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Deep Learning Based Dual-level Bioinspired Model for Parkinson's Disease Detection

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Abstract: Parkinson's disease is a neurological ailment that disrupts a patient's speech, physical, and psychological behavioural characteristics. In order to diagnose this illness, a range of factors such as vocal core frequency ranges, tonal aspects in the voice, frequency Cepstral Coefficients of Melody (MFCCs), and Vocal Fold Features are collected and examined for numerous individuals. Current models utilised for this objective are very intricate or fail to account for multiorgan factors, hence restricting their scalability and suitability for clinical applications. The proposed work focuses on development of a new bioinspired Dual-level feature selection model based on ensemble classifiers to overcome the current limitations of identifying Parkinson's disease. The proposed model gathers patient information from many sources, such as voice patterns, physical activity patterns, and psychological patterns. These datasets are then processed using a dual-level Genetic Algorithm (DLGA) Model, which helps identify highly distinct inter-class features. The selection of these classifiers depends on their testing-accuracy efficiency in real-world clinical situations. The proposed model, when compared with several state-of-the-art models, achieved a 3.5% increase in classification accuracy, an 8.3% reduction in classification latency, a 5.9% improvement in classification precision, and a 2.4% improvement in classification recall. Owing to these benefits, the model is valuable for a diverse range of clinical applications.

Keywords: *Parkinson Disease, Ensemble Classifier, Deep learning, Genetic Algorithm*

1. Introduction

Parkinson's disease, commonly referred to as PD, is a progressive disorder that impacts the brain and nervous system and greatly reduces the standard of life for numerous elderly adults globally [1]. In order to meet the intrinsic variability, the symptoms may manifest differently in an individual. Tremors are the most prominent manifestation experienced by individuals with Parkinson's disease, occurring during the patient's sleep. Additional symptoms encompass hand tremors, limb stiffness, and challenges with ambulation or maintaining an upright posture. The

symptoms of the neurological disorder Parkinson's can generally be categorised into two main groups: motor manifestations, which are related to movements, and non-motor manifestations, which are unrelated to movement. Individuals with non-motor manifestations are more prone to suffering negative impacts compared to those primarily experiencing motor impairment. Non-motor manifestations, with motor manifestations, encompass cognitive impairment, indications of sadness, sleep disturbances, and anosmia. As per the rankings by the US Centre for Disease Control and Prevention (CDC) on causes of mortality, health issues associated with Parkinson's disease currently hold the 14th position in the country. The aetiology of the neurological disorder Parkinson's (PD) remained mysterious. The annual economic burden of Parkinson's illness (PD) in the United States is projected to surpass $52 billion. This figure incorporates the expenses associated with medical care, contributions to welfare, and the income that has been foregone. Undoubtedly, the global prevalence of Parkinson's disease (PD) exceeds 10 million individuals. According to reference [2], it is crucial to prioritise the early identification of Parkinson's disease. This allows for effective treatment and greatly reduces discomfort. Hence, it is imperative to promptly and identify Parkinson's disease (PD) to decelerate the advancement of the ailment and maybe enable individuals to get disease-modifying drugs upon their availability. Parkinson's disease (PD) is characterised by involuntary repetitive movement of the hands and feet, known as tremors, which are beyond the patient's control. Currently, there is no reliable method available to diagnose Parkinson's disease (PD) [2]. Conversely, there is frequently a confluence of diagnostic techniques and symptoms that coexist.

2. Literature Review

Researchers have explored a diverse range of biomarkers in order to identify Parkinson's disease at its first stages and impede its advancement. While there are several drugs available to treat symptoms of Parkinson's condition, none of them possess the ability to decelerate or halt the advancement of the ailment. Speech data, gait patterns [7],

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force tracking data [8], smell recognition data [9], and impulsive cardiovascular oscillations [10] have all been utilised as sources of knowledge for various techniques involving the use of Type-2 Fuzzy AHP (T2F AHP) [7] to aid in the identification of Parkinson's disease (PD). The sawtooth-based pitch estimator [11] is a technique employed to assess speech impairments caused by different forms of Parkinson's disease. This method employs the sawtooth-inspired pitch predictor algorithm, which necessitates the use of a smartphone to capture voice data.

