Journal of Diabetes Science and Technology
Volume 3, Issue 5, September 2009

ORIGINAL ARTICLES

Experimental Evaluation of a Recursive Model Identification Technique for Type 1 Diabetes

Daniel A. Finan, Ph.D.,[1,2,3] Francis J. Doyle III, Ph.D.,[1,2] Cesar C. Palerm, Ph.D.,[1,2,4] Wendy C. Bevier, Ph.D.,[2] Howard C. Zisser, M.D.,[1,2] Lois Jovanovič, M.D.,[1,2] and Dale E. Seborg, Ph.D.[1,2]

Abstract

Background:

A model-based controller for an artificial β cell requires an accurate model of the glucose–insulin dynamics in type 1 diabetes subjects. To ensure the robustness of the controller for changing conditions (e.g., changes in insulin sensitivity due to illnesses, changes in exercise habits, or changes in stress levels), the model should be able to adapt to the new conditions by means of a recursive parameter estimation technique. Such an adaptive strategy will ensure that the most accurate model is used for the current conditions, and thus the most accurate model predictions are used in model-based control calculations.

Methods:

In a retrospective analysis, empirical dynamic autoregressive exogenous input (ARX) models were identified from glucose–insulin data for nine type 1 diabetes subjects in ambulatory conditions. Data sets consisted of continuous (5-minute) glucose concentration measurements obtained from a continuous glucose monitor, basal insulin infusion rates and times and amounts of insulin boluses obtained from the subjects' insulin pumps, and subject-reported estimates of the times and carbohydrate content of meals. Two identification techniques were investigated: nonrecursive, or batch methods, and recursive methods. Batch models were identified from a set of training data, whereas recursively identified models were updated at each sampling instant. Both types of models were used to make predictions of new test data. For the purpose of comparison, model predictions were compared to zero-order hold (ZOH) predictions, which were made by simply holding the current glucose value constant for p steps into the future, where p is the prediction horizon. Thus, the ZOH predictions are model free and provide a base case for the prediction metrics used to quantify the accuracy of the model predictions. In theory, recursive identification techniques are needed only when there are changing conditions in the subject that require model adaptation. Thus, the identification and validation techniques were performed with both "normal" data and data collected during conditions of reduced insulin sensitivity. The latter were achieved by having the subjects self-administer a medication, prednisone, for 3 consecutive days. The recursive models were allowed to adapt to this condition of reduced insulin sensitivity, while the batch models were only identified from normal data.

continued →

Author Affiliations: [1]Department of Chemical Engineering, University of California, Santa Barbara, California; [2]Sansum Diabetes Research Institute, Santa Barbara, California; [3]Currently with Department of Informatics and Mathematical Modeling, Technical University of Denmark, Denmark; and [4]Currently with Medtronic Diabetes, Northridge, California

Abbreviations: (AR) autoregressive, (ARMA) autoregressive moving average, (ARMAX) ARMA with exogenous inputs, (ARX) autoregressive exogenous input, (CGMS) continuous glucose monitoring system, (CHO) carbohydrate, (RMSE) root mean square error, (ZOH) zero-order hold

Keywords: artificial β cell, insulin sensitivity, linear dynamic models, recursive estimation, type 1 diabetes

Corresponding Author: Dale E. Seborg, Ph.D., Professor, Department of Chemical Engineering, University of California, Santa Barbara, CA 93106-5080; email address seborg@engineering.ucsb.edu

Abstract cont.

Results:

Data from nine type 1 diabetes subjects in ambulatory conditions were analyzed; six of these subjects also participated in the prednisone portion of the study. For normal test data, the batch ARX models produced 30-, 45-, and 60-minute-ahead predictions that had average root mean square error (RMSE) values of 26, 34, and 40 mg/dl, respectively. For test data characterized by reduced insulin sensitivity, the batch ARX models produced 30-, 60-, and 90-minute-ahead predictions with average RMSE values of 27, 46, and 59 mg/dl, respectively; the recursive ARX models demonstrated similar performance with corresponding values of 27, 45, and 61 mg/dl, respectively. The identified ARX models (batch and recursive) produced more accurate predictions than the model-free ZOH predictions, but only marginally. For test data characterized by reduced insulin sensitivity, RMSE values for the predictions of the batch ARX models were 9, 5, and 5% more accurate than the ZOH predictions for prediction horizons of 30, 60, and 90 minutes, respectively. In terms of RMSE values, the 30-, 60-, and 90-minute predictions of the recursive models were more accurate than the ZOH predictions, by 10, 5, and 2%, respectively.

Conclusion:

In this experimental study, the recursively identified ARX models resulted in predictions of test data that were similar, but not superior, to the batch models. Even for the test data characteristic of reduced insulin sensitivity, the batch and recursive models demonstrated similar prediction accuracy. The predictions of the identified ARX models were only marginally more accurate than the model-free ZOH predictions. Given the simplicity of the ARX models and the computational ease with which they are identified, however, even modest improvements may justify the use of these models in a model-based controller for an artificial β cell.

J Diabetes Sci Technol 2009;3(5):1192-1202