

Multimodal Parkinson's Disease Detection Using Gait and DaTSCAN Biomarkers: A Comparative and Explainable Machine Learning Approach

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Abstract—Parkinson's disease (PD) is a progressive neurological disorder that is commonly diagnosed through clinical examination, assessment of motor symptoms, and medical history. This study focuses on whether machine-learning techniques can use DaTSCAN imaging biomarkers and gait measurements from the Parkinson's Progression Markers Initiative (PPMI) database to classify Parkinson's disease. To create this dataset we selected some features from gait features and striatal DaTSCAN measurements from 281 participants. We used three models: Logistic Regression, Random Forest and Support Vector Machine using gait-only, DaTSCAN-only, and combined gait–DaTSCAN feature groups. Hyperparameter tuning was performed to identify the best configuration for each model and feature group. Used SHAP explanations to check which features influenced the most in the prediction. The best approach was the SVM that used both walking and DaTSCAN data achieving 84.21% accuracy and a test ROC-AUC of 0.8979 and also achieved a cross-validated ROC-AUC of 0.9579. SHAP analysis showed that putamen measurements and striatal asymmetry were among the most influential features in the final model. MDS-UPDRS Part III scores were positively associated with the predicted probability of Parkinson's disease (Spearman's $\rho = 0.5076$, $p < 0.001$). The overall results indicate that it is possible to provide information by using biomarkers in conjunction with explainable machine learning, which may aid decision making, in the future regarding the diagnosis of Parkinson's disease.

Index Terms—DaTSCAN, explainable artificial intelligence, gait analysis, machine learning, Parkinson's disease, SHAP.

I. INTRODUCTION

Parkinson's disease (PD) is a progressive neurological disorder that primarily impacts both the movement and the balance, which makes daily activities more difficult. The disease is commonly assessed through clinical examination, motor assessment, medical history, and standardized rating scales [1]. However, disease severity and symptoms will differ from person to person, and some of the systemic examination will rely on subjective findings or individual response. This situation has led to a requirement for objective measurements as well as computer-based techniques that can provide additional information for PD detection and assessment.

Gait is an important motor characteristic related to Parkinson's disease. Walking speed, mobility, and postural stability in different walking conditions may provide useful information about motor impairment [2], [3]. These changes can be quantitatively measured and analysed by using machine learning techniques to identify if gait features can distinguish individuals with PD from those without the disease. Gait-based machine learning methods have shown potential, although their performance may vary across datasets depending on the type of gait measures used and the features that are used to analyze the gait [2].

DaTSCAN provides another important source of information for Parkinson's disease-related analysis. It provides information on the availability of the dopamine transporter in the caudate and putamen. Reductions in striatal binding are associated with dopaminergic abnormalities and can provide useful

information for distinguishing participants with dopaminergic deficits from those without such deficits. Previous PPMI-based research has reported reduced striatal and contralateral putamen-specific binding ratios in individuals with PD, supporting the use of dopamine transporter imaging as an important biomarker in Parkinson's disease research [4].

Gait and DaTSCAN provide complementary information about Parkinson's disease. Gait measurements reflect observable motor performance, whereas DaTSCAN provides information about changes in the brain's dopaminergic system [5]. Combining these modalities may therefore provide a more comprehensive representation of disease-related changes. However, multimodal integration can be challenging when the dataset is relatively small and class-imbalanced [5], [12]. Therefore, it's important to assess each of the different modalities individually to determine whether their combination provides additional predictive value.

Another crucial problem in medical machine learning is understanding why a model produces a particular prediction. A model might have almost perfect classification performance with a poor understanding of what contextual information about the biomarker influenced its performance. This lack of transparency can make it difficult to assess the usefulness of machine learning models in medical research. Explainable artificial intelligence (XAI) techniques can help address this problem by providing information about the contribution of individual features to model predictions. One such method is SHapley Additive exPlanations (SHAP), which can be applied to explore the effects of each component of a model on its predictions [6].

