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Parkinson's Disease Prediction Using Wave Frequency Data with Enhanced Graph Neural Networks

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Abstract: With disproportionately high rates among the elderly, Parkinson's disease (PD) ranks as the world's second most common degenerative neurological ailment. For better treatment outcomes, early detection of PD is crucial, as the majority of symptoms do not manifest until the illness has progressed significantly. In this research we propose parkinson's disease prediction using wave frequency data with enhanced graph neural networks (E-GNN). The dataset was collected from Kaggle repository. After collecting the dataset we use Improved Biased K-Means Clustering algorithm for preprocessing. After preprocessing we use Biased Binary Bat with ElasticNet algorithm for feature selection. After feature selection we use Enhanced Graph Neural Network algorithm for parkinson's disease classification. This E-GNN incorporates advanced enhancements in both architecture and training methodology, pushing the boundaries of accuracy in predicting Parkinson's disease. The integration of cutting-edge techniques within the E-GNN framework enables the model to capture intricate relationships and dependencies within the data, ultimately resulting in more precise and reliable predictions.

Keywords: Biased Binary Bat, ElasticNet, Graph Neural Network, Improved Biased K-Means Clustering, Parkinson's disease

I. Introduction

In terms of global prevalence, Parkinson's disease ranks second among neurodegenerative disorders, after only Alzheimer's [1]. More than one million individuals in North America are impacted by PD [2]. Motor skills, particularly the ability to talk and write, are impacted by Parkinson's disease. It incorporates the dysfunction and eventual death of neuronal cells, which are crucial components of the brain [3]. The two regions of the brain responsible for the regulated, smooth motions are the corpus striatum and Substantial Ingra. A loss of normal motor function results from a drop in dopamine production in the brain [4]. There will likely be more people diagnosed with PD as a result of the growing population. Despite the availability of medicine, PD remains untreatable [5]. Therefore, in order to aid patients and enhance their quality of life, an early diagnosis is crucial. PD symptoms include a lack of suppleness in the muscles, a sluggish gait, problems with balance and coordination, a weakened voice, and changes in mood [6].

As far as Parkinson's disease severity measures go, the Unified Parkinson's Disease Rating Scale (UPDRS) has replaced all others. No impairment is indicated by a UPDRS score of 0, whereas significant impairment is indicated by a score of 176. The UPDRS scale is based on the three items that are stated below [7]. Among these three considerations, the third one has a scale from 0 (no symptoms) to 108 (extreme motor impairment). The UPDRS scale is useful for predicting the severity of Parkinson's disease [8].

Clinical intervention, including necessary physical visits for monitoring and observation, at regular intervals, is necessary to make a definitive decision since, as of yet, there is no laboratory or blood test for diagnosing and tracking the course of PD [9–11]. Eighty percent of the dopamine has been used up by the time these physical diagnostics reach a determination. Similarly, PD identification by brain and neurological scans necessitates high-tech equipment and trained medical professionals [12–14]. Additionally, the most prominent signs of PD, according to specialists, are dysarthria (difficulty with articulation), monotone (low pitch), dysphonia (defective voice), hypophonia (low loudness), and gait variability [15–17]. Since almost 90% of PWP display a vocal issue, dysphonia analysis is crucial for the early diagnosis of PD by the observation of vocal traits. Researchers have created a number of noninvasive PD diagnostic methods based on machine learning (ML) that can aid medical professionals up to five years before clinical diagnosis [18–19]. Not only can PD be detected early using voice-based diagnostic technologies, but it also doesn't need costly gear, clinical visits, or medical experts [20-22].

The main contribution of the paper is:

- Data preprocessing using Improved Biased K-Means Clustering

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- Feature selection using Biased Binary Bat with ElasticNet
- Classification using Enhanced Graph Neural Network

The remainder of this paper is structured as follows. Numerous authors address a variety of PD diagnosis strategies in Section 2. The proposed model is shown in Section 3. Section 4 summarizes the results of the investigation. Section 5 concludes with a discussion of the result and future work.

1.1 Motivation of the paper

The worldwide effect and prevalence of Parkinson's disease (PD) on the elderly makes early identification all the more urgent, and this study seeks to meet that need. The article presents a thorough technique that uses wave frequency data. It starts with a preprocessing algorithm called Improved Biased K-Means Clustering and then moves on to feature selection using Biased Binary Bat with ElasticNet. The heart of the matter is an Enhanced Graph Neural Network that incorporates state-of-the-art architectural and training technique upgrades for PD classification. This state-of-the-art method seeks to outperform conventional models by capturing complex data linkages, resulting in more accurate and dependable predictions. By improving treatment techniques and paving the way for earlier diagnoses, this study hopes to transform PD prediction and ultimately lead to better patient outcomes.

II. Background Study

AlZubi, A. A., et al [1] a deep brain simulator (DBS), an Internet of Things (IoT) sensor device, was implanted into the patient's brain in order to collect brain characteristics for this investigation. Following the DBS discussion and making use of medical data authorized by the Florida and institutional review boards, this research evaluates the provided HTSMNN system's efficiency. It also considers the impact of deep brain simulation on the Parkinson's tremor database.