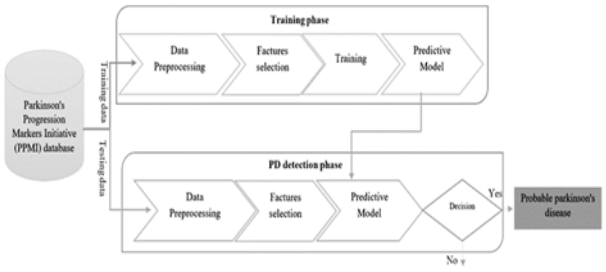

Fig.1. depicts a model that integrates Parkinson Progression Measures (PPMs) with mathematical modelling [10].

This method evaluates the extent of disorder severity. In order to accomplish this, a wide range of feature sets with significant variations are retrieved.The SWIPE technique was successfully applied to distinguish between persons having Parkinson's disease and individuals in good health, yielding positive results. However, to attain effective noise resistance and lower the signal-to-noise ratio at the same time, a more effective technique is needed. S. Kim et al [12] suggests an early diagnosis approach for Parkinson's disease by taking advantage of the characteristics of compressed speech. The information presented indicates that the implementation of Wrappers selection of subsets is deemed appropriate due to the minimal dimension of the feature that was chosen and the possibility of increased PD detection capabilities. A. Prado et al [13] suggested a technique that uses a single-dimensional artificial neural network (1D NN) with gait data. However, voice recordings' susceptibility to background noise frequently compromises the accuracy of diagnosing Parkinson's disease (PD) using speech and gait analyses, leading to a high rate of both missed and false alarms. In this sense, both of these kinds of questions are accurate. The associated gait monitoring and assessment are completed online. For this purpose, extra space is needed for walking around as well as special equipment [14]. [15]

M. Ricci et al [15] suggest employing wavelet analysis in interpretation to assess data from Parkinson's disease patients who wore smartwatches. This technique demonstrated exceptional precision in detecting bradykinesia, dyskinesia, and tremor symptoms throughout testing. C. Laganas et al [16] offers a method for using smartphone touchscreen typing to identify motor dysfunction in Parkinson's patients. The method that has been suggested makes use of touchscreen typing metrics to identify motor symptoms associated with Parkinson's disease. Descriptive statistical measures like covariance, skewness, and kurtosis, as well as temporal data, are examples of these metrics. For the purpose of making predictions of Parkinson's disease (PD) in [17], they also combine information from all of these different sources, combining imaging, genetics, and clinical data, with demographic data. Parkinson's disorder is a degenerative neurological condition. In some research that are occasionally quoted, it was even taken into consideration as a component of the Parkinson's disease diagnostic techniques. A description of the diagnostic technology for Parkinson's disease (PD) can already be found in reference u. To ascertain if a person has the condition or not, it uses handwritten data that they have submitted.

Research has already shown that if information on age and gender are included in the flow of decision-making, both its accuracy rate for diagnosing Parkinson' s disease increases. In line with the results of the experiments conducted in [15, 16], it is suggested that Temporal Self-Attention models be applied to improve Parkinson's disease diagnosis accuracy. A correct and early diagnosis of PD is critical, since it can provide substantial clues that may impede the development talked about above. To handle this problem, a variety of data-driven approaches have evolved over time for more accurate screening and diagnosis in Parkinson's disease. The ingredients Didn't more than that Just for the record to set themselves apart from model-based detection methods, data-driven techniques have only needed to prove they could make something out of available past data. Moreover, model-based detection methods rely on having a computational analytical model in the past when such detections were made. It has been discovered that machine learning is capable of being used as a rapid diagnostic tool for Parkinson's disease. And both educational institutions and corporate enterprises have suddenly started to look into the topic in recent years. This investigation is being carried out through the utilisation of residual network (ResNet) and its variation approaches [17, 18, 19, 20]. All of these investigations are being carried out in recent times. It is via the utilisation of data-driven approaches that machine learning (ML) has brought about a dramatic transformation in the extraction and processing of relevant data from Parkinson's disease (PD) biomarkers. In addition, the techniques of machine learning provide pertinent information that assists in the identification and categorization of PD, which in turn speeds up the process of decision-making. Through the application of a number of different machine learning strategies, the problem of diagnosing Parkinson's disease has been attempted to be solved in published research. Measures of dysphonia were employed by researchers in [21] in order to differentiate

