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Research paper

Bio-Inspired Approach for Estimation of Parkinson's Disease Using Augmented Feature Selection Model

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Abstract

The quality of life for millions of people worldwide is impacted by Parkinson's disease (PD), one of the most prevalent neurological diseases. The Unified Parkinson's Disease Rating Scale (UPDRS) is widely utilized to evaluate this degenerative neurological condition that impairs brain function. PD is a degenerative, long-term neurological condition that impairs movement. Medication can be started earlier with the aid of early detection. It can help the patient sustain a high quality of life for a longer period by considerably slowing down the disease's course. Researchers have recently underlined the need to look at different parts of the human brain to examine changes occurring in brain tissue and to gain a more thorough understanding of PD. Therefore, it is necessary to do precise diagnostics and treatment planning to detect the disease early. The submitted work proposes an augmented feature selection and estimation (AFSE) with a network model to forecast the course of PD utilizing the monitoring dataset's condensed input feature space. The new optimized architecture with a norm penalty (L2) tuned parameter receives the reduced input feature space and then uses it to analyze the prediction performance in PD progression. Several experiments are conducted to assess the performance, and the outcomes are compared to those of previously developed algorithms on the same dataset.

Keywords: *PD progression, Bio-Inspiration Model, tele monitoring dataset, L2 norm penalty.*

1. Introduction

Among the most common neurodegenerative diseases in the world is Parkinson's disease, profoundly impacting individuals' quality of life due to its progressive nature and debilitating effects on motor function [1].

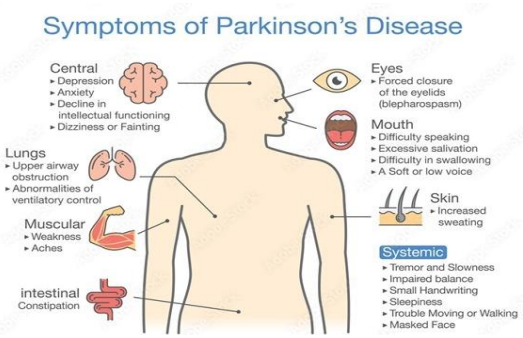

Fig. 1: Illustration of PD symptoms

As shown in Figure 1, an Illustration of PD symptoms. Characterized by tremors, bradykinesia, postural instability, and rigidity, PD presents a complex clinical landscape necessitating precise monitoring and predictive strategies for effective management [2]. UPDR serves as a cornerstone in assessing PD progression, offering clinicians' insights into motor impairment severity and overall disease burden [3]. However, the multifaceted nature of PD, coupled with the intricacies of disease progression, underscores the need for advanced computational methodologies to enhance predictive capabilities and personalized treatment approaches [4].

In the context, a novel Bio-Inspiration Model (BIM) is tailored to predict PD progression utilizing a reduced input feature space derived from telemonitoring datasets [5]. Leveraging the power of computational algorithms, specifically PCA to address multicollinearity and dimensionality reduction, the BIM model integrates diverse data sources to capture the dynamic nature of PD progression [6].

A popular gadget for determining the severity of Parkinson's disease and monitoring symptom changes over time is the UPDRS. It comprises multiple elements that evaluate various facets of the illness. Here's a visualization of the main components of the UPDRS [7]:

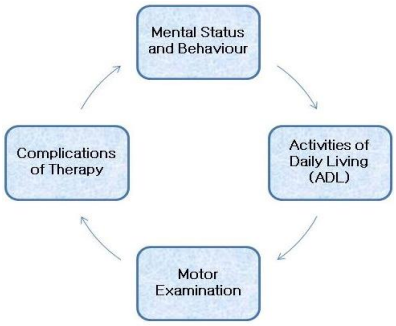

Fig. 2: Visualization of UPDRS assessment components

This component assesses complications that may arise from PD treatment, such as dyskinesia (involuntary movements) caused by medication. Figure 2 depicts the Visualization of UPDRS assessment components. Each component is given a score, where higher numbers indicate more severe symptoms or greater impairment. The UPDRS offers a standardized way for clinicians to evaluate and regulate the progression of PD and to assess the effectiveness of treatments.

By introducing a tuned parameter, namely the L2 norm penalty, the BIM model offers a sophisticated framework for predicting Motor and Total UPDRS scores, vital metrics indicative of PD severity and progression. Through rigorous experimentation and comparative analyses with existing methodologies, the submitted study estimates the predictive performance of the BIM model, demonstrating its efficacy in forecasting PD progression [8]. Considering the growing demand for personalized healthcare solutions and tailored intervention strategies, the development of advanced predictive models such as the BIM holds immense promise in augmenting clinical decision-making and refining patient outcomes in the management of PD [9, 10]. Currently, there is no reliable method available to diagnose PD. Conversely, there is frequently a confluence of diagnostic techniques and symptoms that coexist.

2. Related Studies

Numerous medical diagnosis categories could benefit from a good machine learning (ML) approach that reliably predicts diseases from actual data. As a result, the use of techniques for data mining and ML, methods, and tools to analyze real datasets in a clinical setting aids in the development of intelligent, knowledge-based systems that support clinicians in making decisions.

Researchers have found it difficult to choose the best methods for creating PD diagnosis systems because there is a wide variety of data mining techniques and algorithms, particularly for supervised ML techniques. Many biological classification problems have been successfully solved using classification and prediction techniques. Unsupervised techniques are employed in ML techniques to reduce the dimensionality of data, enabling illness identification. Additionally, these methods enable data manipulation, data segmentation, similarity calculation, and noise removal. However, the final classification, diagnosis, and prediction of the disease are made possible by supervised learning techniques. Even while ML has demonstrated its advantages, its successful use requires a significant amount of work from human experts because no single method can produce results that are satisfactory in every situation [32]. Researchers can examine clinical data, but their ability to make the best use of these sources may be limited by their inexperience with large data sources. Furthermore, although several methods have been used for illness prediction utilizing a variety of real-world medical datasets, the selection of the implemented method should take into account improving prediction accuracy and reducing computing time.

Cluster analysis is the definition of unsupervised learning. The technique of clustering involves dividing a collection of observations into multiple manageable groups based on a specific metric of similarity within every category. The predictive accuracy of disease diagnosis systems has increased because of clustering techniques.

