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Comparative Analysis of Regression Models for the Progression Prediction of Parkinson's Disease

Bikram Kar[1], Bikash Kanti Sarkar[2]
Department of Computer Science and Engineering, Birla Institute of Technology

Abstract: ***Parkinson's Disease (PD) is a progressive neurological disease affecting the movement system, speech and quality of life. To make a proper clinical assessment and treatment planning, you need a proper monitoring of the disease progression. Voice biomarkers may be important in determining the severity of PD, as speech loss is a one of the early signs of the condition. In this work, several machine learning regression models are compared for the prediction of PD progression by using speech-based biomedical features extracted from UCI Parkinson's Telemonitoring dataset. The proposed framework is based on the prediction of motor_UPDRs and total_UPDRs scores, clinically important indices that are employed to measure the severity level of the disease. The Linear Regression, SVR (Support Vector Regression), KNN, Random Forest Regressor, and XGBoost Regressor models were implemented and evaluated. To elevate the predictive ability, model training was preceded with preprocessing techniques like feature selection and irrelevant attribute removal, and feature scaling. The efficiency of models was evaluated by RMSE, MAE and R^2 value. The experimental results show that ensemble learning methods greatly outperform the traditional regression methods when predicting PD progression. The model that best performed for both prediction tasks was the Random Forest Regressor out of all evaluated models. The model achieved RMSE of 2.9769, MAE of 2.1621 and R^2 of 0.9200 for total_UPDRS prediction. Likewise, the prediction of the motor_UPDRS model by the Random Forest model had an RMSE value of 2.3975, an MAE value of 1.7491, and an R^2 value of 0.9099. The results emphasize that ensemble-based machine learning models perform better to capture non-linear relationships between the speech biomarkers and can be a good basis for automated prediction of the PD progression.***

Keywords: Parkinson's Disease (PD), UPDRS Prediction, Regression Models, Speech Biomarkers.

I. INTRODUCTION

Parkinson's Disease or PD is a neurological abnormality which mainly affects the brain and nervous system. The disease manifests itself with symptoms including tremor, rigidity, bradykinesia, posture related issues, and speech impairments. Recent clinical studies indicate that PD is one of the most rapidly expanding neurological ailments in the world and it has high impact on the quality of life among elderly people. World Health Organisation (WHO) has recently released reports that show the prevalence of PD has risen rapidly over the past 20 years and more than 8.5 million people are currently suffering from the disease worldwide. In addition, the Global Burden of Diseases has indicated that the incidence of disability and mortality due to PD is steadily rising, thereby making it a significant public health problem in the world. Therefore, it is crucial to have early diagnosis and follow-up surveillance of disease activity and progression for effective treatment planning and patient management. Impaired speech is regarded as one of the prominent signs of this disease. Jitter, shimmer, harmonicity and pitch instability can be used to provide information on neurological deterioration because of vocal variations. Therefore, speech has become a topic of interest in recent years for the creation of a non-invasive and cost-effective monitoring system for PD. There are several clinical studies which have demonstrated that almost 70%–90% of people suffering from PD have speech abnormalities at some point throughout the course of the disease. Clinicians use UPDRS score to measure the acuteness and progression of PD. In particular, Motor_UPDRS and total_UPDRS scores are significant to assess motor dysfunction and total disease severity. Classical clinical evaluation methods are however time taking and have to be conducted several times in the hospital. As machine learning methods evolve, automatic prediction systems utilizing biomedical speech signals are becoming a promising alternative for ongoing monitoring of diseases. Various studies have examined machine learning methods to detect and classify PD. But most of the current literature primarily emphasizes on classification of disease instead of the prediction of disease progression based on regression. Furthermore, a few studies performed a thorough comparison of the various regression models, based on speech biomarkers, when predicting UPDRS scores. Thus, a good benchmarking scheme to compare the performance of various regression techniques for accurate disease progression prediction is required. Here, speech bio-markers are used to implement a comparative study on various benchmark regression-based models.

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Different regression-based approaches like-Linear Regression, SVR, KNN, Random Forest Regressor and XGBoost Regressor are trained and tested for the prediction of both UPDRS scores. The experimental results confirm the successful use of ensemble learning, specifically Random Forest, for mapping the nonlinear relationships between the speech biomarkers and indicators of disease severity.