between patients who were diagnosed with Parkinson's disease and those who were healthy. The SVM is based on the concept of deducing nonlinearity from a "kernel," and therefore can only be applied to classifying four dysphonic characteristics which are linked with Parkinson' s disease (PD). That discussed in [6] employed random forest (RF), support vector machine, and neural network models using acoustic properties of speech to identify Parkinson's disease. Even so, research has already proven that the RF and SVM are both showing promising results in early diagnosis of other long-term disorders like Parkinson's disease (PD). By comparison with three other classifiers (including Decision Trees, Regression and DMneural), one can see that the most effective tool for detecting Parkinson's disease was a neural network; its accuracy rate reached 92.9 %. Founded on this, Neural Networks are also now known as the most reliable method of diagnosing Parkinson's disease. The remaining classifiers were DM neural, decision trees and regression. Deeply learning Recently, great attention has been paid to applying deep-learning algorithms for assisting in the diagnosis of parkinson's disease (PD) [3, 23]. This is possible because these algorithms can deal with massive quantities of data and high levels of accuracy, while making only a small number of assumptions about the distribution. The Freezing of Gait (FOG) [23, 24,25] employing a Long Short Term Memory Model (LSTM) to recognize motion detected occurrences that indicated foreshadowed falls among Parkinson's disease patients at high risk for tripping or dropping down suddenly without warning. Empirical evidence has shown that the LSTM outperforms SVM in detecting FOG. Despite this, the classification models currently implemented in clinical practice are limited on both scores. These drawbacks arise due to the complex nature of these models, or because they do not cover such factors as various organ characteristics.

The next part will talk about a possible answer to this problem in the form of a suggestion: creating a unique dual-level bioinspired feature selection model that uses ensemble classifiers. This model's accuracy, precision, memory, and latency are all looked at to see how well it works. It is then put up against a number of new methods. As the study comes to an end, some background information about the proposed model is given, along with some suggestions for how to make it more useful while used in clinical settings.

3. Proposed Methodology

Existing Parkinson's detection models are overly complex, or fail to consider multi organ feature interactions, making them not suitable for widespread applicability. In this section, a novel approach Dual-level bioinspired ensemble feature selection is proposed which bypasses these restrictions to detect Parkinson's disorders. Figure 2 illustrates the flow diagram of the proposed model. Initially, patient datasets are collected from multiple sources, including voice, physical activity, and psychological patterns. These datasets are then filtered employing the dual-level genetic algorithms (DLGA) model, which assists in identifying highly variant inter-class features. A composite classification layer that integrates classifier from Naive Bayes (NB), Deep Forest (DF), Multilayer Perceptron (MLP), 1D Convolution Neural Network (CNN), and Logistic Regression (LR) is employed for analysing these features. The selection of these classifiers is based on their performance in experimental accuracy conditions.

The model first gathers Voice Samples (VS), EEG readings, and Physical activity datasets from various sources. It then collects Mel Frequency Cepstral Coefficients (MFCC), iVectors, Wavelet Coefficients, and Fourier Coefficients. This is done to enable the representation of input samples in several domains. In order to construct MFCC Vectors, the input samples that have been gathered are quantized using equation 1.

$$\boldsymbol{Q_a} = \frac{\boldsymbol{N_a - min\,(N_a)}}{\boldsymbol{(N_a)\ - min\,(N_a)}} \qquad (\mathbf{1})$$

Where, N_a represents the normalised samples' real value, and Qa their quantized levels. Equation 2 estimates Mel scales for each input sample,

$$\boldsymbol{M_a} = \mathbf{4} * \boldsymbol{f_s} * \left(\mathbf{1} + \frac{\boldsymbol{Q_a}}{\boldsymbol{f_s}}\right) \qquad (\mathbf{2})$$

Where, f_s is the sampling frequency, and is decided by periodicity of collected samples.

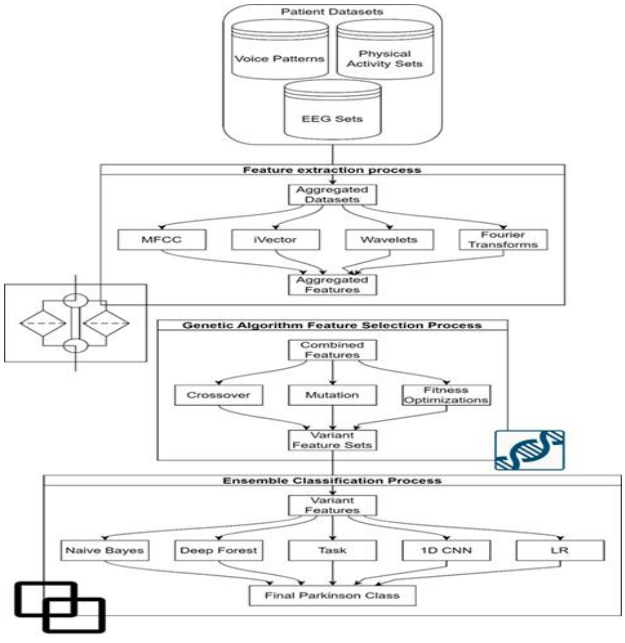

Fig. 2. Proposed bioinspired computing model's overall flow for Parkinson disease identification