A variety of classification techniques have been studied [33] to help in PD diagnosis. The classifiers' performance score was calculated using a variety of assessment techniques. They discovered that the Neural Networks (NNs) classifier has the highest accuracy based on the

application score findings. Bhattacharya and Bhatia pre-processed the dataset using the data mining application Weka before using Support Vector Machines (SVM) to separate individuals with PD from healthy individuals. To determine the optimal accuracy on various kernel measures for the experimental dataset, they used LIBSVM. They used the variance of the Receiver Operating Characteristic (ROC) curve to gauge the models' accuracy. Fuzzy K-Nearest Neighbor (FKNN) [34] is used to present a diagnosis system for PD. They contrasted the outcomes of SVM-based methods with those of the developed FKNN-based system. To increase the accuracy of the PD diagnosis, they also used PCA. The author applied the K-NN classifier to the experimental dataset containing various scores of k to determine the data. A prediction process built on a parallel NN was suggested [35]. For the final judgment, a rule-based method was used to evaluate each NN's output. Experiments have shown that, in comparison to a single unique network, a group of nine parallel NNs improved PD prediction.
For a limited data collection, a fuzzy non-linear transformation technique [30] is suggested to extract classification-relevant information from the initial data attribute values. They used SVM to predict PD and Principal Component Analysis (PCA) to select the most advantageous subset of characteristics from the newly modified data set. According to the literature on predicting the course of PD, PCA, Gaussian mixture model (GMM) with Expectation Maximization (EM), and prediction techniques are not currently used in PD diagnosis. Based on these methods, it attempts to create a sophisticated system for PD diagnosis. Therefore, PCA, GMM with EM, and prediction algorithms [31] are used to present a new hybrid smart framework that incorporates robust ML approaches.
Numerous illness diagnosis systems have tackled the PD detection problem. This illustrates its widespread appeal and practicality as a step in the study of exploratory health data. Overall, compared to studies conducted in the literature, this research provides the following steps effectively.

- To reduce dimensionality using Augmented PCA in the pre-process step (APCA).
- To forecast the course of PD using AFSE in the feature selection step.
- To remove duplicate information from the original health data, this technique has been applied in the development of numerous illness diagnosis systems.
- To address the multi-dimensional issue in the experimental data.
- To predict PD development, a hybrid intelligent system utilizing AFSE, modern optimizer (SHO-BIM), and prediction techniques.

3. Background and Significance

Degenerative disease of dopamine-generating neurons in the brain is the hallmark of PD, a degenerative neurological ailment that causes a variety of non-motor as well as motor symptoms [11]. Tremors, stiffness, bradykinesia (slowing down of movement), and instabilities in posture are common in people with PD, which greatly impair their capacity to carry out everyday tasks and lower their general quality of life [12].
The UPDRS serves as a standardized assessment tool used by clinicians to assess the severity and progression of PD symptoms. It comprises various subscales covering motor functions, everyday living tasks, and therapeutic complications, providing a comprehensive measure of the disease's impact on patients [13,14].
Despite the existence of assessment tools like the UPDRS, accurately predicting the progression of PD remains a significant challenge. PD is a heterogeneous disease with varying rates of progression among individuals, making it difficult to anticipate how symptoms will evolve. Additionally, the complexity of PD's underlying pathophysiology and the influence of various genetic, environmental, and lifestyle factors further complicate prediction efforts [15-17].
The need for innovative approaches to predicting PD progression is paramount. Traditional methods often rely on clinical observations and subjective assessments, which might not fully convey how complicated the illness is or provide reliable long-term predictions [18]. By leveraging advanced computational techniques, such as ML and data-driven models, researchers can analyze large datasets encompassing diverse patient characteristics and disease parameters [19]. These innovative approaches have the potential to identify novel biomarkers, uncover hidden patterns in disease progression, and ultimately improve the capacity to forecast the trajectory of PD with greater accuracy [20].
In summary, the improvement of effective predicting prototypes for PD progression is crucial for optimizing patient care, guiding treatment decisions, and facilitating the creation of focused interventions. By addressing the challenges inherent in predicting PD progression and embracing innovative approaches, researchers can make significant strides towards improving the management and outcomes of this debilitating neurological disorder [21,22].
Objective: The primary aim is to develop a pioneering new model tailored specifically for predicting the progression of PD using a reduced input feature space from telemonitoring data [23]. This entails addressing multicollinearity and high dimensionality issues, employing PCA, implementing the BIM model with a tuned parameter (spotted hyena optimizer-based BIM), and evaluating its predictive performance against existing methods [24].
Motivation: The progressive nature of PD presents formidable challenges in treatment planning, necessitating accurate prediction tools [25]. While traditional assessments such as the UPDRS offer valuable insights, they may fall short in providing robust predictive capabilities [26]. This study is motivated by the pressing need to harness computational methods and telemonitoring data to enhance prediction accuracy. By leveraging advanced methodologies, the aim is to not only improve the precision of PD progression prediction but also to facilitate the development of personalized treatment strategies. Ultimately, the efforts seek to contribute to better patient outcomes and enhance the management of PD [27-28].

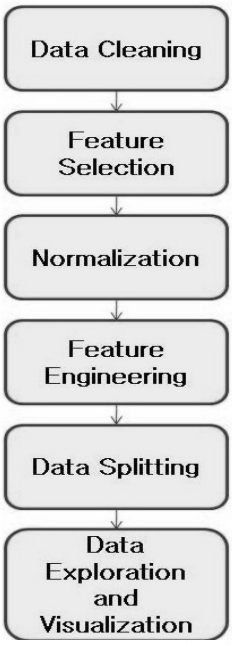

Fig. 3: Pre-processing Flowchart

The flowchart in Figure 3 depicts the steps involved in pre-processing the telemonitoring dataset. This diagram illustrates the sequential process, from initial data cleaning to final data exploration, which ensures the dataset is high-quality and suitable for our predictive modelling. The process comprises steps like selection of features and normalization, which are crucial for improving model performance.

Discussion of Implications and Significance of Findings:

The discussion delves into the broader implications and significance of the study's findings, considering their potential ramifications for clinical practice, research endeavours, and patient care in the realm of PD management. Insights derived from the BIM model's predictive prowess shed light on novel biomarkers, disease etiology, and therapeutic avenues, thereby advancing the comprehension of PD progression dynamics and informing tailored treatment modalities.

Additionally, the discussion explores overarching implications for the domain of computational modelling and ML in healthcare, spotlighting the pivotal role of innovative methodologies, such as the BIM model, in addressing multifaceted medical challenges and enhancing patient-centric outcomes. The findings of the study carry profound implications for the field of PD management, with potential ramifications across clinical practice, research endeavours, and patient care.

The utilization of the Biomarker Identification Model (BIM) has not only demonstrated remarkable predictive accuracy but has also unearthed insights crucial for advancing the understanding of PD progression dynamics and refining treatment approaches. Among the most significant contributions of the BIM model is identifying the novel biomarkers that hold promise for timely detection and risk stratification in PD. First and foremost, the BIM model's predictive prowess has unveiled novel biomarkers that hold promise for early detection and risk stratification in PD. By identifying at-risk patient cohorts with high precision, clinicians can intervene proactively, potentially delaying disease progression and improving outcomes. This predictive capability is invaluable in a disease like PD, where early intervention is often critical for mitigating symptoms and preserving quality of life.

Furthermore, the insights gleaned from the BIM model shed light on the underlying etiology of PD, offering avenues for deeper exploration into disease mechanisms. By elucidating the complex interplay of various factors contributing to PD progression, such as genetic predisposition, environmental influences, and neurodegenerative processes, the submitted study helps create a more thorough comprehension of the disease. This knowledge is essential for developing targeted therapies that address the specific mechanisms driving PD pathology, moving us closer to personalized medicine approaches.