Chen, Z., et al [3] Symptoms of Parkinson's disease, both motor and non-motor, can often coincide. A sign of this was autonomic dysfunction. The financial burden on PD patients grows, motor dysfunction becomes worse, and patients' quality of life gets drastically poorer. Research into the pathophysiological underpinnings of autonomic dysfunction, which have so far remained a mystery, has to be a top priority for future studies.

Demrozi, F., et al [5] by transitioning to a goal-directed gait that was less affected by PD, individuals with PD able to overcome the pathophysiological reasons of the disease, such as the loss of spontaneous movement, via the use of external cueing, a non-pharmacologic approach of FoG. Detection and the transmission of cueing stimuli were two aspects of technology that have been proposed several times.

Haq, A. U., et al [8] these authors research established a reliable strategy for PD prediction. For both PD and healthy person classifications, the system's development team used the support vector machine (SVM) classifier. The L1-Norm support vector machine was used for feature selection in order to achieve accurate target classification of PD and healthy persons. Features must be appropriate and highly related for this strategy to work.

Kamran, I., et al [11] these authors put out a method for the early diagnosis of PD that makes use of handwriting samples given by those who have the disease. The author was able to increase the accuracy of the diagnosis by increasing the sample size using various data augmentation approaches and by combining multiple PD handwriting datasets. Utilizing an end-to-end deep transfer learning approach, the author successfully transferred previously acquired information to the domain of handwriting samples, yielding promising outcomes. These authors findings show that the suggested strategy was superior to the state-of-the-art approaches used today.

Kaur, S., et al [13] among neurological illnesses, Parkinson's disease was second in prevalence only to Alzheimer's disease. Among the many body processes affected, speech was the most susceptible. As a result, the speech study for Parkinson's disease diagnosis served as the basis for other tactics for optimum trial numbers. Doctors can now make more precise and faster diagnosis with the help of optimal deep learning for PD patient identification.

Moetesum, M., et al [16] these authors looked at the potential of visual features of handwriting to predict the onset of Parkinson's disease. Although much of the prior work has been on spatio-temporal, kinematic, and pressure-related elements, the author use Convolutional Neural Networks to derive static visual attributes from handwriting. This was not to say that feature-rich online tools were useless; rather, it was to show that visual data in handwriting might be helpful in finding a solution to this problem. Combining online and offline characteristics might provide interesting outcomes.

Nilashi, M., et al [17] the purpose of this research was to provide a novel hybrid approach to Parkinson's disease diagnosis by using machine learning methods. The UPDRS diagnosis was obtained by constructing prediction models using ANFIS ensembles.

2.1 Problem definition

This research dives into the pressing issue of Parkinson's disease (PD), a neurodegenerative disorder that is second

most common in the world and disproportionately impacts the elderly. One important drawback of GNNs is the challenge of scalability. As the size of the graph or the complexity of relationships increases, GNNs can struggle to efficiently handle and process the information. This can lead to increased computational requirements and longer training times, making the model less practical for large-scale datasets. The primary objective is to enhance the precision of PD predictions. This is being accomplished by incorporating cutting-edge methods into the GNN architecture. Predictions will be safer and more accurate as a result of the model's improved understanding of complicated data connections and relationships.

III. MATERIALS AND METHODS

In this section, the dataset was collected from Kaggle repository. After collecting the dataset we use Improved Biased K-Means Clustering algorithm for preprocessing. After preprocessing we use Biased Binary Bat with ElasticNet algorithm for feature selection. After feature selection we use E-GNN algorithm for parkinson's disease classification.

3.1 Dataset collection

The dataset was collected from Kaggle website https://www.kaggle.com/datasets/naveenkumar20bps1137/parkinsons-disease-detection Thirteen individuals, including twenty-three with Parkinson's disease (PD), contributed to this dataset by providing a variety of biological voice measures. Each column in the table indicates a distinct vocal measure, and there are 195 unique audio recordings of these people's voices (the "name" column). Differentiating between healthy and PD persons is the main objective of the data, with the "status" column set to 0 for healthy and 1 for PD.

