Characterizing the Impact of Diet on Glycemic Variability in Type 1 and Type 2 Diabetes: A Hidden Markov Model Approach

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ABSTRACT

Type 1 diabetes and type 2 diabetes stem from varying causes and typically necessitate distinct management approaches. However, managing blood glucose in both cases is crucial, and diet influence in both cases is an important factor to understand for the optimal management of glycemic variability. Blood glucose management is important for individuals with both diabetes. This study employs the use of a Hidden Markov Model to analyze the intricate interplay between dietary habits and resulting glucose variability in individuals with both type 2 and type 1 diabetes conditions to prevent and reduce long-term complications. The HMM framework helps in characterizing the probabilistic relationships between these factors, providing more insight into the influence and effect of dietary choices on glucose dynamics. We aim to identify patterns and potential predictors of glucose fluctuations by examining transition probabilities between different glycemic states. A comparative analysis between type 1 and type 2 diabetes populations will demonstrate the similarities and differences in the impact of diet on glycemic control. This study contributes to a deeper understanding of the relationship between diet and glucose control. This work focuses mainly on informing the development of personalized dietary interventions for improved diabetes management, which involves a broad focus on utilization of data-driven approaches including continuous glucose monitoring and advanced statistical modeling to ultimately develop an optimal approach towards diabetes care. This study is also helpful in optimal nutritional therapy for type 1 and type 2 patients by understanding the likelihood stages in the ICU admission times.

1 Introduction

Diabetes management remains a significant public health challenge, with type 1and type 2 diabetes affecting millions of individuals. The International Diabetes Federation's 10th Diabetes Atlas estimates 537 million adults (20-79 years) had diabetes in 2021, with a projection of 700 million by 2045.Diabetes mellitus often occurs alongside other chronic conditions, a phenomenon known as comorbidity, which contributes to the complications involving its management and impacts overall health outcomes. These chronic conditions, coupled with risks of severe complications like cardiovascular disease, neuropathy, and nephropathy, emphasize the need for effective glycemic control.

Hidden Markov Models and their derivatives are extensively employed in the modeling of dynamical systems [15, 5]. This reference constitutes a foundational work in the discipline and serves as an excellent introduction to Hidden Markov Models. These models are exceptionally well-suited for the representation of sequential data, wherein the underlying system responsible for generating the observations is presumed to possess hidden states. Although these hidden states are not directly observable, they exert an influence on the observed data. The HMM framework improves the modeling of probabilistic relationships between the hidden states and the observed data, thus enabling the derivation of inferences regarding the hidden states and the prediction of future observations. The maintenance of optimal glycemic control poses a significant challenge for individuals with diabetes, as it is characterized by dynamic and complex glucose regulation, as explained by [8, 4] .[14] justifies the use of single-layer hmm when enough training data is available. [3, 7] . discuss machine learning approaches for diabetes prediction. A dynamic system that employs a machine learning approach is vital for optimal control of diabetic conditions; the study makes use of both. Recent studies have highlighted the potential of hidden Markov models in demonstrating the complex and stochastic nature of glucose regulation in diabetes, as detailed by [2] . According to [6] , observations can be considered as multidimensional vectors, and maximum likelihood estimation training can be pursued using the Expectation-

Maximization iterative algorithm to facilitate the Hidden Markov Model. This unsupervised training process allows the HMM to cluster data points that represent similar stages of the disease into the same state, driven by the statistical similarity of biomarker measurements within each cluster. The effective application of multi-layer Hidden Markov Models for modeling glucose dynamics in diabetes is thoroughly explained by [8]. Comparing different Hidden Markov Models applied to type 1 diabetes patients, as discussed by [8], is beneficial for model framework development. The Markov assumption's validity was also confirmed by [9], justifying the model's construction based on this property, given that the consistent nature of the type 1 diabetes dataset is explained by [8, 9], which focuses on defining three diabetic states and their application to real-world data. [10] work clarifies classifying high-risk and low-risk samples for effective HMM training, including the usage of 10-fold cross-validation for optimal model performance [11], which lays its emphasis on improving data quality collected from patients using wearables in free-living conditions, moving beyond controlled environments. [5] gave an explanation on how to simulate the data for modal validity and training robustness, which is significant for the real world applications of the model. [1] explains the way to classify the clinical stages of type 2 diabetes using a variant of the hidden Markov model. [12] helped to arrive at a global optimum using different initialization and improve the reliability of the model. [16] explains how to facilitate data-driven decision-making for a real-world scenario. Finally, the research by [13] demonstrates the integration of Hidden Markov Models with other machine learning techniques, such as reinforcement learning, which further enhances the capabilities of disease progression modeling and decision support for diabetes management.

