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Predicting Type 1 Diabetes Progression Using Deep Learning on Continuous Glucose Monitoring Data

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ABSTRACT

This study presents a predictive framework for assessing the progression of Type 1 Diabetes by leveraging key glycemic variability metrics, Dynamic Stress Factor, Mean Amplitude of Glycemic Excursions, Mean of Daily Differences, Continuous Overall Net Glycemic Action alongside patient age. Two modeling approaches are explored: a machine learning model using a Random Forest Classifier and a deep learning model based on Recurrent Neural Networks. Patients are classified into three clinically significant categories: Stage 2 Type 1 Diabetes, Stage 1 Type 1 Diabetes, and Low Risk. After addressing class imbalance with Synthetic Minority Oversampling Technique, the Random Forest model achieved 99.6% accuracy, while the RNN model reached 100% accuracy on the test dataset.

Feature importance analysis revealed that Dynamic Stress Factor and Continuous Overall Net Glycemic Action were the most predictive features, emphasizing the critical role of glycemic volatility in early diabetes detection. In contrast, static parameters like age and mean glucose showed minimal contribution. These findings underscore the effectiveness of deep learning models in capturing temporal glucose patterns and support the clinical utility of time-series-based metrics for personalized diabetes management. The proposed framework offers a promising tool for improving early diagnosis, guiding intervention strategies, and enhancing clinical decision support in Type 1 Diabetes care.

1. Introduction

Type 1 Diabetes (T1D) is a lifelong autoimmune disorder characterized by the destruction of pancreatic β-cells, resulting in absolute insulin deficiency and the need for continual glycemic monitoring to avert acute and chronic complications[1, 2]. Traditionally, diagnosis and management have depended on fasting glucose, hemoglobin A_1c, the presence of islet autoantibodies, and oral glucose tolerance tests (OGTT). While these approaches remain the clinical gold standard, they are limited by invasiveness, cost, intra-individual variability, and infrequent sampling, which can obscure transient excursions that contribute to vascular injury as mentioned Monnier et al.[3] and Rodbard[4].

In recent years, there has been growing interest in leveraging machine learning techniques or deep learning models to monitor and predict T1D progression. By analyzing glucose dynamics and physiological stress responses, these data-driven approaches offer the potential for earlier, more accurate, cost-effective detection and classification of disease stages.

In recent years, continuous glucose monitoring (CGM) has emerged as a powerful tool to capture real-time glucose dynamics, enabling calculation of variability metrics—such as mean amplitude of glycemic excursions (MAGE), coefficient of variation (CV), and time-in-range (TIR)—that more closely reflect the metabolic milieu by Battelino et al.[6] and Breyton et al.[7] Concurrently, advances in machine learning and deep learning have unlocked new possibilities for early detection and risk stratification in T1D, by integrating CGM traces with physiological signals and demographic data[8, 9, 10]. These algorithms can identify subtle patterns of dysglycemia before clinical deterioration, offering the promise of truly personalized intervention.

A prospective investigation by Furushima[14] assessed the utility of continuous glucose monitoring (CGM) for quantifying glycemic variability—specifically the mean amplitude of glycemic excursions (MAGE)—in adult sepsis patients admitted to intensive care units. Building on earlier work linking MAGE to ICU mortality[15] and demonstrating the feasibility of CGM in critical care settings[16], there study enrolled patients anticipated to require at least 48 hours of intensive support. Interstitial glucose levels were recorded continuously over the first two days of ICU admission via the FreeStyle Libre system, and MAGE was computed from these data. The primary endpoint was 90-day all-cause mortality; secondary outcomes included 90-day ICU-free days and urinary 8-isoprostaglandin $F_2\alpha$—a marker of oxidative stress—measured 48 hours after CGM initiation. Among the 40 participants, non-survivors exhibited significantly higher MAGE than survivors (median 68.8 mg/dL [IQR 39.7–97.2] vs. 39.3 mg/dL [IQR 19.9–53.3], $p = 0.02$). In multivariate analysis, elevated MAGE independently predicted increased 90-day mortality ($p = 0.02$), higher oxidative stress ($p = 0.03$), and fewer ICU-free days ($p = 0.03$).

These findings suggest that MAGE, as measured by CGM during the early phase of critical illness, may serve as a meaningful indicator of glycemic variability and is more strongly associated with mortality outcomes than other glycemic indices. The study highlights the potential of CGM-derived MAGE as a prognostic marker in septic patients and its relevance to oxidative stress and overall disease severity.

In 2023, Chrzanowski[18] conducted a study highlighting the increasing role of Continuous Glucose Monitoring (CGM) in diabetes care, which generates vast amounts of valuable health data. Despite its importance, researchers often struggle with accessing and analyzing CGM data due to reliance on proprietary software and the complexity of managing large datasets. To bridge this gap, public domain tools have emerged, among which *GlyCulator* stands out. The latest version, *GlyCulator 3.0*, is a free, open-access platform designed to streamline the processing, storage, and analysis of CGM files from all major systems, eliminating the need for data preprocessing. It converts raw files into a standardized GlyQ format, strips personal identifiers, and supports manufacturer-independent analysis. Users can set custom analysis periods, conduct data quality checks, impute missing values, and compute glycemic variability indices (GVIs) in line with the 2019 international consensus. The platform also produces comprehensive reports and allows for integration with external statistical tools, making CGM data more accessible and functional for both clinical and research applications.

A landmark prospective study by Akasaka et al.[20] followed 65 non-diabetic CAD patients after PCI for 12 months, measuring MAGE via CGM and endothelial function via reactive hyperemia index (RHI). They showed that higher MAGE was independently associated with adverse cardiovascular events (CV death, MI, unstable angina, revascularization) and that combining MAGE with RHI further stratified risk.

A more recent ambulatory-setting study by Tateishi et al.[21] used flash glucose monitoring (FGM) to assess intradaily MAGE and related it to invasive intracoronary ACh-induced vasomotion (a gold-standard for coronary endothelial function) in chronic CAD patients, confirming that greater glycemic excursions correlate with poorer endothelial responses.
Patients with elevated glycemic variability (MAGE ≥65 mg/dL) exhibited significantly higher levels of high-sensitivity C-reactive protein (0.18 ± 0.13 mg/dL vs. 0.10 ± 0.11 mg/dL, $p = 0.006$) and impaired endothelial function, as indicated by lower RHI values (0.51 ± 0.22 vs. 0.64 ± 0.21, $p = 0.035$), compared to those with lower MAGE (<65 mg/dL). The incidence of cardiovascular events was highest among patients with both high MAGE and low RHI (46.7%) and lowest among those with both low MAGE and high RHI (6.6%) ($p = 0.014$). The receiver operating characteristic (ROC) curve analysis confirmed the predictive value of MAGE, RHI, and their combination for cardiovascular events, with area under the curve (AUC) values of 0.780, 0.727, and 0.796, respectively.