The Parkinson's Progression Markers Initiative (PPMI) is an international observational study designed to investigate clinical, imaging, genetic, and biospecimen-based biomarkers associated with Parkinson's disease and its progression [4]. The study provides standardized clinical and imaging information that can be used to investigate potential biomarkers and develop computational approaches for Parkinson's disease research. In this study, PPMI data were used to construct a participant-level dataset containing gait and DaTSCAN measurements. This dataset was used to investigate whether these two types of biomarkers provide useful information for Parkinson's disease classification.

Three machine learning algorithms were evaluated in this study: Logistic Regression, Random Forest, and Support Vector Machine (SVM). considered: gait-only, DaTSCAN-only, and combined gait-DaTSCAN features. To assess the performance of models and to determine the optimal model configuration, cross-validation and hyperparameter tuning were implemented. This comparative design allows the predictive value of each modality to be examined separately and determines whether combining gait and DaTSCAN features provides complementary information.

The study also includes clinical validation using MDS-UPDRS Part III [7]. The clinical aspects of Parkinson's disease measured by the MDS-UPDRS Part III were not used as input features in the machine learning models. Instead, they were analysed separately to investigate whether the probability of Parkinson's disease predicted by the model was associated with motor symptom severity. This separation prevented the clinical assessment measure from being used both as a model input and as a validation measure.

II. RELATED WORK

Previous studies have investigated Parkinson's disease detection using gait-based machine learning. Gait-related characteristics such as walking speed, mobility, stride-related measurements, and postural stability have been used to distinguish individuals with Parkinson's disease from those without the disease. These studies indicate that gait analysis can provide objective information about motor impairment. But the reported performance varies according to the dataset, gait features and the method for machine learning [2].

DaTSCAN-based methods have also been examined for Parkinson's disease classification. Dopamine transporter imaging provides information about dopaminergic activity in the caudate and putamen regions of the striatum. PPMI-based research has reported reduced striatal and putamen-specific binding ratios in individuals with Parkinson's disease, supporting the use of dopamine transporter imaging as an important biomarker [4]. These measurements provide useful information about dopaminergic abnormalities in the caudate and putamen.

Multimodal machine learning has received increasing attention because information from different sources, such as clinical, imaging, and biological data, may provide complementary information about Parkinson's disease. However, small sample sizes, class imbalance, feature redundancy, and integration complexity can affect the performance of multimodal approaches [5], [12]. Therefore, combining multiple modalities does not necessarily guarantee improved predictive performance and must be evaluated experimentally. In addition, explainable artificial intelligence (XAI) has become increasingly important in healthcare machine learning because it can help identify how individual features influence model predictions. SHapley Additive exPlanations (SHAP) is one method used to interpret these feature contributions [6].

Previous research has examined gait analysis, DaTSCAN-based classification, multimodal data integration, and explainable machine learning for Parkinson's disease. However, many studies focus on a single modality or use complex integrated models. We still need a comparison of gait and DaTSCAN data from the same people, in the same tests.

Few studies have directly compared gait-only, DaTSCAN-only, and combined gait–DaTSCAN features using several classical machine-learning methods while also examining feature importance and clinical relevance [2], [4]–[6]. This study addresses this gap by testing Logistic Regression, Random Forest and SVM models using PPMI data. SHAP is used to explain the models, while MDS-UPDRS Part III scores are used as a measure to check clinical relevance. This framework enables a comparison of predictive performance, feature contributions, and the relationship between model predictions and motor impairment.

III. MATERIALS AND METHODS

The methodology used in this study investigates Parkinson's disease classification using gait and DaTSCAN biomarkers together with classical machine learning techniques. The complete workflow includes data collection, participant-level dataset preparation, feature selection, preprocessing, model training, hyperparameter tuning, performance evaluation, explainability analysis, and clinical validation. The primary objective is to compare the

predictive information provided by gait and DaTSCAN measurements separately and to determine whether their combination provides additional predictive value for Parkinson's disease classification.

