MDPI

Article

Constructing artificial features with Grammatical Evolution for the motor symptoms of Parkinson's Disease

Aimilios Psathas[1], Ioannis G. Tsoulos[2,*], Nikolaos Giannakeas[3], Alexandros Tzallas[4] and Vasileios Charilogis[5]

[1] Department of Informatics and Telecommunications, University of Ioannina, Greece;pint00141@uoi.gr
[2] Department of Informatics and Telecommunications, University of Ioannina, Greece; itsoulos@uoi.gr
[3] Department of Informatics and Telecommunications, University of Ioannina, Greece; giannakeas@uoi.gr
[4] Department of Informatics and Telecommunications, University of Ioannina, Greece; tzallas@uoi.gr
[5] Department of Informatics and Telecommunications, University of Ioannina, Greece; v.charilog@uoi.gr
* Correspondence: itsoulos@uoi.gr

Abstract: This study introduces a set of features designed to capture the motor symptoms of Parkinson's Disease (PD) through detailed motion analysis, with a specific focus on how these symptoms change before and after medication. The features reflect key aspects of patient movement, such as tremor intensity, slowness, rigidity, instability, and irregularity in motion patterns. By quantifying how consistently and smoothly a patient performs specific tasks, the features provide insight into motor control quality and neurological function. Crucially, they are labeled according to the patient's state—before and after receiving medication—allowing for a clear comparison of treatment effects. This enables not only objective tracking of symptom severity, but also evaluation of medication responsiveness. These features address a fundamental clinical need: moving beyond subjective observation toward continuous, data-driven monitoring of disease progression and therapeutic effectiveness in Parkinson's Disease. In the current work the impact of feature construction using Grammatical Evolution on previously mentioned features in evaluated. We compare traditional neural architectures (MLP with ADAM, MLP with Genetic Algorithm, and RBF networks) against models trained on artificially constructed features. The results demonstrate a substantial reduction in classification error when 2 to 5 constructed features are used, achieving the lowest error rate (14.33%) with four generated features (FC4GEN), compared to 38.65% for the best baseline model (RBF). These findings highlight the effectiveness of evolutionary feature construction in enhancing classification accuracy.

Keywords: Machine learning; Evolutionary algorithms; Genetic Programming; Grammatical Evolution

Received:
Revised:
Accepted:
Published:

Citation: Psathas, A.; Tsoulos, I.G.; Tzallas, A.; Charilogis, V. . Constructing artificial features with Grammatical Evolution for the motor symptoms of Parkinson's Disease. *Journal Not Specified* **2025**, *1*, 0. https://doi.org/

1. Introduction

Global health systems face a significant and growing challenge in the form of neurodegenerative diseases. These conditions cause severe motor and cognitive impairment and are characterized by a progressive disruption of the structure and function of neurons. As the world's population ages, neurodegenerative diseases like Parkinson's and Alzheimer's disease are becoming more common. These conditions have a significant negative impact on patients' quality of life and are becoming more and more expensive. Innovative methods of early detection, assessment, and treatment are required for these difficult disorders.

A common neurodegenerative disease that primarily affects the motor system is Parkinson's disease (PD). Tremor, bradykinesia (slow movement), rigidity, and postural instability are classic clinical presentations. Non-motor symptoms like mood disorders, sleep disorders, and cognitive impairment are frequently present as well. Since there are

no particular biological tests that can result in an early diagnosis, PD diagnosis primarily depends on clinical evaluation, despite the fact that the condition's symptom profile is complex. As a result, slow symptom progression leads to misdiagnosis or delay, which leads to ineffective treatment, poor patient outcomes, and a lower quality of life [1].

The early detection and monitoring of Parkinson's disease (PD) could be greatly aided by recent technological advancements, particularly in the fields of machine learning (ML) and the internet of things (IoT). IoT sensors such as smartwatches, wearable health monitors, and others allow continuous and non-intrusive monitoring of motor activities, tremor frequencies, and gait abnormalities in real-time. These tools enable an evaluation of a patient's health while they are engaging in their regular activities and continue to gather large amounts of data outside of the typical clinical settings. One can more accurately identify early indicators of Parkinson's disease and enable early interventions by using machine learning techniques on this data [2,3]. For example, ML algorithms can analyze speech patterns, motor skills, and other non-motor symptoms and differentiate subtle patterns that could foretell the full-blown expression of the disease.

The pursuit of accurate, quantitative, and real-time measurement of Parkinson's disease (PD) motor symptoms has been the prime interest of computational neurology. It is rich in the current state-of-the-art research that utilizes diverse sensor modalities and machine learning (ML) methodologies. Pioneering work has validated the potential of smartphone sensor-derived composite scores, like the mobile Parkinson Disease Score (mPDS), that highly correlate to the conventional standards, such as the MDS-UPDRS, and that are capable of tracking intraday symptom variation as well as response to therapy [4]. In the same line, smartphone-enabled active tests as well as passive monitoring during clinical trial protocols have been shown to be realistic, reliable, and highly sensible, usually uncovering abnormalities even among those patients rated as normal on specific items of the UPDRS during the clinic evaluation [5].