A randomized crossover study by Imai et al.[22] investigated the acute effects of consuming snacks at different times of day on glucose excursions in 17 patients with T2D. Participants, equipped with continuous

glucose monitoring (CGM) devices, followed a controlled meal schedule over four days. On two of these days, they consumed a 75-kcal biscuit either shortly after lunch (1230 h) or in the mid-afternoon (1530 h), with the sequence randomized across participants.

Results indicated that mid-afternoon snacking significantly reduced glycemic variability. Specifically, the mean amplitude of glycemic excursions (MAGE) and the standard deviation of glucose levels were both significantly lower when snacks were consumed at 1530 h compared to 1230 h ($P < 0.01$). Additionally, the incremental area under the curve (iAUC) for post-dinner glucose was significantly reduced with mid-afternoon snacking, though overall mean glucose levels remained similar between the two conditions.

These findings suggest that delaying snack consumption to the mid-afternoon, allowing a greater temporal separation from lunch, may help attenuate postprandial glucose excursions and improve glycemic control in patients with T2D.

In the TrialNet[28] Pathway to Prevention Study, Wilson et al.[23] employed seven-day CGM assessments alongside standard oral glucose tolerance tests in 105 autoantibody-positive relatives of type 1 diabetes probands. By stratifying participants into stage 1 (normal OGTT) and stage 2 (abnormal OGTT) groups, they demonstrated that several CGM metrics—including time above 140 mg/dL (≥ 5% and ≥ 8%) and time above 160 mg/dL (≥ 5% and ≥ 8%)—were significantly associated with progression to clinical (stage 3) type 1 diabetes over 12 months. Earlier work by Steck et al.[24] similarly showed that CGM can detect "dysglycemia" in high-risk youth: antibody-positive children spent a greater proportion of time above 140 mg/dL and exhibited increased glycemic variability compared to antibody-negative peers, suggesting that CGM metrics may identify early dysglycemic states before conventional diagnostics do.

The study by Tokutsu et al.[25] focused on the average IQR (AIQR) and its relationship with key CGM parameters, with the primary endpoint being the correlation between AIQR and time in range (TIR) over 24 hours. Among patients with T2DM, a higher AIQR was significantly associated with poorer glycemic control, showing a negative correlation with TIR and positive correlations with time above range (TAR), mean interstitial glucose, standard deviation (SD), coefficient of variation (CV), and mean of daily differences (MODD). Notably, T2DM patients who achieved a TIR >70% exhibited significantly lower AIQR values compared to those who did not. The receiver operating characteristic (ROC) analysis identified an AIQR cutoff of 28.3 mg/dL as predictive of achieving this TIR threshold. No significant association was found between AIQR and hypoglycemic events.

Shivaprasad et al.[26] compared glycemic variability (GV) in patients with fibrocalculous pancreatic diabetes (FCPD) and type 2 diabetes (T2D) using continuous glucose monitoring (CGM). In a matched cohort study of 61 patients per group, FCPD patients showed significantly higher GV indices—including MAGE, SD, CONGA, MODD, and %CV—as well as hyperglycemia markers such as time above 180 mg/dL and HBGI. Hypoglycemia indices did not differ significantly. The findings highlight greater postprandial glucose excursions in FCPD, suggesting the need for tailored glycemic management strategies.

Mao et al.[27] conducted a prospective observational study to characterize perioperative glycemic profiles and variability following different types of pancreatic surgery using continuous glucose monitoring (CGM). Mao's study addressed a previously unexplored area critical for both perioperative glucose management and understanding the development of new-onset diabetes mellitus (NODM) after pancreatectomy. Eighteen patients were grouped based on surgical type: control (CTRL), pancreaticoduodenectomy (PD), distal pancreatectomy (DP), and total pancreatectomy (TP). CGM devices were applied immediately postoperatively to monitor glycemic metrics, including mean glucose value (MGV), coefficient of variation (CV), mean of daily difference (MODD), continuous overall net glycemic action (CONGA), and time in hyperglycemia or hypoglycemia (TAR/TBR).

Results showed that TP was associated with the highest MGV, CV, MODD, CONGA, and TAR, indicating significantly elevated glucose levels and glycemic variability compared to other groups ($P < 0.001$). PD and DP exhibited intermediate MGV and CV values, higher than the control group but lower than TP. Notably, PD and DP demonstrated glycemic variability measures closer to those of the control group.

These findings underscore the utility of CGM in perioperative glucose monitoring and reveal distinct glycemic patterns based on surgical type, with total pancreatectomy posing the highest risk for glycemic instability.

Building on this foundation, our study applies a suite of algorithms to analyze key parameters related to glucose regulation and stress responses to predict the progression of T1D. By leveraging a combination of dynamic glucose measurements and physiological reactions to stress, this approach promises a more accurate and efficient means of identifying individuals at risk for T1D, potentially enabling pre-symptomatic intervention[8, 28, 11, 12].

2. Objectives

The main objective of this study is to develop a model that can predict the progression of Type 1 Diabetes using the following key parameters:

- DySF (Dynamic Stress Factor): This parameter quantifies the impact of stress on glucose regulation and its potential role in triggering or exacerbating T1D.
- MAGE (Mean Amplitude of Glucose Excursions): This metric evaluates the variability and frequency of glucose excursions, offering insights into glycemic control and stability.
- MODD (Mean of Daily Differences): MODD helps assess daily glucose fluctuations and overall glucose stability, indicating how well glucose is regulated.

- CONGA (Continuous Overall Net Glycemic Action): CONGA tracks the cumulative effect of glucose fluctuations over time, offering a comprehensive view of overall glycemic trends.
- Patient Age: Age may influence the progression of T1D, and including this parameter allows for more accurate predictions, especially when considering age-related physiological changes.

3. Methodology

This study aims to predict the progression of Type 1 Diabetes using parameters such as DySF, MAGE, MODD, CONGA, and age. Patients will be categorized into Stage 2, Stage 1, or Low Risk groups based on their diabetes-related autoantibodies and OGTT results. A Random Forest Classifier and Recurrent Neural Networks (RNNs) are employed to analyze the relationship between these parameters and diabetes progression. Feature importance is utilized to identify the most critical parameters for predicting diabetes progression and assisting clinicians in early intervention for better patient outcomes.

3.1 DATA COLLECTION AND PREPROCESSING

The raw dataset utilized for this study is obtained from clinic patient data[5] that recorded Continuous Glucose Monitoring Systems (CGMs) in conjunction with clinical data for more than a hundred patients. It shows time-series glucose measurements recorded every 5 minutes over a continuous period of more than 5 days, along with the patients' ages. To ensure patient privacy and confidentiality, all patient names have been replaced with unique subject numbers, allowing for easy distinction between individual data without compromising sensitive personal information. A sample of the dataset is provided in Table 1.