A. Dataset Details

The first step in this process is data collection. The dataset used in this study was obtained from the Parkinson's Progression Markers Initiative (PPMI) [4]. A participant-level master dataset was prepared by combining gait assessment and DaTSCAN measurements. After data preparation, the final dataset contained 281 participants, including 47 participants with Parkinson's disease and 234 participants without Parkinson's disease.

The final dataset included 15 predictive features. Six features were obtained from gait assessments, while nine features were derived from DaTSCAN measurements. The target variable represented the diagnostic class, with Parkinson's disease as the positive class and non-Parkinson's disease as the negative class.

B. Data Preprocessing:

The participant-level dataset was divided into training and testing sets using an approximately 80:20 split. There were 224 participants selected for training and 57 participants selected for testing. The training data were used for the model development, for cross-validation, and for hyperparameter tuning. The testing data were kept separate for final evaluation.

Missing values were replaced using median imputation. The imputation step was included within the machine learning pipeline to reduce the possibility of information leakage. All the models that require scaled input features were standardized after the imputation.

C. Feature Groups

To compare the information provided by gait and DaTSCAN, three separate feature groups were created. The first group, **gait-only**, included six features: GAITTUG1, GAITTUG2, GAITASTUS, GAITASTDUAL, GAITASTSUBS, and GAITASTMIS. The second group, **DaTSCAN-only**, included nine features: STRIATUM_L_REF_CWM, STRIATUM_R_REF_CWM,

CAUDATE_L_REF_CWM,
CAUDATE_R_REF_CWM,
PUTAMEN_L_REF_CWM,
PUTAMEN_R_REF_CWM,
STRIATUM_ASYMMETRY,
CAUDATE_ASYMMETRY, and
PUTAMEN_ASYMMETRY. The third group combined all six gait features with the nine DaTSCAN features, giving a total of 15 features. Each group was tested separately so that the performance of gait information, DaTSCAN information, and their combination could be compared. This helped determine whether using both types of information together offered any improvement in PD classification.

D. Machine Learning Models

The algorithms used in this study were logistic regression, random forest, and Support Vector Machine (SVM). We chose logistic regression as a simple linear baseline model. Random Forest was selected because it can capture nonlinear relationships and interactions between features [8]. SVM was included because of its ability to identify a decision boundary between PD and non-PD classes, particularly in high-dimensional feature spaces [9]. Each algorithm was trained using the gait-only, DaTSCAN-only, and combined gait–DaTSCAN feature groups. This led to nine combinations of models and features, and these were compared on the basis of their performance.

For the linear SVM, the decision function is represented as

$$f(x) = w^T x + b$$

where w is the weight vector, x is the input feature vector, and b is the bias term.

E. Model Training and Evaluation

The model was trained, and hyperparameters were tuned using 5-fold stratified cross-validation. The cross-validation was performed with five folds, shuffling and random state 42. The dataset had a low number of PD participants compared to non-PD participants, so the stratification was used to maintain a similar class distribution across the folds. Model performance was evaluated using accuracy, precision, recall, F1-score, and ROC-AUC. The confusion matrices were also computed to analyze the correct and incorrect classifications. Hyperparameter tuning

was conducted for each model-feature combination, and the resulting best hyperparameters for each model were chosen based on their cross-validation ROC-AUC.

The last model was the combined gait–DaTSCAN SVM with the highest cross-validation ROC-AUC of 0.9579. The major parameters were the linear kernel, $C=0.01$, balanced class weights, and probability estimation.

F. Explainability and Clinical Validation

To understand the contributions of individual features to the model predictions, SHapley Additive exPlanations (SHAP) was applied to the final combined gait–DaTSCAN SVM [6]. The final classifier was a linear SVM, and for this reason a linear SHAP explainer was applied. To obtain a global ranking of feature importance, mean absolute SHAP values were computed and plots were produced to visualize the model behavior.

