

## A discrete salp swarm algorithm with weights and Lévy flights: application for Parkinson's disease detection

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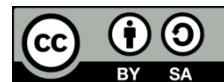
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### ABSTRACT

A new hybrid algorithm named discrete salp swarm algorithm that integrates effectiveness of weights, Lévy flights, and an excellent classifier, support vector machine (SVM), has been proposed to predict Parkinson's disease. In the proposed algorithm, salp swarm algorithm (SSA) is used as a feature selection tool, which targets to reduce the noise in features of the speech PD dataset to improve the SVM classifier's prediction accuracy. The efficacy and usefulness of the proposed discrete salp swarm algorithm with Lévy flights have been meticulously assessed against the speech PD dataset in terms of G-mean, accuracy, F-measure, specificity, sensitivity, and precision measures. DWLSSA has achieved values of the measures, 97.76%, 98.75%, 98.77%, 97.37%, 98.15%, and 99.39% respectively. Comparison of DWLSSA with other nature inspired algorithms applied to predict Parkinson's shows that the proposed DWLSSA performs better. It can be also said that DWLSSA can be an alternative for solving the NP-hard problems.

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## 1. INTRODUCTION

Parkinson's is a disorder of the nervous system. Brain cell loss is the leading cause of it. Walking problems, controlling of hands, trembling, stiffness, and tremors are the symptoms of Parkinson's disease. Failure to coordinate nerve cells results in the inability to send the signals to each other. No availability of proper cure suggests timely diagnosing of the Parkinson's disease. The variation in patterns of handwriting and speech is beneficial in diagnosing Parkinson's in its earlier stages. The correlation between the minimum and maximum frequencies of speech patterns and variations in frequency measures of patients have proved beneficial in diagnosing Parkinson's. Sakar *et al.* [1] prepared a dataset of the vowels 'a' and 'o' phonemes of the Parkinson's patients.

A dataset based on the handwriting patterns generated while drawing menders and spirals in the clock and anti-clockwise directions by a group of healthy people and patients. This dataset was generated by Pereira *et al* [2]. The data size increases with the time, introduces various problems for researchers. It is tough to pre-process this big size data as the number of examples and features increases. A big size of data is always susceptible to more noise. So, it is crucial to remove this noise to improve the prediction rate. Therefore, feature selection is always an important task in the prediction process. Feature selection process

chooses significant features from the dataset and produces a subset. Then, this subset is given to a classifier like SVM which can predict better. It also removes complexity, computational cost and, reduces the dimensionality of the problem. In this paper, a discrete SSA embedded with weights and Lévy distribution (DWLSSA) is introduced to predict the Parkinson's disease using the dataset prepared by [1], [3], and [4]. The contributions of the introduced DWLSSA include:

- i. An enhanced version of the basic SSA is introduced with two improvements.
- ii. Firstly, we have added the weights to improve the exploration and exploitation of the basic SSA. This will improve the searching efficiency of basic SSA to handle the local optima problem.
- iii. Secondly, Lévy Flights are used to enhance the effectiveness and accuracy of the foraging process.
- iv. Lévy flights improve the searching ability of the agent by its short and long-distance walking and jumping in the search space. Lévy flights improve searching in both nearby and far area of the search space.
- v. The speech PD dataset was used to analyze the DWLSSA's performance. According to the data, the basic SSA's performance has improved dramatically when compared to its most recent peers.

Feature selection is favored for the pre-processing task of selecting an optimal subset of the attributes from the actual dataset [5]. The research in nature-inspired algorithms (NIAs) has increased significantly in last decades. NIAs try to generate effective and optimal solutions by removing not useful solutions with the help of a fitness function. Genetic algorithm (GA) [6], firefly algorithm (FA) [7], cuckoo search (CS) [7], bat algorithm (BAT) [8], ant colony optimization (ACO) [9], gravitational search (GSA) [10], artificial bee colony (ABC) [11], grey wolf optimization (GWO) [12], crow search algorithm (CSA) [13], cuttlefish algorithm (CFA) [14], whale optimization algorithm (WOA) [15] and salp swarm algorithm [16] are some of the nature-inspired algorithms proposed for finding the optimal solutions of various problems. NIAs are used for several optimization tasks in different domains [17].

The rest of the paper is organized as follows: Section 3 describes the basic SSA followed by SVM, weight factor, Lévy flights, the proposed DWLSSA algorithm, and fitness function. Results with discussion are given in section 4. Finally, authors conclude the work and suggest several directions for future work followed by acknowledgements and references.