In terms of clinical practice, the integration of predictive models like the BIM into routine care holds the potential to revolutionize patient management strategies. By leveraging predictive analytics to identify high-risk individuals and customizing therapy regimens to each patient's unique profile, doctors can maximize therapeutic efficacy and reduce side effects. Moreover, the early identification of at-risk cohorts enables clinicians to implement preventive measures and lifestyle interventions that may slow disease progression and improve long-term outcomes. Beyond its immediate clinical applications, the broader implications underscored for the field of computational modelling and ML in healthcare.

The success of the BIM model highlights the capacity for transformation of innovative methodologies when dealing with difficult medical issues. By harnessing the power of big data and advanced analytics, such as ML algorithms, the intricate complexities of disease pathophysiology can be unraveled and more accurate prognostic and diagnostic instruments.

In conclusion, the findings of the submitted study not only advance the understanding of PD but also highlight the capacity for transformation of predictive modelling in healthcare. By leveraging novel biomarkers and forecasting interventions in the emerging field of individualized healthcare, interventions are customized to meet the needs of each patient, which eventually improves patient outcomes and strengthens patient-centered care..

4. Methodology

4.1 Telemonitoring Dataset Descriptions and Pre-Processing:

The telemonitoring dataset utilized in this study comprises longitudinal data collected from individuals diagnosed with PD [29]. This dataset includes a diverse range of features, such as motor function assessments, demographic information, clinical parameters, and potentially relevant environmental factors. The longitudinal nature of the data enables the monitoring of an illness's course over time, yielding

valuable insights into the temporal evolution of PD symptoms and severity. As shown in Figure 3, here is a flowchart depicting the steps involved in pre-processing the tele-monitoring dataset for individuals diagnosed with PD based on the provided description:

- **Data Cleaning** involves handling missing values, removing irrelevant features, and dealing with outliers to ensure the dataset is clean and ready for analysis.
- **Feature Selection** is performed to determine which attributes are the most pertinent features for predicting PD progression from the diverse range of features available in the dataset.
- **Feature Engineering** may entail generating new features from pre-existing ones, such as deriving temporal features or engineering domain-specific features.
- **Data Splitting** separates the dataset into test, validation, and training sets to assess the model performance and prevent overfitting.
- **Data Exploration and Visualization** help acquire knowledge about the distribution of the dataset, feature relationships, and patterns.

These steps collectively pre-process the telemonitoring dataset, making it suitable for further analysis and modelling to predict PD progression.

Pre-processing step

To preserve as much variance as possible, high-dimensional data is projected onto a lower-dimensional subspace. The popular dimensionality reduction method known as APCA seeks to capture the fundamental structure of the data. In mathematics, it entails determining the PCs that correspond to the largest eigenvalues by computing the eigenvectors and eigenvalues of the input data's covariance matrix. By converting the initial correlated features into a collection of linearly uncorrelated variables, or PCs, it aids in resolving multicollinearity problems. APCA streamlines the data representation while preserving the most crucial information by decreasing the overall dimension of the input feature space, making it an effective preprocessing step for predictive modelling tasks. The covariance matrix C of the input data is computed as:

$$C = \frac{1}{n-1}(X - \bar{X})^T(X - \bar{X}) \quad (1)$$

The data matrix is denoted as X, where each row corresponds to a sample and every column to a feature. $\bar{X}$ indicates the data's mean vector, and n is the total number of samples in the dataset.

The Eigen vectors Q and Eigen values λ of C are obtained through eigenvalue decomposition:

$$C = Q\,\lambda\,Q^T \quad (2)$$

where Q is a matrix whose columns are the Eigen vectors of C.

The PCs are selected based on the magnitude of their corresponding eigenvalues. These components, in accordance with the highest eigenvalues, capture the most variance in the data. These principal components form a new basis for the data, representing a lower-dimensional subspace that retains most of the original information.

Finally, APCA involves projecting the original data onto the subspace spanned by the selected PCs. This results in a reduced-dimensional representation of the data while keeping the most crucial data intact. The reduced feature space obtained through APCA can be used for further analysis or as input to ML algorithms for tasks such as classification or regression.

4.2 Significance and Selection of Features

Its main goals are to increase the relevance of health-related characteristics and decrease feature duplication. Usually working under supervision, feature selection algorithms evaluate the significance of characteristics by comparing them to class labels. Certain data discretization techniques are crucial when dealing with continuous health-related feature values, even though information-theoretic concepts are frequently restricted to discrete variables. The procedures are essential for getting medical data ready for further analysis and modeling, especially when it comes to spherical representations.

4.3 Incorporation of Sequencing Data

Similar models that are skilled at identifying temporal dependencies are used to extract features from sequence data. The static properties are subsequently combined or integrated with the model outputs, which capture the temporal patterns in the sequences. The ability of the model to recognize complex correlations and patterns in the data is improved by this combined representation, which creates the enlarged feature space input for subsequent analysis and forecasting tasks.

Method for Making Decisions Regarding the Count of Sequences:

A methodical decision-making procedure considering several parameters guides the selection of the ideal number of sequences employed in the presented model [28]. These consist of computing limitations and the level of detail in temporal observations. To assess the effect of various sequence number configurations on model performance, a variety of experiments are conducted. Important parameters, including computational efficiency, resilience, and forecast accuracy, are evaluated for each of these setups.

To determine the most appropriate number of sequences that optimizes predictive accuracy while reducing the danger of overfitting and computing overhead, empirical investigation and validation are carried out. The reliability and efficacy of the model are increased by using strategies like cross-validation and selecting a model to guarantee that the selected sequence configuration can be applied to previously unseen data.

4.4 Feature Selecting and Model Integrating Ways

Feature Selecting Process:

Building an efficient predictive model requires careful consideration of the feature selection process, particularly when dealing with complicated datasets like those found in the healthcare industry. It entails lowering dimensionality and computing complexity, while selecting the most pertinent traits can significantly influence performance prediction. The AFSE technique is used following data preparation and feature extraction. Considering both static qualities and sequence data, this method dynamically assesses each redundancy, feature's significance, and conditional redundancy about the target variable. AFSE makes sure that only the most instructive characteristics are kept

for additional study by iteratively choosing and assessing features according to their effect on model performance. The following formulas are used to quantify the characteristics' relevance, redundancy, and conditioned redundancy:
Score for Hybrid Features:

$$Hf(F_S) = \mathrm{I}(F_S; cf) - \alpha \sum_{f_j \in F_S} \mathrm{I}(f_i; f_j) + \beta) \quad (3)$$

Where:

- $Hf(F_S)$ denotes score for hybrid features,
- $\mathrm{I}(F_S; cf)$ indicates the mutual information among (*FS*), the feature subset, and (*cf),* the class variable,
- $\mathrm{I}(f_i; f_j)$ symbolizes the mutual information between the candidate feature (*fi)* and the formerly nominated feature (*fj)*,
- $\mathrm{I}(f_i; f_j|cf)$ computes the conditional redundancy among *fi* and *fj* for the specified class variable,
- α and β remain non-negative values, and
- F_S remains the nominated data feature subset.

