

Enhancing Arousal Level Detection in EEG Signals through Genetic Algorithm-based Feature Selection and Fast Bit Hopping

Abstract

Background: This study explores a novel approach to detecting arousal levels through the analysis of electroencephalography (EEG) signals. Leveraging the Faller database with data from 18 healthy participants, we employ a 64-channel EEG system. **Methods:** The approach we employ entails the extraction of ten frequency characteristics from every channel, culminating in a feature vector of 640 dimensions for each signal instance. To enhance classification accuracy, we employ a genetic algorithm for feature selection, treating it as a multiobjective optimization task. The approach utilizes fast bit hopping for efficiency, overcoming traditional bit-string limitations. A hybrid operator expedites algorithm convergence, and a solution selection strategy identifies the most suitable feature subset. **Results:** Experimental results demonstrate the method's effectiveness in detecting arousal levels across diverse states, with improvements in accuracy, sensitivity, and specificity. In scenario one, the proposed method achieves an average accuracy, sensitivity, and specificity of 93.11%, 98.37%, and 99.14%, respectively. In scenario two, the averages stand at 81.35%, 88.65%, and 84.64%. **Conclusions:** The obtained results indicate that the proposed method has a high capability of detecting arousal levels in different scenarios. In addition, the advantage of employing the proposed feature reduction method has been demonstrated.

Keywords: Arousal level, feature selection, genetic algorithms, machine learning

Submitted: 16-Dec-2023

Revised: 30-Mar-2024

Accepted: 12-Apr-2024

Published: 25-Jul-2024

Introduction

The recognition of arousal levels plays a pivotal role in enhancing human-machine interaction by enabling machines to emulate human emotional attributes more accurately. Arousal, a fundamental aspect of human emotional experience, significantly influences decision-making processes. It is mediated by the limbic system, which impacts brain signals, notably observable through electroencephalography (EEG) signals. Despite the advancements in EEG signal analysis for arousal recognition, challenges persist in achieving real-time detection and distinguishing real arousal from superficial expressions, such as those in lie detection scenarios.

Recent studies have primarily concentrated on two main avenues: traditional machine learning methods, which necessitate explicit feature selection (FS) and extraction, and deep learning approaches, which automate these procedures but

demand significant data and computational resources. Notably, methods such as linear and nonlinear estimation have been applied to categorize brain signals, with varying degrees of success in real-time application and accuracy in emotional state recognition, including stress, anxiety, and joy.^[1-6] Furthermore, novel approaches using deep belief networks and enhanced capsule network-based models have shown promising results in emotion classification through EEG signals, achieving high accuracy in distinguishing between positive, negative, and neutral emotions.^[7-13] Despite these advancements, a gap remains in effectively processing EEG signals for arousal detection in real-time applications, necessitating an exploration of new feature extraction and selection algorithms.

This study introduces a novel method that integrates frequency-based features with an advanced feature reduction technique to classify arousal levels from EEG signals efficiently. Our proposed method is designed to overcome the limitations

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How to cite this article: Sheikhian E, Ghoshuni M, Azarnoosh M, Khalilzadeh MM. Enhancing arousal level detection in EEG signals through genetic algorithm-based feature selection and fast bit hopping. *J Med Sign Sens* 2024;14:20.

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Access this article online

Website: www.jmssjournal.net

DOI: 10.4103/jmss.jmss_65_23

Quick Response Code:



of existing techniques by ensuring higher accuracy and real-time processing capabilities. We chose this approach based on preliminary findings suggesting that frequency-based features, when optimally reduced, could provide a more accurate and computationally efficient means of recognizing arousal states. This method stands to significantly improve real-time arousal detection, offering enhanced decision-making support, better environmental interaction for individuals, and facilitating precise therapeutic interventions. By focusing on the efficacy of new feature extraction and selection algorithms, this study aims to bridge the gap in real-time arousal detection, underscoring the potential of our approach over existing methodologies.

Materials and Methods

This section begins by presenting the database utilized in the study. Subsequently, it delineates the different phases of the proposed methodology, encompassing feature extraction, FS, and the classification function. A schematic representation of the proposed method is depicted in Figure 1.

