A New Metaheuristic Approach to Diagnosis of Parkinson's Disease Through Audio Signals

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***Abstract*—Parkinson's disease is accepted as one of the most important diseases in the world. Parkinson's disease can be diagnosed in various conventional techniques. Recently, these techniques have been replaced by artificial intelligence systems. This study proposes a feature selection and classification technique for Parkinson's disease based on speech signals using a meta-heuristic algorithm. The proposed method selects the features from the data set including speech signal data that most accurately represent the problem using the efficient search strategies of the immune plasma algorithm (IPA). The experimental results are promising compared to other competing methods for diagnosing Parkinson's disease in the literature.**

***Index Terms*—Feature selection; Immune plasma algorithm; Machine learning; KNN; Parkinson.**

I. INTRODUCTION

Parkinson's disease is a neurological disorder, associated with motor symptoms such as slow movement, tremors, difficulty walking and balance problems, and also various nonmotor complications such as cognitive impairment, mood problems, sleep disorders, and pain [1]. In many cases, Parkinson's disease is the second most common neurological disease after Alzheimer's disease [2]. Furthermore, currently there is no known cure for Parkinson's disease [3]. However, patients' quality of life can be enhanced by early diagnosis of Parkinson's disease [4]. According to the World Health Organisation (WHO) 2022 report, 5.8 million people have suffered disability due to Parkinson's disease, with an increase of 81 % worldwide between 2000 and 2019 [1]. The WHO also revealed that 329,000 people died from Parkinson's disease between 2000 and 2019, an increase of more than 100 % between 2000 and 2019 [1]. As a result, early detection of Parkinson's disease is critical for human life, as it can help prevent deaths and enhance patient quality of life.

Current diagnostic methods for Parkinson's disease are limited. Unfortunately, current general diagnostic methods used for other diseases, such as blood tests, cannot be used to definitively diagnose Parkinson's disease [5]. Existing methods may be time-consuming and expensive, and are also prone to diagnostic errors. Parkinson's disease can be detected through audio signals. The diagnostic method developed based on audio signals is quite effortless and can be more efficient and effective compared to existing methods.

In recent years, promising results have been achieved with diagnostic methods developed using machine learning [6]–[10]. Consequently, machine learning methods have become one of the increasingly used medical approaches for various diseases. Therefore, the successful results obtained from other studies have become one of the main motivations for our study to achieve success in diagnosing Parkinson's disease using machine learning methods.

In the literature, several studies have used machine learning methods for the diagnosis of Parkinson's disease. Furthermore, recent studies in the literature on Parkinson's diagnosis with machine learning use data sets that include audio signal data. Nakkas [11] proposed a feature selection and SMOTE-based method for the diagnosis of Parkinson's disease. Badem, Turkusagi, Caliskan, and Çil [12] proposed a method to detect Parkinson's disease using machine learning approaches and artificial bee colony algorithm (ABC)-based feature selection. Adamu, Abdullahi, Junaidu, and Hassan [13] proposed a new hybrid version of the chaotic crow search algorithm (CCSA) and the particle swarm optimisation algorithm (PSO) for feature selection. Elmanakhly, Saleh, and Rashed [14] proposed an improved binary version of the equilibrium optimiser algorithm (EO) to overcome the challenging feature selection problems in their study. Luo, Wang, Li, Chen, Lv, and Yi [15] proposed the rough hypercuboid (RH) approach and the binary particle swarm optimisation (BPSO) algorithm (RH-BPSO). Rajammal, Mirjalili, Ekambaram, and Palanisamy [16] proposed a grey wolf algorithm (GWO)-based feature selection method for the diagnosis of Parkinson's disease. Anila, Kumar, Rani, Kantipudi, and Jayaram [17] proposed a new deep neural network (DNN) model based on the long short-term memory (LSTM) design to diagnose Parkinson's disease through audio signals. The limitations of these studies are presented in Table I.

In 2020, the immune plasma algorithm (IPA) [18] was introduced to the literature. The IPA algorithm models the plasma treatment procedures used during the COVID-19 pandemic. IPA has been reported to achieve more effective results than eight competing algorithms, including the genetic

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algorithm [19], the particle swarm optimisation [20], the differential evolution algorithm [21], and the artificial bee colony algorithm [22], which are widely known in the literature.

TABLE I. THE LIMITATIONS OF THE STUDIES ABOUT PARKINSON DISEASE.