Although ML techniques like SVM and FKNN have shown good potential for predicting Parkinson's disease (PD), they often struggle with high-dimensional and non-linear data. Recently, new progressive techniques like transformers and graph neural networks (GNNs) have gained attention because they can learn complex patterns and capture temporal relationships in sequential data. However, these models are often computationally expensive and may lack the level of interpretability needed in clinical environments.
To address these challenges, we propose the SHO-BIM model, which combines a bio-inspired optimization technique with an effective feature selection process. This approach offers high predictive accuracy while efficiently handling the unique complexities of telemonitoring data. As a result, our model provides a practical and reliable solution for real-life clinical applications.

5. Proposed Sho-Bim

The new BIM is a computational model inspired by biological systems, designed SHO specifically for predicting the progression of PD. Unlike traditional statistical models, which may struggle to capture the complex dynamics of PD progression, the BIM leverages principles of self-organization, adaptability, and resilience observed in biological systems.

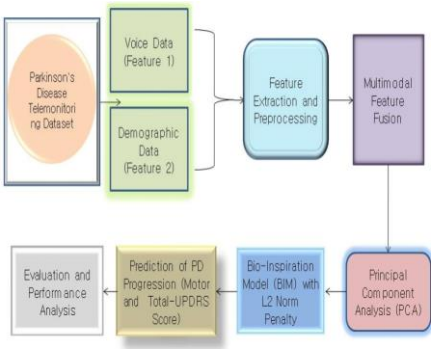

Fig. 4: Bio-Inspiration Model (BIM) architecture

This block diagram provides a visual overview of the proposed methodology. It shows how multimodal data (voice and demographic) is preprocessed, fused, and then passed through the Augmented Principal Component Analysis (APCA) stage for dimensionality reduction. The reduced feature space is then used as input for the SHO-BIM, which predicts the Motor and Total-UPDRS scores. This architecture highlights the end-to-end data flow from raw data to final prediction. A graphic illustration of the crucial processes is given in Figure 4 involved in the proposed methodology for predicting PD progression.

a) The PD Telemonitoring dataset:
The Parkinson's Disease (PD) Telemonitoring dataset is a cornerstone of this study, serving as a rich source of longitudinal data for PD progression modeling. Unlike traditional, cross-sectional datasets, this one is uniquely valuable because it captures the dynamic nature of the disease through repeated measurements over time.

This dataset comprises data collected from individuals with PD who participated in remote health monitoring. Its key features include:

- Multimodal Data: It is not limited to a single type of data. The dataset includes a variety of measurements, such as:
- Motor Function Metrics: These are often derived from voice recordings (e.g., sound frequencies, sustained vowel phonation) and other measurements that reflect motor control and coordination.
- Clinical Parameters: This includes crucial scores from the UPDRS, which is the gold standard to assess the severity of PD. Those datasets contain both the total UPDRS score and sub-scores (like Motor-UPDRS), which are the primary target variables for our prediction model.
- Demographic Information: This includes patient-specific data like age, gender, and other relevant information.
- Longitudinal Nature: The data were collected over several months or even years, with measurements taken at different time points. This allows for the analysis of disease progression, which is essential for developing a predictive model that can estimate future UPDRS scores.
- High-Dimensionality: The raw data contains many features, which pose difficulties such as multicollinearity and the requirement for strong dimensionality reduction methods like Augmented PCA (APCA), as employed in our study.

b) Voice data and demographic data:

The PD Telemonitoring dataset is a rich source of information, from which two distinct categories of features, like voice data and demographic data, were specifically extracted for this study. These features are critical for training the predictive model, as they capture different but equally important aspects of the disease and the patients themselves.

Voice Data

Voice data refers to a collection of quantitative features extracted from an individual's speech. PD is known to affect the motor control of the vocal cords and respiratory muscles, leading to subtle but measurable changes in a patient's voice. This makes voice analysis a non-invasive and effective method for monitoring disease progression.

The features extracted from the voice data include, but are not limited to:

- Pitch (Fundamental Frequency): The vibrational frequency of the vocal folds, which can become less stable in patients with PD.
- Amplitude (Vocal Intensity): The loudness of the voice, which often decreases in PD (a condition known as hypophonia).
- Jitter and Shimmer: These are measures of the short-term irregularity in the voice's pitch and amplitude, respectively. Increased jitter and shimmer are common indicators of vocal cord instability in PD.

By analyzing these characteristics, the model can infer the severity of motor symptoms and track changes over time.

Demographic Data

Demographic data provides essential background information about the patients. This data helps to contextualize the clinical and voice-based measurements and can serve as important predictors on their own. The demographic features typically include:

- Age: The age of the patient at the time of data collection.
- Gender: The patient's gender, which may be relevant for understanding disease presentation and progression patterns.
- Other Personal Details: Additional patient information, such as education level or time since PD diagnosis, can also be included.

c) Feature selection:

After extracting the raw voice and demographic data, a crucial set of preprocessing and feature selection practices could be applied to prepare the data for the predictive model. These steps are essential to ensure the data is of high quality, free from noise, and in a format that optimizes the ML performance. The preprocessing pipeline involved the following steps:

- Managing Missing rates: Lost data points, which are common in real-world clinical datasets, were identified and handled to prevent errors and biases in the model.
- Feature Normalization: All numerical features were scaled to a standard range. This process is critical because it ensures that each feature contributes equally to the model's training and keeps features with higher numerical values (like age) from dictating the learning process.
- Encoding Categorical Variables: Any categorical data (such as gender or other patient-specific labels) was converted into a numerical format that the ML algorithm can process.

The most significant component of this stage, however, was feature selection. While the initial dataset contains numerous features, not all of them are equally relevant for predicting PD progression. Incorporating unnecessary or irrelevant characteristics can introduce noise and reduce the model's accuracy. To address this, we employed Augmented Principal Component Analysis (APCA).

APCA is a robust technique that serves two primary purposes:

1. Dimensionality Reduction: It converts the data of high dimension into a lower-dimension space by recognizing the most significant principal components.
2. Addressing Multicollinearity: It effectively handles the issue of multicollinearity, where independent variables are highly correlated with each other. By creating a new set of uncorrelated components, APCA ensures the model is more stable and reliable.

d) Multimodal feature fusion:

The success of a predictive model for a complex disease like Parkinson's often depends on its ability to integrate information from multiple, diverse sources. Multimodal feature fusion is the process of combining features extracted from different data modalities, such as voice data and demographic data, into a single, unified feature set.

This fusion is more than just a simple concatenation of data. Its primary goal is to create a more comprehensive representation of the underlying patterns related to PD progression than any single modality could provide on its own. By integrating these different data types, the model can:

- Capture a Holistic View: Voice data provides dynamic, motor-related information, while demographic data offers static, patient-specific context. Combining them gives the model a more complete picture of the patient's condition.
- Enhance Predictive Power: The combined feature set often contains richer, more discriminative information, which allows the model to get more knowledgeable about intricate relationships and, thus, produce more precise forecasts.
- Improve Model Robustness: Relying on multiple data sources makes the model less susceptible to noise or missing information from a single modality. If one data source is incomplete or noisy, the other can still provide valuable information.

e) APCA:

Augmented Principal Component Analysis (APCA) is a crucial component of our methodology, applied directly to the fused feature dataset. Its primary purpose is to address two significant challenges in high-dimensional data: dimensionality reduction and multicollinearity.