Database

To examine the proposed method, we first introduce the dataset. Next, the devised approach is implemented on the dataset, and the resultant findings are showcased.

In this article, the Faller paper dataset has been used.^[14] The data related to this database consist of real-time EEG signals during arousal, which have been used to change the arousal of an individual from the rightward side of the Yerkes–Dodson curve to its leftward side toward the optimal performance state. Specifically, a brain–computer interface (BCI) has been used, which dynamically stores the electroencephalography (EEG) signal information. A boundary avoidance task refers to a sensorimotor operational pattern executed as an aerial navigation task within virtual reality, creating conditions where arousal is intensified and quickly leads to failure. The data have been recorded according to a BCI system, and the goal is to change the individual’s arousal level by reducing the target.

In total, 18 healthy participants (aged 19–33 years, all right-handed, 4 females) with natural or corrected-to-normal vision participated in this study. They were also familiarized with the virtual reality three-dimensional flight simulation platform through the control of virtual aircraft for a minimum of 60–120 min before the experiment, either on the same day of the experiment or the day before. Each subject has to move approximately once every 2 s during a box. A weighted sum of three sinusoids with various frequencies and amplitudes along the gait axis models the trajectory that the moving boxes create. The difficulty of the experiment is adjusted by reducing the size of the boxes at regular intervals (every 30 s) during each trial. Therefore, user-controlled flight during each trial (up to 90 s) can be divided into three distinct periods of the same box trajectory but with varying difficulties continuously adjusted. Figure 2 represents the trajectory and the size of the boxes.

During the protocol execution, various signals, such as the 64-channel brain signal (20–10) and cardiac systems, were recorded, and finally, the changes induced in the extracted features from the mentioned signals are presented in various graphs.

Data preprocessing

To create a suitable dataset for classification to detect arousal levels, the signal of each individual within a 2 s interval where the target is observed is considered the input signal, and the target size in this experiment is considered the label of the signal that in this paper, to address the issue of imbalanced classes (classes with limited data), only the signals related to targets 1 and 2 are considered. After aligning the data and removing irrelevant signals, 252 2-s signals (64 channels) are obtained, with 150 instances belonging to Class 1 and 102 instances belonging to Class 2, and considering that the sampling frequency of the brain signal is 256 Hz, the final signal $X = [x_1, x_2, \dots, x_{252}]$ has $252 \times 64 \times 512$ dimension and the signal of each X_i has 64×512 dimension and the final label vector has a dimension of 252×1 .

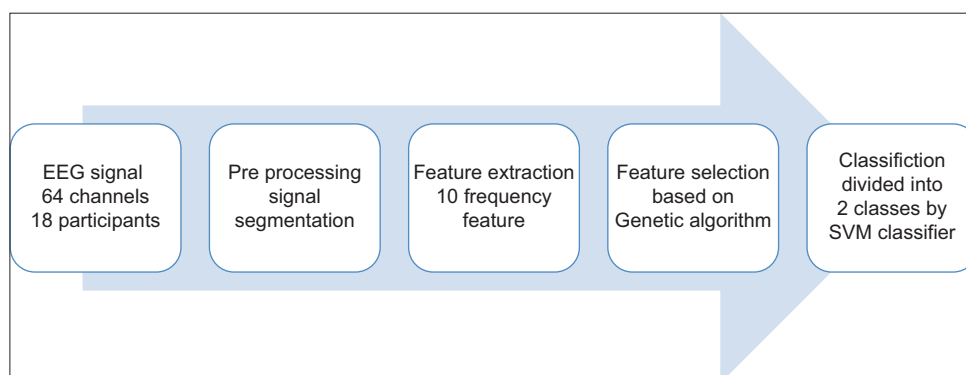


Figure 1: Diagram of proposed methodology. EEG – Electroencephalography, SVM – Support vector machine