A. Major Contribution

- Multiple machine learning regression models, including classical and ensemble-based approaches, are implemented and evaluated.
- Performance of the used regression models are presented by using RMSE, MAE, and R^2 score to ensure reliable comparative analysis.
- Results of this study shows that the Random Forest based regression model achieves strong predictive ability compared to other evaluated approaches.

RELATED WORKS

There have been several studies that have investigated the use of machine learning and speech-based biomedical analysis for predicting progression of PD based on the Parkinson's Telemonitoring dataset. Only a few existing researches have been targeting UPDRS scores prediction with regression and ensemble learning methods. One of the earliest telemonitoring frameworks for predicting the progression of PD that uses speech signal processing and biomedical voice measurements was introduced in [1]. Their work showed the usefulness of voice biomarkers for the estimation of the motor_UPDRS and total_UPDRS scores. In the study by Sakar et al. [2] they explored the use of machine learning methods for PD assessment based on speech data sets, and concluded that speech impairment can be a good measure of disease severity. They concluded that biomedical voice analysis is a key factor in the development of automatic disease monitoring systems. Little et al. [3] presented the nonlinear speech signal analysis for PD identification and monitoring. The study showed that the measurements of dysphonia (jitter and shimmer) provide important information about neurological deterioration. Arora et al. [4] introduced a machine learning based Telemonitoring system for PD used an speech based features and a smartphone. Their structure allowed them to monitor the diseases remotely and proved the value of mobile health technologies in clinical evaluation. In the context of Parkinson's Telemonitoring dataset, Eskidere et al. [5] used regression-based machine learning techniques to estimate the UPDRS scores. Several predictive algorithms were evaluated and the superiority of the nonlinear regression models was shown. Hlavnička et al. [6] studied the speech disorders in PD using acoustic analysis and machine learning methods and results show that there is a strong correlation between speech biomarkers and disease progression and motor impairments. Hemmerling et al. [7] suggested ways to extract features from speech for use in analysing the severity of PD and showed that machine-learning approaches could be used to classify and predict disease stages using recordings of speech. Ali et al. [8] applied ensemble learning models to predict the progression of PD and found that the boosting-based and Random Forest models show a significant improvement in prediction compared to the traditional regression models. Peker et al. [9] built a hybrid machine learning model for the early analysis of Parkinson's progression based on biomedical voice measurements. They combined feature selection and disease classification mechanisms for better disease assessment. Anter et al [10] have presented an intelligent optimization-based regression framework to predict the impact of PD based on voice features. The results showed that the ensemble regression approach could be used for estimating UPDRS score. García-Ordás et al. [11] investigated machine-learning based SBP prediction based on speech biomarkers and telemonitoring data. According to the study, ensemble learning techniques outperforms the other techniques for disease progression assessment. Khedimi et al. [12] introduced the framework for predicting the progression of PD based on voice biomarkers, which is based on deep learning. They employed multimodal learning and attention-based architectures to enhance their prediction accuracy. Varghese et al. [13] employed machine learning techniques on speech data for PD severity estimation and showed regression analysis was successfully applied for predicting the UPDRS score. Sajal et al. [14] presented a telehealth monitoring system for PD based on wearable and voice based biomedical systems. Their work pointed out the relevance of ML to remote health applications. Pechprasarn et al. [15] used regression and ensemble learning methods to predict the motor_UPDRS and total_UPDRS scores using the Parkinson's Telemonitoring dataset. They concluded that voice biomarkers have the potential to be important for disease progression analysis. Aich et al. [16] introduced biomedical speech data-driven deep neural network-based PD prediction models. They showed that this deep learning architectures could be used for better prediction performance. Grover et al. [17] studied feature engineering and ensemble learning methods for monitoring PD progression and found that ensemble-based models have better performance than traditional regression models. While there has been a number of studies investigating PD prediction and monitoring with machine

learning techniques, there is limited research that directly compares a number of different regression models for predicting motor_UPDRS and total_UPDRS scores by speechbased biomarkers. Hence this research work gives a comparative study between the various regression techniques to find the optimum model for the prediction of progression of PD.