Table 1: Continuous Glucose Monitoring data per one Subject

Reading #	Subject ID	Age	Glucose Display Date	Glucose Display Time	Glucose mg/dL
1	254469	44	2/19/2016	4:30:00 AM	125
2	254469	44	2/19/2016	4:35:00 AM	130
3	254469	44	2/19/2016	4:40:00 AM	134
…	…	…	…	…	…
101	254469	44	2/19/2016	12:45:00 PM	78
102	254469	44	2/19/2016	12:50:00 PM	74
…	…	…	…	…	…
701	254469	44	2/21/2016	3:39:00 PM	106
702	254469	44	2/21/2016	3:44:00 PM	109
…	…	…	…	…	…
1804	254469	44	2/25/2016	10:49:00 AM	98
1805	254469	44	2/25/2016	10:54:00 AM	99
1806	254469	44	2/25/2016	10:59:00 AM	98

The data Continuous Glucose Monitoring Systems (CGMs) collected from 105 patients are categorized into three distinct patient groups, as outlined in Table 2. These categories include patients diagnosed with Stage 1 and Stage 2 Type 1 Diabetes, as well as those classified as low risk for diabetes. The classification criteria for each group are as follows:

1. Stage 2 Type 1 Diabetes: Patients in this group possess two or more diabetes-related autoantibodies and exhibit abnormal results on the Oral Glucose Tolerance Test (OGTT), indicating a more advanced stage of the disease.
2. Stage 1 Type 1 Diabetes: Similar to Stage 2, these patients have two or more diabetes-related autoantibodies; however, their OGTT results are normal, suggesting they are in an earlier stage of the disease or a pre-diabetic state.
3. Low Risk: This group consists of patients who test negative for all diabetes-related autoantibodies and demonstrate normal OGTT results. These individuals are considered to be at minimal risk of developing Type 1 Diabetes.

Table 2: Patient Data

Subject ID	Age	Glucose Recorded date	Classification	
194887	51	6/6/2015	Type 1 Diabetes Stage 1	53 patients
522200	14	5/28/2015	Type 1 Diabetes Stage 1	
169216	20	1/19/2016	Type 1 Diabetes Stage 1	
254469	44	2/19/2016	Type 1 Diabetes Stage 1	
421349	29	1/11/2017	Type 1 Diabetes Stage 1	
…	…	…	…	
233598	26	3/30/2016	Low Risk	10 patients
252007	50	5/27/2016	Low Risk	
147666	21	12/16/2015	Low Risk	
…	…	…	…	
361760	8	10/12/2016	Type 1 Diabetes Stage 2	42 patients
241923	17	8/14/2015	Type 1 Diabetes Stage 2	
298664	39	6/27/2017	Type 1 Diabetes Stage 2	
120342	23	5/10/2016	Type 1 Diabetes Stage 2	

3.2 INITIAL DISTRIBUTION OF DATA

The dataset is analyzed to understand the distribution of Low Risk, Stage 1, and Stage 2 number of patients. The number of instances in each class is illustrated in Figure 1 that reveals a significant imbalance in the number of instances across the three categories, which can pose a challenge for deep learning models:

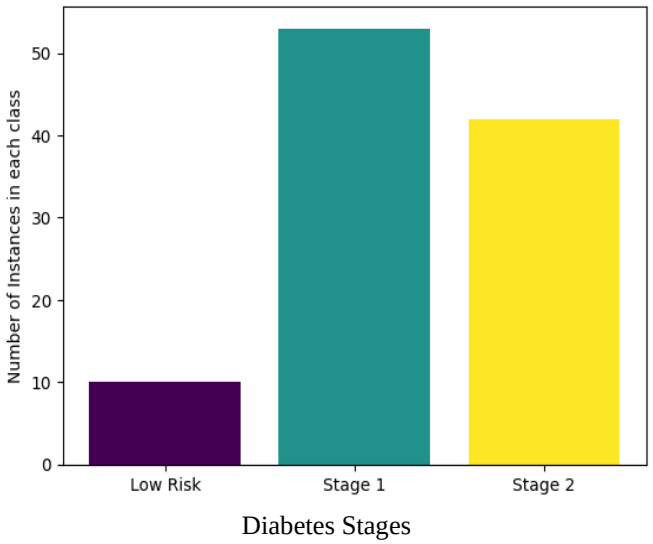

Figure 1: The number of patients per categories

This class imbalance is crucial in machine and deep learning, particularly when working with models that rely on large amounts of data to learn effective patterns. When one class has a substantially smaller number of instances compared to others, the model tends to develop a bias toward the majority classes in this case, Stage 1 and Stage 2. This happens because the model "learns" more from the features in the majority classes. As a result, the Low Risk category, with only 10 instances, is underrepresented and not sufficiently learned by the model.

This bias leads to poor model performance when trying to predict the Low Risk category. Since the model has had limited exposure to the characteristics of the Low-Risk class, it is more likely to misclassify new, unseen data points from this group.

Such an imbalance is especially concerning in a clinical setting where early detection of the disease stage is crucial for effective management and intervention. Therefore, addressing this issue becomes a priority to ensure the model's fairness and accuracy across all patient categories.

3.3 DATASET BALANCING

To address class imbalance, the Synthetic Minority Oversampling Technique (SMOTE) is employed to balance the dataset, thereby improving model performance and classification accuracy across all classes. SMOTE effectively handles the issue of imbalanced data by generating synthetic instances for the minority class. This process begins by identifying the nearest neighbors of each data point in the minority class, and new synthetic points are created along the line connecting the original data point and its neighbor. These synthetic instances help ensure a more diverse representation of the underrepresented class, reducing the risk of bias toward the majority class. Consequently, the model's ability to accurately classify the minority class is significantly enhanced.

The synthetic data points created by SMOTE are similar to, but not identical to, the original data. This increases the diversity within the minority class, allowing the model to learn more varied patterns. Unlike simple oversampling, which involves duplicating existing minority class instances, SMOTE prevents overfitting by generating new and distinct instances. This distinctiveness helps improve the model's generalization ability, making it more robust and less likely to overfit to the minority class. By balancing the class distribution, SMOTE enhances the performance of classification models, particularly for the minority class, and reduces bias toward the majority class.

Figure 2 illustrates the dataset after applying SMOTE to achieve balance. Following the application of SMOTE, the class distribution is significantly more balanced, with each class having an equal number of instances: Class 1 (Low Risk) has 4900 instances, Class 2 (Stage 1) has 4900 instances, and Class 3 (Stage 2) has 4900 instances.

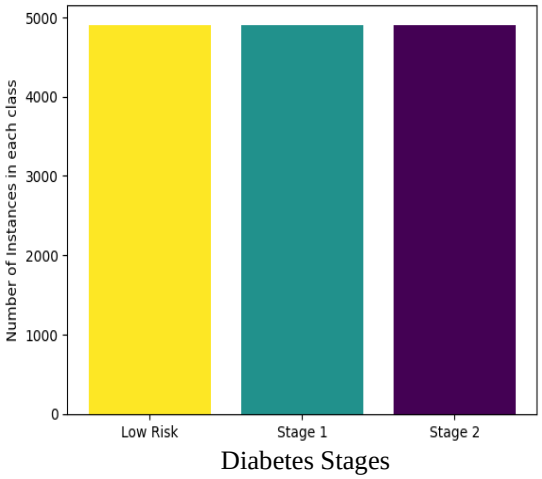

Figure 2: Distribution of Patients per Category After Applying SMOTE

3.4 DYNAMIC STRESS FACTOR, DYSF

The Dynamic Stress Factor is an insightful metric introduced by Rawlings et al.[13] to address a critical limitation of traditional glucose monitoring approaches. Conventionally, Hemoglobin A1c (HbA1c) has served as the benchmark for evaluating long-term glycemic control. However, HbA1c effectively captures average blood glucose levels over a two- to three-month period; it fails to reflect daily glucose fluctuations, such as rapid rises or drops that can significantly affect a patient's well-being. Notably, patients with similar HbA1c values may exhibit vastly different glucose variability profiles, meaning that HbA1c alone is not always a sufficient indicator of glycemic stability or risk.