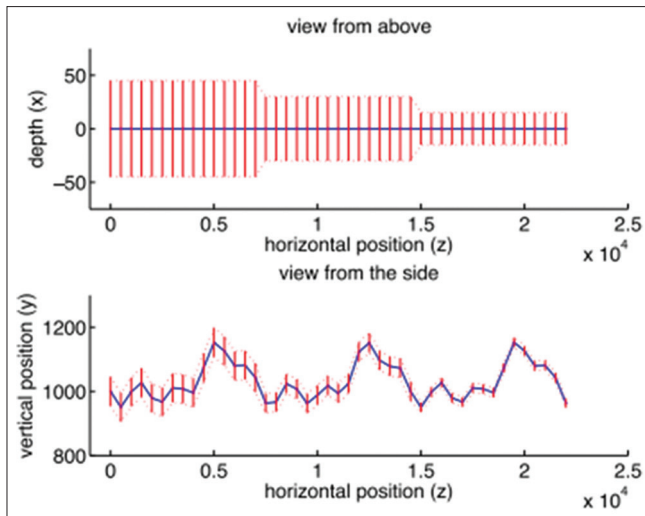


Figure 2: Recorded signal of virtual position as a function of horizontal position^[15]

Feature extraction

Selecting appropriate features is pivotal for optimizing the performance of any classification system. Various methods are available for pattern recognition in EEG signals, among which extracting features in the frequency domain is notably prominent. This approach is widely acknowledged for its effectiveness in discerning various brain activities. At this stage, the time domain signal is mapped to the feature domain. In this research, the frequency domain is utilized for feature extraction. Specifically, the spectral estimation of the signal for each instance and each channel is first computed using the Fourier transform. Subsequently, rhythmic activities are divided into different frequency bands. Based on frequency ranges, eight types of waves can be identified: delta (δ) (0.5–3 Hz), theta (θ) (4–7 Hz), alpha (α) (8–12 Hz), beta (β) (15–30 Hz), β_1 (7.5–12 Hz), β_2 (12.5–15.5 Hz), β_3 (16–31 Hz), and high β (32–100 Hz), which are written from low to high frequencies. In addition, two ratios, θ/α and θ/β , are considered two ratios that can represent useful features. Finally, 10 features are extracted from each signal, and considering the data being 64 channels, the resulting feature vector has a dimension of 640.

Feature selection

FS is a pivotal aspect of the proposed classification system, warranting special attention. To address this, we have employed a genetic algorithm (GA) to tackle the FS problem. Initially, we formulated the FS conundrum as a multiobjective optimization problem with three objectives. In this formulation, features contributing to enhanced classification accuracy are accorded a higher probability of survival. We have incorporated a rapid bit-string mutation technique, which eschews the constraints of traditional bit-string mutations, thereby bolstering efficiency.

Moreover, we have implemented both a mutation operator and a crossover operator to expedite convergence and

enhance overall performance. In addition, we have devised a solution selection strategy to identify the most suitable feature subset.

In the GA framework, each candidate solution for the problem, or chromosome, is encoded as a vector. In our approach, we utilize a binary bit-string to represent the chromosome, where “1” indicates FS and “0” denotes otherwise. To illustrate, considering a dataset D as an example, chromosome i in the population is encoded by a bit-string from D , as described in Eq. 1:^[16]

$$X_i(t) = (x_{i,1}, x_{i,2}, \dots, x_{i,j}) \quad (1)$$

$$x_{i,j} = \{0,1\}, j = 1, 2, \dots, D. i = 1, 2, \dots, N.$$

where $X_i(t)$ represents the i^{th} chromosome in the t^{th} generation, and N denotes the initial population.

Cost or fitness function

The fitness cost serves as a pivotal metric for assessing the performance of each sample or feature. To harness the benefits of both wrapper and filter approaches in FS, our cost function takes into account not only the classification error rate but also the distance metric. Moreover, we incorporate the ratio of selected features as the third objective to facilitate superior dimensionality reduction.