Clinical validation was performed using MDS-UPDRS Part III scores as an independent clinical measure [7]. Spearman's rank correlation was used to compare the predicted probability of Parkinson's disease with the available MDS-UPDRS Part III scores. The Mann–Whitney U test was also used to compare the scores for Part III of the MDS-UPDRS between the actual PD and non-PD groups.

IV. EXPERIMENTAL RESULTS

Experimental results are demonstrated using model performance, feature-group comparison, final model evaluation, and explainability analysis. The results highlight the relative contribution of gait and DaTSCAN biomarkers and examine whether the model predictions are associated with clinical motor impairment.

A. Participant Distribution

The final dataset contained 281 participants, including 47 participants with Parkinson's disease and 234 participants without Parkinson's disease.

The class distribution is shown in Figure 1.

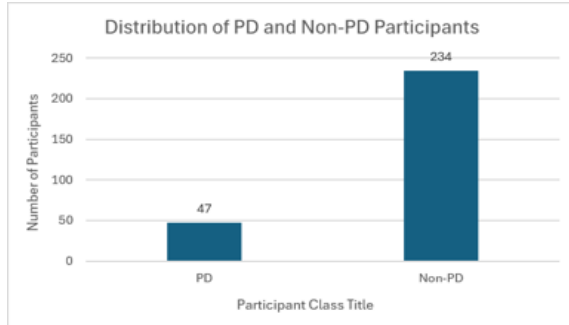


Fig. 1. Distribution of Parkinson's disease and non-Parkinson's disease participants.

The figure shows that the dataset was imbalanced, with a considerably larger number of non-Parkinson's disease participants. Thus, the accuracy was interpreted together with precision, recall, F1-score, and ROC-AUC. This was especially relevant because an accurate model may not detect enough cases of PD.

B. Baseline Model Performance

The baseline experiments showed a clear difference in performance across the three feature groups. The gait-only models produced weak results, with ROC-AUC values ranging from 0.3989 to 0.5106. These results indicate that the selected gait features provided limited discrimination between the PD and non-PD groups in the present dataset.

The models that included DaTSCAN worked significantly better. The ROC-AUC performance for logistic regression, random forest, and SVM was 0.8872, 0.8894, and 0.9043, respectively. The DaTSCAN-only SVM achieved the best baseline test performance, with an accuracy of 85.96%, precision of 57.14%, recall of 80.00%, F1-score of 0.6667, and ROC-AUC of 0.9043.

The combined feature group was also satisfactory, with ROC-AUC values of 0.8809 for logistic regression, 0.8830 for random forest, and 0.8872 for SVM. However, the combined models did not improve upon the best DaTSCAN-only baseline model.

C. Hyperparameter-Tuned Performance

The DaTSCAN-only and combined models also performed well after hyperparameter tuning, and the gait-only models still performed poorly. The

combined gait–DaTSCAN SVM model achieved the highest cross-validation ROC-AUC of 0.9579.

The tuned DaTSCAN-only logistic regression model gave the best ROC-AUC of 0.9021 on the independent test set. It achieved an accuracy of 87.72%, a precision of 60.00%, a recall of 90.00%, and an F1-score of 0.7200. The tuned DaTSCAN-only SVM resulted in a similar performance, with a test ROC-AUC of 0.9000 and the same accuracy, recall, and F1-score.

Table I. Comparison of tuned model performance across feature groups.

Feature Group	Model	CV ROC-AUC	Test ROC-AUC
Gait-only	Logistic Regression	0.6027	0.4702
Gait-only	SVM	0.6155	0.5277
Gait-only	Random Forest	0.5953	0.4936
DaTSCAN-only	Logistic Regression	0.9558	0.9021
DaTSCAN-only	SVM	0.9567	0.9000
DaTSCAN-only	Random Forest	0.9453	0.8872
Combined	Logistic Regression	0.9553	0.8979
Combined	SVM	0.9579	0.8979
Combined	Random Forest	0.9460	0.8830

Table I compares the performance of the tuned models across the three feature groups. The gait-only models performed relatively poorly, while the DaTSCAN-only and combined models showed much better ROC-AUC scores. The combined SVM had the highest cross-validation ROC-AUC (0.9579), while the DaTSCAN-only Logistic Regression gave the best test ROC-AUC (0.9021).