## 2. LITERATURE REVIEW

A brief review of some recent research done for feature selection using nature-inspired algorithms based on Parkinson's disease is presented in this section. Pereira *et al.* [18] proposed a cuckoo search algorithm to selecting features from a dataset. They introduced various transfer functions to map continuous results to discrete results. They compared it with traditional BAT, FA, and PSO. Emary *et al.* [19] proposed a wrapper based binary GWO for feature extraction from different medical datasets. The algorithm used KNN for classification. Zawbaa *et al.* [20] proposed a wrapper-based ant lion optimizer. They have tested the algorithm on 18 datasets. Results attained are compared with GA and PSO. Results prove this approach very good. Saroj and Jyoti [21] introduced a multi-objective genetic algorithm (MOGA) for feature extraction. They have tested the algorithm on seven different datasets with an SVM classifier. It has produced results with reasonable classification accuracy. Sharawi *et al.* [22] gave a wrapper-based whale algorithm (WOA) for feature extraction. They tested the algorithm on 16 datasets and compared it with GA and PSO. The results proved it a good approach. Zawbaa *et al.* [23] introduced a chaotic ant lion optimizer (CALO) for feature extraction. They have tested the algorithm on different medical datasets. Results were compared with GA, PSO, and ALO algorithms and produced better results. Dash [24] proposed a harmony search algorithm with Pareto optimization (AHS GS) for a high-volume dataset. Again, he compared results with GA and PSO. AHS GS has proved itself better there. Nayak *et al.* [25] proposed an elitism based MODEA for feature extraction. Twenty three benchmarked datasets are used for testing. Results are compared with MECY-FS and MECY-FS-U algorithms. This algorithm has produced best results compared to the other algorithms. We do not have any method which can solve any optimization problem efficiently [26]. A method works well for a problem may not be best for other problems. This phenomenon has motivated us to improve SSA algorithm for predicting Parkinson's.

## 3. MATERIAL AND METHODS

### 3.1. Salp swarm algorithm

The salp swarm algorithm was proposed by [15]. The basic salp swarm is given in Algorithm 1 [15] and described here. The SSA imitates the foraging behaviour of the salps in different oceans. In oceans, salps form a swarm called as salp chains. In SSA, the salp which remains at the front of the chain is named as leader salp. Remaining salps are named as followers. The position of each salp in the swarm is determined based on the  $d$ -dimensional search space, where  $d$  represents the number of the variables in the problem. So, here a two-dimensional matrix  $A$  is used to store the position of the salps in the swarm. The goal of the salp

swarm is to search a food source  $FD$  in the search space. The math's model for salp swarm algorithm is described below. The leader salp updates its position using (1).

$$A_i^1 = \begin{cases} FD_i + r_1((u_i - l_i) \times r_2 + l_i) & r_3 \geq 0 \\ FD_i - r_1((u_i - l_i) \times r_2 + l_i) & r_3 < 0 \end{cases} \quad (1)$$

Where  $A_i^1$  and  $FD_i$  are the position of the leader at the  $i^{th}$  position and food source position at the  $i^{th}$  position respectively. Here  $u_i$  and  $l_i$  are the bounds at the  $i^{th}$  position. The  $r_1$ ,  $r_2$ , and  $r_3$  are some random numbers. SSA uses a parameter  $r_1$  to balance the exploitation and exploration of the search space. Following (2) is used to calculate  $r_1$ .

$$r_1 = 2e\left(\frac{4i}{T}\right)^2 \quad (2)$$

Where  $i$  is current iteration and  $T$  is total number of iterations respectively. The follower updates its position using (3). Here,  $A_i^j$  is the current place of the  $j^{th}$  follower salp in  $i^{th}$  dimension.

$$A_i^j = \frac{1}{2}(A_i^j + A_i^{j-1}) \quad (3)$$

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### Algorithm 1. Basic salp swarm algorithm

Initialize the parameters: total number of salps, max. Iterations, salp's position, and best fitness.

Initialize the salps positions  $A_i$  ( $i = 1, 2, \dots, n$ )

While ( $t < \text{max iterations}$ )

Determine the fitness value of each salp

$F = \text{best salp}$  ((search-agent))

Update the value of  $r_1$  parameter using (2)

For every salp ( $A_i$ )

If ( $i == \text{leader}$ )

Update leader position using (1)

Else

Update follower position using (3)

End if

End for

Reposition salp which go out search space

$t=t+1$

End While

return  $F$

### 3.2. Support vector machine

Support vector machine is one of the techniques available for classification and regression [27]. SVM is exceptionally accepted for classification due to its ability to manage categorical and continuous variables. The SVM uses a hyperplane in multidimensional space to represent different classes. The iterative generation of hyperplane minimizes the errors. The SVM has following concepts:

- i. Support vectors-The data points closed to the hyperplane is known as support vectors. A line that separates the data points is defined with the help of the support vectors.
- ii. Hyperplane-The line which separates the input variables is known as a hyperplane. In SVM, hyperplane is used to split the points in their respective variable space based on their class.
- iii. Margin-Margin is a distance between nearby data points and the line. A large margin is measured as a good margin.