The formula of the cost function is shown in Eqs. 2 and 3:^[16,17]

$$f = D + E_{\text{Classifier}} + \alpha \quad (2)$$

$$\alpha = \frac{N_{\text{Selected feature vector}}}{N_{\text{All feature vector}}} \quad (3)$$

where α is the feature rate and is calculated from the number of features in the feature vector selected in each chromosome to the total number of extracted features. D is the distance metric, which section “The hybrid operator” describes this parameter. $E_{\text{Classifier}}$ is also the error rate obtained for classifying the train set with the feature vector selected in each chromosome.

The hybrid operator

GAs possess the capability to evade local optima through the utilization of crossover and mutation operators, thereby exploring a broad search space when selection pressure is aptly managed. However, their efficacy in fine-tuning near local optima is limited, often leading to prolonged running times. To enhance their fine-tuning capabilities, hybrid GAs (HGAs) have been developed across various applications, such as the traveling salesman problem, graph partitioning problem, and image compression.

In a HGA, chromosomes undergo refinement through appropriate local search operations. We introduce a HGA tailored for the FS problem. The fundamental concept

behind our HGA is to integrate problem-specific local search operations within a GA framework.^[18]

The objective function

The primary objective of the objective function is to minimize the classification error rate. In addition, we incorporate the distance metric as the second objective. The aim of the distance metric is twofold: to maximize the distance between samples from different classes (Db) and to minimize the distance between samples within the same class (Dw).

Eqs. 4-7 provide the objective function:^[16,17]

$$D = \frac{Dw}{Db} K, L=1,2 \quad (4)$$

$$Db = \frac{1}{L} \frac{1}{K} \sum_{l=1}^L \sum_{k=1}^K d_{l,k} \quad (5)$$

$$Dw = \frac{1}{K} \sum_{k=1}^K d_{k,k} \quad (6)$$

$$D_{a,b} = \frac{1}{N} \frac{1}{M} \sum_{i=1}^N \sum_{j=1}^M \|F_{a,i} - F_{b,j}\|^2 \quad (7)$$

where K and L are the number of the classes, and F is the feature vector selected in each chromosome. N and M are also the number of the samples in the class a or b, respectively. $\| \cdot \|$ is the Euclidean distance.

Fast bit mutation

In bit-string mutation, the algorithm randomly selects some genes with a mutation probability of P and alters their original values. When applied to FS, basic bit-string mutation gradually reduces the size of the feature set while maintaining a balanced ratio of selected features. Specifically, if the ratio of selected features is relatively low, most chromosomes encode zeros (0). Consequently, randomly selected genes are likely to be zeros, leading to an expansion in the feature set size through mutation. A slow pace of feature reduction results in a sluggish evolutionary or FS process.

Moreover, in our approach, we employ both regular crossover and uniform crossover. In uniform crossover, each gene in the offspring chromosomes is independently selected from either parent. Since no preference is given to either parent, roughly half of the genes in the offspring chromosomes originate from the first parent and the remainder from the second parent. Notably, the regular crossover operator yields two complementary offspring, yet in our method, only one is chosen.

By applying the proposed FS method from among 640 input features, those with more information are selected for classification. After the features are selected and normalized,

a classification function is used to separate the two classes. The classification process is based on initially dividing the data into two groups: training and testing. We used the leave-one-out (LOO) cross-validation for this experiment design. Therefore, the train and test sets depended on the employed LOO technique. After determining the training data and unknown coefficients, the classification function is determined using the training data, whose labels are also specified. In other words, the classification function is trained at this stage, and its parameters are specified for classifying the classes. After the classification function is determined, it is applied to the test data. In this stage, the unlabeled data are fed into the predetermined classification function, and the obtained labels from the classifier are compared with the actual labels to determine the accuracy of the function.

The classification function

Support vector machine (SVM) stands out as one of the prominent machine learning methods, introduced by Wapnick *et al.* in the 1990s. This method employs principles known as structural risk minimization (SRM) to minimize model error, contrasting with other methods such as artificial neural networks that utilize empirical risk minimization principles. Typically, SVMs are utilized for binary or multiclass classification and regression tasks. Essentially, SVMs approximate the regression function by utilizing a set of linear functions.