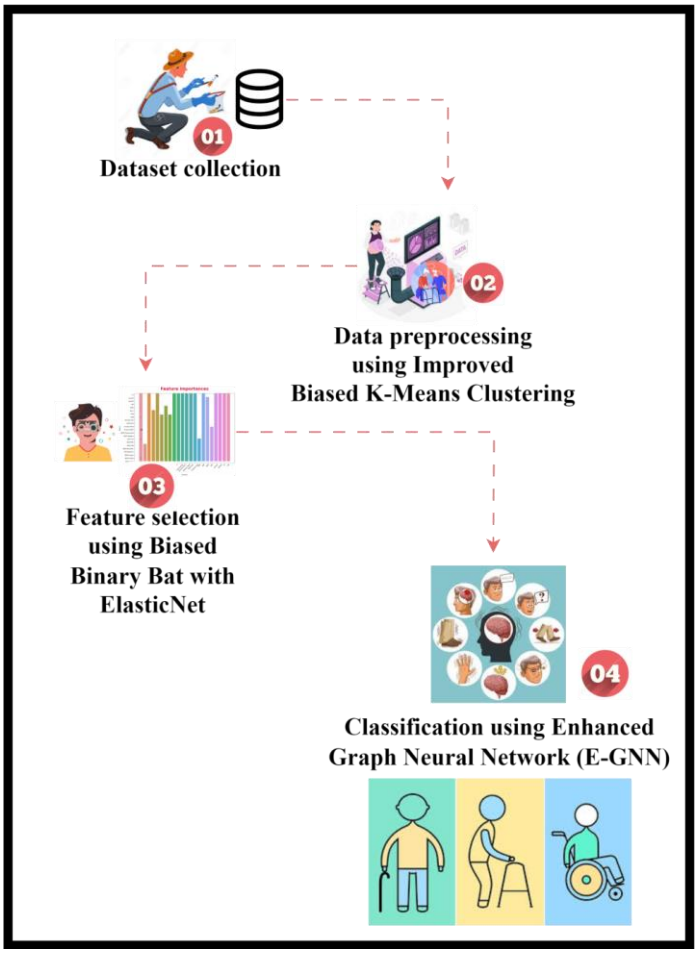

Figure 1: Proposed work flow architecture

3.2 Dataset preprocessing using Improved Biased K-Means Clustering

After collecting the dataset we use Improved Biased K-Means Clustering algorithm for data preprocessing.

In the preprocessing step of dataset preparation, the Improved Biased K-Means Clustering (IBKMC) technique is used to improve the dataset's structure and get it ready for further analysis. By using biases as clustering guidelines, this technique improves upon the classic K-Means Clustering method referred by Wang, X. et al. (2020). The bias factor guarantees a more precise and focused grouping of data points, and it effectively splits the information into clusters based on similarities.

To classify data samples into different categories, the IBKMC clustering method employs distance measures. It locates a partition that satisfies this criterion in order to minimize the squared error between the points of a cluster and its empirical mean. Put the n data samples $O = \{O_1, O_2, \dots, O_n\}$ into K groups and think about it. The set C is defined as C_i, where i ranges from 1 to k+}. The goal of IBKMC clustering is to minimize the total squared errors across all k clusters. This goal is articulated in the following way:

$$J(C) = \sum_{i=1}^{k} \sum_{O_l \in C_i} (O_l - Z_i)^2 \text{ --------- (1)}$$

In IBKM clustering, the cluster centroids are first set at random. We assign data samples to the cluster that is geographically nearest to them by measuring their distances from the relevant centroid. Each cluster's centroid updated by taking an average of all data samples inside that cluster. When all of the end criteria have been satisfied, the procedure of data sample splitting into the appropriate clusters is repeated using the updated cluster centroids. Computer vision, pattern identification, and information retrieval are just a few of the several fields that can greatly benefit from the IBKMC method. For more complicated models, it's a common pre-processing step to provide a starting setup.

In spite of its widespread use and many benefits, IBKMC has some drawbacks caused by its rigid assumptions and methods of operation. Initialization sensitivity is a major issue with IBKMC. When using IBKMC to minimize the total intra-cluster distances, essentially doing a local search around the original centroids. Consequently, cluster centroids' initial arrangement has a significant impact on IBKMC performance. Furthermore, IBKMC is prone to local optima traps because of its operational mechanisms and the unpredictability of centroid initialization. our limitation of IBKMC clustering is a driving force for our study.

The IBKMC model uses k-means foraging behaviors to conduct search operations. Every k-means in a IBKMC swarm represents a different starting solution, and the process of starting a swarm is totally random. The light intensity is used to construct a fitness score, which is derived from the objective functions of each k-means. People living in close proximity to those with bright lights attract k-means with lower light intensities, as mentioned before.

$$X_i^{t+1} = X_i^t + \beta_0 e^{-\gamma r_{ij}^2}\left(X_j^t - X_i^t\right) + \alpha_t \varepsilon_t \text{ ------- (2)}$$

In this context, k-means *i* and *j* are symbolized by lower and higher light intensities, correspondingly, whereas X_i^t and X_j^t reflect the current placements of k-means i and j at the tth iteration. The initial attractiveness parameter is denoted by β_0, and r_{ij} is the distance between k-means i and j. The coefficient of light absorption is denoted by γ. A uniform distribution is used to produce the randomization coefficient α_t, whereas a Gaussian distribution is used to create the vector of random numbers ε_t.