To fill this gap, DySF is developed as a complementary metric that quantifies glycemic volatility that is, the frequency and magnitude of large, rapid transitions in blood glucose levels within short timeframes. Specifically,

DySF measures the daily weighted number of large, monotonic transitions (either increasing or decreasing) that occur within one hour. This measure allows for a more nuanced and individualized assessment of a patient's glucose dynamics, providing insight into the extent of stress their body undergoes due to abrupt glucose fluctuations. Such insights are particularly valuable for early detection of instability, proactive intervention, and tailored treatment planning in diabetes care.

In this study, DySF is computed for a cohort of 105 subjects across various stages of Type 1 Diabetes, leveraging data collected via Continuous Glucose Monitoring (CGM) systems. These systems record glucose readings at consistent intervals (typically every five minutes) over several days, offering rich, time-series data for in-depth analysis. Each recorded glucose value is categorized into predefined discrete bins: 40, 80, 120, 160, 200, 240, 280, and 320 mg/dL. A transition is identified whenever the glucose reading shifts from one bin to another as shown in Figure 3 for four different subjects 194887, 254469, 169126, and 294413 selected randomly.

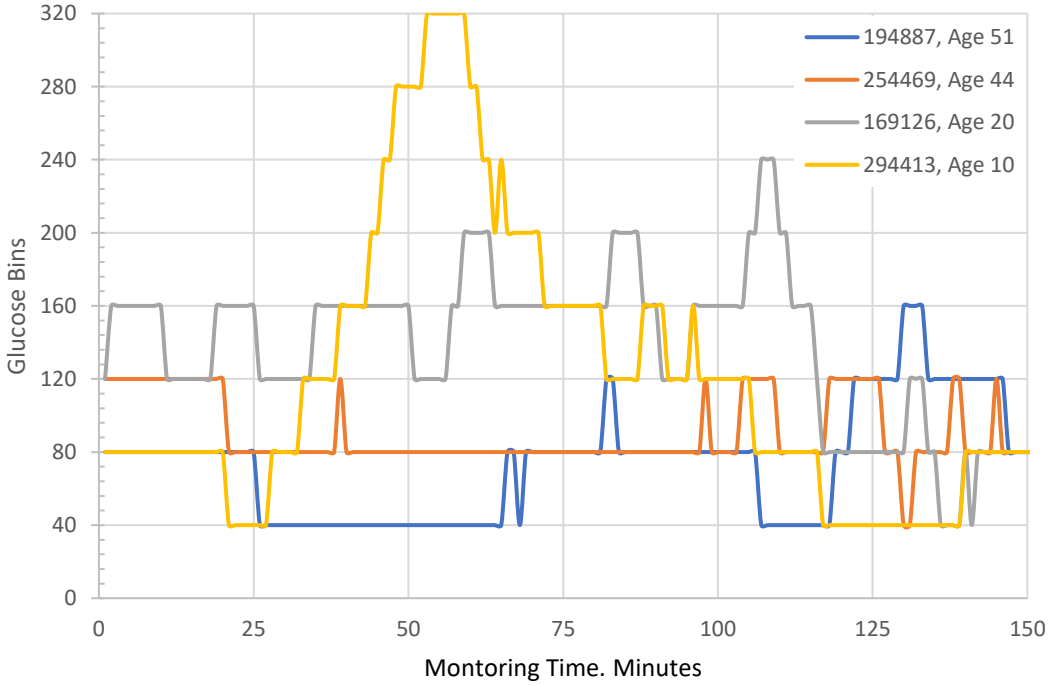

Figure 3: Continuous Glucose Monitoring distributed into bins

The calculation of DySF begins by initializing the DySF value to zero. As the CGM data is processed, each time a transition between glucose bins is detected, the magnitude of the transition, the absolute difference between two consecutive glucose readings, is computed. This magnitude is then weighted based on the time elapsed between the two readings, with the weight calculated as the reciprocal of the time difference. This is further normalized by multiplying by 60, effectively converting the metric to reflect changes per hour.

The weighted magnitude of each bin transition is then accumulated into the total DySF value. As a result, DySF becomes a dynamic, patient-specific indicator that increases with both the number and the severity of glucose level changes. Larger, more frequent transitions contribute more significantly to the overall DySF, thus painting a more accurate picture of the glycemic stress experienced by each patient.

The final DySF values computed for each patient reflect the cumulative impact of these glucose transitions over the monitoring period. This dataset, including DySF scores for each individual, is summarized in Table 3, offering critical insights into the relationship between glucose volatility and the progression or risk level of Type 1 Diabetes.

3.3 MEAN AMPLITUDE OF GLUCOSE EXCURSIONS, MAGE

The MAGE is a widely used metric in diabetes research and clinical practice to quantify the degree of blood glucose variability (Furushima et al., 2021). It focuses specifically on the major swings in glucose levels both upward and downward throughout a given period, rather than capturing all fluctuations. This makes MAGE especially useful in identifying significant glycemic instability, which may be masked by average glucose readings such as HbA1c.

In this research, MAGE is computed by first identifying local maxima and minima in a sequence of glucose measurements taken over several days. These extrema represent the peaks and valleys in a patient's glucose levels. A local maximum is recorded when a glucose value is higher than its immediate neighbors, while a local minimum is noted when the value is lower than its surrounding values.

Once the local peaks and troughs are found, the amplitude of each glycemic excursion, defined as the absolute difference between paired maxima and minima. These amplitudes reflect the magnitude of significant glucose changes. The mean of these amplitudes is calculated to obtain the MAGE value.

This MAGE value provides a single number that summarizes the average size of the most pronounced glucose excursions, giving clinicians and researchers an effective tool to assess the severity of glycemic variability. Elevated MAGE values are often associated with poorer glucose control and a higher risk of diabetes-related complications. The values of MAGE for each individual is summarized in Table 3.