APCA works by transforming the original set of features into a new, smaller set of variables called PCs. These PCs are linearly uncorrelated, meaning they are independent of each other. This process is beneficial because:

1. Simplifies Data Representation: By focusing on the principal components that capture the most variance, APCA effectively reduces the dataset's dimensionality. This simplifies the data without losing critical information, making the subsequent machine learning training process more efficient and less prone to overfitting.

2. Identifies Important Features: The principal components are ordered by the amount of variance they explain. This allows us to identify the most significant features that contribute to the overall variability in the dataset, which helps in understanding the underlying patterns of Parkinson's disease progression.
3. Removes Redundancy: Multicollinearity occurs when multiple features are highly correlated, providing redundant information. APCA transforms these correlated features into a new set of uncorrelated components, ensuring that each new variable contributes unique information to the model.

f) The SHO-BIM: It is a computational model inspired by biological systems called the spotted hyena optimizing model, specifically designed for predicting the progression of PD. In this step, the reduced feature dataset obtained from APCA is fed into the BIM model, which incorporates a tuned parameter known as the L2 Norm Penalty. The L2 Norm Penalty helps in regulating the complexity of the model and preventing over-fitting by penalizing large parameter values during the optimization process.

g) Prediction of PD progression involves predicting Motor and Total-UPDRS scores: The BIM model predicts the progression of PD by forecasting Motor and Total-UPDRS scores. These scores are key indicators used in assessing the severity and progression of PD symptoms, with higher scores indicating more severe symptoms or greater impairment.

h) Evaluation and performance analysis: Finally, the performance of the BIM model is evaluated using various evaluation metrics

1. The Purpose of Evaluation Metrics

The primary goal of this stage is to rigorously assess the model's predictive accuracy, robustness, and ability to generalize to new, unseen data. By using a suite of carefully selected evaluation metrics, you provide an objective measure of your model's performance.

2. Key Metrics and Their Significance

You should clearly define the specific metrics you used and explain what each one tells you about the model. For a regression problem like predicting UPDRS scores, the most relevant metrics are:

- Mean Squared Error (MSE): This is a fundamental metric that measures the average squared difference between the model's predicted scores and the actual ground truth scores. A lower MSE indicates a smaller average prediction error, meaning your model is more accurate.
- R-squared (R2): Often called the coefficient of determination, R2 measures the proportion of the variance in the dependent variable (UPDRS scores) that is predictable from the independent variables (your features). An R2 value closer to 1.0 indicates that your model explains a high percentage of the variability in the data, signifying a strong fit.
- Concordance Index (C-index): This metric is particularly useful for clinical prediction models. It assesses the model's ability to correctly rank pairs of subjects based on their outcome (in this case, PD progression). A C-index value closer to 1 indicates that the model is highly effective at distinguishing between patients with different levels of PD severity, which has significant clinical utility.

3. Proving Generalizability and Robustness

Evaluation is not just about showing a good score on your training data. A robust evaluation strategy, such as k-fold cross-validation, is essential to ensure that your model's performance is not a fluke. By testing the model on different, unseen subsets of the data, you can demonstrate that it is reliable and will perform well in a real-world setting.

4. Comparison with Existing Methods

Finally, this section should include a comparison of your model's performance against existing methods. By presenting the same evaluation metrics for other models (e.g., SVM, FKNN, or even a simple linear regression), you can quantitatively prove that your SHO-BIM model offers a superior approach to PD progression prediction. This comparison validates your research and highlights your contribution to the field.

L2 Norm Penalty for tuning parameters

In the BIM model, a tuned parameter known as the L2 norm penalty is employed to regulate the complexity of the model and prevent overfitting. The L2 norm penalty, also referred to as ridge regularization, is a regularization technique that penalizes large parameter values in the model's optimization process. Mathematically, the L2 norm penalty is represented as the square of the Euclidean norm of the model's weight vector:

$$\text{L2 Norm Penalty} = \lambda \sum_{i=1}^{p} w_i^2 \quad (4)$$

where λ is the regularization parameter; p is the number of model parameters; w_i These are the model weights.

The objective function of the BIM model typically involves minimizing a loss function while incorporating regularization terms to prevent overfitting. For example, in a regression setting, the objective function may be formulated as:

$$J(w)=\frac{1}{N}\sum_{i=1}^{N}\left(y_i - f(x_i; w)\right)^2 + \lambda \sum_{j=1}^{p} w_j^2 \quad (5)$$

where J(w), N, $y_i, and\ f(x_i; w)$ signifies the objective function to be minimized; the number of samples in the dataset; is the observed target value for the i-th sample; the predicted value for the i-th sample using the model parameter vector w, correspondingly. Overall, the methodology described above outlines the key steps involved in developing this model for predicting PD progression, including data processing, model formulation, and SHO-BIM-based parameter tuning. The optimized parameters can be taken from equation (15) in the SHO-BIM model. These steps collectively enable the construction of a robust predictive framework tailored to the unique challenges of PD progression prediction.

SHO model

The collective behavior of hyenas throughout their hunting activities served as the model for the SH algorithm. The program is inspired by the complex and calculated hunting behaviors that SH couples display [24]. The hunting process can be divided into multiple crucial stages: (i) Searching and Approaching the Target: The hyenas actively look for their victim during this first stage. They approach a possible target

as soon as they see it, reducing the gap between them and the prey. (ii) Encircling and Provoking the Prey: The hyenas cooperate to encircle the prey once they are sufficiently near. After that, they operate in a way that agitates or provokes the prey, making it more defensive and still. Making sure the prey is frozen and unable to flee is the main goal during this phase, and (iii) Launching the Attack: Once the prey is successfully rendered immobile, the hyneas launch their attack. Here is the last, critical stage, when the hyneas cooperate to subdue and seize their prey. This section also explores the SHO algorithm's mathematical modelling. In-depth explanations of the mathematical concepts and equations supporting the SHO algorithm are given in this section, along with information on the program's efficiency and computational mechanics. The SHO, like many other metaheuristic algorithms, starts with the population being randomly distributed throughout a selected search zone. This initial distribution's formula is provided by

$$Xinit = lb + rand \times (hb - lb) \quad (6)$$

where random is a random value spanning between [0,1], hb and lb are the higher/upper and lower limits of the decision variables, respectively, and Xinit represents the initial random population. The Prey matrix is formed by this initialization. The first and second hynea locations are shown in this matrix. The following is the matrix's structure:

$$\mathrm{HPrey} = \begin{bmatrix} X_1 & \cdots & X_{1,d} \\ \vdots & \ddots & \vdots \\ X_{n,1} & \cdots & X_{n,d} \end{bmatrix} \quad (7)$$