With IBKMC, its attraction mechanism is the main benefit. Subgroups of the k-means swarm form automatically in response to attractiveness-based motions; these subgroups then swarm to a singular mode or local optimal solution. In theory, if the population is large enough relative to the number of local optimums, the subdivision ability in IBKMC can identify all optimums at once and reach the global optimums. Multimodal and very nonlinear optimization problems tackled by the IBKMC model because to its ability to autonomously partition data sets. These characteristics are consistent with the clustering issues addressed in this research, which include datasets exhibiting nonlinearity and several local optima traps.

3.3 Feature selection using Biased Binary Bat with ElasticNet

After preprocessing, we use Biased Binary Bat with ElasticNet algorithm for feature selection.

Feature selection in the dataset is performed using the Biased Binary Bat with ElasticNet technique. Binary Bat Algorithm and ElasticNet, a regularization approach, are combined in this method referred by Chatra, K. et al. (2019). It takes into account the significance and association of traits while evaluating and weighting them, and it biases the selection process to maximize for significant qualities in forecasting Parkinson's disease. In order to find the most important variables to analyze later, the method uses ElasticNet, which combines L1 and L2 regularization, to find a compromise between sparsity and feature significance.

Microbats rely on echolocation to aid them in their nighttime meal search. They are able to differentiate between predators and prey by using the echolocation technique. Bats will make a series of short, loud pulses to get their attention. It is possible to calculate the distance to an object by timing the return and arrival times of the pulses that hit it. Here are a couple of the first phases of the bat algorithm:

$$\mathbf{fr_i} = \mathbf{fr_{min}} + (\mathbf{fr_{min}} - \mathbf{fr_{max}}) \text{ --------- (3)}$$

$\mathbf{fr_i}$ Represents the frequency of the bats at iteration i

$\mathbf{fr_{min}}$ And $\mathbf{fr_{max}}$ are minimum and maxi mum frequencies, respectively.

$$\mathbf{v_i^j(s)} = \mathbf{v_i^j(s-1)} + [\hat{\mathbf{p}}^{\mathbf{j}}(\mathbf{s-1})]\mathbf{fr_i} \text{ --------- (4)}$$

$\mathbf{v_i^j(s)}$ is the velocity of the bat for the j[th] decision variable at iteration ss.

$\hat{\mathbf{p}}^{\mathbf{j}}$ is the currently optimal global value for the decision variable jj.

$$\mathbf{p_i^j = p(s-1) + v_i^j(s)} \text{ ---------- (5)}$$

$\mathbf{p_i^j}$ is the position of the bat for the j[th] decision variable at iteration ss.

$\mathbf{p(s-1)}$ is the previous position.

The currently optimal global value for the decision variable *j* is denoted by $\hat{\mathbf{p}}^{\mathbf{j}}$. To provide some randomness to the answers, random walks are performed. For this, if the criterion rand > r_i is fulfilled, the best solution out of all the ones now available is chosen and then subjected to a random walk.

$$p_{new} = p_{old} + \epsilon \bar{L}(s) \text{ ---------- (6)}$$

p_{new} is the new position of the bat.

ϵ is a constant.

$\bar{L}(s)$ is the average loudness at iteration ss.

$$\mathbf{L_i(s+1) = aL_i(s)} \text{ ---------- (7)}$$

$\mathbf{L_i(s+1)}$ is the loudness of the bat at the next iteration.

a is a constant.

$$\mathbf{r_i(s+1) = r_i[1 - exp(-\gamma s)]} \text{ ---------- (8)}$$

The variables α and γ are constants. By using a transfer function, one can get the bat algorithm's binary variant:

$$\mathbf{S(v_i^j) = \frac{1}{1+exp^{-v_i^j}}} \text{ ---------- (9)}$$

Then Eq. 10 can be replaced by

$$\mathbf{p_i^j = \begin{cases} 1, & if S(v_i^j) > rand \\ 0, & otherwise \end{cases}} \text{ ---------- (10)}$$

To address feature selection issues in high dimensions, EN regularization modifies multiple linear regression methods. To improve the prediction accuracy, the EN uses two penalty terms—the L1-norm and the L2-norm—to automatically choose variables and perform continuous shrinkage. In the same way that a stretched fishing net catches "all big fish," or important predictors, this method discards the remainder.

If we use the linear regression approach, we can represent the equation for the response variable y as $\hat{y} = \beta_0 + \beta_1 x_1 + \cdots + \beta_p x_p$, given p predictors $x_1, \ldots, x_p$. The coefficients ($\beta = [\beta_0, \ldots, \beta_p]$) obtained by minimizing the sum of the squares of the error residuals, as shown in Equation (11). Instead of using SSE, the coefficients are calculated by minimizing the L function (Eq (12)) when the number of observations is less than the feature space dimensions:

$$SSE = \|Y - X\beta\|^2 \text{ ---------- (11)}$$

$$L = SSE + ap\|\beta\|_1 + a(1-p)\|\beta\|^2 \text{ ---------- (12)}$$

Where ‖β‖_1 and ‖β‖^2 are calculated with Eq (13 and 14)

$$\|\beta\|_1 = \sum_{p=1}^{p} |\beta_p| \text{ ---------- (13)}$$

$$\|\beta\|^2 = \sum_{p=1}^{p} \beta_p^2 \text{ ---------- (14)}$$

3.4 Classification using Enhanced Graph Neural Network

After feature selection, we use Enhanced Graph Neural Network algorithm for PD classification.