Study	Method	Limitations
[11]	RFE	The synthetic minority oversampling technique (SMOTE) applied in this study generates synthetic data that corrupt the original distribution in the data set. This can lead to overfitting problems. Moreover, the recursive feature elimination (RFE) method removes the least important features in each iteration, potentially increasing the errors introduced in one step in the following steps. Therefore, choosing such error-prone methods may not be appropriate for diagnostic techniques that affect human lives.
[12]	ABC	In this study, the most fundamental version of the ABC algorithm is used. In the fundamental version of ABC, the risk of getting stuck in local optima is high. Several new versions of ABC have been proposed to avoid local optima.
[13]	CCSA and PSO	In this study, a hybrid method is developed by combining the search strategies of two optimisation algorithms. To prevent the hybrid method from getting stuck at the local minimum point, a new method is applied to the model to increase its complexity.
[14]	EO	In EO, as in most other metaheuristic algorithms, the risk of getting stuck in local minima is high. In this study, new methods are implemented in Basic EO to minimise local minima. As a result, the complexity of the feature selection process has increased.
[15]	RH-BPSO	In this study, a highly complex method is studied to avoid local optimum, which is one of the major disadvantages of PSO.
[16]	GWO	In this study, the mutation process is added to the GWO algorithm to improve the search feature of the method. Furthermore, the k value in the k-nearest neighbour (KNN) machine learning method was also adaptively optimised to improve the success of the model. In this study, different methods were applied to the optimisation algorithm to overcome the local minima problem and a more complex method was used to select the features.
[17]	LSTM-DNN	DNN models may not be appropriate for low-size data sets. DNN models often require high system specifications.

The current success of IPA is the main motivation for this study, which shows that it can also be successfully used for the diagnosis of Parkinson's disease. The advantages of IPA over current methods suggest that it can be successfully applied as a feature selection method for the diagnosis of Parkinson's disease from audio signals. Moreover, IPA's improved search capabilities and local minimum avoidance suggest that it can overcome the limitations of the studies mentioned in Table I and achieve more successful results than the results obtained from these studies.

In this study, a new wrapper model has been proposed that uses machine learning techniques and IPA-based feature selection to diagnose Parkinson's disease from speech signals. In the proposed model, a data set that contains speech signals is used to diagnose Parkinson's disease. Using the efficient search strategies of the IPA, the subset of features that best represents the problem is determined, and the success of the diagnosis is improved.

The contributions of this study to the literature can be summarised as follows:

– A novel AI-based Parkinson's disease diagnosis method is developed using the proposed IPA for the first time;

– A method is introduced that uses the robust search mechanism of the IPA for the diagnosis of the disease based on audio signals with feature selection;

– The optimal values of the parameters for the IPA for the diagnosis of Parkinson's disease are determined based on audio signals.

The proposed method is presented in Section II. Experimental results are presented in detail in Section III. In Section IV, an overall evaluation of the study is presented.

II. PROPOSED METHOD

This section introduces the proposed method, which uses the metaheuristic immune plasma algorithm (IPA) for search operations. Subsequently, a proposed feature selection method based on the IPA is presented. In this study, the "Parkinsons" data set from the UCI Machine Learning Repository was used [23], [24]. This data set consists of various acoustic measurements from 31 individuals. Of these 31 individuals, 23 are Parkinson's patients and 8 are healthy. The data set includes 23 features and 195 samples.

A. Immune Plasma Algorithm (IPA)

The COVID-19 disease, which emerged in Wuhan, China, in 2020, has spread rapidly throughout the world and has become a global pandemic. It has been observed that one of the most effective methods for individuals infected with the disease to recover quickly is immune plasma treatment. In this treatment, antibodies taken from the blood of individuals who have previously been infected with the coronavirus and recovered from the disease are transferred to the coronavirus patient. This strengthens the immune system of infected individuals, alllowing them to fight the coronavirus more effectively and recover from the disease more easily. Inspired by immune plasma treatment in 2020, Aslan and Demirci [18] developed IPA and introduced it to the literature. IPA consists of four main phases: generating the initial population, infection spread, plasma transfer, and donor update. The pseudocode of the IPA algorithm is given in Algorithm 1. Algorithm 1 shows that the IPA algorithm consists of initialisation, infection distribution, plasma transfer, and donor update phases [18], [25]–[31].

Algorithm 1. Pseudocode of the immune plasma algorithm.