In addition to smartphones, specific PD symptoms have been targeted with special-purpose sensors. Quantification of bradykinesia, the PD hallmark, has been achieved successfully with gyrosensors during tapping tests, demonstrating strong correlations with clinical ratings [6]. Tremor measurement has been automated with body-worn accelerometers combined with Hidden Markov Models, classifying tremor type and severity reliably [7]. Moreover, inertial sensors have been used to detect and classify complex gait disorders such as Freezing of Gait (FOG) reliably [8]. Even speech has been targeted in the remote monitoring paradigm, where off-the-shelf speech tests analyzed with signal analysis combined with regression models are capable of tracking PD progression with clinically helpful accuracy [9]. Notably, incorporation of the resulting objective measures into standard care has been shown to improve significantly the resulting clinical outcomes, including the UPDRS as well as quality-of-life scores [10]. Latest advances still investigate the integration of sensor data and advanced ML. Research has looked into the integration of speech signals along with ensemble classifiers such as AdaBoost [11] as well as the processing of gait as well as tremor data obtained from off-the-shelf wearable devices. Still missing, though, is an integrative, high-fidelity method for tracking the subtle kinematics of hand movement, a key domain for the measurement of bradykinesia as well as tremor—beyond controlled smartphone tasks.

This work contributes to this vibrant body of research through the proposal of a unifying methodology grounded in a bespoke SmartGlove system that would allow in-depth analysis of hand movement. Our contribution is tripartite:

- Innovation and pilot use of the SmartGlove, a sensor- rich tool to capture high-accuracy, multi-parameter kinematic output of the hand.

- Construction of a holistic, multiple-component feature selection framework that goes beyond single technologies by integrating statistical significance (t-tests), ensemble learning (Random Forest), and analysis of variance (PCA) to pick the most discriminating, non-redundant biomarkers.
- The recognition of essential attributes—especially non-linear dynamics and spectral traits—that are notably proficient in differentiating motor states in Parkinson's Disease patients both prior to and following medication, offers an enhanced array of digital biomarkers for prospective diagnostic and monitoring applications.
- **(EDO PREPEI NA MPEI GRAMMATICAL EVOLUTION)**

By emphasizing the rich data space of hand kinematics and adopting a rigorous, multi-faceted analytical framework, this research hopes to improve the accuracy and completeness of objective PD evaluation. Briefly stated, the key innovation of this work lies in the combination of a specially crafted data-capture device with an upper-level analytical framework. Contrast this with previous work, which has employed repurposed consumer devices or targeted a very limited set of symptoms, and our specially developed SmartGlove presents a previously unmatched, high-fidelity view of hand motion's rich kinematics. Coupled with our multi-modal feature choice methodology, this system doesn't merely replicate clinical scores but uncovers a novel class of physiologically enlightening biomarkers—specifically in the non-linear dynamic range—that are hidden under conventional analysis. This end-to-end machine learning model is a significant advancement toward precise, data-based neurology from correlation against clinical scales to the detection of underlying digital biomarkers for Parkinson's disease.

The remainder of this paper follows this organization: Section 2 outlines the materials and methods utilized with a detailed description of the system architecture of the SmartGlove system, the process of data acquisition related to individual exercises of the hands, and the overall feature extraction process. Section 3 details the multi-faceted feature choice strategy and the composite scoring system used to determine the best biomarkers. Finally, Section 4 discusses implications of the research results, points out limitations of the study, and suggests directions of future research.

2. Materials and Methods

2.1. Preliminaries

Grammatical Evolution procedure can be considered as a genetic algorithm, where the chromosomes are sets of randomly chosen integers. These integers represent production rules of the provided BNF grammar [12]. BNF grammars are usually expressed as sets having the form $G = (N, T, S, P)$, where

- The set N contains the non-terminal symbols of the grammar.
- The set T includes the terminal symbols of the grammar.
- S denotes the start symbol of the grammar, with $S \in N$.
- P is the set of production rules of the grammar.

The Grammatical Evolution procedure utilizes an extended version of the initial BNF grammar by adding enumeration in the the production rules. As an example of an extended BNF grammar consider the grammar shown in Figure 1. The notation < > is used to enclose the non - terminal symbols of the grammar. The value d denotes the dimension of the input data. The Grammatical Evolution procedure starts from the start symbol of the program and gradually it creates valid programs in the underlying language, using the production rules of the grammar. The general scheme of the production procedure has as follows:

- **Get** the next element V from the chromosome that is under processing.