In constructing an SVM model, the user defines parameters C and ϵ . The parameter C serves as a regularization parameter, ranging from zero to infinity. Larger values of C imply that SVM does not tolerate errors in training data, leading to a complex model and reduced generalization ability. Conversely, as C approaches zero, the model can tolerate higher error levels, resulting in a simpler model. The parameter ϵ , also ranging from zero to infinity, plays a crucial role in determining support vectors and consequently the model's performance. While large values of ϵ reduce the number of support vectors (desirable), excessively widening the ϵ range is not advisable. Conversely, very small values of ϵ lead to selecting numerous support vectors, increasing the risk of overfitting.

The linear regression problem in SVM can be extended to nonlinear regression through the use of kernel functions, which map data to a feature space where linear regression can be applied. Various kernel functions, including polynomial kernels and radial basis function (RBF) kernels, have been introduced.

SVM is an efficient learning system rooted in the theory of constrained optimization, employing the principle of SRM to achieve a globally optimal solution. In SVM regression models, a smooth function approximates the dependent variable y , which is a function of multiple independent

x variables. Similar to other regression problems, the relationship between independent and dependent variables is assumed to be expressed by a linear function $f(x)$, along with some allowable error ϵ .^[19]

$$f(x) = w^T \cdot \phi(x) + b \tag{8}$$

(1) If W is the coefficient vector, b is the coefficient of the regression function, and ϕ is the kernel function, then the goal is to find a functional form for $f(x)$. This is achieved by training the SVM model with a set of samples (the training set). This process involves the successive optimization of the error function.

Performance criteria

To compare different methods with various features, it is necessary to first specify a set of criteria for comparison. To conduct a more detailed examination of the criteria, we first define a set of variables based on the confusion matrix.

- True negative (TN): The count of samples belonging to Class 1 that are correctly classified as Class 1
- False negative (FN): The count of samples belonging to Class 1 that are incorrectly classified as Class 2
- False positive (FP): The count of samples belonging to Class 2 that are incorrectly classified as Class 1
- True positive (TP): The count of samples belonging to Class 2 that are correctly classified as Class 2.

Using these variables, we have utilized the following criteria:

Accuracy = (TP + TN)/total, sensitivity = TP/(TP+FN), specificity = TN/(TN+FP).

Through the implementation of the suggested FS methodology, from an initial set of 640 input features, 100 features enriched with more significant information are identified for classification purposes using a GA. Following the selection and normalization of these

features, the SVM classification function is employed to differentiate between two classes, utilizing SVM with three distinct kernels: linear, RBF, and polynomial. The classifier operates on a foundational process where, initially, data are segregated into training and testing cohorts, and the validation is conducted using the LOO cross-validation technique.

Results

The presented results indicate the classification performance of the system for distinguishing between different levels of arousal (two levels). These results have been examined on EEG signals, and the experiments have been conducted in two ways. The first experiment is individual centric, meaning that the experiment is conducted independently for each individual, and the results are reported separately for each person. In this context, the performance of the proposed FS method has been evaluated and compared with other methods to assess its impact. In the second experiment, data from all individuals has been combined, and the data from 17 individuals are considered training data, whereas the remaining data from one individual are used as test data, and the final results are reported based on this setup. The results obtained from each of the experiments will be analyzed further.

Performing the experiment on each individual separately

In this case, all stages are carried out for each individual separately, independently of other individuals. The results of the LOO cross-validation obtained for each individual are presented in Tables 1-3. Figure 3 shows the LOO method used for validating each individual. As illustrated in the figure, during each step of the LOO cross-validation, a single sample is isolated for the test set, whereas the remaining samples constitute the training set. In this iterative process, a classifier is developed using the training set. Subsequently, the performance of the developed classifier is evaluated using the isolated test sample, as