Initialisation:
  Assign values to the control parameters *P S*, *D*, *NoD*, and *NoR*.
  Set initial population using (1).
  Set x_{best} as the best individual of the PS individuals.
Repeat
  Infection Distribution Phase:
    Generate the x_k^{inf} for each individual by using (2).
  if $f(x_k^{inf}) < f(x_k)$, **then** update x_k^{inf} with x_k .
  if $f(x_k^{inf}) < f(x_{best})$, **then** update x_k^{best} with x_k^{inf}.
  Plasma Transfer Phase:
    Choose the donor and receiver in the population based on fitness function.
  Set the dose control vector to *1*.
  For all receivers x_k^{rcv}, generate the x_k^{rcv-p} by using (4). (t_{cr}) + 1
  if receiver dose is *1*, **then**
    if $f(x_k^{rcv-p}) < f(x_m)$, **then** Update x_k^{rcv} with x_k^{rcv-p} and dose + *1*.
    else

17: Update x_k^{rcv} with x_m^{dnr}. Set dose to *0*.
18: **else**
19: **if** $f(x_k^{rcv-p}) < f(x_m^{dnr})$, **then** Update x_k^{rcv} with x_k^{rcv-p}.
20: **else** Set dose to *0*.
21: **end if**
22: **if** $f(x_k^{rcv}) < f(x_{best})$, **then** Update x_{best} with x_k^{rcv}.
23: **Donor Update Phase:**
24: For all donors:
25: **if** $(t_{cr}/t_{max}) < rand(0, 1)$, **then** Update $x_m^{dnr}$by using (5).
26: **else** Update x_m^{dnr} by using (1).
27: **if** $f(x_m^{dnr}) < f(\mathrm{x_{best}})$, **then** Update x_{best} with x_m^{dnr}.
28: **Until** $(t_{cr} < t_{max})$.

Generating Initial Population: In IPA, each individual in the population is a potential candidate solution. Assuming that the problem to be solved has *D* different decision parameters, the *PS* population is formed using the equation shown in (1)

$$x_{kj} = x_j^{min} + rand\,(0,1)\left(x_j^{max} - x_j^{min}\right). \tag{1}$$

In this equation, x_k is the generated individual, x_{kj} is the j^{th} parameter of x_k, x_j^{min}, and x_j^{max} represent the lower and upper limits of the j^{th} parameter of the individual. *rand*(*0*, *1*) represents a random number between *0* and *+1* [18], [25]–[31].

Infection Spreading Phase: In IPA, the spread of disease in the population is carried out in the infection spreading phase. Individuals are infected according to (2)

$$x_{kj}^{\mathrm{inf}} = x_{kj} + rand\,(-1,+1)\left(x_{kj} - x_{mj}\right). \tag{2}$$

In this phase, the infection spreads to every individual in the population to expand the search space of IPA. In the equation, x_{kj}^{inf} represents the value of the j^{th} parameter of the infected x_k individual, which is randomly selected, x_{mj} is the value of the j^{th} parameter of the x_{mj} individual, which is randomly selected from the population, x_k and x_m have to be different individuals, *rand*(*−1, +1*) represents a random number between −1 and +1 [18], [25]–[31].

The immune response of the infected individual to infection is evaluated using the fitness function. The individual's immune memory is updated according to (3), where $f(x_k^{inf})$ is the immune response of the infected individual x_k^{inf} to the infection, and $f(x_k)$ is the immune response of the individual x_k

$$x_{kj} = \begin{cases} x_{kj}^{inf} & ;\ \text{if}\ f\left(x_k^{inf}\right) < f\left(x_k\right), \\ x_{kj}^{inf} & ;\ \text{if}\ f\left(x_k^{inf}\right) \geq f\left(x_k\right). \end{cases} \tag{3}$$

Here, if the response of the infected individual x_k^{inf} to the infection is smaller than the response of the individual x_k to the infection, the parameter value changed in the infection spreading phase of the individual x_k is updated. Otherwise, the parameter value of the individual x_k before infection is not changed [18], [25]–[31]

Plasma Transfer Phase: In IPA, the process of transferring plasma to infected individuals is modelled in the plasma treatment phase. After individuals are infected in the infection spreading phase, the IPA identifies *NoD* (Number of Donor) individuals with the best immune response to infection and *NoR* (Number of Receiver) individuals with the worst immune response as donor and receiver individuals, respectively. The *NoD* and *NoR* numbers are control parameters that take a fixed value at the beginning of IPA. Plasma transfer is performed according to (4)

$$x_{kj}^{rcv-p} = x_{kj}^{rcv} + rand\,(-1,+1)\left(x_{kj}^{rcv} - x_{mj}^{dnr}\right). \tag{4}$$

In (4), x_k^{rcv} represents a randomly selected receiver individual, x_m^{dnr} represents a randomly selected donor individual, and x_{kj}^{rcv-p} represents the new value of the j^{th} parameter of the x_k^{rcv} individual after plasma transfer. Additionally, x_{kj}^{rcv} and x_{mj}^{dnr} represent the j^{th} parameters of the x_k^{rcv} receiver and x_m^{dnr} individuals, respectively. In the plasma transfer phase, a randomly selected donor from among the donors transfers plasma to all [18], [25]–[31].