3.4 MEAN OF DAILY DIFFERENCES, MODD

The Mean of Daily Differences (MODD) is a clinically relevant metric used to evaluate the intra-day variability of blood glucose levels in individuals with diabetes. Unlike average glucose measures or HbA1c which provide a broader view of long-term glycemic control. MODD offers a more detailed insight into daily glucose fluctuations, helping to identify instability in blood sugar patterns that may not be apparent through other metrics. To calculate MODD, glucose data is collected as a time series over multiple consecutive days. Each glucose reading is associated with a specific timestamp. The data are processed to enable grouping by individual days. For each day, the maximum and minimum glucose values are identified, representing the daily range of glucose excursions. The difference between these two values, the daily glucose range, is computed to quantify that day's glycemic variability. Once all daily differences are calculated, the MODD is obtained by taking the average of these daily ranges over the entire observation period. This final value serves as a summary of how much, on average, a patient's glucose levels vary within a single day. A high MODD suggests significant daily fluctuations in glucose levels, potentially requiring changes in insulin dosage, dietary habits, or physical activity. In contrast, a low MODD indicates more stable and consistent glucose control. As such, MODD is a powerful tool for clinicians seeking to personalize and optimize diabetes treatment plans, making it an essential complement to traditional glycemic indicators. Table 3 presents the calculated values of MODD for each patient.

3.5 CONTINUOUS OVERALL NET GLYCEMIC ACTION, CONGA

CONGA is a widely used metric for assessing short-term glycemic variability, which reflects how quickly and how often a person's blood glucose levels change over a specific period. Unlike average glucose measures, CONGA captures the dynamic nature of glucose fluctuations, offering clinicians and researchers a more detailed understanding of the stability of a patient's glycemic control.

To calculate CONGA, the first step is to determine the differences between each pair of consecutive glucose readings in a time-series dataset. These differences represent the immediate changes in glucose levels over time. By taking the absolute values of these differences, the calculation accounts for the magnitude of each fluctuation whether the glucose level increased or decreased.

The total CONGA value is then computed as the sum of all these absolute differences, indicating the cumulative glucose variability across the monitoring period. Additionally, the mean of these differences provides an average measure of how much glucose levels typically fluctuate between time points, offering a normalized indicator of volatility.

Clinically, higher CONGA values suggest greater instability in glucose control, which may be associated with increased risk of hypoglycemia, hyperglycemia, or the need for therapeutic adjustments. Conversely, lower CONGA values reflect more stable glucose patterns, which are generally associated with better diabetes management. Thus, CONGA plays a vital role in continuous glucose monitoring by helping to evaluate both the effectiveness of treatment strategies and the patient's risk profile for glycemic complications. The values of CONGA per patient are presented in Table 3.

Table 3: Key Glucose and Stress-Related Parameters

Subject ID	Age	MAGE	MODD	CONGA	Mean Glucose	DySF	Classification
172537	53	21.52	70.5	3.44	89.66	6.28	Type 1 Diabetes Stage 1
205062	53	17.58	81.6	4.27	106.05	9.23	Type 1 Diabetes Stage 1
248473	30	18.48	83.33	3.2	99.64	2.12	Type 1 Diabetes Stage 1
294413	10	30.6	130.86	4.49	97.24	7.4	Type 1 Diabetes Stage 1
300501	10	22.49	85.67	3.82	93.41	10.01	Type 1 Diabetes Stage 1
…	…	…	…	…	…	…	…
269261	14	17.96	56.86	4.69	100.03	4.29	Low Risk
148508	17	19.85	93	4.65	96.87	5.17	Low Risk
104498	20	11.88	49.38	2.18	100.19	2.59	Low Risk
…	…	…	…	…	…	…	…
361760	8	16.46	69.71	2.93	92.36	4.44	Type 1 Diabetes Stage 2
404334	9	22.66	83.86	4.37	93.76	8.33	Type 1 Diabetes Stage 2
288070	10	22.96	121	3.4	111.31	6.51	Type 1 Diabetes Stage 2
421654	11	16.22	86.4	3.04	85.08	5.18	Type 1 Diabetes Stage 2
…	…	…	…	…	…	…	…

4. Data Analysis

The data analysis phase of this research plays a critical role in uncovering meaningful insights and patterns from continuous glucose monitoring (CGM) data, aimed at predicting the progression of Type 1 Diabetes (T1D). The dataset used in this study includes time-series glucose measurements collected at 5-minute intervals over several consecutive days, along with key clinical variables such as patient age. Patients were categorized into three distinct groups.

The data analysis process also included extensive preprocessing steps, feature extraction, and statistical evaluations. These helped identify patterns indicative of disease progression and provided the foundation for developing both machine and deep learning models.

4.1 MACHINE LEARNING APPROACH

In this study, five different machine learning models were evaluated for their ability to predict clinical outcomes based on key features, including Logistic Regression, Support Vector Classifier, Gaussian Naive Bayes, Decision Tree, and Random Forest Classifier. Among them, the Random Forest Classifier demonstrated the highest accuracy, outperforming the other models in terms of predictive performance. To further enhance its effectiveness, hyperparameter tuning was conducted to determine the most suitable configuration. The optimal parameters included enabling bootstrap sampling, setting class weights to address imbalance, a maximum tree depth of 30, and 200 estimators. These settings significantly reduced the risk of overfitting and improved the model's generalization capability on unseen data.

To gain deeper insights into the model's behavior and to better understand the impact of various parameters, several visualizations are created before and after training the model. Before training the model, feature importance analysis is conducted shown in Figure 4. This analysis identified the most influential features in predicting the target variable. Understanding these relationships helped fine-tune the model, ensuring it focused on the most critical predictors for more accurate outcomes.

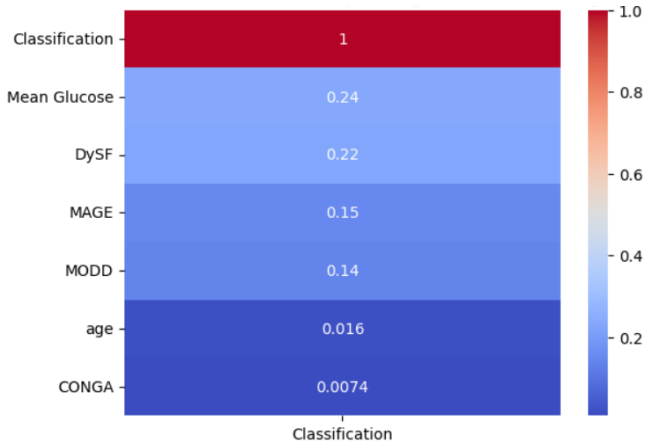

Figure 4: Feature Correlation before upscaling and Model Training

The dataset is divided into two subsets: 80% for training and 20% for testing. This split allowed the model to be evaluated on unseen data, providing a realistic estimate of its performance in practical settings. One of the key hyperparameters influencing model performance is the number of estimators, which refers to the number of trees in the Random Forest model. Each tree contributes a vote toward the final prediction, and increasing this number generally enhances the model's overall performance and stability. More trees help reduce variance and improve generalization, making the model less prone to overfitting. However, increasing the number of estimators also raises computational costs and training time. There is typically a point of diminishing returns, where adding more trees results in minimal performance gain. Therefore, tuning this parameter requires balancing accuracy with computational efficiency. A visualization of the accuracy plot with varying numbers of estimators shown in Figure 5 demonstrates that increasing the number of estimators improved the model's performance, though beyond a certain point, adding more trees showed diminishing returns and potential overfitting. With this configuration, the model achieved an accuracy of 99.6% on the test dataset, indicating exceptional predictive capability. The high accuracy demonstrates the model's robustness in predicting outcomes even in the presence of complex data and potential noise.