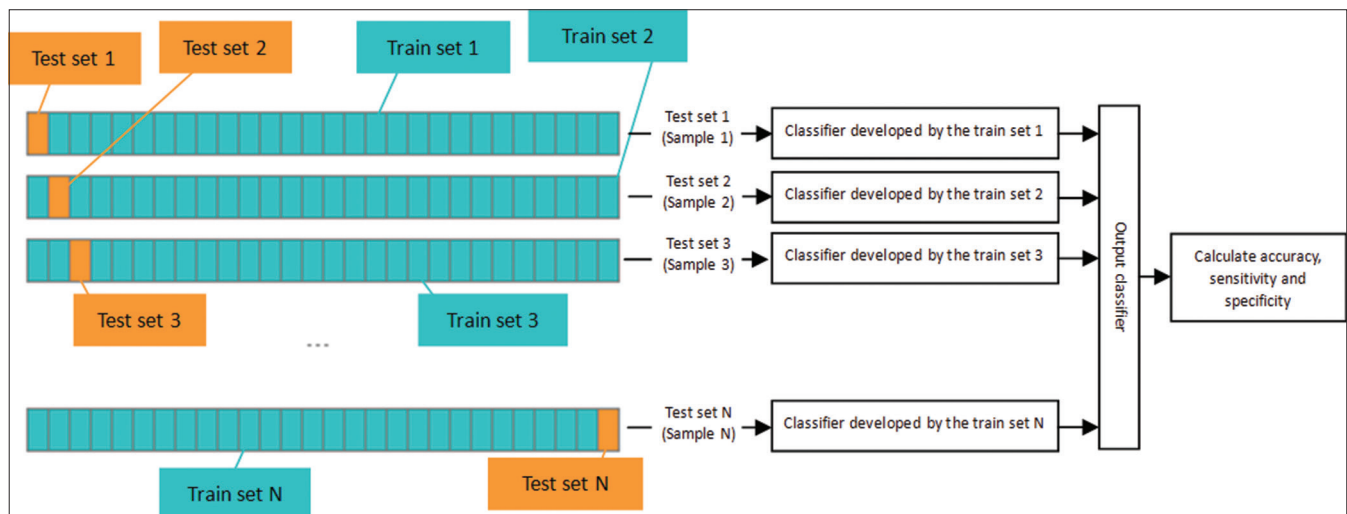


Figure 3: The leave-one-out method used for validating each individual

Table 1: The classification accuracy of the proposed method for 18 people and using 3 different kernels

Subjects	All features			Selected features		
	Linear SVM	Polynomial kernel	RBF kernel	Linear SVM	Polynomial kernel	RBF kernel
1	0.86	0.86	0.86	0.95	0.95	0.96
2	0.70	0.69	0.72	0.81	0.83	0.83
3	0.78	0.75	0.75	0.89	0.89	0.87
4	0.87	0.84	0.87	0.94	0.94	0.96
5	0.91	0.90	0.93	0.98	0.95	0.93
6	0.62	0.54	0.54	0.73	0.71	0.75
7	0.72	0.71	0.78	0.85	0.86	0.89
8	0.84	0.82	0.81	0.91	0.93	0.90
9	0.82	0.75	0.81	0.84	0.84	0.84
10	0.83	0.81	0.79	0.92	0.93	0.94
11	0.81	0.76	0.81	0.95	0.92	0.98
12	0.88	0.84	0.86	0.95	0.91	0.96
13	0.73	0.70	0.70	0.97	0.92	0.97
14	0.61	0.63	0.64	0.82	0.83	0.89
15	0.83	0.78	0.83	0.93	0.90	0.92
16	0.80	0.79	0.79	0.86	0.88	0.87
17	0.80	0.81	0.84	0.97	0.94	0.94
18	0.81	0.82	0.83	0.97	0.93	0.95
Average	0.79	0.77	0.79	0.92	0.91	0.93

SVM – Support vector machine; RBF – Radial basis function

Table 2: The classification sensitivity of the proposed method for 18 people and using 3 different kernels