In IPA, the end of the plasma transfer phase is decided according to the immune responses produced by the x_k^{rcv-p} and x_k^{rcv} individuals against infection [18]. In this phase, dose control is carried out according to the response of the receiver individual to treatment. If the fitness value of x_{kj}^{rcv-p} exceeds the fitness value of x_{mj}^{dnr}, the dose transfer is performed until it passes.

Donor Update Phase: In plasma treatment, the immune response of donors to infection can change over time. This is modelled in IPA in the donor memory control phase. In IPA, the decision on whether or not to update donors is based on the time-dependent change in donors' immune responses to infection, the ratio of the total evaluation number (t_c) to the maximum evaluation number (t_{max}). Accordingly, if the value of $(t_{cr})/(t_{max})$ is less than a randomly selected number between 0 and 1, the x_m^{dnr} donor is completely updated according to (1). Otherwise, the x_m^{dnr} donor's all parameters are updated according to (5) and the donor's immune memory is controlled [18], [25]–[31]

$$x_{mj}^{dnr} = x_{mj}^{dnr} + rand\,(-1,+1)\left(x_{mj}^{dnr}\right). \tag{5}$$

B. Feature Selection

Feature selection is a crucial process in machine learning that involves identifying and selecting the most relevant features from a data set [32]. The features are the variables that are used to describe the data. In machine learning, feature selection can be used to improve the performance of a model by removing irrelevant or redundant features. In feature selection, filtering, wrapper, and hybrid methods are the three most common approaches [33].

In filtering methods, features are selected or extracted without using any classification method [34]. In filtering methods, each feature is assigned a statistical importance value (chi-square, correlation, etc.) and the features are ranked according to these values [35]. In wrapper feature selection methods, classification algorithms and meta-heuristic algorithms can be used to find the most appropriate feature set [36]. In wrapper methods, candidate feature subsets are generated using metaheuristic algorithm search strategies and evaluated by testing them in a classifier [37]. In the hybrid feature selection method, both filter and wrapper methods are used together to achieve the most optimal feature

subset [38]. This approach can lead to better results, but it may also require more processing time compared to the other two methods.

C. *Proposed IPA-based Feature Selection on The Parkinson's Disease*

In this section, the diagnosis of Parkinson's disease is described using IPA-based feature selection in audio signal data. The data set used in the study consists of 195 samples and 22 attributes, as described in the previous section. The data extraction process consists of data preprocessing, feature selection, and classification. In the first phase, the data set is preprocessed. The data set was determined to have no missing data. Subsequently, normalisation was applied to the data using the min-max normalisation method. To ensure data integrity, synthetic data insertion or data removal was performed. After the preprocessing phase, the feature selection process is performed with IPA. The proposed IPA-based feature selection is described in detail below.

In the IPA-based feature selection phase, the population size, *D*, *NoD*, and *NoR* values are initialised and remain constant throughout the algorithm search process. Then, individuals with $D = 22$ are created from the 22 features of the "Parkinsons" data set, according to (1). Each parameter value of the created individuals is randomly generated between 0 and 1. Each initial individual with 22 parameters represents a potential solution. The parameter value of each potential solution is compared to the threshold value of 0.5. If the parameter value of an individual is greater than 0.5, that parameter value is assigned a value of 1, and if it is less than 0.5, it is assigned a value of 0. The process of selecting features based on the threshold value is shown in Fig. 1.

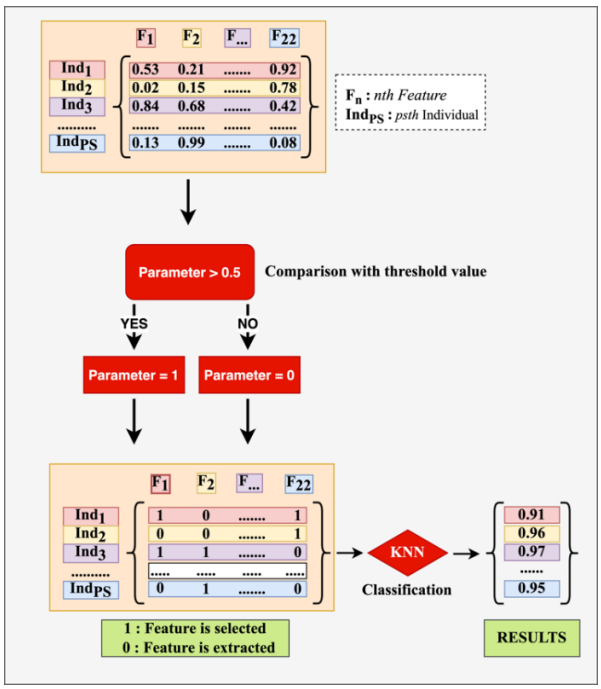

Fig. 1. Feature selection by threshold value.