II. DATASET DESCRIPTION

A. *Dataset Source*

Related data was taken from the UCI Machine Learning Repository, one of the most popular data sets repositories for machine learning and biomedical research data sets. This dataset is used to predict PD progression based on biomedical features extracted from speech. The data set includes a set of voice measurements collected from PD patients during sessions of telemonitoring. These biomedical voice characteristics can help analyze voice impairments during neurological deterioration. The data is made up of several features of the speech signal from Parkinson patients, recorded across various sessions. The main use of the dataset is to determine the severity of PD based on clinically relevant scores provided by UPDRS.

B. *Target Variables*

In this study two clinically relevant target variables were taken into account:

- motor_UPDRS

The score is obtained from the motor examination part of the UPDRS score, which is used to assess the severity of motor dysfunction in patients with PD.

- total_UPDRS

The overall severity of PD is indicated by this score, taking into account a number of clinical aspects, such as motor symptoms and non-motor symptoms.

Multiple machine learning regression models were used in an independent prediction of both target variables to assess the ability of speech biomarkers to track the progression of PD.

III. PROPOSED METHODOLOGY

Here, the proposed approach for predicting the progression of PD using multiple regression models from machine learning is presented. The proposed framework deals with the use of speech-based biomedical attributes derived from the dataset to estimate the severity of PD in terms of motor_UPDRS and total_UPDRS scores. The proposed system consists of four main steps those are data preprocessing, feature scaling, splitting the data into training sets and testing sets, implementing the regression models and evaluating the model's performance.

A. *Overall Framework*

The detail framework of the proposed methodology is illustrated in Fig. 1. Initially, the data is collected from the repository. The dataset then undergoes preprocessing and feature scaling before being divided into training and testing subsets. Subsequently, multiple regression models are trained and evaluated using standard regression performance metrics.

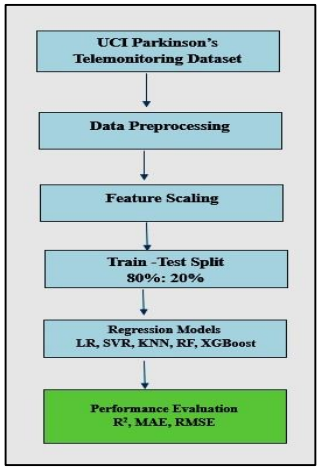


Fig. 1. Overall Framework of the Proposed Methodology

B. *Data Preprocessing*

Data preprocessing is significant in enhancing the quality and reliability of machine learning approaches. In this work, some preprocessing operations were done prior to model training. First the attributes subject and test_time were dropped from the data. The subject attribute is only used to identify the individual and is not used in the severity prediction of the disease; test_time is temporal information not used in the present study. Unnecessary attributes were removed from the dataset and the missing value analysis was performed to find any missing or inconsistent data in the dataset. The experimental analysis showed that there were no missing data in the dataset, and it ensure integrity and consistency. The dataset has different numerical ranges in the features, therefore feature standardization was conducted with the StandardScaler technique. Standardization converts the features into a standard scale with zero mean and unit variance, which has significant improvement on the performance of distance-based and optimization-based regression algorithm like SVR and KNN.

C. *Regression* Models

In this work, several regression models were applied here and tested to study the efficacy of various machine learning strategies to predict the PD progression. The models selected are traditional regression models as well as advanced ensemble learning models.

Linear Regression

Linear Regression is the basic supervised learning algorithm that is applied into predictive analysis. Using the model, a linear relationship between the independent variables and the target variable is found, with the aim of minimizing the prediction error.

Linear Regression is mathematically represented as:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \epsilon \quad (1)$$

where $y$denotes the predicted output, $x_1, x_2, \ldots, x_n$represent the input features, βindicates regression coefficients, and ϵdenotes the error term.

Support Vector Regression (SVR)

The purpose of SVR is to find the "best" regression hyperplane which minimizes the prediction error while simultaneously keeping the largest margin. SVR can be used to model nonlinear relationships that may be found in biomedical data sets using kernel functions.

The mathematical representation of SVR is given as:

$$f(x) = w^T \phi(x) + b \quad (2)$$

where $\phi(x)$represents nonlinear feature transformation, $w$denotes the weight vector, and $b$is the bias parameter.