Table II. Best hyperparameter configurations selected by grid search.

Feature Group	Model	Best Hyperparameter Configuration	CV ROC-AUC
Gait-only	Logistic Regression	$C = 0.01$; solver = liblinear; class weight = balanced	0.6027
Gait-only	SVM	$C = 0.01$; kernel = RBF; gamma = 0.001; class weight = balanced	0.6155
Gait-only	Random Forest	n_estimators = 500; max_depth = 3; min_samples_leaf = 1; max_features = sqrt; class weight = balanced	0.5953
DaTSCAN-only	Logistic Regression	$C = 0.1$; solver = liblinear; class weight = balanced	0.9558
DaTSCAN-only	SVM	$C = 0.01$; kernel = linear; class weight = balanced	0.9567
DaTSCAN-only	Random Forest	n_estimators = 200; max_depth = None; min_samples_leaf = 1; max_features = sqrt; class weight = balanced	0.9453
Combined	Logistic Regression	$C = 0.1$; solver = liblinear; class weight = balanced	0.9553
Combined	SVM	$C = 0.01$; kernel = linear; class weight = balanced	0.9579
Combined	Random Forest	n_estimators = 200; max_depth = None; min_samples_leaf = 4; max_features = sqrt; class weight = balanced	0.9460

Table II shows the best hyperparameter settings found through grid search for each model and feature group. The search covered factors such as regularization, kernel type, tree complexity, and class weighting. The combined SVM performed best, with a cross-validation ROC-AUC of 0.9579 using a linear kernel, $C = 0.01$, and balanced class weights. Since the models were selected based on cross-validation ROC-AUC rather than test-set results, this configuration was chosen as the final model.

D. ROC Curve Analysis

The ROC curves provide a visual comparison of the model's ability to distinguish Parkinson's disease from non-Parkinson's disease participants. As can be seen in Fig. 2, the gait-only models are clustered near the diagonal reference line, indicating that their classification performance is poor.

The other models (the DaTSCAN only and the combined) display curves that stay higher than the diagonal. These models also show strong ROC-AUC values, which means there is more discriminative information in the DaTSCAN measurements in this dataset than the selected gait measurements.

The DaTSCAN-only logistic regression, DaTSCAN-only SVM, and combined SVM demonstrate particularly high discrimination. The combined SVM

was selected as the final model because it achieved the highest cross-validation ROC-AUC.

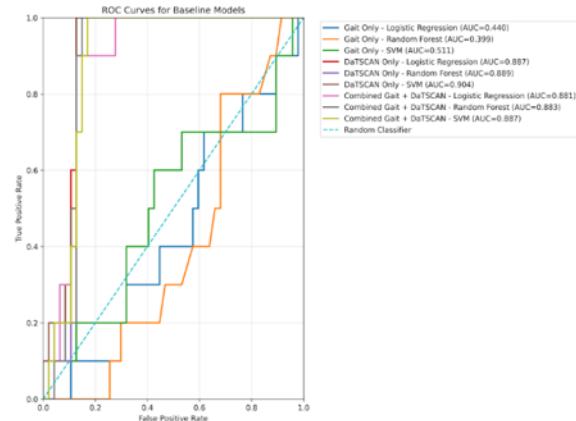


Fig. 2. ROC curves of the baseline models across gait-only, DaTSCAN-only, and combined gait–DaTSCAN feature settings

E. Performance Comparison Across Feature Settings

The best test ROC-AUC results for each feature setting are compared in figure 3. The best test ROC-AUC results for each feature setting are compared in figure 3. The ROC-AUC of the best gait-only model was 0.5277, while that of the best DaTSCAN-only model was 0.9021. The highest combined feature model was 0.8979.