Thus, the parameters of the candidate solution are transformed from continuous values to binary values. Parameter 1 represents the selection of the attribute corresponding to that parameter. Parameter 0 represents the unselection of the feature from the data set. The obtained feature subset is classified using a KNN classifier with 10-fold cross-validation.

In this study, the classifier's average accuracy is obtained by averaging the accuracy values from 10 runs of the 10-fold cross-validation technique. Consequently, the classification accuracy serves as the fitness value for the candidate solution. The entire IPA-based feature selection process described is presented in Fig. 2.

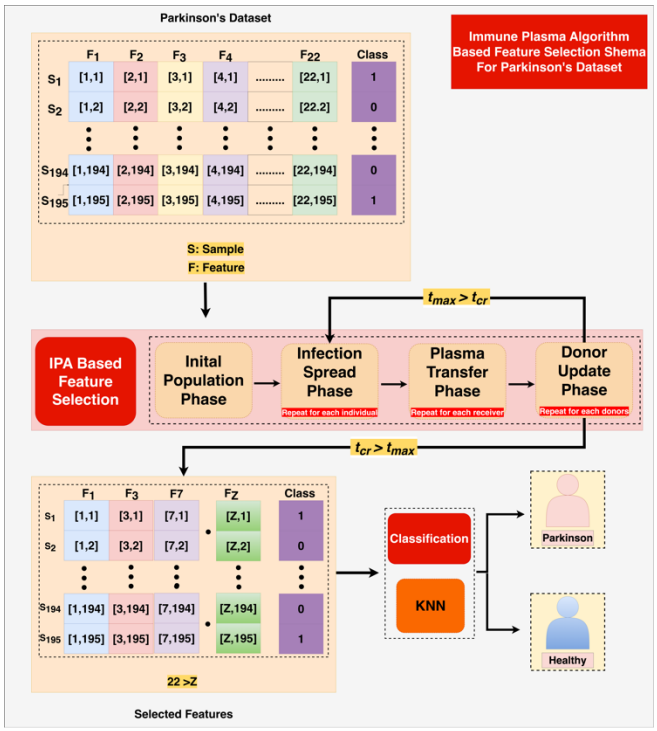

Fig. 2. The proposed IPA-based feature selection process for the data set.

The process of generating a new feature subset based on the threshold value is applied in the same way for each new candidate solution created in the infection spread, plasma transfer, and donor update phases of the IPA. The best fitness value and corresponding solution are stored in memory and updated whenever a better solution is found. Once the maximum evaluation number is reached, the final best fitness value represents the best achievable accuracy for the classification of Parkinson's disease. The corresponding best solution set represents the feature subset with the optimal representation power for the Parkinson's data set. In this study, the experimental results were obtained and reported through this method.

III. EXPERIMENTAL RESULTS

All experimental results were obtained in the MATLAB R2021a environment using the MATLAB programming language. The results were reported from a system with a 2.4 GHz Intel i5-6200U processor and 12 GB of RAM memory. To more accurately evaluate the success of the proposed method, in addition to the accuracy value of the classifier, the values of precision, sensitivity, specificity, and F-Score, along with the standard deviation values of these values, are presented in this study.

In the proposed method, the KNN classifier was selected as the main classifier. The reason for choosing the KNN classifier is that KNN is a simple and fast classifier. The value of k neighbourhood in the KNN classifier affects the success of the classification. Since the value of k = 5 is often preferred

in the literature, the neighbourhood value was determined as 5 in our proposed method. To test the proposed method and obtain reliable results, 10.000 evaluations were performed using the 10-fold cross-validation technique for each IPA parameter set, respectively. Each run was independently repeated 10 times to obtain the average results. The average and standard deviation values of the performance comparison of the IPA control parameters obtained as a result of the experimental study are presented in Table II. In Table II, *acc*, *P*, *Sn*, *Sp*, and *F* represent the accuracy, precision, sensitivity, specificity, and F-score values, respectively.

TABLE II. SCORES OF THE PROPOSED METHODS ACCORDING TO IPA CONTROL PARAMETERS.

