\frac{d\mathbf{x}_t}{dt} = f^{(uva)}(\mathbf{x}_t, \mathbf{u}_t, \mathbf{p}), \qquad (6)$$

where the dynamics are a function of the current state, time-varying inputs, and static parameters, respectively.⁵ The evolution from state x_{t-1} to x_t involves integrating these dynamics over the time increment Δ_t , which in this work we assume is always one so that:

$$\boldsymbol{x}_{t+1} = \int_{t}^{t+1} f^{(uva)}(\boldsymbol{x}_{t'}, \boldsymbol{u}_{t}, \boldsymbol{p}) dt'$$
 (7)

$$\triangleq \mathtt{UVA-step}(\boldsymbol{x}_t,\boldsymbol{u}_t,\boldsymbol{p}). \tag{8}$$

Results

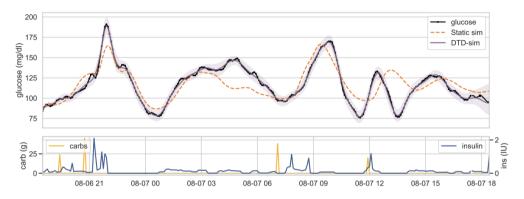


Figure 3: Static UVA/Padova lacks the capacity to describe real CGM data. Top: model fit comparison of static UVA/Padova simulator and dynamic DTD-sim model for a full day of CGM data. Bottom: corresponding insulin and carbohydrate data. Without varying parameters in time and accounting for data noise, the T1D simulator model does not describe observed data.