Subjects	All features			Selected features		
	Linear SVM	Polynomial kernel	RBF kernel	Linear SVM	Polynomial kernel	RBF kernel
1	0.88	0.89	0.89	0.97	0.99	0.99
2	0.86	0.89	0.89	0.85	0.96	0.98
3	0.86	0.89	0.89	0.93	0.98	0.99
4	0.85	0.88	0.88	0.94	0.98	0.98
5	0.58	0.77	0.85	0.88	0.88	1
6	0.68	0.85	0.80	0.89	0.88	0.92
7	0.70	0.84	0.88	0.85	0.82	0.94
8	0.83	0.88	0.89	0.98	0.98	0.99
9	0.81	0.90	0.85	0.95	0.98	1
10	0.83	0.92	0.87	0.99	1	1
11	0.81	0.93	0.83	0.91	0.98	0.98
12	0.86	0.92	0.91	0.97	1	1
13	0.89	0.91	0.89	0.93	1	1
14	0.81	0.92	0.91	0.90	1	1
15	0.88	0.93	0.90	0.96	0.99	1
16	0.84	0.91	0.91	0.88	0.97	0.99
17	0.87	0.88	0.92	0.99	1	1
18	0.82	0.89	0.89	0.85	0.96	0.99
Average	0.87	0.85	0.86	0.92	0.95	0.98

SVM – Support vector machine; RBF – Radial basis function

depicted in Figure 3. This process is repeated for each sample in the dataset, allowing for a comprehensive assessment. Finally, accuracy, sensitivity, and specificity metrics are computed based on the results obtained from all steps of the LOO cross-validation.

In addition, the results are presented in two scenarios: using all features and using features extracted by the GA.

As evident from the obtained results, the efficacy of the proposed feature reduction method is markedly apparent.

Furthermore, the effectiveness of the proposed feature reduction approach has been assessed against three other FS methods, alongside a baseline approach where no FS is applied. The compared methods encompass FS based on principal component analysis, FS based on evolutionary

algorithms,^[20] and the nondominated sorting multiobjective organism search algorithm.^[8]

The numerical outcomes for the proposed approach are succinctly presented in Table 4, where the average performance across 18 individuals is compared. In this analysis, it is presumed that all stages (preprocessing, feature extraction, and classifier) remain constant, with the sole differentiation found in the dimensionality reduction and FS phases. Subsequently, the proposed approach is evaluated based on accuracy, sensitivity, and specificity criteria.

A conspicuous observation emerges from the results: utilizing all features yields the lowest classification performance, underscoring the challenge posed by high dimensionality. Conversely, the proposed dimensionality reduction method showcases superior performance compared to the other examined methods.

Performing the experiment on the combination of all individuals' data

In this scenario, data from all individuals have been combined, and the data from 17 individuals are considered training data, whereas the remaining data from one individual are used as test data, and the final results are reported based on this setup. The results obtained from this scenario are presented in Table 5. The results in the *i*th row correspond to the scenario where the *i*th individual is used as the test, and the data from the remaining 17 individuals are combined.

Conclusions

It is imperative to underscore that the proposed method represents a significant advancement in the field of arousal level detection using EEG signals. By employing a 640-dimensional feature vector derived from the Faller

Table 3: The classification specificity of the proposed method for 18 people and using 3 different kernels

Subjects	All features			Selected features		
	Linear SVM	Polynomial kernel	RBF kernel	Linear SVM	Polynomial kernel	RBF kernel
1	0.87	0.89	1	0.91	0.99	1
2	0.82	0.86	0.86	0.90	0.97	0.98
3	0.79	0.86	0.86	0.90	0.97	0.98
4	0.82	0.89	0.89	0.94	0.98	0.99
5	0.88	0.87	0.89	1	1	1
6	0.80	0.83	0.89	0.91	0.99	0.97
7	0.83	0.88	0.87	0.99	1	1
8	0.80	0.89	0.89	0.89	0.98	0.98
9	0.78	0.86	0.88	0.93	0.99	1
10	0.84	0.82	0.90	0.81	0.90	0.98
11	0.81	0.88	0.90	0.92	1	1
12	0.84	0.85	0.91	0.89	0.96	0.97
13	0.83	0.88	0.92	0.93	1	1
14	0.82	0.88	0.91	0.87	0.95	1
15	0.87	0.85	0.91	0.88	0.94	0.96
16	0.84	0.83	0.90	0.90	0.98	0.99
17	0.79	0.84	0.90	0.87	0.95	0.98
18	0.83	0.80	0.87	0.96	0.99	0.99
Average	0.85	0.86	0.88	0.96	0.99	0.99