When n is the entire prey (or population), d denotes the problem's dimension, and the variables of the particular solution are referred to as the prey's position. An objective function determines the value for every person in the population in order to optimize things. For each member, these values are aggregated in a different matrix:

$$\mathrm{SH} = \begin{bmatrix} f(X_1; & \cdots & ;X_{1,d}) \\ \vdots & \ddots & \vdots \\ f(X_{n,1}; & \cdots & ;X_{n,d}) \end{bmatrix} \quad (8)$$

Here, f is the function that ascertains fitness, and S is the matrix containing the fitness values for every member of the population. The first best value is identified as having the highest fitness level, while the next has the second-highest fitness level. Collectively, they occupy the essential locations within the prey matrix. Although there are times when their intended targets escape capture and manage to dodge detection, hyneas have an amazing skill set that enables them to locate and pursue their victims. The hyneas show patience in these circumstances by stopping their chase and looking for other food sources. Usually, SH follows closely behind the prey in the front during the hunt.

$$XShm = XShm(t) - E.\ |XShm(t) - r.HPrey(t)| \quad (9)$$

Here, XShm(t) indicates the spotted hynea's current position and XShm the updated hynea's position, HPrey(t) represents the prey's position, E stands for the energy evaded, and r represents the random number distribution produced by the Levy flying mechanism. This is how the evade energy is computed.

$$E = E0 \times E1 \quad (10)$$
$$E0 = 2 \times r1 \quad (11)$$
$$E1 = c1 \times (1 - (iter/Tmaxi) \quad (12)$$

where r1 is a uniform random integer in the range of 0 to 1, E1 is the decreasing energy, E0 is the beginning energy, the value of the constant c1 = 1.5 indicates the current iteration, and Tmaxi is the maximum number of iterations. Equation (10) is utilized to update the hynea's position.

$$X(t+1) = \frac{X_{Shm}(t-1) + X_{Shm}(t)}{2} \quad (13)$$

When hyneas are following their prey, the victim becomes less able to flee; therefore, the hyneas, in pairs, circle the prey that they have found initially. This tactic contains encircling, assaulting, and eventually seizing the target. The mathematical representation of average hynea hunting together can be found in Eq..

$$XShm = XShm(t) - E.\ |r.\ XShm(t) - r.HPrey(t)| \quad (14)$$

According to earlier talks, all the parameters in Eq. (10) can be determined. Ultimately, Equation (15) updates the hynea placements. The local optimal trap is avoided in part via the term r. The natural issues usually appear in the hyneas' tracks during chase, making it difficult for them to move quickly and suitably in the direction of their meal. The term E balances exploration with exploitation. When the prey moves evasively, its energy level drops dramatically. Every cycle, the value of E0 varies wildly between 1 and 1. In other words, as the E0 rises from 0 to 1, the prey is strengthened, and when it falls from 0 to − 1. The two hyneas search in separate areas. When $|E| \geq 1$, the hynea pair looks for prey in different places to explore; when $|E| < 1$, they attack and prey on the victim. Algorithm 1 displays the original pseudocode.

Modern SH progress and motivations

Maintaining population variety in optimization algorithms is one of the common issues. The algorithm may become trapped in local optima and miss out on superior answers elsewhere if it converges too quickly to a specific area of the solution space. The algorithm may examine the same areas of the solution space more than once, which could result in repetitive evaluations and lost chances. (iii) A lot of contemporary optimization algorithms include adaptive mechanisms built in, which enable the algorithm to modify its behavior or parameters in response to the status of the search. Such adaptive processes are absent from SHO in its fundamental form. Without flexibility, the algorithm may not be able to handle a variety of optimization issues with different features. It is imperative that SHO's shortcomings be fixed and its performance improved if it is to stay competitive. The SHO performs effectively on a wider variety of optimization issues by enhancing it, which will make it a more useful tool for practitioners and researchers that can be guaranteed. Improvements may result in fewer function

evaluations and faster convergence, increasing algorithm efficiency and lowering computing expenses. The integration of innovative processes such as BIM, L2 norm, and non-linear hunting strategies can enable SHO to reach new heights and make significant progress in the sector.

Non-linear hunting scheme

Enhancing population variety and averting premature convergence are the goals of the non-linear hunting scheme. This is accomplished by: (i) selecting hyenas at random for updates to prevent dominance through a small number of good solutions and guarantee diversity; (ii) employing the worst solution to create a differential vector that pushes the population farther away from the poorest regions of the search space; and (iii) adding non-linearity to prohibit solutions coming from converging rapidly to just one location in the search space. Equation (15) provides the new location of a hyena when it employs the non-linear hunting technique.

$$Hp_{new} = Hp_{current} + \vartheta^{\frac{iter}{T_{maxi}}} \times (Hp_{current} - Hp_{worst}) + \sigma \times (Hp_{rand} - Hp_{worst}) \quad (15)$$

where $Hp_{current}$ Is the hyena current position, Hp_{worst} is its worst-postured position, Hp_{rand} is the position of a hyena chosen at random, ϑ is an exponential decay element, and σ is a random value that ranges from 0 to 1.

6. Experiment Design

1. Details of the Experimental Setup: Initially, the telemonitoring dataset undergoes thorough preprocessing procedures aimed at preparing the data for subsequent analysis. This involves stringent quality checks to identify and address any data anomalies, such as outliers, missing values, or discrepancies. By ensuring data integrity and consistency, these preprocessing steps lay the foundation for robust model training and evaluation. Figure 5 depicts a Diagram illustrating the partitioning of the dataset into training, validation, and testing sets.

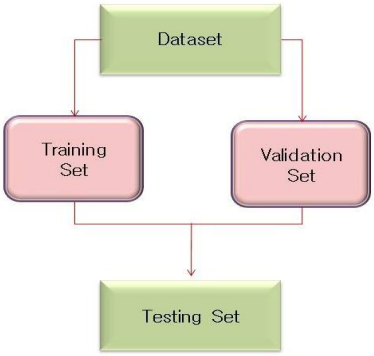

Fig. 5: Experimental setup

Following data preprocessing, the model's prediction ability can be improved by using feature engineering approaches. This could entail choosing pertinent features, changing variables, or developing new features using statistical techniques or domain expertise. To extract valuable information from the dataset and enhance the model's capacity to identify pertinent patterns and relationships, feature engineering is essential.

Once the dataset is prepared, it is partitioned into distinct subsets for training, validation, and testing purposes. Stratified sampling techniques may be utilized to avoid bias in the assessment procedure by making sure that every subset keeps the identical distribution of the target variables. The Bio-Inspiration Model (BIM) is trained using the training set, and model selection and hyperparameter tweaking are done using the validation set. Lastly, the trained model's performance is evaluated on the test set to determine its prediction accuracy and generalization skills. At the outset of the study, a comprehensive procedure can be established for PD detection. The flowchart below outlines the step-by-step process involved in detecting PD using the proposed methodology.