The outcomes of this research will allow the creation of targeted interventions, laying its focus mainly on optimization of dietary behaviours to enhance glycemic control in individuals diagnosed with type 1 and type 2 diabetes. It is imperative to examine specific characteristics and apply them to simulate data derived from the modal. Analyzing the dynamic interactions between dietary intake and glycemic variability can help us to discover valuable insights that support personalized treatment strategies. This research has an advanced approach than existing studies by applying a hidden Markov model to both type 1 and type 2 patients with similar hidden state diet and comparing the control it has on glycemic level. By including relevant medical expertise, this study will propose novel analytical frameworks to demonstrate the distinct progression pathways of type 1 and type 2 diabetes, providing a more comprehensive and insightful way of understanding the disease trajectories and thereby the need for the development of tailored interventions for a significant improvement in the patient outcomes. This methodology offers a comprehensive framework for addressing the three fundamental challenges of Hidden Markov Models, which includes the solutions, the minimization of local optima and lastly the implementation of the Baum-Welch algorithm with diverse initializations.

Key components of this study include the following:

- The outcomes of this research will contribute to the development of targeted interventions designed to optimise dietary habits, which enhance insulin adherence and ultimately improve glycemic control for individuals with type 1 and type 2 diabetes.
- The proposed model focuses on capturing the latent states of dietary behaviors and insulin management, along with their impact on observed blood glucose levels over time. This will be achieved using the expectation-maximization technique within a Hidden Markov Model.
- By modeling the temporal patterns and transitions of these factors, we can gain valuable insights for designing personalized and tailored treatment strategies.

2 Materials and Methods

2.1 Materials

The authors used secondary data on type 2 Diabetes Mellitus as utilized by Zhu, which included 100 Type1 patients with 5-12 days of data each. The authors randomly selected 50 patients with a total of 900 follow-up data points for their analysis. This study also used data from 12 Type-1 diabetes patients from a Chinese source (ShanghaiT1DM). The dataset consisted of 572 glucose level readings taken every 15 minutes over 143 hours for each patient analysis was carried out using a Hidden Markov model With one hidden layer and one Emission layer. The hidden layer is categorized into unbalanced and balanced dietary regimens. A balanced diet is defined for Type 1 and Type 2 diabetes patients by daily consumption that includes the following food groups: fruits (such as kiwi and apple), vegetables, proteins, moderate grain intake, and other items such as milk, corn soup, and wax gourd. The emission layer comprises three states: Hypo (CGM < 70), Normal (70 ≤CGM ≤150), and Hyper (CGM > 150).

2.2 Methods

2.2.1 Forward backward and Viterbi algorithm

For a single-layer Hidden Markov Model, the following are the inputs of the model.

- π1,π2: The initial probability vectors for the hidden states in Type1 and Type2 patients respectively.
- T1,T2: The transition probability matrix for the hidden layer. T1[i][j] ,T2[i][j] represent the probability of transition from dietary state i to dietary state j in the type 1 patient type 2 patient, respectively.
- E1,E2: The emission probability matrix. E1[i][j], E2[i][j] represent the probability of observing the glucose level j given that the current state of the diet is i. This links the hidden dietary state to the observed glucose level in type1 and type2 patients, respectively.
- N1, N2: the number of possible diet states in type 1 and type2 patients, respectively.
- O1, O2: The observed sequence of glucose levels of type 1 and type 2 with size L1 and L2 respectively

2.2.2 Algorithm Design and Implementation

Initialization:

$\alpha 11(i) = \pi 1i * E1i(O11)\beta 1L1(i) = 1$ for $i = 1, 2, ..., N1\alpha 21(i) = \pi 2i * E2i(O21)$

$\beta 2L2(i) = 1$ for $i = 1, 2, ..., N2$

Induction:

$\alpha 1l1+1(j) = N1\ i=1[\alpha 1l1(i) * T1(i, j)] * E1(j, O1l1+1)$ for $l1 = 1, 2, ..., L1 - 1 and j = 1, 2, ..., N1$