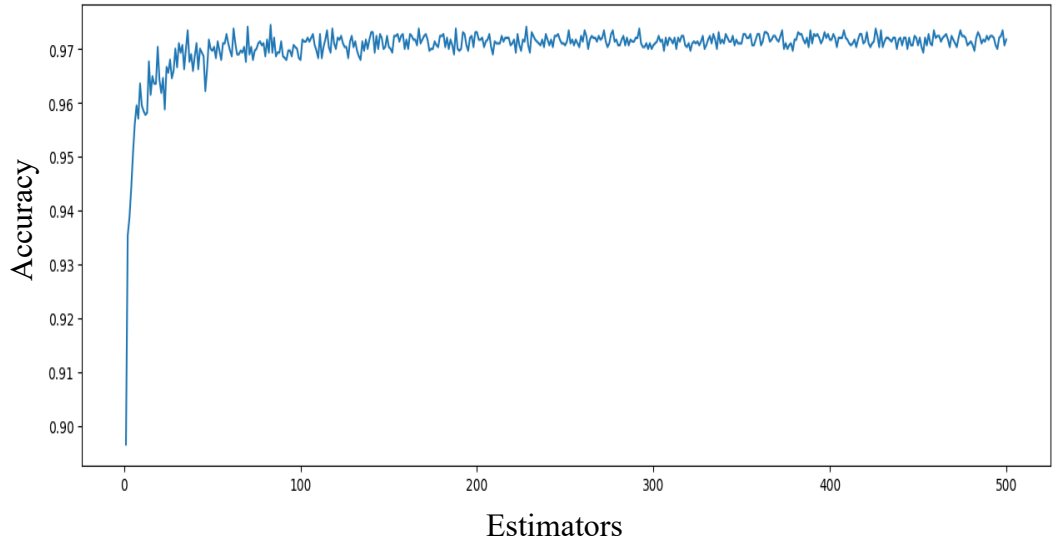

Figure 5: Number of Estimator vs Accuracy for a Random Forest Classifier

After training the model, the feature importance analysis revealed that DySF is the most important predictor for diabetes status, as shown in Figure 6. This clinical marker exhibited a strong influence on the model's decision-making process, reinforcing its significance in predicting outcomes. Conversely, features such as CONGA and MAGE, which are commonly used to measure glycemic variability, are found to be less important in this specific model. This aligns with the understanding that not all glycemic variability measures contribute equally to predictive accuracy for certain clinical outcomes.

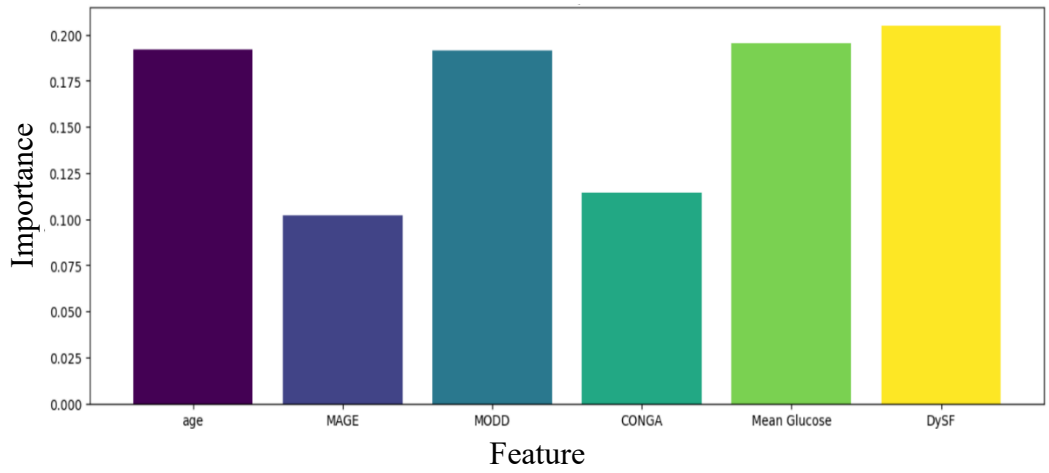

Figure 6: Feature Importance

Another crucial hyperparameter is the minimum samples split that determines the minimum number of samples required to split an internal node as shown in Figure 7. It serves as a regularization technique to control the complexity of the model and prevent overfitting. A lower value allows the algorithm to create more splits, leading to deeper trees that may capture subtle patterns but risk overfitting to noise. Conversely, a higher value leads to shallower trees that may generalize better to new data. Selecting an appropriate value is crucial and often guided by cross-validation to ensure a balance between model complexity and generalization.

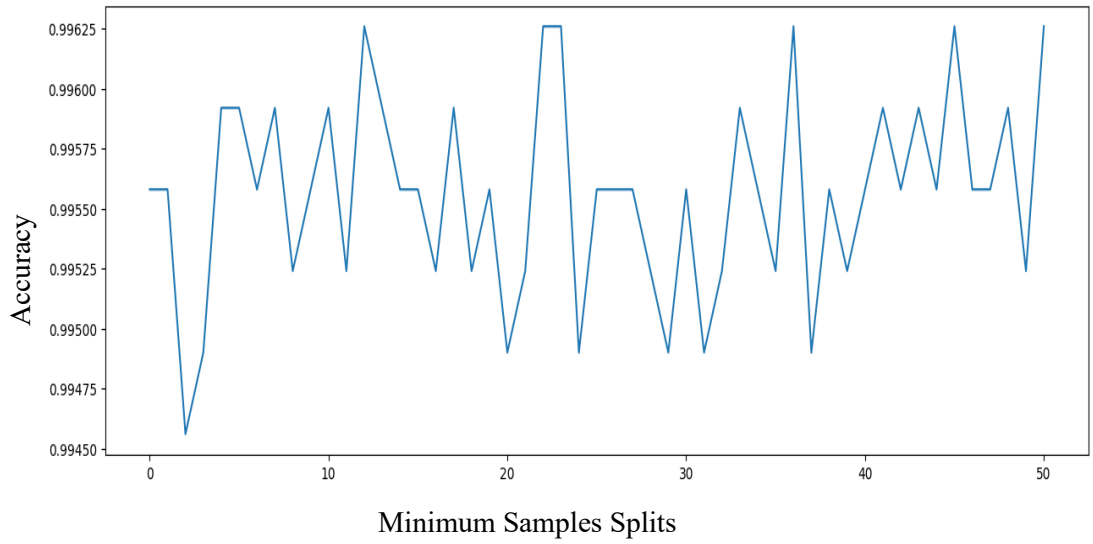

Figure 7: Minimum Sample Splits Vs Accuracy for a Random Forest Classifies

4.2 NEURAL NETWORK MODEL DEVELOPMENT

To enhance the prediction of Type 1 Diabetes (T1D) progression across its three clinical stages, this study incorporates a deep learning approach using Recurrent Neural Networks (RNNs). These models are designed to analyze the temporal relationships among key physiological indicators: DySF (Dynamic Stress Factor), MAGE (Mean Amplitude of Glucose Excursions), MODD (Mean of Daily Differences), CONGA (Continuous Overall Net Glycemic Action), and patient age. As a specialized form of neural network, RNNs are particularly effective in processing sequential data, making them well-suited for glucose monitoring time series where patterns evolve over time.