Figure 1. An example of an extended BNF grammar.

```
S::=<expr>   (0)
<expr> ::=  (<expr> <op> <expr>)  (0)
          | <func> ( <expr> )    (1)
          |<terminal>            (2)
<op> ::=     +      (0)
          | -       (1)
          | *       (2)
          | /       (3)
<func> ::=   sin  (0)
          | cos  (1)
          |exp   (2)
          |log   (3)
<terminal>::=<xlist>                (0)
          |<dlist>.<dlist> (1)
<xlist>::=x1    (0)
          | x2 (1)
          .........
          | xd (d-1)
<dlist>::=<digit>                  (0)
          | <digit><digit>            (1)
          | <digit><digit><digit>     (2)
<digit>  ::= 0 (0)
          | 1 (1)
          | 2 (2)
          | 3 (3)
          | 4 (4)
          | 5 (5)
          | 6 (6)
          | 7 (7)
          | 8 (8)
          | 9 (9)
```

- **Select** the next rule using the equation Rule = V mod NR. The symbol NR denotes the number of production rules for the under processing non – terminal symbol.

A full working example of the production procedure is the chromosome

$$x = [9, 8, 6, 4, 16, 10, 17, 23, 8, 14]$$

with $d = 3$. After a series of steps, the function $f(x) = x_2 + \cos(x_3)$ is produced for the grammar of Figure 1. The production steps are shown in Table 1.

2.2. The feature construction method

The technique of feature construction produces artificial features for classification or regression problems as non - linear transformations of the original ones. The new features are evaluated using a machine learning technique, such as artificial neural networks [14,15] or a Radial Basis Function (RBF) networks [27,28]. This method was presented initially in [16]. Also, this method was used in many areas, such as Spam Identification [17], Fetal heart classification [18], signal processing [19,20] etc. The process has the following steps:

1. **Initialization** step.
   (a) **Obtain** the train data for the current problem. The train data have M pairs (x_i, t_i), $i = 1..M$. The dimension of each vector x_i is d**.** The values t_i are the expected outputs for each pattern.

Table 1. A series of production steps for the example chromosome.

String	Chromosome	Operation
<expr>	9,8,6,4,16,10,17,23,8,14	9 mod 3 = 0
(<expr><op><expr>)	8,6,4,16,10,17,23,8,14	8 mod 3 = 2
(<terminal><op><expr>)	6,4,16,10,17,23,8,14	6 mod 2 = 0
(<xlist><op><expr>)	4,16,10,17,23,8,14	4 mod 3 = 1
(x2<op><expr>)	16,10,17,23,8,14	16 mod 4 = 0
(x2+<expr>)	10,17,23,8,14	10 mod 3 = 1
(x2+<func>(<expr>))	17,23,8,14	17 mod 4 = 1
(x2+cos(<expr>))	23,8,14	23 mod 2 = 2
(x2+cos(<terminal>))	8,14	8 mod 2 = 0
(x2+cos(<xlist>))	14	14 mod 3 = 2
(x2+cos(x3))		

(b) **Define** the parameters of the genetic algorithm: N_g stands for the the number of allowed generations, N_c represents the number chromosomes, p_s defines the selection rate and p_m the mutation rate.

(c) **Set** as N_f the number of features that will construct the Grammatical Evolution procedure.

(d) **Initialize** the chromosomes in the population. Each chromosome is considered as a set of randomly chosen positive integers.

(e) **Set** $k = 1$, as the generation counter.

2. **Genetic step**

(a) **For** $i = 1, \ldots, N_c$ **do**

i. **Produce** using the Grammatical Evolution procedure a set of N_f artificial features for the corresponding chromosome g_i. These features are produced using the grammar of Figure 1.

ii. **Transform** the original dataset using the previously constructed features. The new training set is denoted as $(x_{g_i,j}, t_j)$, $j = 1, ..M$

iii. **Train** a machine learning model denoted as C using the new training set. The fitness f_i for the corresponding chromosome is defined as:

$$f_i = \sum_{j=1}^{M} \left(C\left(x_{g_i,j}\right) - t_j\right)^2 \tag{1}$$

In the proposed method the RBF network is used as the machine learning model, since the time required for its training is significantly lower than other models, such as neural networks.

iv. **Perform** the selection procedure. During this procedure the chromosomes are firstly sorted according to their fitness values and the best $(1 - p_s) \times N_C$ of them are copied intact to the next generation. The rest of the chromosomes will be substituted by new chromosomes produced during the procedures of crossover and mutation.

v. **Perform** the crossover procedure. During this procedure $p_s \times N_c$ new chromosomes are produced. For every pair of $(\tilde{z}, \tilde{w})$ of new chromosomes, two two distinct chromosomes (z, w) are selected from the current population. The selection is performed using the tournament selection. The new chromosomes are produced from the old ones using the one - point crossover procedure, which is graphically outlined in Figure 2.

vi. **(OK)Perform** the mutation procedure: for each each element of each chromosome, a random number $r \in [0, 1]$ is selected. The underlying element is altered randomly when $r \leq p_m$.

(b) **EndFor**

3. **Set** $k = k + 1$
4. **If** $k \leq N_G$ goto **Genetic** Step, else terminate the process and obtain the best chromosome g^* with the lowest fitness value.
5. **Transform** the corresponding test set, using the N_f features obtained for chromosome g^*.
6. **Apply** a machine learning model to the constructed test set and report the associated test error..