$\beta 1l1(i) = N1\ j=1 T1(i, j)E1(j, o1l1+1)$ for $l1 = L1 - 1, L1 - 2, ..., 1$ and $1 \le i \le N1$

START

$\pi 21$

$\pi 22$

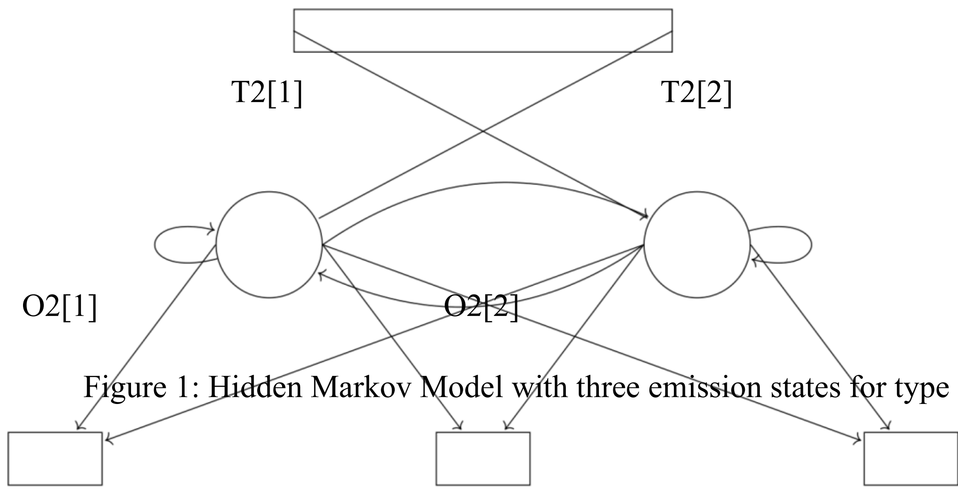

Figure 1: Hidden Markov Model with three emission states for type 2

$\alpha 2l2{+}1(j) = N2\ i{=}1[\alpha 2l2(i) * T2(i, j)] * E2(j, O2l2{+}1)$ for $l2 = 1, 2, ..., L2 - 1 and j = 1, 2, ..., N2$

$\beta 2l2(i) = N2\ j{=}1 T2(i, j) E2(j, o2l2{+}1)$ for $l1 = L2 - 1, L2 - 2, ..., 1$ and $1 \leq i \leq N2$

Termination:

$P(O1|\lambda 1) = N1$

$i{=}1\alpha 1L1(i)\ P(O2|\lambda 2) = N2\ i{=}1\alpha 2L2(i)$

Initialization:

$\delta 11(i) = \pi 1i * E1i(O1)$ for $i = 1, 2, ..., N1$ $\psi 11(i) = 0$

$\delta 21(i) = \pi 2i * E2i(O2)$ for $i = 1, 2, ..., N2$ $\psi 21(i) = 0$

Induction:

$\delta 1l1(j) = \max[\delta 1l1{-}1(i) T1(i, j)] E1j(O1l1)$ for $j = 1, 2, ..., N1$ for $l1 = 2, ..., L1{-}1$

$\delta 2l2(j) = \max[\delta 2l2{-}1(i) T2(i, j)] E2j(O2l2)$ for $j = 1, 2, ..., N2$ for $l2 = 2, ..., L2{-}1$

Termination:

P1 $*$= max($\delta L1(i)$)

for$i$ = 1, ..., $N1$ $P2$*=max[$\delta L2(i)$] for$i$ = 1, ..., $N2$

2.2.3 Baum-Welch algorithm design and implementation

Input: O1, O2: Observed glucose level sequences for Type 1 and Type 2 patients respectively.

Output: π1, π2: Initial state probability vectors for Type 1 and Type 2.

T1, T2: Transition probability matrices for Type 1 and Type 2.

E1, E2: Emission probability matrices for Type 1 and Type 2.

Initialization:

- Set initial guesses for π1, π2, T1, T2, E1, E2.
- Set iteration counter k = 0.
- Set initial log-likelihoodL(k)= −∞

Repeat until convergence:

1. E-step (for Type 1 and Type 2 patients):

- Compute the forward and backward probabilities using Observation and the current parameters.
- Compute the state probabilities and transition probabilities using the forward and backward probabilities

2. M-step (for Type 1 and Type 2 patients):

- Update Initial probabilities and Transition matrix using state occupation probabilities.
- Update emission matrix using state occupation probabilities and observations.