Unlike traditional machine learning algorithms, such as Random Forests, which are highly accurate and data-efficient but limited in capturing temporal dependencies, Recurrent Neural Networks (RNNs) offer a more advanced representation learning framework. This enables them to automatically extract and interpret dynamic features from raw sequential inputs, a critical advantage in clinical applications where time-based variability plays a key role in signaling disease progression. While the Random Forest Classifier demonstrated excellent performance, achieving 99.6% accuracy in classifying individuals into Stage 1, Stage 2, or Low Risk categories, the integration of RNNs adds significant value by modeling complex, non-linear

relationships over time and enhancing the model's ability to generalize. Leveraging both approaches in parallel not only strengthens the predictive framework but also provides a more comprehensive understanding of disease progression through complementary modeling perspectives. In this study, the RNN model is trained on a balanced dataset to ensure robust learning across all classes.

4.3 MODEL ARCHITECTURE

The neural network is implemented using a Sequential architecture designed to effectively classify patients into one of three diabetes categories. The model begins with an input-dense layer consisting of 256 units and a ReLU activation function. This layer receives input based on the number of features in the training dataset. To prevent overfitting, a dropout layer with a rate of 0.2 is applied immediately after. The architecture continues with a second dense layer containing 128 units, also using ReLU activation, followed by another dropout layer with a rate of 0.2. A third dense layer with 64 units and ReLU activation is then added to further refine the feature extraction process. Finally, the network concludes with an output-dense layer comprising 3 units, each corresponding to one of the diabetes categories (Stage 1, Stage 2, or Low Risk). This layer uses a SoftMax activation function to output a probability distribution over the three categories, enabling the model to make a definitive classification decision.

4.4 TRAINING CONFIGURATION AND HYPERPARAMETERS

To ensure optimal model performance and stability during training, several key configurations and hyperparameters were carefully selected. The Adam optimizer is used with a learning rate of 0.0001, which provides an adaptive learning process that adjusts the step size during gradient descent. This choice is particularly beneficial in deep learning applications, where maintaining a balance between convergence speed and stability is essential.

The loss function chosen for this task is categorical cross-entropy, which is specifically designed for multi-class classification problems. Since the model aims to classify patients into one of three distinct categories, Stage 1, Stage 2, or Low Risk, this loss function is well-suited to measure the difference between the predicted class probabilities and the actual class labels.

Accuracy is employed as the primary evaluation metric, offering an intuitive measure of the model's overall correctness in classification. To further enhance model generalization and prevent overfitting, early stopping is integrated into the training process. Early stopping monitored the validation loss and halted training if no improvement is observed over five consecutive epochs. Moreover, it automatically restored the best-performing model weights recorded during training, ensuring the final model reflected the most optimal state encountered.

The data is partitioned into training, validation, and testing sets in the ratio of 90%, 5%, and 5% respectively. This split allowed the model to learn from the majority of the dataset while being validated and tested on unseen data to assess its generalization capabilities.

The performance of the model was evaluated through a combination of metrics and visualizations, providing a comprehensive understanding of how well it learned to classify the progression stages of Type 1 Diabetes. A key performance indicator is the accuracy-over-epoch curve, which illustrated a consistent and steady improvement in classification accuracy as training progressed.

Initially, at epoch 5, the model achieved 95% accuracy, indicating a strong baseline performance with only a short training duration. As the number of epochs increased, the model continued to refine its internal parameters, leading to an improvement in classification capability. By epoch 20, the accuracy rose to 98%, reflecting the model's enhanced ability to capture more complex patterns in the dataset. Ultimately, at epoch 80, the model reached 100% accuracy on the test dataset, signifying perfect classification performance. This final result, also depicted in Figure 9, underscores the model's ability to fully differentiate between patients in Stage 1, Stage 2, and Low Risk categories without any misclassification.

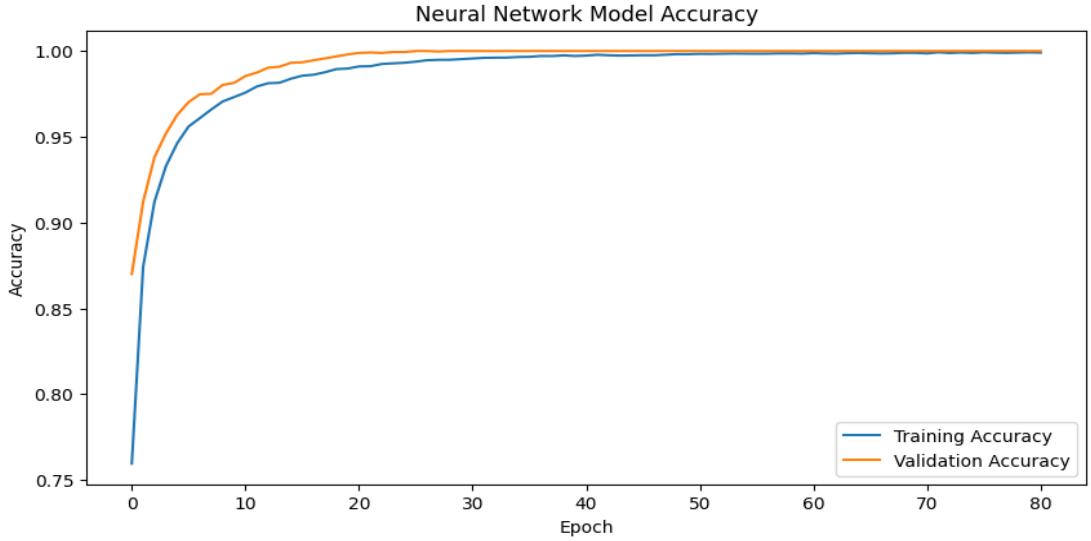

Figure 8: Neural Network Model Accuracy

The accuracy graph effectively visualizes this learning progression, showing a smooth and incremental increase in accuracy with each epoch, and demonstrating the benefits of well-configured training strategies such as early stopping and dropout regularization. These mechanisms helped prevent overfitting while allowing the model to generalize well to unseen data.

Further validation of model reliability is provided by the confusion matrix shown in Figure 9, which showed the classification across all three target classes. Each instance is correctly predicted, and no errors are observed in any category. This reinforces the strength of the model's predictions and the quality of the data preprocessing techniques used, such as SMOTE for balancing class distribution.