K-Nearest Neighbors Regressor

KNN Regressor is a non-parametric statistical learning model used to predict the target value using the K-nearest neighbours. For each data point, the algorithm computes the distance between the point and the rest of the data sample set, and predicts the target value as the mean of the closest data points. KNN regression works well for the detection of local patterns and nonlinear relationships between speech biomarkers that are related to the progression of PD. The prediction function of KNN regression can be mathematically expressed as:

$$\hat{y}(x) = \frac{1}{} \sum_{i \in N_K(x)} K \qquad y_i \quad (3)$$

where $\hat{y}(x)$represents the predicted output for the input sample x, Kdenotes the number of nearest neighbors, and $N_K(x)$represents the set of Knearest neighboring samples. The predicted value is computed as the average of the target values of the nearest neighbors.

Random Forest Regressor

Random Forest Regressor is an ensemble machine learning method that is based on numerous decision trees, each of which models the target variable with a different random forest. Random subsets of data and features are used to train each decision tree, and the final prediction is the average of the predictions of all the decision trees. Random Forest is highly suitable for predicting the progression of PD for its ability to model the complex nonlinear relationships and its power to handle noisy biomedical data.

The mathematical representation of Random Forest regression is given as:

$$N1 = \sum_{i=1} \qquad T_i(x) \quad (4)$$

where $\hat{y}$represents the final predicted output, Ndenotes the total number of decision trees in the forest, and $T_i(x)$represents the prediction generated by the i^{th}decision tree for the input sample x. The final prediction is obtained by averaging the outputs of all individual trees.

XGBoost Regressor

XGBoost is a popular boosting-based ensemble learning algorithm for regression and predictive analytics. XGBoost builds decision trees in a sequence such that each new tree tries to explain the errors made by the previous trees. The algorithm includes gradient optimization and regularization to enhance the predictive performance and avoid overfitting. XGBoost is a popular model for biomedical prediction tasks due to its learning ability and computational efficiency.

The mathematical representation of XGBoost regression is expressed as:

$$\hat{y_i} = \sum_{k=1}^{K} f_k(x_i),\ f_k \in F \quad (5)$$

where $\hat{y_i}$represents the predicted output for the i^{th}sample, Kdenotes the total number of decision trees, and $f_k(x_i)$represents the prediction generated by the k^{th}decision tree. The final prediction is obtained by summing the outputs of all boosting trees sequentially.

D. Evaluation Metrics

In this study, three common regression performance metrics were used to determine the effectiveness of the regression models implemented: RMSE, MAE, and R^2 score.

Root Mean Square Error (RMSE)

RMSE represents the root of the mean squared error (MSE) between the actual and forecasted values. The smaller RMSE values are the better the prediction.

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2} \quad (6)$$

Mean Absolute Error (MAE)

The mean of the absolute represents differences between actual and predicted values. The smaller the MAE value, the more accurate the prediction.

$$MAE = \frac{1}{n}\sum_{i=1}^{n} |y_i - \hat{y}_i| \quad (7)$$

R^2 Value

R^2 value represents the percentage of variance in the target variable that is explained by the regression model. The higher the R2 value, the better the fit and prediction of the model.

$$R^2 = 1 - \frac{\sum(y_i - \hat{y}_i)^2}{\sum(y_i - \bar{y})^2} \quad (8)$$

IV. RESULTS AND DISCUSSIONS

A. Results and Discussion Experimental Setup

This work was carried out using Python and Google Colab notebook with various libraries such as Scikit-learn, XGBoost, NumPy, Pandas, Matplotlib, and Seaborn. Experiments were conducted with the Parkinson's Telemonitoring dataset from UCI Machine Learning Repository. To preprocess the data, the following attributes were eliminated: subject#, test_time and standardization of features was done by StandardScaler. Here, 80-20 train-test split was used to perform this experiment. The performance of the regression models was evaluated by RMSE, MAE and R^2 score.

1) Performance Analysis for total_UPDRS Prediction

Table 1 presents the performance evaluation of the regression models for total_UPDRS prediction.