Compute the log-likelihood:

$L^{k+1} = \sum_{l1=1}^{L1} log\,(\sum_{i=1}^{N1})\alpha^{k}_{i}$

$L^{k+1} = \sum_{l2=1}^{L2} log\,(\sum_{i=1}^{N2})\alpha^{k}_{i}$

L(k+1) given the updated parameters for both Type1 and Type2 patients respectively.

Check for convergence:

If

|L(k + 1) −L(k)| ≤ threshold

then

stop.

otherwise

Increment k: k = k + 1. The Baum-Welch algorithm yields refined parameters for the Hidden Markov Model.

2.2.4 Simulation

The simulation was performed to know the behaviour of the dietary habits, using the Markov technique for the hidden layers. A sample sequence 10,000 was generated from the original data to check the modal validity.

3 Result and Discussion

3.1 Initial Probability Vectors

The probabilities of 0.49423113 and 0.50576887 represent the likelihoods of initiating in each of the two hidden states within the dietary layer of the Hidden Markov Model designed for the study of Type 1 Diabetes. This initial probability distribution indicates a slightly higher propensity to begin in an unbalanced dietary state for cases related to Type 1 diabetes. Similarly, the probabilities of 0.4785436 and 0.5214564 correspond to the likelihoods of initiating in each of the two hidden states within the same layer for the context of Type 2 Diabetes. While both models indicate a slightly higher initial probability of an unbalanced state, this difference is more pronounced in the Type 2 diabetes model.

3.2 Hidden layer transition probability matrices

In both Type 1 and Type 2 diabetes, the dietary transition probabilities are contingent solely on the current state, whether balanced or unbalanced, without consideration of prior dietary states.

3.2.1 Type 1

Within the framework of Type 1 diabetes, an individual presently in a Balanced state manifests a 53.31% likelihood of maintaining this state and a 46.69% likelihood of transitioning to an Unbalanced state. Conversely, if the individual is in an Unbalanced state, there exists a 46.76% probability of transitioning to a Balanced state and a 53.24% probability of remaining Unbalanced.

$$\begin{bmatrix} 0.5331 & 0.4669 \\ 0.4676 & 0.5324 \end{bmatrix}$$

3.2.2 Type 2

In the context of Type 2 diabetes, a patient currently in a Balanced state has a 51.13% probability of remaining there and a 48.87% probability of transitioning to an Unbalanced state. If the patient is in an Unbalanced state, the probabilities are

45.57% for transitioning to a Balanced state and 54.43% for remaining Unbalanced.

$$\begin{bmatrix} 0.5113 & 0.4887 \\ 0.4557 & 0.5443 \end{bmatrix}$$

3.3 Emission probabilities

Among individuals diagnosed with Type 1 diabetes, adherence to a nutritious diet is correlated with enhanced glycemic control. Specifically, individuals adhering to a healthful dietary regimen demonstrate an increased likelihood of attaining normal glucose levels (38.24%) compared to those with unhealthy dietary patterns (23.45%). Nonetheless, many patients adhering to a healthy diet may still encounter episodes of atypical glucose levels. This suggests that dietary modifications alone may be insufficient for optimal glycemic management. Consequently, it is often necessary to adopt a comprehensive strategy incorporating adjudicative therapies such as insulin administration, physical activity, and lifestyle modifications to achieve and maintain desired glycemic control in individuals with Type 1 diabetes.

$$\begin{bmatrix} 0.2029 & 0.4147 & 0.3824 \\ 0.2453 & 0.5202 & 0.2345 \end{bmatrix}$$

Within the cohort of patients with Type 2 diabetes, a nutritious diet similarly correlates with improved glycemic regulation. Specifically, individuals following a healthful diet are more likely to achieve normal glucose levels (31.45%) than those with suboptimal dietary habits (21.14%). However, many patients adhering to a healthier diet may still experience atypical glucose levels, indicating that dietary strategies alone may not suffice for optimal glycemic regulation. Therefore, it is frequently necessary to implement a holistic approach that includes additional interventions, such as insulin therapy, exercise, and lifestyle alterations, to effectively manage and sustain target glycemic outcomes in individuals with Type 1 diabetes.

$$\begin{bmatrix} 0.3857 & 0.2998 & 0.3145 \\ 0.4352 & 0.3534 & 0.2114 \end{bmatrix}$$

Additionally, when comparing both types of diabetes, patients with Type 1 diabetes exhibit a higher propensity to experience hypoglycemic episodes than those with Type 2, regardless of their dietary practices.