SVM – Support vector machine; RBF – Radial basis function

Table 4: Investigating the performance of the proposed feature reduction method and comparing it with other methods

References	Feature reduction	Classifier	Accuracy		Specificity		Sensitivity	
			Minimum	Maximum	Minimum	Maximum	Minimum	Maximum
-	All features	Linear	61.79	91.55	58.86	89.63	78.71	88.81
		RBF	54.89	93.14	80.75	92.66	86.21	100
[18]	Evolutionary algorithm	Linear	-20	6	-20	6	-20	6
		RBF	-20	7	-20	7	-20	7
[20]	Search for symbiotic organisms	Linear	-2.1	7.2	-2.1	7.2	-2.1	7.2
		RBF	-19.5	2.99	-19.5	2.99	-19.5	2.99
The proposed method	Genetic algorithm	Linear	73.79	98.75	85.26	99.23	81.72	100
		RBF	75.96	98.87	92.85	100.52	96.28	100

RBF – Radial basis function

Table 5: Investigating the performance of the proposed method to detect the level of arousal by considering the combination of all people's data and evaluating it on one person

Subjects	All features			Selected features		
	Accuracy	Sensitivity	Specificity	Accuracy	Sensitivity	Specificity
1	0.89	0.88	0.80	0.92	0.91	0.89
2	0.74	0.71	0.77	0.86	0.83	0.87
3	0.80	0.90	0.70	0.87	0.91	0.77
4	0.81	0.87	0.76	0.86	0.87	0.86
5	0.58	0.85	0.54	0.71	0.88	0.78
6	0.51	0.65	0.69	0.71	0.79	0.80
7	0.67	0.53	0.78	0.87	0.83	0.87
8	0.85	0.86	0.74	0.88	0.89	0.83
9	0.83	0.85	0.73	0.89	0.89	0.84
10	0.75	0.81	0.70	0.83	0.87	0.81
11	0.84	0.96	0.76	0.88	0.86	0.85
12	0.84	0.99	0.72	0.89	0.91	0.83
13	0.84	0.85	0.75	0.88	0.90	0.87
14	0.70	0.62	0.75	0.78	0.82	0.87
15	0.84	0.81	0.69	0.87	0.91	0.80
16	0.79	0.85	0.72	0.81	0.88	0.81
17	0.83	0.85	0.73	0.85	0.90	0.82
18	0.82	0.88	0.71	0.84	0.88	0.80
Average	0.7783	0.8130	0.7449	0.8135	0.8865	0.8464

database's 64-channel EEG signal, our method demonstrates a robust ability to classify arousal levels in different scenarios. The utilization of a GA for FS, formulated as a multiobjective optimization problem, signifies a novel approach in this domain.

This methodology notably outperforms existing methods, as evidenced by a minimum 4% improvement in average accuracy, sensitivity, and specificity in the first scenario. In the second scenario, despite the challenges of combining data from multiple subjects, the method still maintains commendable accuracy and sensitivity.

However, potential limitations include the method's dependency on high-dimensional data and the complexity of the GA, which may necessitate substantial computational resources. Furthermore, the study's narrow focus on a specific age group and the utilization of data from a video game task could constrain the generalizability of the findings.

The study's design, focused on two distinct scenarios (individual and combined data), was chosen to validate the method's effectiveness across different levels of data complexity. This approach ensures the method's robustness and applicability in real-world scenarios where individual variability can play a significant role.

Overall, this research contributes a valuable and efficient tool for arousal level detection, with implications for enhancing machine understanding of human emotional states. Future research could explore the method's applicability to other age groups and settings, potentially broadening its utility.

Financial support and sponsorship

Nil.

Conflicts of interest

There are no conflicts of interest.

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