Table 1. Performance Comparison for total_UPDRS Prediction

Model	RMSE	MAE	R^2 Score
Linear Regression	9.7012	8.0336	0.1507
SVR	6.5824	4.7966	0.6090
KNN	6.0798	4.1797	0.6664
Random Forest	2.9769	2.1621	0.9200
XGBoost	3.2938	2.4536	0.9021

The performance of the models is evaluated by calculating the mean square error (MSE), mean absolute error (MAE), and R2 score. The results indicate that the model with the lowest RMSE and MAE and highest R2 value is the Random Forest Regressor, which has an R2 score of 0.9200. XGBoost also resulted in competitive performance but Linear Regression had the least performance because of the nonlinearity in the data.

2) Performance Analysis for *motor*_UPDRS Prediction

Table 2 presents the comparative performance of the regression models for motor_UPDRS prediction.

Table 2. Performance Comparison for motor_UPDRS Prediction

Model	RMSE	MAE	R^2 Score
Linear Regression	7.5094	6.3654	0.1165
SVR	4.9437	3.7189	0.6171
KNN	4.5618	3.2058	0.6740
Random Forest	2.3975	1.7491	0.9099
XGBoost	2.7242	2.0383	0.8837

Similar observations were obtained for motor_UPDRS prediction, where Random Forest again achieved the highest prediction accuracy with an R^2 score of 0.9099, followed by XGBoost.

3) *Graphical* Analysis

The graphical analysis along with this, also confirms the efficiency of the regression models applied. As shown in the Actual vs Predicted plot in Fig. 2, the predicted UPDRS values by the Random Forest Regressor are in good agreement with the actual values, which means that the model optimally captures the nonlinear relationships of the features and has a good prediction ability. The residual plot in Fig. 3 displays the residual values, which are randomly distributed around the zero-reference line with no systematic pattern, showing that there is little bias in the predictions and the performance is stable. Moreover, the residual error distribution shown in Fig. 4 suggests that the majority of prediction errors lie around the zero value and that the distribution is very close to normal distribution, which confirm reliability and robustness of the RF regression model for prediction the progression of PD.