To forecast the occurrence of Parkinson's disease using the preprocessed and feature-selected data, an Enhanced Graph Neural Network is used during the classification phase. In an effort to outperform more traditional models, this state-of-the-art E-GNN integrates novel architectural and training process upgrades. E-GNN design, which is able to grasp intricate data connections and relationships, the model, can identify patterns that might indicate the presence of Parkinson's disease. Integrating state-of-the-art methods into the E-GNN improves prediction accuracy for Parkinson's disease classification and ensures a more nuanced understanding of the complex data structure.

According to the research, real-world graphs have underlying structures. We divide the original input graph G_o into two parts: $G_o = G_s + \Delta G$, so we can comprehend the predictions made by a E-GNN model. In this case, Gs stands for the anticipated explanatory graph that makes a substantial contribution to the E-GNN predictions, whereas ΔG encompasses the remaining edges that are unrelated to the current job. Maximizing the mutual information between the underlying structure and the E-GNN predictions allows the following r to identifyG_s:

$$\mathbf{\max_{G_s} MI(Y_o, G_s) = H(Y_o) - H(Y_o|G = G_s)} \text{ ---------- (15)}$$

In this case, Y_o represents the output of the GNN model fed G_o . When the E-GNN model is fed only the explanatory graph G_s, the mutual information measures how likely it is that prediction Yo will be correct. The whitebox explanation's conventional forward propagation-based approaches provide the idea for this. If, for instance, the E-GNN prediction is significantly altered after eliminating an edge (i,j), then it's clear that this edge is crucial and need to be part of Gs. A E-GNN model can exclude it as a useless edge if it doesn't meet certain criteria. The goal is the same as reducing the conditional entropy $H(Y_o|G = G_s \dashv)$ *as* $H(Y_o)$ is solely connected to the E-GNN model whose parameters are set during the explanation step.

Nevertheless, with 2^M possible values for G_s , the aforementioned objective function cannot be optimally

optimized directly. Since the edges chosen from the initial input graph G_o are assumed to be conditionally independent, we can relax our assumptions and think of the explanatory graph as a Gilbert random graph. The selected edge is denoted by the binary variable $e_{ij} \in V \times V$, where $e_{ij} = 1$ in the case when the edge (i, j) is chosen and 0 in all other cases. The random graph variable is denoted as G. If we assume the following, we can factorize the probability of a graph G as:

$$\mathbf{P(G)} = \prod_{(\mathbf{i,j})\in\boldsymbol{\varepsilon}} \mathbf{P(e_{ij})} \text{ ------ (16)}$$

A simple example of $P(e_{ij})$ is the Bernoulli distribution $e_{ij} \sim Bern(\theta_{ij})$.The likelihood that the edge (i,j) exists in G is denoted as $P(e_{ij} = 1) = \theta_{iji}$. In light of this loosening, we might reframe the goal as:

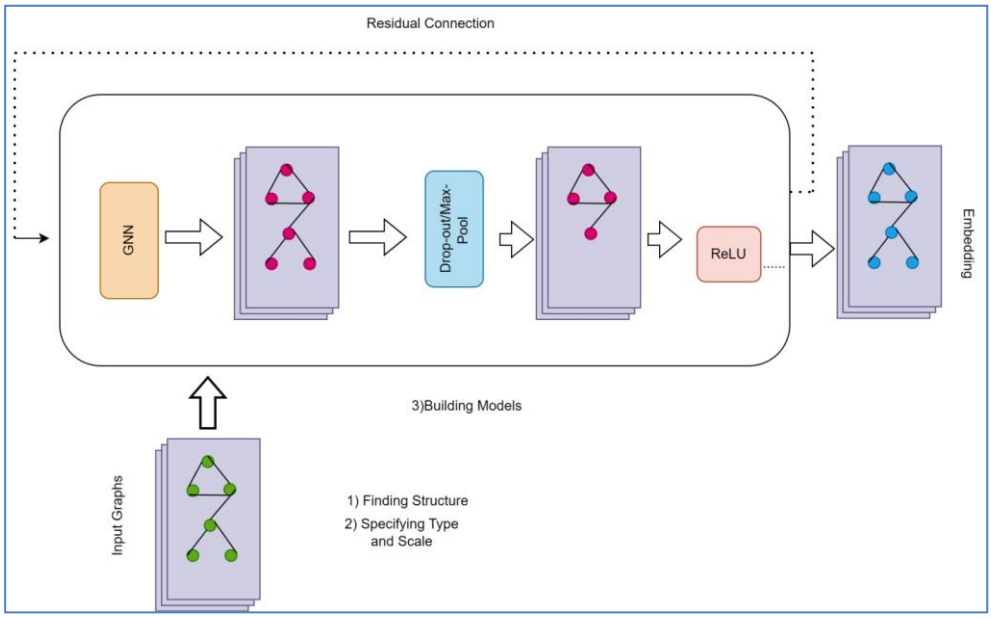

Figure 2: GNN architecture

$$\min_{G_s} \mathbf{H(Y_o|G} = \mathrm{G_s}) = \min_{G_s} \mathbb{E}_{G_s}[\mathbf{H(Y_o|G} = \mathrm{G_s})] \approx \min_{\ominus} \mathbb{E}_{G_s \sim q(\ominus)} \mathbf{H(Y_o|G} = \mathrm{G_s}) \text{ ---------- (17)}$$