The SVM aims to find a sizeable marginal hyperplane by dividing the datasets into classes. SVM does this as per the following steps; in the first step, SVM iteratively generates hyperplanes, separating the classes in the possible way. Then, SVM chooses the hyperplane, which separates the classes accurately.

### 3.3. Weight factor

Inertia weight is introduced in PSO by Kennedy and Eberhart [28] to balance exploitation and exploration of the search space. This inspiration motivated us to apply a weight ( $w$ ) to both the leaders and the followers in the SSA. The weight expands global search in the initial steps to address premature convergence. It also does an outstanding local search at the later stages. The mathematical equation for weight ( $w$ ) [29] is given (4).

$$W = \left(1 - \frac{Ces}{MCes}\right)^{1 - \tan(\pi \times (rand - 0.5) \times \frac{S}{MCes})} \tag{4}$$

Where *Ces* is the current evaluation and *MCes* is the maximum evaluations respectively. And, *S* is used as an independent continuously changing variable. Based on the above, the equations for updating leader and followers are changed as (5) and (6).

$$A_i^1 = \begin{cases} FD_i + w \times r_1((u_i - l_i) \times r_2 + l_i)r_3 \geq 0.5 \\ FD_i - w \times r_1((u_i - l_i) \times r_2 + l_i)r_3 < 0.5 \end{cases} \tag{5}$$

$$A_i^j = w \times \frac{1}{2}(A_i^j + A_i^{j-1}) \tag{6}$$

**3.4. Lévy flight**

French Lévy introduced a probability distribution named as Lévy flight [30]. The Lévy flight regulates the direction and size of the algorithm's progress. It uses a probability distribution to do this task [31]. In this research, an arbitrary number is generated, which is based on a probability distribution given in (7) using the Mantegna method [32].

$$levy(x) = \frac{1}{2} \times \frac{a}{|b|^{1-x}} \tag{7}$$

Here, *a* and *b* are normally distributed arbitrary numbers. The value of *a* and *b* are calculated using (8) and (9). The  $\sigma_a$  and  $\sigma_b$  are standard deviation values and computed using (10). The value of *x* is in the range of 1 to 2.

$$a = normal(0, \sigma_a^2) \tag{8}$$

$$b = normal(0, \sigma_b^2) \tag{9}$$

$$\sigma_a = \left[ \frac{\gamma(1+x) \sin \frac{\pi x}{2}}{\gamma \left(\frac{1+x}{2}\right) x^2 \frac{(x-1)}{2}} \right]^{\frac{1}{x}} \tag{10}$$

The long jumps occasionally and small steps associated with Lévy flight enhance the searching ability of the algorithm. The shorter step length helps in searching an optimal solution in the neighbourhood of the current best. On the other hand, the small steps could simultaneously help explore a more extensive search space. The exploitation and exploration in SSA rely heavily on the parameter *r<sub>1</sub>* which affects the timely convergence of SSA. So, the SSA strengthens its exploration capability by integrating randomization/Lévy flights. This random updating of salps' position helps to improve foraging process and avoids trapping in the local optima. A long jump in the Lévy flight increases the step size of the initial population. In turn, it also helps to explore a more prominent search area. The salps' step size is stated using (11).

$$stepsize_i = levy(x) \times (FD_i - levy(x) \times y_i) \tag{11}$$

After computing the step size, the leader salp updates its position using (12) and (13). Once the leader updates his position successfully, the followers update their positions using (14).

$$A_i^1 = \begin{cases} FD_i + r_1((u_i - l_i) \times r_2 + l_i) r_3 \geq 0 \\ FD_i - r_1((u_i - l_i) \times r_2 + l_i) r_3 < 0 \end{cases} \tag{12}$$

$$A_i^1 = A_i^1 + stepsize_i \tag{13}$$

$$A_i^1 = \frac{1}{3}(A_i^1 + A_i^{i-1} + Levy(x)) \tag{14}$$

**3.5. Proposed DWLSSA algorithm**

The proposed algorithm is given in Algorithm 2 and described here. In the proposed DWLSSA algorithm, solutions are generated in the binary form which is either 0 or 1 in a feature selection problem. So, a discrete SSA is developed to use with our problem of research. A vector is used to define a solution. The length of this vector is defined as the number of features available in the real dataset. The solution vector

consists of values in binary 0 or 1. Value 1 indicates the selected solution while 0 indicates not selected solution. Equation (15) is used for continuous to binary mapping of the values.