This comparison demonstrates that the features extracted from DaTSCAN data gave the best predictive performance. Both the feature group together and the DaTSCAN-only setting were competitive, but it did not improve upon the best DaTSCAN-only test ROC-AUC. Therefore, the addition of gait features should be viewed as a complementary approach rather than an automatic performance improvement.

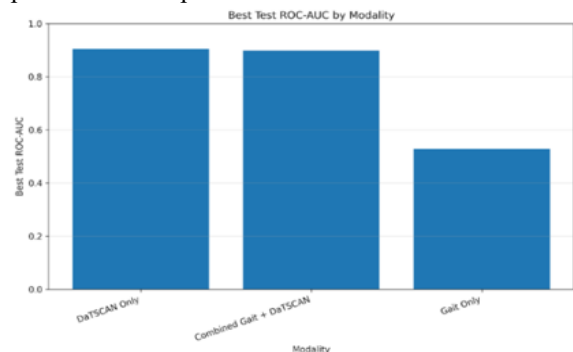


Fig. 3. Comparison of the best test ROC-AUC obtained from gait-only, DaTSCAN-only, and combined feature settings.

F. Final Model Evaluation

The final model was a combination of the gait and DaTSCAN SVM, which had the highest cross-validation ROC-AUC of 0.9579. A linear kernel was used, along with a balanced class weighting.

On the independent test set, the final model achieved an accuracy of 84.21%, a precision of 53.85%, a recall of 70.00%, an F1-score of 0.6087, and an ROC-AUC of 0.8979.

The confusion matrix is shown in Fig. 4. The model correctly classified 41 non-Parkinson's disease participants and 7 Parkinson's disease participants. It incorrectly classified 6 non-Parkinson's disease participants as Parkinson's disease and 3 Parkinson's disease participants as non-Parkinson's disease.

The confusion matrix shows that the model correctly identified 7 of the 10 PD participants in the test set. However, this relatively low precision was due to the relatively high number of false positive predictions.

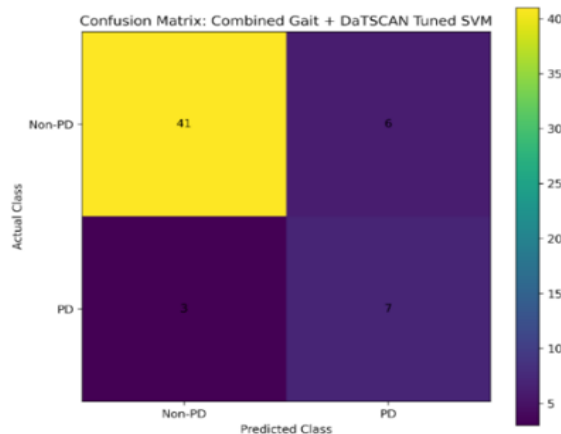


Fig. 4. Confusion matrix of the selected combined gait–DaTSCAN SVM model.

G. SHAP-Based Feature Interpretation

To understand which features contributed most to the predictions of the final combined model, SHAP analysis was performed. The results showed that DaTSCAN-related features dominated the global feature importance ranking.

The top features were PUTAMEN_L_REF_CWM and PUTAMEN_R_REF_CWM, followed by STRIATUM_ASYMMETRY and PUTAMEN_ASYMMETRY. Other influential features included STRIATUM_L_REF_CWM, STRIATUM_R_REF_CWM, and the caudate binding measurements.

Among the gait features, GAITASTDUAL had the highest mean absolute SHAP value, followed by GAITASTMIS and GAITASTUS. This indicates that the model relied mainly on putamen and striatal imaging measurements, while gait features contributed additional information to the prediction process.

The SHAP results describe the internal behavior of the trained model. They should not be interpreted as proof that a feature directly causes Parkinson's disease.