Where $q(\Theta)$ is the distribution of the explanatory graph parameterized by θ's.

Algorithm 1: Enhanced Graph Neural Network

- **Input:**
- Original input graph G_o representing the preprocessed and feature-selected data.
- Parameters of the GNN model.

Steps:

- **Enhanced GNN Classification:**
- Utilize the preprocessed and feature-selected data G_o as input to an Enhanced Graph Neural Network (GNN) for Parkinson's disease classification.

$\mathbf{P(G)} = \prod_{(\mathbf{i,j})\in\boldsymbol{\varepsilon}} \mathbf{P(e_{ij})}$

- Train the GNN model with advanced enhancements in both architecture and training methodology to optimize predictive accuracy.

- **Explanatory Graph Division:**
- Divide the original input graph G_o into two subgraphs: G_s andΔ_G.

- **PGExplainer for Explanatory Graph Identification:**
- Use PGExplainer to find G_s by maximizing the mutual information between the GNN's predictions and the underlying structure G_s .

$$\min_{G_s} \mathbf{H(Y_o|G} = \mathrm{G_s}) = \min_{G_s} \mathbb{E}_{G_s}[\mathbf{H(Y_o|G} = \mathrm{G_s})] \approx \min_{\ominus} \mathbb{E}_{G_s \sim q(\ominus)} \mathbf{H(Y_o|G} = \mathrm{G_s})$$

- **Output:**
- Distribution $q(\Theta)$ providing insights into the explanatory graph parameterized by$\theta's$.

IV. RESULTS AND DISCUSSION

In this section, we present the outcomes of our study on predicting Parkinson's disease using a novel approach that integrates the Biased Binary Bat with ElasticNet feature selection method and a state-of-the-art Enhanced Graph Neural Network architecture.

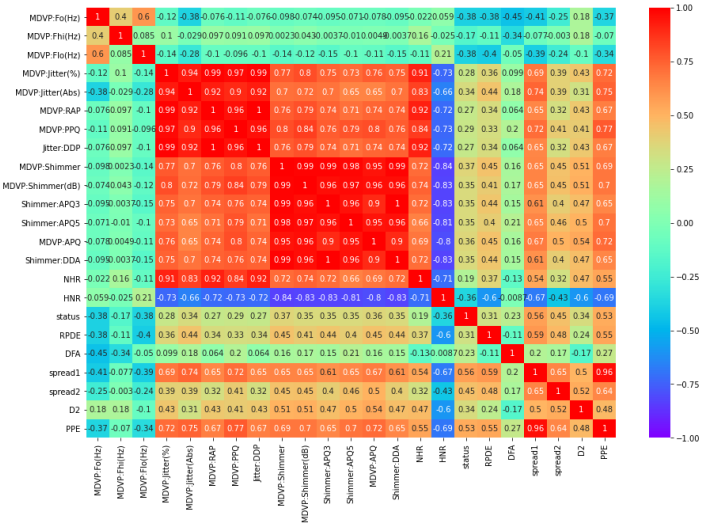

Figure 2: Correlation matrices

The figure 2 shows statistical correlation between the dataset's variables graphically in Figure 2's correlation matrices. When applied to the problem of Parkinson's disease prediction utilizing wave frequency data, these matrices provide important information about the interdependencies and linkages between the characteristics that were chosen for research.