Using these Mel Scales, Cepstrum Values are estimated via equation 3,

$$C_a = ifft[log\ log\ (fft[M_a])\ ] \quad (3)$$

Each cepstrum coefficient has some DC offsets, which are removed via normalizing the signals as per equation 4,

$$Norm_a = \frac{\left(C_a - \sum_{i=1}^{N} \frac{C_{a_i}}{N}\right) * (N-1)}{\sqrt{\sum_{j=1}^{N}\left(C_{a_j} - \sum_{i=1}^{N} \frac{C_{a_i}}{N}^2\right)}} \quad (4)$$

Where, N represents total number of samples present in the cepstrum coefficient sets. To further filter out invariant samples, a triangulation filter is applied as per equation 5,

$$T_a = \sum_{i=0}^{N-1} [Norm_{a_i}]^2 * M_{h_i} \quad (5)$$

Where, M_h is a pre-decided filter bank coefficient set, which is capable of extracting Mel Frequency Components as per equation 6,

$$M_h(i) = \frac{i - f(h-1)}{f(h) - f(h-1)} \quad (6)$$

Based on these values, the MFCCs are extracted via equation 7,

$$MFCC_i = \sum_{m=1}^{M} log\ log\ [T_a(m)] * cos\ cos\ \left[i * \left(m - \frac{1}{2}\right) * \frac{pi}{M}\right] \quad (7)$$

These components are extended via equation 8 for estimation of iVector components,

$$iVector_i = MAX\left(\cup_{j=1}^{N} MFCC_j\right) + [(1,1)_{var} \cdots (1,n)_{var} \vdots \ddots \vdots (n,1)_{var} \cdots (n,n)_{var}\ ] * MFCC_i \quad (8)$$

Here, the value of correlative variance $(n,n)_{var}$ is estimated via equation 9,

$$(n,m)_{var} = \frac{exp\ exp\ \left(\frac{n^2}{2}\right)}{2 * pi * var(n) * var(m)} \quad (9)$$

And the variance levels are estimated via equation 10,

$$var(x) = \frac{1}{N-1} * \sum_{i=1}^{N}\left(x_i - \sum_{j=1}^{N} \frac{x_j}{N}\right)^2 \quad (10)$$

These coefficients are cascaded with approximate & detailed Wavelet components, that are extracted via equations 11 and 12 as follows,

$$w_{i_{approx}} = \frac{x_i + x_{i+1}}{2} \quad (11)$$

$$w_{i_{detail}} = \frac{x_i - x_{i+1}}{2} \quad (12)$$

Finally, Fourier components are extracted via equation 13 as follows,

$$F_i = \sum_{j=0}^{N-1} x_j * \left[cos\ cos\ \left(2 * pi * i * \frac{j}{N}\right) - \sqrt{-1} * sin\ sin\ \left(2 * pi * i * \frac{j}{N}\right)\right] \quad (13)$$

The various coefficients are consolidated to create a Super Feature Vector (SFV), which is depicted in figure 3 as follows,