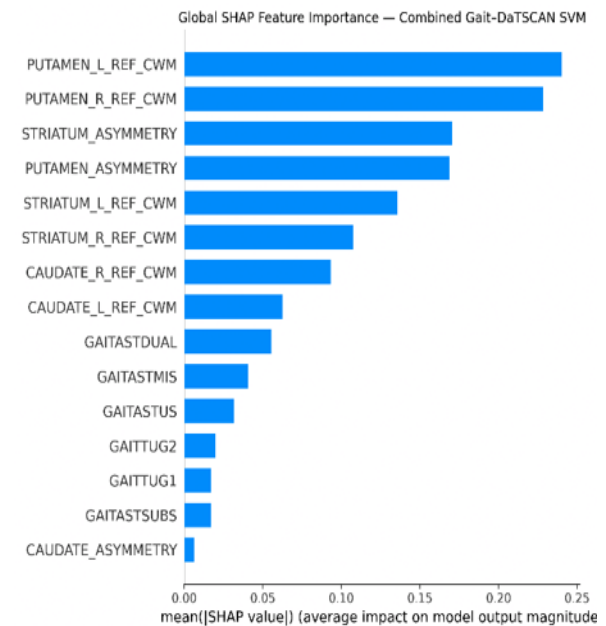


Fig. 5. Global SHAP feature importance for the final combined gait–DaTSCAN SVM model.

H. Clinical Validation

The clinical relevance of the model predictions was examined using MDS-UPDRS Part III scores. The motor impairment showed a positive correlation with the model's predicted PD probability, with a Spearman correlation coefficient of 0.5076 and $p < 0.001$.

The median MDS-UPDRS Part III score was 17 in the PD group and 3 in the non-PD group, and the difference was statistically significant. These findings suggest that the model's predicted probability was associated not only with diagnostic status but also with the level of motor impairment. This gives further clinical validation of the predictive results.

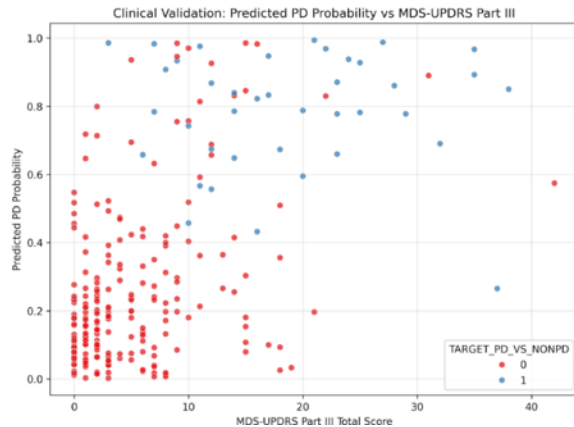


Fig. 6. Relationship between predicted PD probability and MDS-UPDRS Part III total score.

V. CONCLUSION

This study presented a comparative and explainable machine learning approach for Parkinson's disease detection using gait and DaTSCAN biomarkers. Three feature sets (gait-only, DaTSCAN-only, and a combination of gait–DaTSCAN) were tested with logistic regression, random forest, and support vector machine models.

The experimental results showed that DaTSCAN-derived features provided stronger classification performance than the selected gait features. The best DaTSCAN-only model achieved a test ROC-AUC of 0.9021, while the selected combined gait–DaTSCAN SVM achieved a cross-validation ROC-AUC of 0.9579 and a test ROC-AUC of 0.8979. The final model achieved an accuracy of 84.21% and a recall of 70.00%, which indicated that the model was able to capture a significant percentage of the PD participants.

The SHAP analysis showed that putamen measurements and striatal asymmetry were the most influential features in the final model. The additional information provided by gait variables was less influential than the DaTSCAN features in the final model. Clinical validation also showed a correlation between the model prediction of PD probability and MDS-UPDRS Part III scores, showing clinical relevance of the model predictions.

Although these results were encouraging, the study was constrained by a limited sample size in the PD population and class imbalance in the dataset. The results should therefore be validated using larger and

more diverse cohorts. Further research could also be conducted on more gait features, longitudinal data, more sophisticated multimodal fusion methods, and validation with external clinical data. The overall results showed the potential of explainable machine learning to assist in the detection of Parkinson's disease and to gain insight into the imaging and gait characteristics that impact model decisions.

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