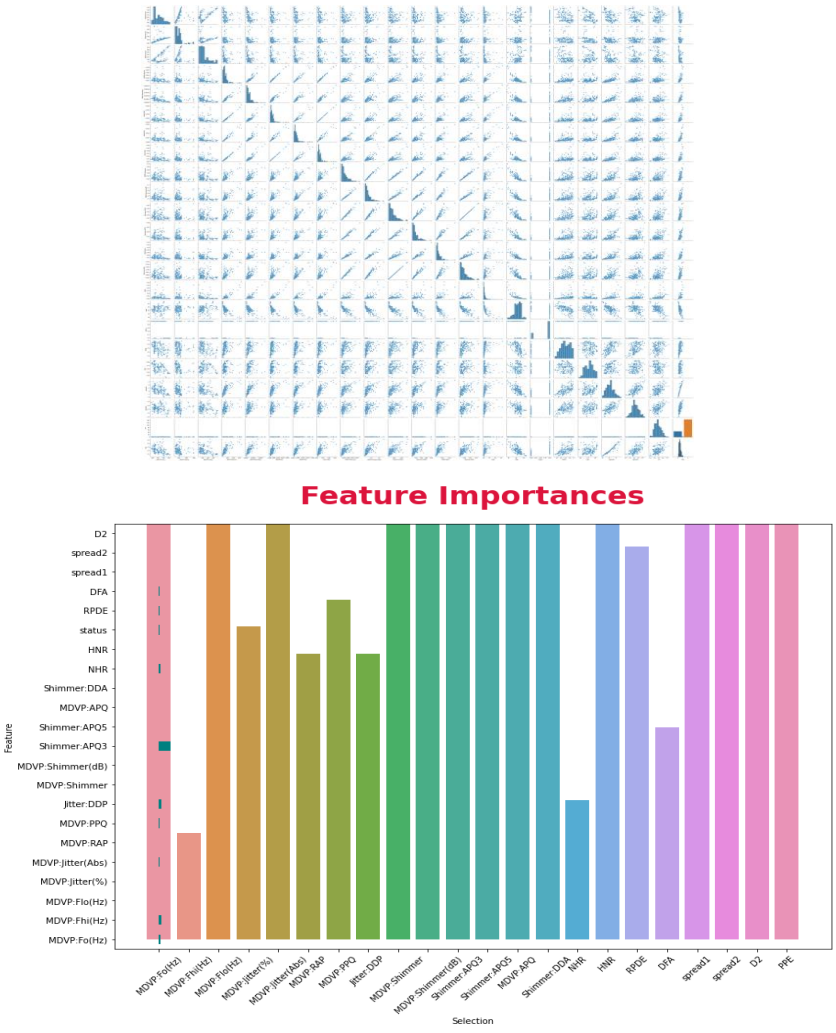

Figure 3: Feature selection

The feature selection procedure, shown in Figure 3, is an important part of improving the dataset and the model's ability to forecast Parkinson's disease. In feature selection, the goal is to keep the most useful variables and remove the ones that aren't. It is possible that this chart shows a graphical depiction of the characteristics' relative importance in determining the model's predicted accuracy.

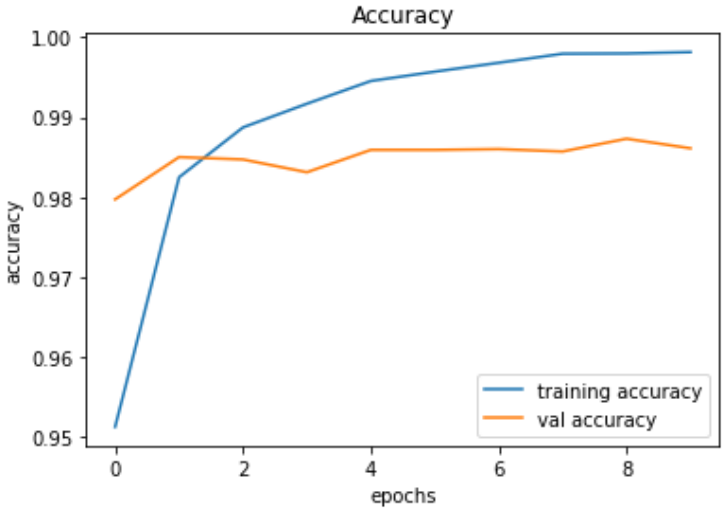

Figure 5: Training accuracy

The figure 5 shows training accuracy the x axis shows epochs and the y axis shows training accuracy value.

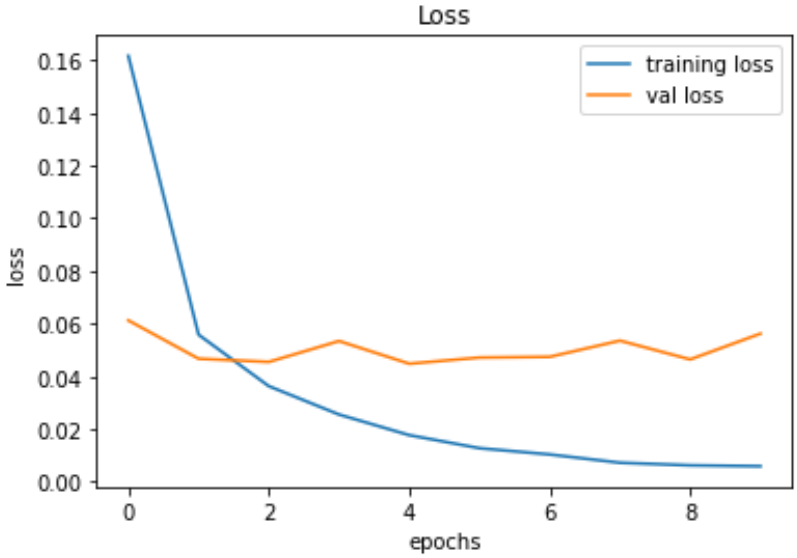

Figure 6: Training loss

The figure 6 shows training loss the x axis shows epochs and the y axis shows loss value.