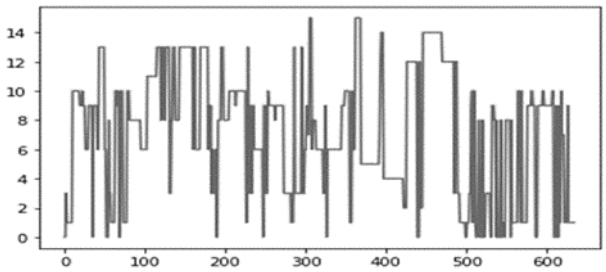

Fig. 3. The SFV generated after combining all Feature Vectors

Table 1. Parameters used for different classifiers

Classifier	Parameter Used
NB	Priors = Featured Selection Variance. Smoothing Value $SV = \frac{Var(F)}{Mean(F)}$ ... (17) Where Var and Mean denote the amounts of variance and average of the attributes that were chosen.
DF	The quantity of estimators = $10 * N_{feat}$ Classification Criteria = Entropy Split Samples = $\frac{N_{feat}}{N_{classes}}$ ... (18) Where, $N_{classes}$ represents number of classes in the datasets Class Weights = Class-based variance levels
MLP	Quantity of concealed levels = $N_{classes}$ Function of activation = Rectilinear unit Adam is the solver type. Learned Value = L_r
1D CNN	Same as MLP but each layer has Max Pooling of sizes 1x4, 1x8, 1x16 and 1x32 with Drop Out and Convolutional feature extraction layers Tolerance = 0.001
LR	Class Weights refer to the variation levels specific to each class. The solver type is linear, and the maximum number of iterations is 10 times the number of features.

4. Comparison & Statistical Analysis

The suggested approach intelligently identifies Parkinson disease kinds using multiple feature extraction, Genetic Algorithm, and ensemble classification. This model was assessed based on classification accuracy (A), precision (P), recall (R), and delay needed to classify patient data from Kaggle & IEEE Data Port. These samples were Normal and Parkinson. Recently suggested classification models T2F AHP [5], TSA [16], and Res Net [18] performed well against the model. From equations 20, 21, 22, and 23, accuracy, precision, recall, and delay were assessed.

$$A = \frac{t_p + t_n}{t_p + t_n + f_p + f_n} \quad (20)$$

$$P = \frac{t_p}{t_p + f_p} \quad (21)$$

$$R = \frac{t_p}{t_p + t_n + f_p + f_n} \quad (22)$$

$$d = \frac{1}{N}\sum_{i=1}^{N} t_{end_i} - t_{start_i} \quad (23)$$

The rates of true positives (t_p), false positives (f_p), true negatives (t_n), and false negatives (f_n) are denoted by the corresponding variables. The dates and time stamps of the beginning and ending processes during processing of N samples are represented by the parameters t_end and t_start, respectively. A grand total of 3000 samples were utilised for the purpose of assessment, with 60% allocated for training, 20% for testing, and the remaining 20% for validation procedures. Table 2 examined the accuracy of this method by comparing it with respect to... The number of test samples (NTS) is as follows:

Table 2. Classification accuracy for identification of Parkinson disease w.r.t. different models

NTS	T2F AHP [5]	TSA [16]	Res Net [18]	Proposed Work
133	81.86	86.25	88.59	95.95
267	81.93	86.75	88.89	95.99
400	81.98	87.25	89.12	96.06
533	82.01	87.56	89.36	96.15
667	82.05	87.75	89.6	96.26
800	82.11	87.88	89.87	96.34
933	82.17	88.17	90.03	96.42
1067	82.23	88.54	90.15	96.48
1200	82.28	88.96	90.21	96.56
1333	82.33	89.28	90.41	96.64
1467	82.38	89.61	90.64	96.7
1667	82.43	89.93	90.94	96.74
2000	82.48	90.26	91.15	96.75
2167	82.53	90.59	91.36	96.76
2333	82.59	90.91	91.57	96.76
2667	82.64	91.24	91.77	96.76
2833	82.7	91.56	91.98	96.84
3000	82.75	91.89	92.19	96.94

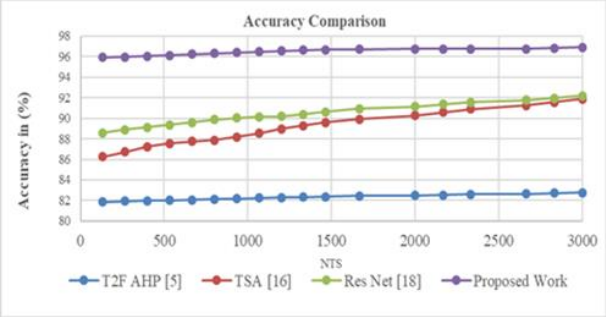

Fig. 4. Accuracy of Parkinson disease classification according to several models

According to this assessment and figure 4, the suggested model demonstrated a 12.4% higher accuracy compared to T2F AHP [5], a 4.5% higher accuracy compared to TSA [16], and a 3.9% higher accuracy compared to Res Net [18]. This indicates that the model is extremely valuable for various real-time classification situations. This is a result of employing a high variance feature selection and ensemble classification procedure. Table 3 examined the precision of categorization in a similar manner.