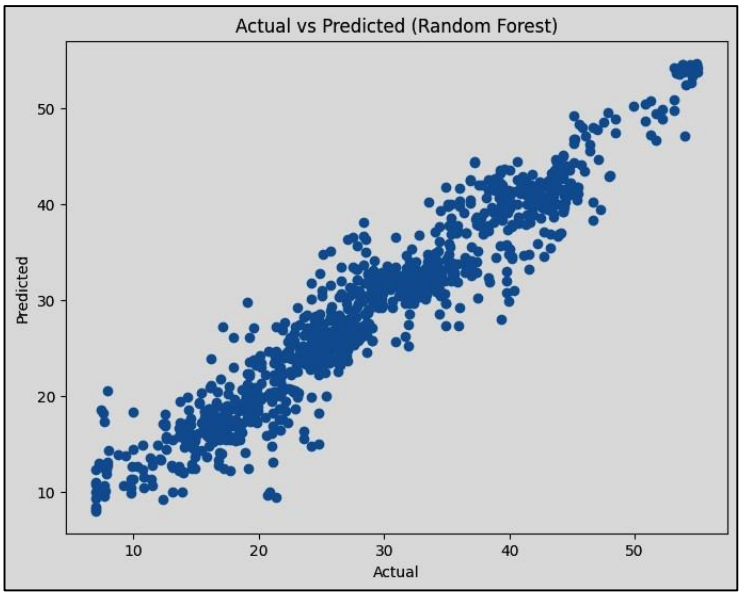


Fig 2. Actual Vs Predicted Cases by Random Forest based Regression Model

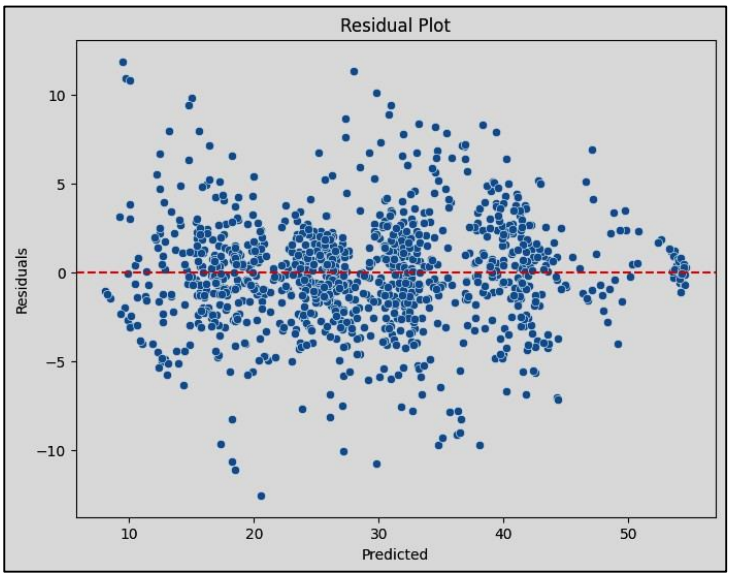


Fig 3. Residual plot of the Random Forest regression model for Total UPDRS prediction.

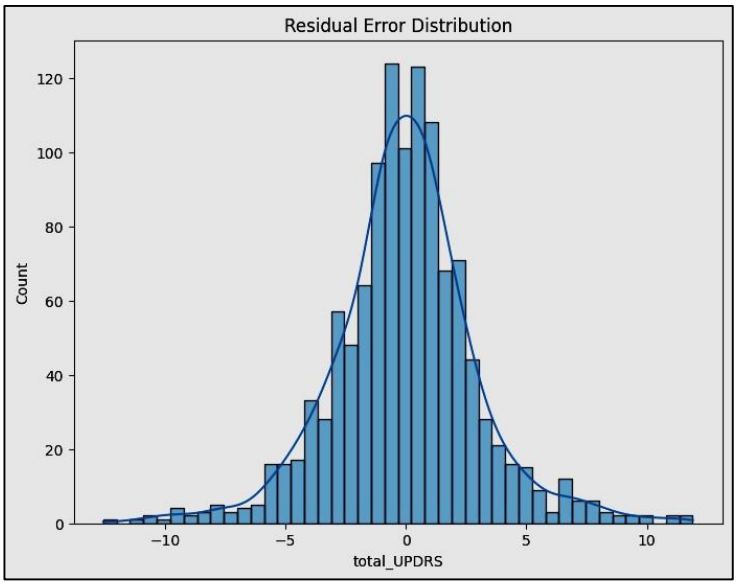


Fig 4. Residual Error Distribution Plot of the Random Forest regression model for Total UPDRS prediction

Results show that the ensemble learning methods are superior to the traditional regression models in predicting the progression of PD. The linear correlation between the speech biomarkers and the UPDRS scores is very nonlinear and thus resulted in poor performance in Linear Regression. Random Forest and XGBoost showed better results in terms of prediction accuracy, largely due to their ability to model complex interactions between the features. Random Forest and XGBoost demonstrated moderate performance, while XGBoost excelled in capturing complex feature interactions, leading to significant improvements in prediction accuracy. Random Forest shows the highest overall prediction accuracy for both prediction tasks and speech biomarkers (jitter, shimmer, HNR, RPDE, DFA, and PPE) suggest that these speech biomarkers have high utility for the prediction of severity and progression of PD.

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V. CONCLUSION

Several regression models were compared to predict the progression of PD using speech biomarkers. Multiple regression techniques were employed and assessed for prediction of the motor_UPDRS and total_UPDRS scores, such as Linear Regression, Support Vector Regression (SVR), K-Nearest Neighbors (KNN), Random Forest Regressor, and XGBoost Regressor. Experimental results showed that the ensemble learning methods are better than the use of the traditional regression methods. The overall performance of the models evaluated was best in the Random Forest regressor with the lowest RMSE and MAE values and the highest R^2 scores for both prediction tasks. Through the graphical analysis, the robustness and stability of the Random Forest model have also been verified by comparing actual values to predicted values and plotting the distribution of the errors between the actual and predicted values. The inferred results suggest that the features extracted from speech (jitter, shimmer, HNR, RPDE, DFA, and PPE) have highly informative patterns, which are related to the severity and progression of PD. Hence, automated voice analysis of PD using machine learning is a feasible, non-invasive and relatively inexpensive method to monitor and assess the progression of the disease.