4.1 Performance evaluation

1. Accuracy: The fraction of samples with the right classification out of all samples. Mathematically:

$$Accuracy = \frac{(TP + TN)}{(TP + FP + TN + FN)} \text{ ---------- (18)}$$

2. Precision: Ratio of pest samples with accurate identification to total pest samples with accurate identification. Mathematically:

$$Precision = \frac{TP}{TP + FP} \text{ ---------- (19)}$$

3. Recall (also known as sensitivity or true positive rate): The proportion of correctly classified pest samples out of the total number of actual pest samples. Mathematically:

$$Recall = \frac{TP}{TP + FN} \text{ ---------- (20)}$$

4. F1 score: A middle ground between accuracy and memory that strikes a harmonic mean. Mathematically:

$$F1\ score = 2 * Precision * Recall\ /\ (Precision + Recall) \text{ --------- (21)}$$

Table 1: Classification performance metrics comparison

	Algorithm	Accuracy	Precision	Recall	F-measure
Existing methods	KNN	93.21	93.65	94.01	94.23
	DCNN	95.35	94.87	95.10	95.07
	CNN	96.11	96.32	96.75	97.14
Proposed methods	E-GNN	98.61	97.11	97.84	98.21

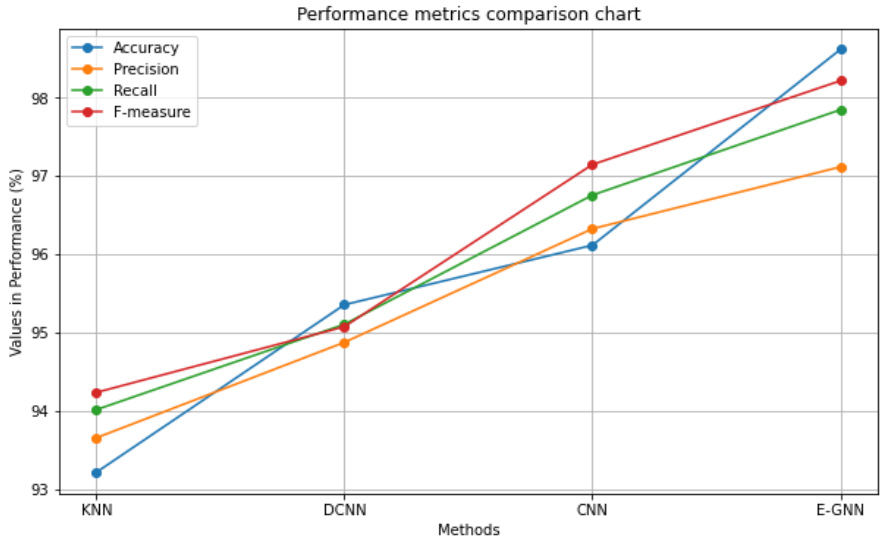

Figure 7: Performance metrics comparison chart

Table 1 and figure 7 show the performance metrics of E-GNN, an established approach for Parkinson's disease prediction, in comparison to KNN, DCNN, and CNN. In comparison to its competitors, the E-GNN achieves an outstanding 98.61% accuracy, which is higher than the scores of KNN (93.21%), DCNN (95.35%),and CNN (96.11%). By properly recognizing affirmative instances with a rate of 97.11%, E-GNN proves its supremacy using the accuracy measure. Recall is another area where E-GNN shines; it achieved 97.84%, proving that it successfully captured all true positives. Impressively, E-GNN achieved an F-measure of 98.21%, which is a balanced performance indicator that takes into account both recall and accuracy. All things considered, our findings demonstrate that the suggested E-GNN is an effective and reliable approach to predicting the onset of Parkinson's disease, outperforming state-of-the-art methods in a number of tests.

V. Conclusion

Finally, this study highlights the need of early diagnosis in treating this common degenerative neurological ailment, especially affecting the elderly, by providing a new and thorough method for predicting the onset of Parkinson's disease. The research breaks new ground in predictive accuracy by using wave frequency data in conjunction with a novel pipeline that includes Enhanced Graph Neural Network for illness classification, Biased Binary Bat with ElasticNet for feature selection, and Improved Biased K-Means Clustering for preprocessing. Improved prediction accuracy is the end result of the E-GNN's state-of-the-art architectural and training procedure upgrades, which help to capture complex data correlations. Our knowledge of Parkinson's disease enhanced by the integration of cutting-edge approaches inside the E-GNN framework. This will lead to better treatment options and better patient outcomes. The proposed E-GNN algorithm successfully predicts the occurrence of Parkinson's disease with a 98.61% accuracy rate, with high precision (97.11%), recall (97.84%), and F-measure (98.21%), demonstrating its resilience and efficacy in real-world clinical settings. This study highlights the need of advanced machine learning techniques for the early detection and treatment of neurological diseases such as Parkinson's disease.

Reference

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