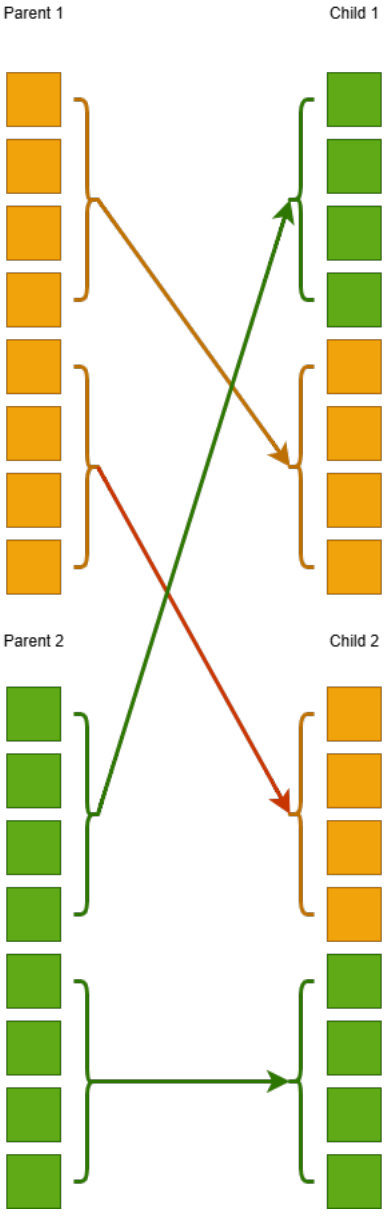

Figure 2. One point crossover method, used in the Grammatical Evolution procedure.

2.3. SmartGlove System and Sources of Data

The system of interest here as a primary data source is the SmartGlove system, a specially developed wearable system that has been created with the intent of telemonitoring

motor symptoms of PD patients. It has been created with the support of the Operational Program of the Epirus Region 2014-2020 and ESPA 2014-2020 with a view of increasing innovative health and biotechnology solutions. The system of SmartGlove has three primary subsystems:

1. Textile Glove: Made of durable, biocompatible materials, the glove has conductive areas on the palm and fingers that aid movement recognition. It is sweat-resistant and can be washed. It is also expected to last longer than 10 years.
2. System on Chip (SoC): The central processing unit encompasses a low-energy microcontroller that incorporates a Bluetooth 5.0 module, facilitating wireless data communication while utilizing minimal energy resources (with a typical operational range of 10-100 meters, contingent upon the surrounding environment).
3. Sensors: The glove contains a multi-modal sensor suite:
4. Flex sensors to measure finger bending.
5. Contact sensors to detect finger-to-palm interaction.
6. A 9-axis Inertial Measurement Unit (IMU), composed of a 3-axis accelerometer, 3-axis gyroscope, and 3-axis magnetometer, to identify hands' orientation and movement. IMU has outputs of up to a sampling rate of 100 Hz and a resolution of 16 bits.

The system is supplemented with a power management circuitry developed for lithium-polymer batteries, as well as with flash memory used for transient storage of data. The SmartGlove complies with the IEC 60601-1 medical electrical apparatus safety standard, thus ensuring reliability for medical applications. The SmartGlove sends data via Bluetooth to the mobPark mobile app supporting Android 6.0+ as well as iOS 11+. The app acts as an intermediary providing the possibility of managing the profile of the users, providing screen-level cues of exercises, as well as capturing sensor data at a sampling rate of 100 Hz. Then the captured data gets securely sent via an encrypted HTTPS connection to a centralized cloud platform like AWS or Azure for storage, processing, and analyzing purposes with a consideration of the General Data Protection Regulation (GDPR).

2.4. Data Collection Exercises

Data recording was at a sampling rate of 100 Hz, selected to efficiently capture tremor frequencies from 4 to 6 Hz and also captures bradykinesia. Measurements were obtained before and after medication administration (i.e., Levodopa) as a means of investigating therapeutic action. Four carefully designed motor tasks were incorporated into the experiment as described next:

- Exercise 1 (**Postural Stability**): Patient sits with their hands resting on their legs with palms facing upwards and counts from 1 to 10. It checks postural stability and resting tremor.
- Exercise 2 (**Coordination**): The patient stands with their hands at shoulder height and counts to ten while attempting to touch their index fingers together. It is intended to assess tremor and coordination when standing for a long time.
- Exercise 3 (**Finger Tapping Speed**): With their palm flat, the participant taps their index finger back and forth against their thumb, then quickly returns to the starting position ten times. It is a traditional metric used to evaluate bradykinesia and motor speed.
- Exercise 4 (**Hand Speed of Closing and Opening**): For ten repetitions, the patient continuously makes a fist with an open palm and returns to an open position as quickly as they can. It checks for bradykinesia and hand rigidity.