$$D_{mn} = \begin{cases} 1, & \text{if } E_{mn} > 0.5 \\ 0, & \text{otherwise} \end{cases} \quad (15)$$

Where  $m$  and  $n$  are search agent and the dimension respectively.  $D_{mn}$  and  $E_{mn}$  are discrete solution vector and continuous position of the search agents. Figure 1 presents an example subset of a solution having eight features dataset. In this "1" signifies the selected features, and "0" signifies not selected features.

0	1	1	0	0	0	1	1
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Figure 1. An example solution subset

### Algorithm 2. Proposed discrete salp swarm algorithm with weights and Lévy flight

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Initialize the parameters: Total number of salps, Max. Iterations, weight, Lévy flight
position of salp and best fitness. Initialize the salps positions A ( $i = 1, 2, \dots, n$ )
While ( $Fes < MaxFes$ )
  Update the values of  $c_1, c_2, c_3$  and weight ( $w$ )
  Determine the fitness value of each salp
   $F = \text{best salp}$  ((search-agent))
  Update the value of  $r_1$  parameter using (2)
  For every salp (A)
    If ( $i == 1$ )
      Update leader position using (16)
    Else
      Update follower position using (18)
    end if
    Update the position of the  $Fes$ 
  End for
  Reposition the salp which go out search space
  Calculate the fitness of each salp and store the
  best salp as  $F$ ,  $Fes = Fes + 1$ 
End while
return  $F$ 

```

The weights and Lévy flights are embedded in the original SSA to propose DWLSSA algorithm. Based on embedding, updating of positions of the leader and follower salps is done using (16)–(18).

$$A_i^1 = \begin{cases} FD_i + (w \times r_1)((u_i - l_i) \times r_2 + l_i) & r_3 \geq 0 \\ FD_i - (w \times r_1)((u_i - l_i) \times r_2 + l_i) & r_3 < 0 \end{cases} \quad (16)$$

$$A_i^1 = A_i^1 + \text{stepsize}_i \quad (17)$$

$$A_i^1 = \frac{1}{5}(A_i^1 + A_i^{i-1} + \text{Levy}(x)) \quad (18)$$

### 3.6. Fitness function

The problem in this research has two objectives to be satisfied. These two objectives are maximizing accuracy and minimizing features. Here, The SVM classifier is used for predicting the Parkinson's after getting the minimal subset of the features by the DWLSSA. So, prediction accuracy of SVM will act as the fitness function to assess the performance of search agents. The fitness function ( $FF$ ) used is given in (19).

$$FF = \alpha \times \text{err} - \text{rate}(E) + \beta \left( \frac{|FS|}{|TF|} \right) \quad (19)$$

Where  $|FS|$  is reduction in features and  $|TF|$  is total number of features respectively. The constants  $\alpha$  and  $\beta$  are controlling parameters having values [ $\alpha = [0, 1]$  and  $\beta = 0.8$ ]. The error rate is represented by  $E$ .

**4. RESULTS AND DISCUSSION**

**4.1. Dataset**

The experiments have been performed using the speech PD dataset available in the UCI library [33], [34]. The dataset consists of voice data of 31 individuals. Out of 31 individuals, 23 individuals were detected with Parkinson's disease (PD). This dataset has 195 voice instances (48 = Healthy, 147 = Patients). The age of individuals ranged between 46 to 85 years. The speech PD stores on an average six phonations of the vowel letters ("a" & "o"). The length of each phonation is 36 seconds. The dataset does not contain any missing values. All features in the dataset were real values. Table 1 describes the features of the dataset.

Table 1. The description of the features of speech PD dataset

Features	Description	Features	Description
MDVP:Fo(Hz)	Average vocal fundamental frequency	MDVP:RAP	---
MDVP:Fhi(Hz)	Maximum vocal fundamental frequency	MDVP:PPQ	---