A. Limitations of the Study

Despite achieving promising results, the present study has several limitations:

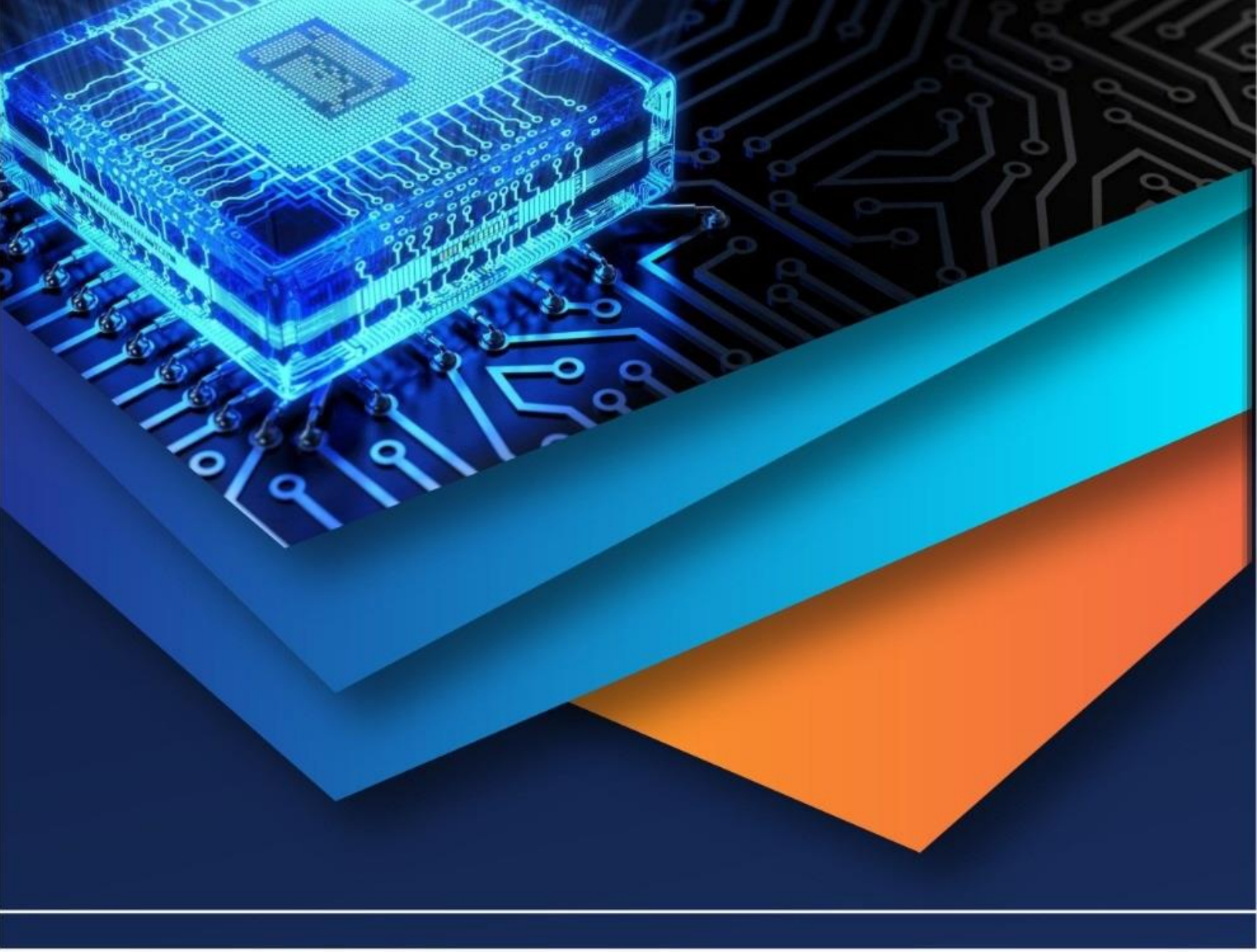
- The experimental analysis was conducted using a single publicly available dataset, which may limit the generalization capability of the developed models.
- Temporal progression information associated with test_time was not considered in the current regression framework.
- Deep learning and hybrid ensemble architectures were not explored in this study.
- Clinical validation using real-time patient monitoring data was not performed.

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