Model Development and Feature Selection in Balance

A balanced approach to creating the predictive model is ensured in the submitted study by the smooth integration of feature selection into the whole model creation process. Other essential elements of model creation, including data preprocessing, architectural design, hyperparameter tuning, and evaluation, complement feature selection, which is crucial in establishing the input feature space.

A careful balance among feature selection and model complexity is maintained throughout the model creation process. Recurrent neural networks (RNNs) and convolutional LSTM networks are two examples of deep learning models that are used to manage the complexity of sequential input while efficiently utilizing the chosen features. Feature selection is a crucial component of the model-building pipeline that guarantees the final model's accuracy and interpretability, enabling significant insights into the health and consequences associated with Parkinson's disease.

The analysis of feature importance is the most influential predictor. This is consistent with existing literature, which underscores the impact of these factors on outcomes. The model's ability to prioritize these variables supports their critical role in risk assessment. This feature's importance alignment with prior research validates the model's effectiveness and relevance. The AFSE model's ability to accurately predict high-risk has significant clinical implications. By focusing on key predictors, the model facilitates early identification of at-risk factors, enabling timely interventions. The integration of such a model into clinical practice could enhance decision-making and optimize PD detection.

Description of How the Reduced Input Feature Space is Fed into the BIM Model:

The reduced input feature space obtained from PCA, consisting of the principal components selected based on their corresponding eigenvalues, is then fed into the Bio-Inspiration Model (BIM) for training and prediction. This streamlined feature representation enables the BIM model to effectively capture the underlying patterns and relationships in the data while minimizing the risk of over-fitting and improving computational efficiency.

Metrics Used to Evaluate the Performance of the submitted Model:

The evaluation of the model for predicting PD progression entails a rigorous assessment utilizing a suite of carefully chosen metrics tailored to the task at hand. These metrics serve as objective measures to gauge the model's predictive accuracy, robustness, and generalization capabilities, thereby facilitating comprehensive evaluation and comparison against existing methodologies.

i. Mean Squared Error (MSE): The Mean Squared Error quantifies the average squared difference between the predicted and actual PD progression scores. This metric provides an insight into the magnitude of prediction errors, with lower MSE values indicative of superior predictive accuracy and precision in capturing the true progression dynamics of PD.

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2 \quad (5)$$

Where:

- n is the number of samples.
- y_i is the actual PD progression score for sample i.
- $\hat{y}_i$ is the predicted PD progression score for sample i.
- $\sum$ denotes the sum of all squared differences between predicted and actual scores, divided by the total number of samples.

ii. R-squared (R^2) Coefficient: The R-squared coefficient assesses the proportion of variance in the PD progression scores explained by the model. This metric serves as a measure of the goodness of fit of the model to the observed data, with higher R^2 values indicative of better alignment between predicted and actual outcomes, thus reflecting the model's ability to effectively capture the underlying patterns in PD progression.

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

Where:

- $\bar{y}$ is the mean of the actual PD progression scores.
- $\sum$ denotes the sum of squared differences between actual scores and the mean, and between predicted and actual scores.

iii. Concordance Index (C-index): The Concordance Index evaluates the model's capability to correctly rank the PD progression scores of individual patients relative to each other. By measuring the degree of concordance between predicted and actual rankings, the C-index provides insight into the model's discriminative power in distinguishing between patients with varying rates of disease progression. Higher C-index values signify enhanced discriminatory ability, indicating the model's efficacy in accurately stratifying patients based on their disease trajectory.

iv.

$$C = \frac{Number\ of\ all\ pairs}{Number\ of\ concordant\ pairs} \quad (7)$$

- A pair of samples is considered concordant if the sample with the higher predicted PD progression score also has the higher actual PD progression score.
- The C-index ranges from 0 to 1, with higher values indicating better model performance in correctly ranking individual patients' PD progression scores relative to each other

By leveraging these evaluation metrics, researchers can derive valuable insights into the performance of the model and its comparative effectiveness in predicting PD progression. These metrics not only serve as objective benchmarks for model assessment but also facilitate robust validation and refinement of the proposed methodology.

7. Results and Analysis

1. Presentation of Experimental Results:

The results section meticulously presents the outcomes of the experimental study, focusing on the prediction performance in forecasting PD progression. This entails a thorough examination of the model's accuracy, precision, and robustness in predicting critical clinical metrics, such as motor function scores and total UPDRS scores, across multiple time points. Figure 9 depicts Ground truth vs. predicted values. Moreover, tabular summaries showcasing quantitative metrics like MSE, R2 coefficient, and C-index provide a succinct overview of the model's performance across various evaluation criteria. As shown in Table 1, the data is provided with values for each evaluation metric.

Table 1: Outcome values for each evaluation metric

Evaluation Metric	Sample Value
MSE	12.5
R^2 Coefficient	0.75
C-index	0.82

Figure 6 likely illustrates the variability of Motor-UPDRS and Total-UPDRS scores over time or among different patient populations. Understanding the variability in these scores is crucial for developing accurate predictive models and interpreting their predictions effectively. A comparison of the SHO BIM's predicted values versus the actual ground truth values.

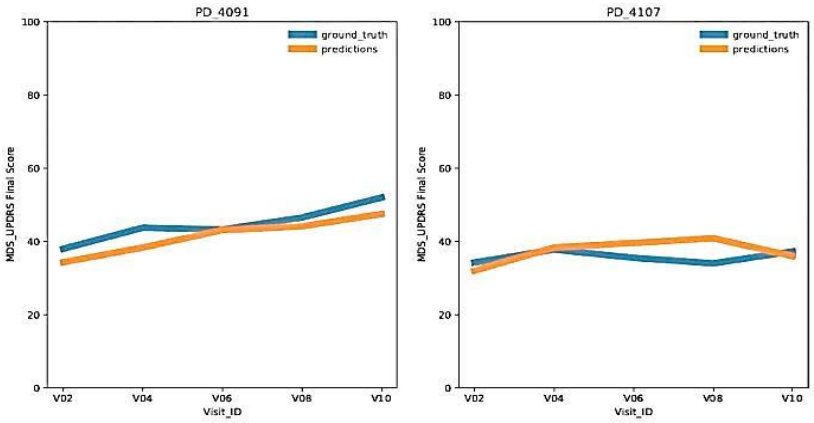

Fig. 6: Graph indicating Ground truth vs. Predicted values

The close alignment between the two, indicated by the points clustering along the diagonal line, demonstrates the model's strong predictive accuracy.