[PS; DS; RS]	*Acc*	*Std.*	*P*	*Std.*	*Sn*	*Std.*	*Sp*	*Std.*	*F*	*Std.*
[10; 1; 1]	0.960	0.005	0.790	0.028	0.860	0.02	0.880	0.015	0.820	0.048
[20; 1; 1]	0.957	0.004	0.830	0.025	0.850	0.028	0.910	0.018	0.830	0.029
[40; 1; 1]	0.957	0.002	0.820	0.023	0.860	0.033	0.910	0.017	0.840	0.023
[10; 1; 2]	0.964	0.004	0.830	0.024	0.880	0.033	0.910	0.015	0.850	0.028
[20; 1; 2]	0.961	0.004	**0.870**	0.025	0.880	0.027	0.930	0.02	0.870	0.028
[40; 1; 2]	0.960	0.006	0.850	0.022	0.920	0.013	0.910	0.018	0.880	0.033
[10; 1; 3]	0.965	0.003	0.850	0.02	0.920	0.035	0.910	0.007	0.880	0.013
[20; 1; 3]	**0.965**	0.003	0.850	0.02	**0.930**	0.026	0.920	0.012	**0.890**	0.03
[40; 1; 3]	0.963	0.003	0.840	0.027	0.910	0.042	0.920	0.007	0.870	0.021
[10; 2; 1]	0.957	0.002	0.80	0.019	0.840	0.022	0.90	0.015	0.810	0.026
[20; 2; 1]	0.956	0.003	0.790	0.021	0.820	0.035	0.890	0.016	0.790	0.026
[40; 2; 1]	0.954	0.004	0.80	0.011	0.860	0.026	0.90	0.011	0.820	0.015
[10; 2; 2]	0.960	0.002	0.810	0.024	0.850	0.03	0.90	0.018	0.830	0.025
[20; 2; 2]	0.959	0.005	0.80	0.019	0.890	0.036	0.890	0.007	0.840	0.029
[40; 2; 2]	0.957	0.005	0.850	0.027	0.860	0.02	0.920	0.024	0.850	0.039
[10; 2; 3]	0.962	0.003	0.840	0.004	0.880	0.011	0.910	0.008	0.850	0.018
[20; 2; 3]	0.960	0.004	0.840	0.013	0.870	0.023	0.920	0.018	0.850	0.033
[40; 2; 3]	0.961	0.003	0.850	0.017	0.880	0.023	**0.920**	0.011	0.860	0.019
[10; 3; 1]	0.959	0.004	0.770	0.021	0.810	0.016	0.880	0.017	0.780	0.035
[20; 3; 1]	0.957	0.004	0.770	0.025	0.780	0.052	0.880	0.029	0.770	0.04
[40; 3; 1]	0.954	0.004	0.80	0.03	0.830	0.042	0.90	0.013	0.810	0.017
[10; 3; 2]	0.960	0.003	0.80	0.03	0.820	0.033	0.90	0.017	0.80	0.037
[20; 3; 2]	0.958	0.004	0.80	0.035	0.830	0.034	0.90	0.022	0.810	0.039
[40; 3; 2]	0.956	0.003	0.830	0.014	0.850	0.022	0.910	0.02	0.830	0.03
[10; 3; 3]	0.960	0.004	0.80	0.018	0.850	0.019	0.890	0.018	0.810	0.032
[20; 3; 3]	0.959	0.004	0.820	0.033	0.860	0.028	0.90	0.031	0.830	0.049
[40; 3; 3]	0.958	0.005	0.830	0.025	0.90	0.021	0.910	0.022	0.860	0.036
Average	**0.959**	**0.004**	**0.820**	**0.022**	**0.863**	**0.028**	**0.904**	**0.017**	**0.834**	**0.030**

Table II shows the average results obtained from 10 independent runs using the 10-fold cross-validation technique for each IPA parameter. When Table II is analysed, it is seen that the best accuracy value obtained with the proposed method is 0.965. For all the sets of IPA parameters, the proposed method achieved the best accuracy result in the set of parameters where the population size is set to 20, the donor number is set to 1, and the receiver number is set to 3. The lowest accuracy value of 0.954 was obtained in the method where the population size is 40, the donor number is 3, and the receiver number is 1. Furthermore, according to Table II, the most successful results were obtained in terms of accuracy, sensitivity, and F-Score values, in addition to the accuracy value, with the same set of parameters compared to other set of parameters. According to Table II, the standard deviation values of the comparison criteria obtained from 10 independent runs for each set of parameters indicate that consistent results can be obtained with the proposed method.

For metaheuristic-based feature selection methods, computation time is a crucial performance metric along with accuracy. Table III shows the average computation times for 10-fold cross-validation and 10 independent runs for each IPA parameter. When the number of selected features presented in Table III is analysed, it is seen that the best selection of features is achieved in the parameter set where the number of populations is 10, the number of donors is 1, and the number of receivers is 3. Furthermore, Table III reveals that the parameter set with the lowest average computation time (fastest results) has a population size of 40, a donor number of 3, and a receiver number of 3. This set exhibits an average computation time of 440.83 seconds, with the longest time being 672.51 seconds.