Table 3. Classification Precision for Identification of Parkinson disease w.r.t. different models

NTS	T2F AHP [5]	TSA [16]	Res Net [18]	Proposed Work
133	79.95	82.81	85.78	94.85
267	80.00	83.17	86.02	94.93
400	80.04	83.43	86.25	95.02
533	80.09	83.65	86.47	95.11
667	80.14	83.89	86.67	95.19
800	80.19	84.18	86.81	95.26
933	80.25	84.51	86.94	95.34
1067	80.30	84.85	87.09	95.40
1200	80.35	85.19	87.28	95.46
1333	80.40	85.50	87.50	95.51
1467	80.45	85.81	87.73	95.54
1667	80.50	86.12	87.95	95.55
2000	80.55	86.43	88.15	95.56
2167	80.60	86.74	88.35	95.58
2333	80.65	87.05	88.55	95.63
2667	80.70	87.36	88.75	95.70
2833	80.75	87.66	88.94	95.79
3000	80.80	87.95	89.13	95.86

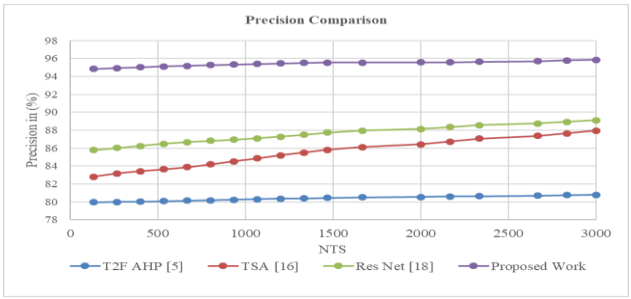

Fig. 5. Precision of classification for the identification of Parkinson's disease with respect to several models

According to this assessment and figure 5, it was noted that the suggested model demonstrated an accuracy improvement of 15.2% compared to T2F AHP [5], 8.3% compared to TSA [16], and 6.5% compared to Res Net [18]. This makes it very valuable for a range of real-time classification applications. This is a result of employing the maximisation of variance method in feature selection, as well as effectively combining ensemble classification approaches. Table 4 tested the recall of categorization in a similar manner.

Table 4. Classification recall for identification of Parkinson disease w.r.t. different models

NTS	T2F AHP [5]	TSA [16]	Res Net [18]	Proposed Work
133	78.95	84.74	86.24	94.25
267	79.01	85.15	86.49	94.32
400	79.05	85.48	86.72	94.40
533	79.09	85.71	86.94	94.49
667	79.14	85.92	87.15	94.58
800	79.20	86.18	87.32	94.66
933	79.25	86.52	87.46	94.73
1067	79.30	86.89	87.59	94.79
1200	79.35	87.23	87.75	94.85
1333	79.41	87.55	87.98	94.91
1467	79.45	87.87	88.22	94.95
1667	79.50	88.18	88.44	94.96
2000	79.55	88.50	88.64	94.98
2167	79.60	88.82	88.84	95.00
2333	79.65	89.14	89.05	95.03
2667	79.71	89.46	89.25	95.08
2833	80.09	89.06	89.27	95.37
3000	80.47	88.66	89.30	95.65

According to the assessment and figure 6, the suggested model demonstrated a 14.5% higher recall compared to T2F

AHP [5], a 6.5% higher recall compared to TSA [16], and a 6.2% higher recall compared to Res Net [18]. This indicates that the proposed approach is extremely valuable for various real-time categorization scenarios. This can be ascribed to the utilisation of highly varied feature sets and the incorporation of multiple classification models when evaluating different types of Parkinson's disease. Table 4 analysed the latency of categorisation in a comparable fashion.

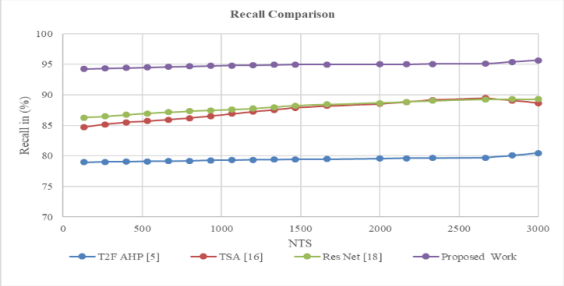

Fig. 6. Classification recall for identification of Parkinson disease w.r.t. different models

According to this assessment and the data presented in Table 5 and figure 7, the suggested model exhibited a 4.5% increase in speed compared to T2F AHP [5], a 5.3% increase compared to TSA [16], and a 5.9% increase compared to Res Net [18]. This indicates that the proposed model is suitable for various real-time high-speed classification situations. This is because of the utilisation of elementary variant feature selection methods, which decrease redundancy in features during classification procedures.