2.5. Feature extraction

Numerous features were taken from the raw sensor data (accelerometer, gyroscope, magnetometer) for each exercise in order to quantitatively describe the motor symptoms of Parkinson's disease. These features were computed using 50% overlap (50 samples, 0.5 seconds) and sliding windows of 100 samples (1 second). These features extracted are as follows:

- Statistical Properties: These characteristics provide a succinct explanation of the signal's variation and distribution. The following properties were calculated: Skewness, Kurtosis, Quartile Deviation, Mean, Standard Deviation, Variance, Minimum, Maximum, Range, Median, and Interquartile Range (IQR).
- Energy Characteristics: These metrics assess the signal's intensity and degree of activity. Signal Magnitude Area (SMA), Root Mean Square (RMS), Total Energy, and Logarithmic Energy are among the features that were extracted.
- Frequency-Domain Features: These are essential for detecting tremors and take into account the signal's spectral characteristics. Included are the following features: Dominant Frequency, Spectral Flatness, Spectral Flux, Spectral Variability, Spectral Entropy, Spectral Centroid, Spectral Spread, and Spectral Roll-on(85%).
- Dynamic and Nonlinear Features: These characteristics specify the signal's temporal fluctuations, complexity, and predictability. The following characteristics are taken into consideration: Mean Absolute Deviation (MAD), Root Mean Square of Successive Differences (RMSSD), Higuchi Fractal Dimension, Lyapunov Exponent, and Sample Entropy.

Since each feature includes specific aspects of motor impairment typical of the disease, such as tremor regularity, movement amplitude, and signal complexity, the selection of features was driven by a large body of literature on PD analysis. The characteristics for Movement Analysis in Parkinson's Disease are outlined in Table 2.

Table 2. Table of Characteristics for Movement Analysis in Parkinson's Disease.

Category	Characteristics	Purpose	Clinical Significance
Central Tendency	Mean, Median	Median Measures the central value of the signal	Detection of bradykinesia (slowed movements)
Dispersion	Standard deviation, Variance, IQR, QD	Quantifies the spread of data	Identifies motion variability (e.g. gravity, tremor)
Range	Minimum/Maximum value, Range	Records extreme values	Assessment of range of motion reduction in patients with Parkinson's disease
Distribution Shape	Skewness, Kurtosis	Describes asymmetry/peakedness of distribution	Correlation with irregular motor patterns
Variability	Coefficient of Variation (CV), MAD, RMSSD	Normalized measures of dispersion	Variability differentiation before after the treatment
Energy	Total energy, Absolute Energy, RMS	Measures signal intensity	Correlation with hypokinesia (reduced motor energy)
Logarithmic Energy	Log Energy	Enhances subtle energy changes	Detection of small changes
Spectral	Spectral Entropy, Centroid	Analyzes frequency distribution	Localization of tremor and rhythmic abnormality
Roll-off	85% Roll-off	Frequency band where 85% of the power is concentrated	Characterization of tremor bandwidth
Dominant Frequency	Dominant Frequency	Identification of peak frequency	Detection of Parkinson's tremor (4-6Hz)
Spectral Shape	Flatness, Flux, Variability, Dispersion	Quantifies the stability of the spectrum	Unstable tremors vs. rhythmic movements
Dynamics	Lyapunov Exponent, Sampling Entropy	Evaluates the chaos/regularity of the system	Degeneration of motor control in Parkinson's
Fractal	Dimension Higuchi	Measures the complexity of the signal	Loss of fine motor control

2.6. Feature Selection Methodology

Feature selection is a critical step in developing accurate and interpretable machine learning (ML) models for Parkinson's disease (PD) detection. In this study, a multi-method scoring approach was applied to identify the most informative features that differentiate

between pre-medication and post-medication states. Instead of relying on a single method, three complementary techniques were employed, and their outputs were combined into a composite score.

2.6.1. Multi-Method Scoring Approach

For each feature, three independent scores were calculated:

- Statistical Significance (Paired T-Test): A paired T-Test was performed between pre- and post-medication measurements. The score was defined as:

$$\text{score}_{T_{\text{test}}} = -\log_{10}(p_{\text{value}} + \epsilon) \tag{2}$$

where ϵ prevents λ zero (DEN BGAZEI NOIMA!!!). A lower p_{value} corresponds to a higher score, indicating stronger statistical significance [21].
- **Model-Based Importance** (**Random Forest**): A Random Forest classifier was trained, and feature importance was derived from the mean decrease in Gini impurity across all trees in the ensemble [22]. The final outcome here is the score_{RF}.
- **Variance Contribution** (**PCA**): Principal Component Analysis (PCA) was applied, and the importance of each feature was computed as the sum of the absolute loadings across all principal components, reflecting its overall contribution to data variance [23]. The outcome of this method is $\text{score}_{\text{PCA}}$.