When the convergence graph is analysed, it is seen that the parameter sets [20; 1; 3] with the most successful result and [40; 3; 1] with the worst result converge close to each other until 0.95. However, after 0.95, it is seen that the parameter set [20; 1; 3] converges faster and better in the 200th evaluation.

The convergence graph for the most and least successful parameter sets is presented in Fig. 3.

TABLE III. AVERAGE NUMBER OF SELECTED FEATURES AND AVERAGE COMPUTATIONAL TIMES.

[PS; DS; RS]	Number of Feature	Average Selected Features	Average Calculation Time (Seconds)
[10; 1; 1]	22	10.7	463.45
[20; 1; 1]	22	10.4	495.37
[40; 1; 1]	22	10.8	494.72
[10; 1; 2]	22	10.9	566.17
[20; 1; 2]	22	11.3	672.51
[40; 1; 2]	22	10.1	513.89
[10; 1; 3]	22	9.9	491.74
[20; 1; 3]	22	11.3	492.45
[40; 1; 3]	22	11.6	497.24
[10; 2; 1]	22	11.7	501.70

[PS; DS; RS]	Number of Feature	Average Selected Features	Average Calculation Time (Seconds)
[20; 2; 1]	22	12.2	504.54
[40; 2; 1]	22	12.1	502.23
[10; 2; 2]	22	11.2	497.18
[20; 2; 2]	22	12.5	497.53
[40; 2; 2]	22	12.5	502.4
[10; 2; 3]	22	10.3	497.19
[20; 2; 3]	22	10.6	482.59
[40; 2; 3]	22	11.5	499.29
[10; 3; 1]	22	11.4	489.07
[20; 3; 1]	22	12.3	493.73
[40; 3; 1]	22	10.8	501.55
[10; 3; 2]	22	11.2	482.04
[20; 3; 2]	22	10.4	503.06
[40; 3; 2]	22	11.8	497.26
[10; 3; 3]	22	11.3	622.20
[20; 3; 3]	22	10.3	545.36
[40; 3; 3]	22	10.7	440.83
Average	**22**	**11.18**	**509.16**

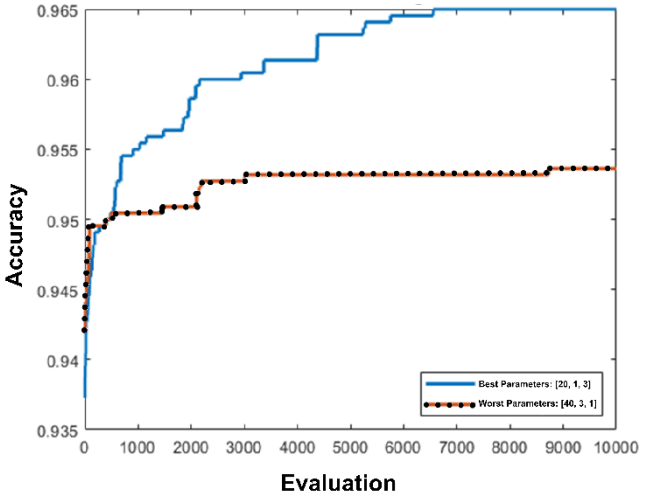

Fig. 3. Convergence plot of the worst and the best IPA parameter set.

In this study, the performance of the proposed feature selection method is compared with the competing filtering methods, including principal component analyses (PCA), relief-based feature selection method, Chi-square test-based feature selection method, and information gain-based feature selection method. Furthermore, the classification results with KNN without feature selection in the "Parkinsons" data set are also reported in Table IV.

For all competing methods, cross-validation and 80 % training and 20 % testing methods were used for classification and the results were reported. Table IV also presents the classification results on the Parkinson's data set without feature selection.

When Table IV is analysed, it is seen that the most successful feature selection method in the classification process performed with 10-fold cross-validation is the information gain-based method. The information gain-based feature selection method has the highest accuracy value of 0.880. In the classification process performed with the train-test method, it is seen that the most successful method is the PCA feature reduction method. PCA obtained the highest accuracy value with 0.970. When the results obtained by cross-validation are evaluated, it is seen that the PCA dimensionality reduction method is the most unsuccessful method. PCA obtained the lowest accuracy value with 0.84. In the train-test split method, it is seen that the Relief-based feature selection method is the most unsuccessful method. The Relief-based feature selection method obtained the lowest accuracy value with 0.920. When classification was performed with the train-test technique without any feature selection in the Parkinson's data set, an accuracy value of 0.950 was obtained. This value, which was quite high in the 10-cross-validation technique, decreased to 0.820. The classification results obtained with the train-test method may be unreliable. Because in the train-test split method, training and testing are not performed with all the data in the data set. In the proposed method, this may be the reason we perform the classification process with cross-validation technique instead of train-test. Thus, although PCA with the train-test method is more successful than the method we proposed in this study, it would be a better approach to prefer the results obtained by cross-validation for better evaluation. Information about the performance of the proposed method can be obtained by comparing it with the results obtained in other studies.