3.4 Simulation Matrices

The following are the results of simulation matrices performed on dietary states of Type 1 and Type 2 diabetic patients in the dataset, and the simulated dietary layer is nearly identical to the actual state.

Type 1

$$\begin{bmatrix} 0.5347859 & 0.4652141 \\ 0.4662312 & 0.5337688 \end{bmatrix}$$

Type 2

$$\begin{bmatrix} 0.5102323 & 0.4897677 \\ 0.4647866 & 0.5352134 \end{bmatrix}$$

3.5 comparison of type1 and type2 dietary transitions and emission

From Figure2, both Type 1 and Type 2 diet transitions show a similar pattern over time with a noticeable dip around the midpoint, which follows

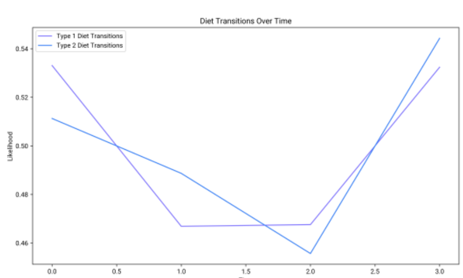

Figure 2: Comparison of dietary transition for type1 and type2 patents

a rise towards the end. This pattern suggests that both type 1 and type 2 patients show a similar nature for the transition between healthy and unhealthy food. Moreover, the similar trend in emission indicates that diet has a significant influence on the glycemic variation, a key point that enlightens and informs our understanding of both type 1 and type 2 diabetes conditions.

4 Conclusion

This Study employs a Hidden Markov Model to examine the influence of dietary patterns on glycemic variability in individuals with Type 2 and Type 1 diabetes. The model highlights that both groups exhibit a slightly higher initial probability of being in an unbalanced dietary state. Irrespective of their initial state, individuals prefer maintaining their existing dietary pattern, although there is a considerable probability of transitioning between the two states. A nutritious diet is considered to improve glycemic control in both kinds of diabetes, which is seen as an increase in the probability of achieving normal glucose levels, but it is insufficient for optimal management. Hence, a more comprehensive approach that includes additional therapies and lifestyle modifications is preferred, mainly due to the elevated risk of hypoglycemic episodes in Type 1 diabetes.

This Study elucidates the intricate relationship between diet and glycemic control, underscoring the necessity for personalised interventions. This research is crucial when considering ICU admissions due to several factors: Glycemic Management in Intensive Care, ensuring stable blood sugar levels is vital for critically ill patients, especially those with diabetes. Patients in the ICU are frequently subjected to intense stress, and the Study's emphasis is on understanding and comprehending how diet affects glucose variability and how this can be used in developing nutritional strategies to minimise or prevent significant fluctuations, followed by issues like hypoglycemia or hyperglycemia. The Hidden Markov Model offers a more personalised insight into diet and glycemic control, which is crucial in ICUs due to varied patient needs and responses. It helps design a customised nutritional plan for optimal glucose management in critical care.

This Study enhances CGM data interpretation by linking dietary factors to glucose trends in type 1 and 2 cases. The Study offers a framework for managing interactions between diet and glycemic variability in these cases. Understanding and analysing the transitions between glycemic states aids in timely diet intervention, which, to a greater extent, prevents glucose fluctuations by predicting transitions from balanced to unbalanced states. It provides key insights for optimising and managing diabetes in critically ill patients.

Despite the current study providing valuable insights into dietary patterns and glycemic fluctuations using a hidden Markov model, several areas require further investigation. To enhance predictive precision, consider refining ”balanced” and ”unbalanced” diet classifications by examining and characterising the roles of macro nutrients and micro nutrients. The research should also further expand on examining many other key factors, such as how diet-induced variability influences HbA1c levels, hypo/hyperglycemic episodes, and diabetes-related complications.

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