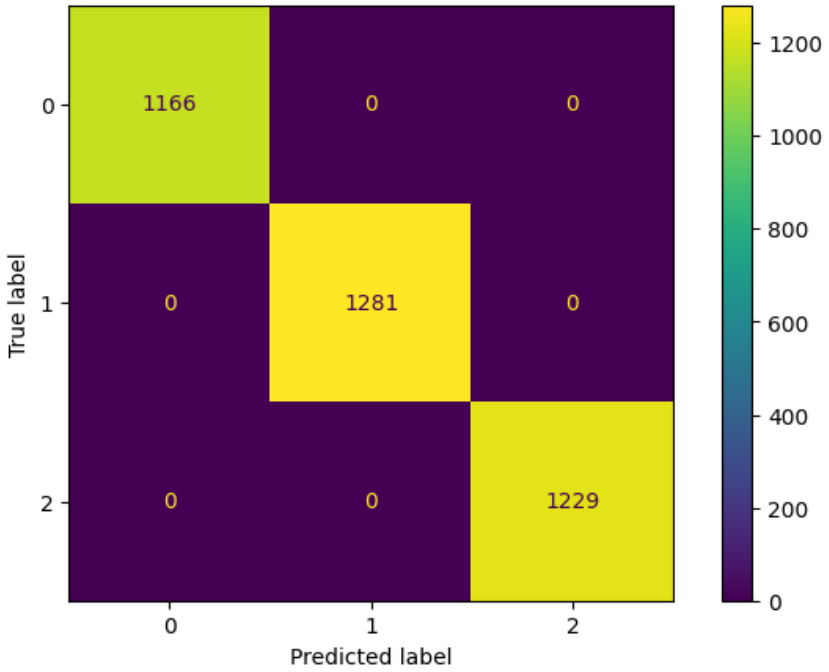

Figure 9: Confusion Matrix

5. Feature Importance Post-Training

Following the training and evaluation of the neural network model, a detailed analysis is conducted to assess the contribution of individual features to the model's predictions. This feature importance analysis aimed to identify which input variables had the greatest influence on the classification of patients into the three categories of Type 1 Diabetes progression: Stage 1, Stage 2, and Low Risk.

The results presented in Figure 10 revealed that Dynamic Stress Factor (DySF) and Continuous Overall Net Glycemic Action (CONGA) are the most influential features in driving the model's predictive performance. Both of these metrics are designed to capture glycemic volatility, the degree to which blood glucose levels fluctuate over time. DySF measures the frequency and magnitude of significant glucose transitions within short periods, while CONGA quantifies the overall variability across consecutive time points. Their strong influence highlights the critical role that temporal patterns in glucose behavior play in identifying early and advanced stages of diabetes, providing a dynamic perspective that traditional static measures fail to capture.

On the other hand, features such as age and mean glucose levels were found to be the least influential in the model's decision-making process. Although age is commonly considered in clinical assessments, this result suggests that it may not offer as much predictive value when combined with more granular, time-series-based glycemic data. Similarly, average glucose levels, while useful for general monitoring, do not reflect the fluctuations that are key indicators of disease progression.

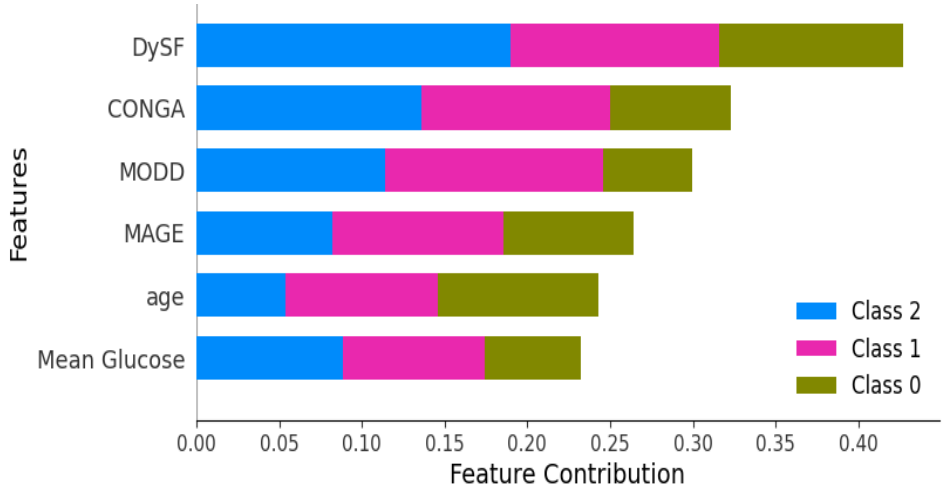

Figure 10: Neural Network model Feature Importance

6. Discussion

The results of this study demonstrate the effectiveness of leveraging dynamic glycemic variability metrics, mostly DySF and CONGA, in predicting the progression of Type 1 Diabetes (T1D). The high performance of both the Random Forest Classifier (99.6% accuracy) and the Recurrent Neural Network (100% accuracy) shine the power of combining machine learning and deep learning models with time-series health data for clinical classification tasks.

One of the most notable outcomes is the strong predictive value of DySF and CONGA, which underscores the importance of glycemic volatility as a critical factor in early detection of T1D. These metrics capture rapid glucose changes and variability that static indicators like age or mean glucose fail to reflect. The minimal contribution of such static features further supports the shift toward using more dynamic, personalized indicators in modern diabetes risk assessment.

The use of SMOTE to address class imbalance is important in achieving high classification performance. Without such preprocessing, models are likely to underperform on minority classes, which are clinically the most urgent to detect early. This step reinforces the importance of careful data preparation in healthcare machine learning applications. The RNN model's superior performance may be attributed to its ability to capture temporal dependencies in glucose fluctuations, which are inherently sequential in nature.

Clinically, the framework presented in this study offers significant advantages. It not only enables earlier and more precise diagnosis of T1D stages but also supports continuous monitoring that could guide personalized interventions. By moving beyond traditional, one-time diagnostic tests to dynamic, data-driven methods, healthcare providers can potentially reduce diagnostic delays, optimize patient outcomes, and tailor treatment strategies more effectively.

These results show that using dynamic glucose data with machine learning and deep learning models can help predict early stages of Type 1 Diabetes more accurately. In the future, we plan to collect more data from a wider range of patients to make the model stronger and more reliable. We also aim to explore ways to make the model easier to understand, so it can be used more confidently by doctors in real-world settings.

7. Conclusion

This research emphasizes deep learning, especially RNNs, for classifying and predicting the progression of Type 1 Diabetes based on high-resolution glycemic variability data. DySF emerged as a key feature, providing dynamic and clinically meaningful insights into disease progression. The findings from this study can assist in creating advanced clinical decision support systems, facilitating early diagnosis, targeted interventions, and personalized treatment strategies for individuals at different stages of Type 1 Diabetes.

Both the Random Forest and RNN models showed high accuracy. Nevertheless, RNNs delivered superior results due to their capability to learn from sequential data. The implementation of SMOTE enhanced classification performance across all categories.

The feature importance analysis identified DySF and CONGA as the strongest predictors, reinforcing the significance of glucose variability in the disease progression.

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