Table 5. Classification delay for identification of Parkinson disease w.r.t. different models

NTS	T2F AHP [5]	TSA [16]	Res Net [18]	Proposed Work
133	112.35	101.52	104.24	101.81
267	112.43	102.03	104.56	101.87
400	112.5	102.46	104.84	101.96
533	112.55	102.77	105.11	102.05
667	112.62	103.03	105.36	102.15
800	112.7	103.29	105.6	102.24
933	112.78	103.68	105.77	102.32
1067	112.85	104.11	105.93	102.39
1200	112.92	104.55	106.1	102.46
1333	112.99	104.93	106.36	102.52
1467	113.06	105.31	106.64	102.56
1667	113.14	105.69	106.94	102.59
2000	113.21	106.08	107.18	102.6
2167	113.28	106.46	107.42	102.62
2333	113.35	106.84	107.66	102.65
2667	113.42	107.22	107.91	102.7
2833	113.5	107.6	108.14	102.78
3000	113.57	107.97	108.38	102.87

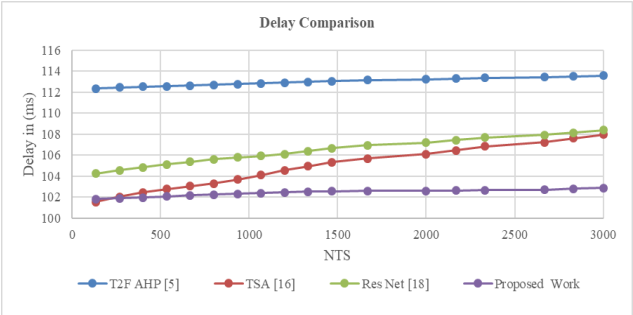

Fig. 7. Classification delay for identification of Parkinson disease w.r.t. diverse models

As a result of these improvements, the suggested approach was shown to be valuable for a diverse range of Parkinson classification applications.

5. Conclusion

The suggested approach utilises multimodal feature extraction, Genetic Algorithm for feature selection, and multidomain feature classifiers to minimise feature redundancy and maximise the performance of Parkinson disease classification. The GA Model has the ability to detect feature sets that have a significant degree of variation, allowing the cascaded classifiers to more effectively identify Parkinson's illnesses. The model produced better results than T2F AHP by 12.4 %, TSA by 4.5 % and Res Net by 39 %. This feature renders it appropriate for a diverse array of real-time classification issues. This is related to the high volatility of feature selection and ensemble categorization. It had 15.2 % better accuracy than T2F AHP, 8.3 % higher precision than the Taiwan Semantic Architecture (TSA) and Res Net of Hong Kong prototype Tom Lee (Res Net = residue network). This advances can be applied to many real-time categorization tasks. But it is for this reason that feature selection uses variance maximization and ensemble classification techniques are successfully combined. Compared to T2F AHP (5), the model has 14.5 % higher recall; compared with TSA [16] and Res Net [18], it offers six percentage points, respectively five percentage point improvements in performance. Consequently, it is of practical use for many real-time categorization applications. This is because a variety of data sets and models are used to derive estimates about Parkinson's disease types. This proposed model ranked higher than four other state-of-the art basics (T2F AHP, TSA and Res Net) by 4.5 %, 5.3 %and 5.9 %. Consequently, it is useful in a number of real-time high-speed classification applications. These procedures utilize simplified variant feature selection methods, to eliminate redundant features. Changes in the model can serve many of Parkinson's classifications. Larger training sets should be used to evaluate the model, and Auto Encoders (AE), Deep

Neural Networks (DNN) and specifically designed Q-Learning algorithms should also be added. In all application situations, bioinspired methods can make the model better at precision, recall and accuracy.

Author Contributions

Pratik S. Deshmukh: Conceptualization, Methodology, Software, Field study, Writing-Reviewing and Editing. **Amit K. Gaikwad**: Field study, Visualization. **Pratik K. Agrawal:** Data curation, Writing-Original draft preparation, Software, Validation.

Conflicts of interest

The authors declare no conflicts of interest.

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