2.6.2. Composite Score Calculation

All three scores were normalized to the $[0, 1]$ range. A final composite score was then computed as a weighted average:

$$\text{Composite Score} = 0.4 \times \text{score}_{T_{\text{test}}} + 0.3 \times \text{score}_{RF} + 0.3 \times \text{score}_{\text{PCA}} \tag{3}$$

This weighting scheme prioritizes statistical significance while also incorporating insights from model-based learning and variance-based analysis.

2.6.3. Selection of best features

Features were ranked according to their composite score, and the top-performing ones were selected for subsequent model development. Representative high-ranking features includes:

- RMSSD from the gyroscope during Exercise 2 (score: 0.663),
- Lyapunov Exponent (score: 0.644),
- Higuchi Fractal Dimension (score: 0.612).

These selected features served as the foundation for later predictive modeling and analysis, aiming to capture the most relevant motor signal characteristics associated with PD symptoms [24,25]. In Table 3 the top 20 features are presented.

Table 3. Top 20 features scored

Exercise	Sensor	Feature Name	Composite Score
2	gyro	rmssd	0.663
2	gyro	lyapunov_exponent	0.644
2	gyro	higuchi_fractal_dimension	0.612
2	gyro	range	0.573
3	acce	higuchi_fractal_dimension	0.469
3	gyro	max	0.452
3	acce	lyapunov_exponent	0.437
2	gyro	spectral_rolloff	0.433
2	acce	sample_entropy	0.422
0	magn	lyapunov_exponent	0.406
0	magn	spectral_variability	0.399
0	magn	higuchi_fractal_dimension	0.399
0	magn	range	0.381
3	magn	rmssd	0.376
0	gyro	rmssd	0.375
2	gyro	std	0.373
3	acce	spectral_flux	0.367
1	gyro	lyapunov_exponent	0.365
1	gyro	rmssd	0.361
1	gyro	max	0.358

3. Results

The code used in the experiments was code in the C++ programming language and for the optimization methods the freely available Optimus programming tool was incorporated [26]. The experiments were conducted on machine with 128GB of ram, running the Debian Linux operating system. Each experiment was executed 30 times and the average classification error was measured and depicted in the related tables and graphs. Also, the 10 - fold cross validation technique was incorporated for the validation of the experimental results. The values for the parameters of the proposed method are depicted in Table 4.

Table 4. The values for the parameters for the current work.

PARAMETER	MEANING	VALUE
N_g	Number of maximum allowed generations.	500
N_c	Number of chromosomes	500
p_s	Selection rate	0.10
p_m	Mutation rate	0.05
H	Number of processing nodes for neural network	10

In the experimental tables the following notation is used:

1. The column DATASET represents the used dataset.
2. The column RBF stands for the application of an RBF neural network [27,28] with 10 processing nodes on the corresponding dataset.
3. The column GEN represents the application of a genetic algorithm [29] on the training process of a neural network with 10 processing nodes.
4. The column PCA stands for the application of the PCA method [30–32] to construct two artificial features from the original ones. Afterwards, a neural network with 10 processing nodes trained using the BFGS method is applied on the new datasets.

5. The column NNC stands for the application of a neural network constructed with Grammatical Evolution [33] on the corresponding dataset.
6. The column GENCLASS represents the usage of a method that constructs classification rules using Grammatical Evolution [34].
7. The column FC2 is used to represent the application of a genetic algorithm to train a neural network on the dataset produced by the construction of two artificial features using the feature construction method.
8. The column FC3 is used to represent the application of a genetic algorithm to train a neural network on the dataset produced by the construction of three artificial features using the feature construction method.
9. The column FC4 is used to represent the application of a genetic algorithm to train a neural network on the dataset produced by the construction of four artificial features using the feature construction method.
10. The row AVERAGE represents the average classification error for all datasets and the corresponding method.

Table 5. Experimental results for various exercises.

DATASET	RBF	GEN	PCA	NNC	GENCLASS	FC2	FC3	FC4
EXERCISE_0	40.86%	39.63%	44.70%	32.57%	25.52%	11.39%	11.06%	10.35%
EXERCISE 1	38.65%	47.61%	47.35%	42.07%	29.98%	20.16%	16.08%	14.84%
EXERCISE 2	37.57%	35.33%	40.46%	35.01%	31.34%	22.50%	19.78%	22.10%
EXERCISE 3	41.64%	39.17%	43.46%	35.88%	29.00%	19.79%	17.39%	19.91%

Table 6. Precision values.

DATASET	RBF	GEN	PCA	NNC	GENCLASS	FC2	FC3	FC4
EXERCISE_0	58.93%	60.30%	55.89%	67.34%	76.09%	88.51%	88.87%	89.82%
EXERCISE 1	61.99%	49.57%	58.12%	59.48%	71.27%	79.45%	83.66%	85.10%
EXERCISE 2	61.61%	72.58%	58.21%	64.62%	69.02%	77.78%	80.27%	78.01%
EXERCISE 3	58.33%	60.80%	56.63%	64.22%	71.52%	80.29%	82.88%	80.30%

Table 7. Recall values.