TABLE IV. RESULTS OF FILTER-BASED FEATURE SELECTION METHODS IN PARKINSON'S DATA SET.

Method	*Acc*	*P*	*Sn*	*F*
PCA/10-Fold Cross-Validation	0.840	0.910	0.890	0.890
PCA/80 % Train + 20 % Test	0.970	**1.00**	0.960	**0.980**
Relief/10-Fold Cross-Validation	0.870	0.920	0.920	0.920
Relief/80 % Train + 20 % Test	0.920	0.910	**1.00**	0.950
Chi-Square/10-Fold Cross-Validation	0.850	0.890	0.940	0.910
Chi-Square/80 % Train + 20 % Test	0.940	0.840	0.930	0.910
Information Gain/Cross-Validation	0.880	0.940	0.910	0.920
Information Gain/80 % Train + 20 % Test	0.950	0.970	0.970	0.970
No Feature Selection/Cross-Validation	0.820	0.870	0.900	0.890
No Feature Selection/80 % Train + 20 % Test	0.950	0.970	0.970	0.970
Proposed Method	**0.965**	0.850	0.930	0.890

Table V shows the results of the comparison of the performance of the proposed method in this study with other recent studies in the literature where classification and feature selection were performed with the same data set. Furthermore, it was ensured that the studies selected for an equitable comparison had performed training and testing with a 10-fold cross-validation technique.

When Table V is analysed, it is seen that the proposed method achieved better results than 10 competitive methods and equal results in one method with an accuracy value of 0.965. Consequently, it proves that effective IPA search strategies are more successful than other competing methods.

In this study, an IPA-based feature selection approach is proposed for the classification of Parkinson's disease based on speech signals. In the proposed method, the effective search strategies of IPA are used to obtain the features that represent the disease. Classification was performed with the KNN classifier with the selected features by IPA. The values

of the comparison criteria obtained were reported and compared with similar studies in the literature. Thus, the proposed IPA-based feature selection approach is significantly successful compared to similar methods.

TABLE V. COMPARISON OF THE PROPOSED METHODS WITH THE COMPETITOR METHODS.

Competing works	Method	Accuracy	Reference
Dinesh and He	Filter-based feature selection, Improved Decision Trees	91.00	[5]
Nakkas	Reductive feature elimination, KNN	96.10	[11]
Adamu, Abdullahi, Junaidu, and Hassan	Hybrid PSO and CCSA, KNN	92.63	[13]
Elmanakhly, Saleh, and Rashed	IBEO, KNN	92.59	[14]
Luo, Wang, Li, Chen, Lv, and Yi	BPSO and the RH approach, C4.5 and NB	87.58	[15]
Rajammal, Mirjalili, Ekambaram, and Palanisamy	GWO with Mutation, Adaptive KNN	95.66	[16]
Anila, Kumar, Rani, Kantipudi, and Jayaram	LSTM-DNN	89.23	[17]
Fayyazzifar and Samadiani	Adaboost, GA	**96.5**	[39]
Goyal, Khandnor, and Aseri	GA, SVM	88.71	[40]
El-Hasnony, Barakat, Elhoseny, and Mostafa	GWO and PSO, KNN	92.00	[41]
Proposed Method	**IPA, KNN**	**96.5**	

IV. CONCLUSIONS

In this study, a feature selection method using IPA is proposed for the classification of Parkinson's disease based on audio signals. The proposed method aims to reach the features that best represent Parkinson's disease by using effective search strategies from IPA. The classification process was conducted using the KNN classifier with features selected by IPA. Each process was separated as a train-test split using the 10-cross-validation method. The results obtained are the average results from running the process 10 times. The results obtained were reported and compared with similar studies in the literature. The experimental results show that the proposed immune plasma-based feature selection approach, with an accuracy value of 0.965, is significantly more successful than the 10 competing feature selection methods proposed in the literature. Additionally, the experimental results show that the proposed IPA-based method successfully identified the most relevant features for Parkinson's disease, reducing the number of features from 22 to an average of 11.18 for all parameters. The proposed IPA-based feature selection method was also compared with commonly used filter-based feature selection and dimensionality reduction methods in the literature. For each method compared, the train-test split and cross-validation methods were applied separately, and the results were reported. The experimental results showed that the method proposed in this study is significantly more successful than five filter-based feature selection and dimensionality reduction methods.

CONFLICTS OF INTEREST

The authors declare that they have no conflicts of interest.

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