MDVP:Flo(Hz)	Minimum vocal fundamental frequency	Jitter:DDP	----
MDVP: Jitter (%)	Several measures of variation in fundamental frequency	Shimmer:APQ3	--
MDVP:Jitter(Abs)		Shimmer:APQ5	---
MDVP:Shimmer	Several measures of variation in amplitude	MDVP:APQ	---
NHR	Two measures of ratio of noise to tonal components in the voice	Shimmer:DDA	---
HNR		MDVP:Shimer	---
RPDE	Two nonlinear dynamical complexity	PPE	---
DFA	Signal fractal scaling exponent	MDVP:RAP	--
Spread1	Three nonlinear measures of fundamental	Class Label	(1) Parkinson's (2) healthy
Spread2	Frequency variation		

**4.2. Evaluation measures**

The performance of the proposed DWLSSA is assessed using the measurements provided by [35]–[37], including Spec, Sens, Acc, Prec, F-measure (FM), and geometric mean (GM). The above-mentioned measures are defined using rules such as true positive (TP): number of Parkinson's patients correctly classified, true negative (TN): number of non-patients Parkinson's correctly classified, false positive (FP): number of patients incorrectly classified as Parkinson patients, and false negative (FN): number of incorrectly classified non-Parkinson patients. Equations (20)–(25) are used to define all evaluation measures based on the above rules.

$$Accuracy (Acc) = \frac{TP+TN}{TP+FN+FP+FN} \times 100\% \tag{20}$$

$$Sensitivity(Sens) = \frac{TP}{TP+FN} \times 100\% \tag{21}$$

$$Specificity (Spec) = \frac{TN}{TN+FP} \times 100\% \tag{22}$$

$$Precision (prec) = \frac{TP}{TP+FP} \times 100\% \tag{23}$$

$$G - mean (GM) = \sqrt{Sensitivity \times Specificity} \tag{24}$$

$$F - measure (FM) = \frac{(\beta_2 + 1) \times Prec \times Sens}{\beta_2 \times Prec + Sens} \tag{25}$$

**4.3. Discussion**

We implemented proposed DWLSSA with a Core i3, 8-GB RAM computer system using MATLAB 15a. The algorithm is executed several times for the Parkinson's dataset using a random population. The results are compared with BCS [18], BGWO [19], CALO [20], GA [21], WOA [22], PSO [38], FFA [39], BMVO [40], SSPA [41], RBMFO [42], and MAKHA [43]. Table 2 and Figure 2 illustrate the detailed classification of results in terms of all evaluation measures used. The results clearly prove DWLSSA better than the algorithms used in comparison.

Table 2. Comparison of the results (measures)

Algorithm	Acc (%)	Sens (%)	Spec (%)	Prec (%)	GM (%)	FM (%)
PSO	95.7	96.8	95.5	96.0	96.2	96.4
GA	93.8	94.3	94.5	95.9	94.4	95.1
FFA	96.3	97.0	96.6	97.0	96.8	96.8
BGWO	97.4	98.0	96.6	98.2	97.3	98.1
DWLSSA	98.7	98.1	97.3	99.3	97.7	98.7
BCS	68.0	69.3	70.2	70.5	69.7	69.9
BMVO	96.1	95.8	96.7	96.9	96.3	96.4
SSPA	80.9	81.9	82.2	83.1	82.1	82.5
RBMFO	89.5	91.2	90.9	91.8	91.1	91.5
WOA	93.1	94.1	94.6	94.9	94.4	94.5
CALO	82.4	83.6	83.9	84.2	83.8	83.9
MAKHA	78.0	79.1	79.8	79.9	79.5	79.5

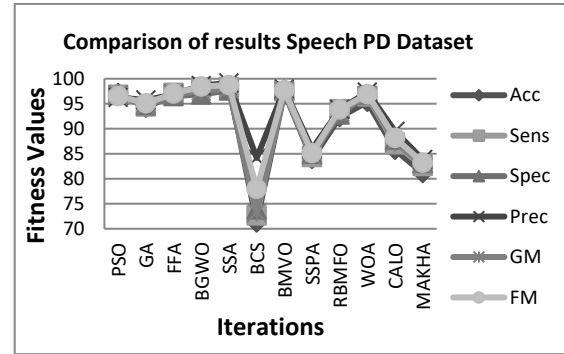


Figure 2. Comparison of results attained using speech PD dataset

## 5. CONCLUSION

This research proposes an enhanced salp swarm algorithm (DWLSSA) to predict Parkinson's disease. The DWLSSA works in two stages. In the first stage, DWLSSA performs the task of extracting the most useful features from the Parkinson's dataset. Support vector machine (SVM) performs the task of prediction using the features extracted in the first stage. The proposed DWLSSA is compared against well-known algorithms like BCS, BGWO, CALO, GA, WOA, PSO, FFA, BMVO, SSPA, RBMFO, and MAKHA applied for feature selection to diagnose Parkinson's disease. The results have demonstrated that the DWLSSA algorithm produces the best quality solution in acceptable time. Also, the SVM produces a very good classification and prediction results.

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