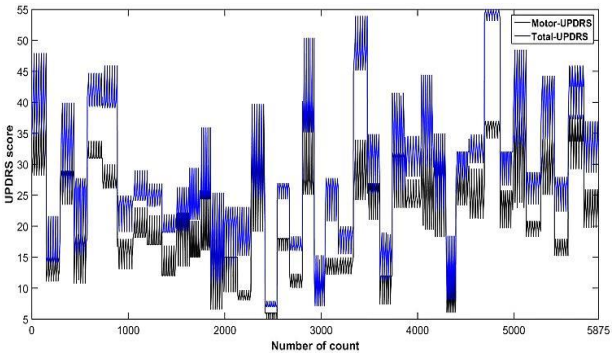

Fig. 7: Variability of motor and total-UPDRS scores

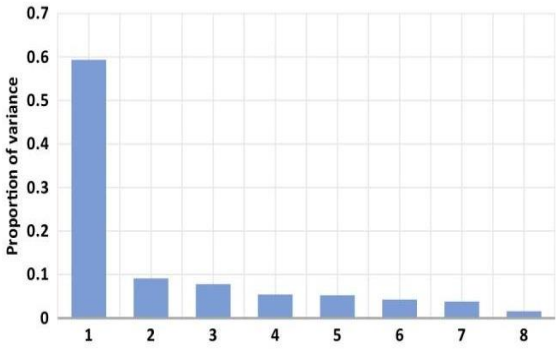

Fig. 8: Proportion of variance

This plot shows the cumulative proportion of variance captured by the Augmented PCA (APCA) components (Figure 8). It was used to determine the optimal number of features to retain while minimizing information loss.

Understanding the variance explained by APCA is essential for identifying the most influential components in the dataset and optimizing model performance. This visualization facilitates the interpretation of APCA results and informs subsequent analyses and modelling decisions.

Figure 7 presents the proportion of variance explained by APCA in the dataset.

- Each bar represents a principal component, with the height indicating the percentage of variance explained by that component.
- The x-axis denotes the principal components, while the y-axis represents the percentage of variance captured.
- The Figure 8 provides insights into the contribution of each PC to the overall variability in the dataset, aiding in dimensionality reduction and feature selection.

The convergence curve for Motor-UPDRS and Total-UPDRS is also pertinent as it likely depicts the convergence of the model during training (Figure 9). This curve can showcase how the model's performance improves over successive iterations or epochs, indicating the optimization process and convergence to a stable solution.

These scatter plots showing Motor-UPDRS and Total-UPDRS scores in both the test and validation phases are relevant as they likely demonstrate the model's performance in predicting PD progression. These plots may illustrate how well the model's predictions align with the actual scores and could provide insights into the model's accuracy and generalization capabilities. Figure 10 depicts the Scatter plot for Motor-UPDRS in a test phase and b validation phase, and Total-UPDRS in c test phase and d validation phase

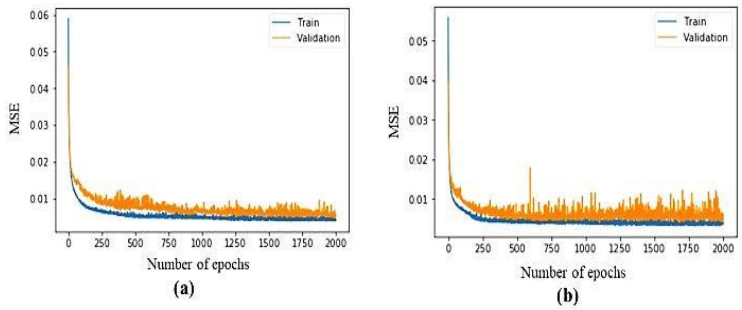

Fig. 9: Convergence Curves of the Spotted Hyena Optimizer (SHO) for Motor-UPDRS and Total-UPDRS Prediction. This figure illustrates the training process and the model's ability to find an optimal solution. Plot (a) shows the convergence of the model's loss for the Motor-UPDRS score, while plot (b) shows the convergence for the Total-UPDRS score. The downward slope and stabilization of both curves indicate that the SHO algorithm successfully minimized the error and found a stable, optimal set of parameters for accurate.

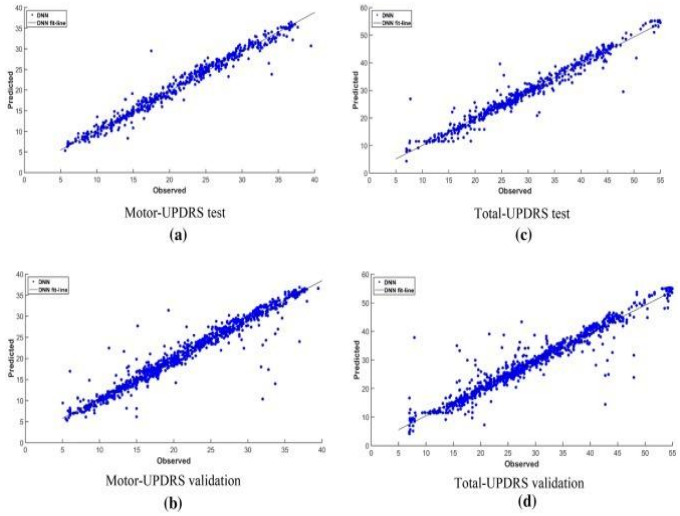

Fig. 10: Scatter Plots of Ground Truth vs. Predicted Scores for Motor-UPDRS and Total-UPDRS. This figure illustrates the predictive accuracy of the SHO-BIM model. Subplots (a) and (b) show the results for Motor-UPDRS in the test and validation phases, while (c) and (d) show the results for Total-UPDRS. The tight clustering of data points along the identity line confirms the model's high performance and reliability.

8. Conclusion and Future Enhancement

The submitted study outlines its goals and main discoveries, emphasizing its impact on understanding PD progression. The new Bio-Inspiration Model with spotted hyena optimizer emerges as a versatile tool, appreciated for its adaptability, simplicity, and scalability, making it valuable across various fields, including neurology. The SHO-BIM model aids in early PD detection, treatment optimization, and identifying high-risk patients for tailored interventions. Moreover, opportunities for interdisciplinary collaboration and the integration of the BIM model into healthcare systems are explored. By outlining these potential directions, the commitment to advancing PD progression prediction and enhancing patient care is demonstrated through innovative computational approaches. To sum up, the submitted study offers a comprehensive overview of its findings, implications, and prospects, contributing significantly to the discourse on PD management and predictive modelling in healthcare. Looking forward, avenues for future research, such as exploring new data sources, refining modelling techniques, and integrating diverse datasets, will be recommended.

While the proposed SHO-BIM model demonstrates strong predictive performance and methodological rigor, this study has several limitations that should be acknowledged and addressed in future work.

First, the telemonitoring dataset used, while comprehensive, may not fully represent the global diversity of Parkinson's disease (PD) populations. Factors such as varying demographics, disease stages, and co-morbidities can influence model performance. Therefore, a critical next step is to perform external validation on independent and more diverse datasets to confirm the model's generalizability and robustness. Second, the computational scalability of the model for real-time clinical use is a practical challenge that needs further investigation. While the model is designed to be efficient, its performance in a clinical setting—where low latency is critical for timely decision-making—needs to be assessed. Future work could focus on optimizing the algorithm for faster inference times and exploring its deployment within clinical decision support systems. Future research could explore collaborations with experts in neuroimaging to incorporate brain imaging data (e.g., MRI or PET scans) into the model. This would allow for a more holistic understanding of PD progression and potentially lead to the discovery of new, significant biomarkers.

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