DATASET	RBF	GEN	PCA	NNC	GENCLASS	FC2	FC3	FC4
EXERCISE_0	58.84%	60.27%	55.85%	68.92%	74.99%	88.25%	88.49%	89.27%
EXERCISE 1	61.90%	76.55%	60.45%	62.56%	71.11%	79.74%	83.92%	85.42%
EXERCISE 2	62.55%	64.58%	58.94%	65.32%	67.42%	77.06%	80.14%	78.04%
EXERCISE 3	58.30%	60.76%	56.67%	65.19%	71.27%	80.12%	82.65%	80.21%

4. Conclusions

Author Contributions: Fo

Funding: This research has been financed by the European Union : Next Generation EU through the Program Greece 2.0 National Recovery and Resilience Plan , under the call RESEARCH – CREATE – INNOVATE, project name “iCREW: Intelligent small craft simulator for advanced crew training using Virtual Reality techniques" (project code:TAEDK-06195).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Jankovic, J., 2008. Parkinson’s disease: clinical features and diagnosis. J Neurol Neurosurg Psychiatry 79, 368.

2. Javaid, M., Haleem, A., Pratap Singh, R., Suman, R., Rab, S., 2022. Significance of machine learning in healthcare: Features, pillars and applications. International Journal of Intelligent Networks 3, 58–73.
3. C., Wang, J., Wang, S., Zhang, Y., 2024. A review of IoT applications in healthcare. Neurocomputing 565, 127017.
4. Zhan, A., Mohan, S., Tarolli, C., Schneider, R.B., Adams, J.L., Sharma, S., Elson, M.J., Spear, K.L., Glidden, A.M., Little, M.A., Terzis, A., Dorsey, E.R., Saria, S., 2018. Using Smartphones and Machine Learning to Quantify Parkinson Disease Severity: The Mobile Parkinson Disease Score. JAMA Neurology 75, 876–880.
5. Lipsmeier, F., Taylor, K.I., Kilchenmann, T., Wolf, D., Scotland, A., Schjodt-Eriksen, J., Cheng, W.Y., Fernandez-Garcia, I., Siebourg-Polster, J., Jin, L., Soto, J., Verselis, L., Boess, F., Koller, M., Grundman, M., Monsch, A.U., Postuma, R.B., Ghosh, A., Kremer, T., Czech, C., Gossens, C., Lindemann, M., 2018. Evaluation of smartphone-based testing to generate exploratory outcome measures in a phase 1 Parkinson's disease clinical trial. Movement Disorders 33, 1287–1297.
6. Kim, J.W., Lee, J.H., Kwon, Y., Kim, C.S., Eom, G.M., Koh, S.B., Kwon, D.Y., Park, K.W., 2011. Quantification of bradykinesia during clinical finger taps using a gyrosensor in patients with Parkinson's disease. Medical & Biological Engineering & Computing 49, 365–371.
7. Rigas, G., Gatsios, D., Fotiadis, D.I., Tsakanikas, V., Tsilikis, I., Konitsiotis, S., 2012. Assessment of Tremor Activity in the Parkinson's Disease Using a Set of Wearable Sensors. IEEE Transactions on Information Technology in Biomedicine 16, 478–487.
8. Djuric-Jovicic, M., Jovicic, N.S., Radovanovic, S.M., Stankovic, I.D., Popovic, M.B., Kostic, V.S., 2014. Automatic Identification and Classification of Freezing of Gait Episodes in Parkinson's Disease Patients. IEEE Transactions on Neural Systems and Rehabilitation Engineering 22, 685–694.
9. Tsanas, A., Little, M.A., McSharry, P.E., Ramig, L.O., 2010. Accurate telemonitoring of Parkinson's disease progression by noninvasive speech tests. IEEE Transactions on Biomedical Engineering 57, 884–893.
10. Farzanehfar, P., Woodrow, H., Braybrook, M., McGregor, S., Evans, A., Nicklason, F., Horne, M., 2018. Objective measurement in routine care of people with Parkinson's disease improves outcomes. NPJ Parkinson's Disease 4, 10.
11. Bukhari, S.N.H., Ogudo, K.A., 2024. Ensemble Machine Learning Approach for Parkinson's Disease Detection Using Speech Signals. Mathematics 12, 1575.
12. J. W. Backus. The Syntax and Semantics of the Proposed International Algebraic Language of the Zurich ACM-GAMM Conference. Proceedings of the International Conference on Information Processing, UNESCO, 1959, pp.125-132.
13. M. O'Neill, C. Ryan, Grammatical evolution, IEEE Trans. Evol. Comput. **5,**pp. 349–358, 2001.
14. C. Bishop, Neural Networks for Pattern Recognition, Oxford University Press, 1995.
15. G. Cybenko, Approximation by superpositions of a sigmoidal function, Mathematics of Control Signals and Systems **2**, pp. 303-314, 1989.
16. Dimitris Gavrilis, Ioannis G. Tsoulos, Evangelos Dermatas, Selecting and constructing features using grammatical evolution, Pattern Recognition Letters **29**,pp. 1358-1365, 2008.
17. Dimitris Gavrilis, Ioannis G. Tsoulos, Evangelos Dermatas, Neural Recognition and Genetic Features Selection for Robust Detection of E-Mail Spam, Advances in Artificial Intelligence Volume 3955 of the series Lecture Notes in Computer Science pp 498-501, 2006.
18. George Georgoulas, Dimitris Gavrilis, Ioannis G. Tsoulos, Chrysostomos Stylios, João Bernardes, Peter P. Groumpos, Novel approach for fetal heart rate classification introducing grammatical evolution, Biomedical Signal Processing and Control **2**,pp. 69-79, 2007
19. Otis Smart, Ioannis G. Tsoulos, Dimitris Gavrilis, George Georgoulas, Grammatical evolution for features of epileptic oscillations in clinical intracranial electroencephalograms, Expert Systems with Applications **38**, pp. 9991-9999, 2011
20. A. T. Tzallas, I. Tsoulos, M. G. Tsipouras, N. Giannakeas, I. Androulidakis and E. Zaitseva, Classification of EEG signals using feature creation produced by grammatical evolution, In: 24th Telecommunications Forum (TELFOR), pp. 1-4, 2016.
21. Tukey, J.W., 1977. Exploratory Data Analysis. Addison-Wesley.
22. Patel, S., Lorincz, K., Hughes, R., Huggins, N., Growdon, J., Standaert, D., Akay, M., Dy, J., Welsh, M., Bonato, P., 2009. Monitoring Motor Fluctuations in Patients With Parkinson's Disease Using Wearable Sensors. IEEE Trans. Inform. Technol. Biomed. 13, 864–873.
23. Guyon, I., Elisseeff, A., 2003. An Introduction to Variable and Feature Selection. Journal of Machine Learning Research 3, 1157–1182.
24. Goetz, C.G., Tilley, B.C., Shaftman, S.R., Stebbins, G.T., Fahn, S., Martinez-Martin, P., Poewe, W., Sampaio, C., Stern, M.B., Dodel, R., Dubois, B., Holloway, R., Jankovic, J., Kulisevsky, J., Lang, A.E., Lees, A., Leurgans, S., LeWitt, P.A., Nyenhuis, D., Olanow, C.W., Rascol, O., Schrag, A., Teresi, J.A., Van Hilten, J.J., LaPelle, N., 2008. Movement Disorder Society-sponsored revision of the Unified Parkinson's Disease Rating Scale (MDS-UPDRS): Scale presentation and clinimetric testing results. Movement Disorders 23, 2129–2170.
25. Chen, Z., Pang, M., Zhao, Z., Li, S., Miao, R., Zhang, Yifan, Feng, Xiaoyue, Feng, Xin, Zhang, Yexian, Duan, M., Huang, L., Zhou, F., 2020. Feature selection may improve deep neural networks for the bioinformatics problems. Bioinformatics 36, 1542–1552.
26. I.G. Tsoulos, V. Charilogis, G. Kyrou, V.N. Stavrou, A. Tzallas, Journal of Open Source Software **10**, 7584, 2025.

27. J. Park and I. W. Sandberg, Universal Approximation Using Radial-Basis-Function Networks, Neural Computation **3**, pp. 246-257, 1991.
28. G.A. Montazer, D. Giveki, M. Karami, H. Rastegar, Radial basis function neural networks: A review. Comput. Rev. J **1**, pp. 52-74, 2018.
29. Reynolds, J., Rezgui, Y., Kwan, A., & Piriou, S. (2018). A zone-level, building energy optimisation combining an artificial neural network, a genetic algorithm, and model predictive control. Energy, 151, 729-739.
30. Burcu Erkmen, Tülay Yıldırım, Improving classification performance of sonar targets by applying general regression neural network with PCA, Expert Systems with Applications **35**, pp. 472-475, 2008.
31. Jing Zhou, Aihuang Guo, Branko Celler, Steven Su, Fault detection and identification spanning multiple processes by integrating PCA with neural network, Applied Soft Computing **14**, pp. 4-11, 2014.
32. Ravi Kumar G., Nagamani K., Anjan Babu G., A Framework of Dimensionality Reduction Utilizing PCA for Neural Network Prediction. In: Borah S., Emilia Balas V., Polkowski Z. (eds) Advances in Data Science and Management. Lecture Notes on Data Engineering and Communications Technologies, vol 37. Springer, Singapore. 2020.
33. I.G. Tsoulos, D. Gavrilis, E. Glavas, Neural network construction and training using grammatical evolution, Neurocomputing **72**, pp. 269-277, 2008.
34. Nikolaos Anastasopoulos and Ioannis G. Tsoulos and Alexandros Tzallas, GenClass: A parallel tool for data classification based on Grammatical Evolution, SoftwareX, 16, 100830, 2021.