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Article

Adaptive Genetic Selection of Heart Rate Variability and Electrocardiographic Morphology Features for Cognitive Stress Detection Using Multi-Classifier Evaluation

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Abstract

Cognitive stress detection based on electrocardiogram (ECG) is challenged by the high dimensionality of multichannel analysis, redundancy between heart rate variability (HRV) and morphological descriptors, and variability in classifier performance. We developed and evaluated a cognitive stress classification framework based on a standardized ECG acquisition protocol, the integration of HRV and morphological descriptors extracted from 12 leads, and an adaptive feature selection strategy using a binary genetic algorithm with explicit penalization of dimensionality. Seventy healthy students aged 18–25 years participated, and cognitive stress was induced using a task based on PMA-R Factor R. The initial dataset included 27 descriptors per lead, and the proposed dimensionality reduction method was compared with two reference schemes: no dimensionality reduction and conventional principal component analysis (PCA) with a 99% cumulative explained variance threshold. Performance was assessed over 30 data splits using five classifiers: logistic regression, linear support vector machine (SVM), radial basis function SVM (SVM-RBF), k-nearest neighbors (KNN), and decision tree. The best trade-off between parsimony and predictive performance was achieved with $\lambda = 0.05$, yielding a compact subset of 11 features on average and a mean AUC of 0.830. In the final comparison, the adaptive strategy achieved the best overall performance with SVM-RBF (AUC $= 0.830 \pm 0.047$; specificity $= 0.814 \pm 0.115$), outperforming both the full feature set and PCA. These findings indicate that penalized genetic selection validated across multiple classifiers is an effective strategy for identifying compact, discriminative, and robust feature subsets for ECG-based cognitive stress classification.

Keywords: stress classification; heart rate variability; ECG morphology; adaptive feature selection; genetic algorithm; multichannel ECG

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1. Introduction

Mental and emotional stress represents a major public health concern because of its effects on mental health, cognitive function, cardiovascular health, and overall functional performance [1–4]. In addition, stress assessment based solely on self-reported measures has important limitations, as its manifestation varies across individuals, fluctuates over time, and depends strongly on context. As a result, there has been increasing interest in physiological monitoring strategies for stress assessment [1,4,5]. In this context, heart rate variability (HRV) and electrocardiogram (ECG) morphology have gained relevance as non-invasive biomarkers for stress evaluation because they can reflect changes in cardiac activity [6,7].

The reviewed literature indicates that mental stress alters cardiac markers associated with autonomic regulation. Reported findings include reductions in HRV parameters related to parasympathetic activity [8–10], a decrease in nonlinear dynamics during cognitively demanding tasks [11], and the possibility of distinguishing between stress and rest conditions using short or ultra-short ECG recordings [12–16]. Nevertheless, a recent review noted that, despite growing interest in HRV as an AI-supported stress biomarker, consistent methodological frameworks and standardized protocols are still needed to improve comparability between studies and strengthen the clinical validity of reported findings [5].

ECG-based stress analysis has mainly followed two directions: HRV descriptors and features directly derived from the ECG waveform. Although HRV has been widely studied in the time, frequency, and nonlinear domains, not all descriptors exhibit consistent discriminative ability under acute stress conditions [8,12,14–16]. In parallel, ECG morphological descriptors have been considered an additional source of physiological information with potential value for stress assessment [6,17–19]. In this regard, several recent studies have explored high-dimensional feature spaces, for example, by using 93 HRV features extracted from ECG signals to discriminate between stress and non-stress conditions [20]. However, increasing the number of descriptors does not necessarily improve discriminative performance. Consequently, classical dimensionality reduction techniques such as principal component analysis (PCA) have been used to compact the feature representation and facilitate classification in physiological signal-based problems [21–23]. In addition, several studies have shown that feature selection or reduction can improve model efficiency, reduce redundancy, and preserve the discriminative capacity of the most informative features [2,20]. Despite these advances, at least two important limitations remain: there is no consensus on how many and which descriptors are truly necessary to identify stress, and classification performance may vary with the selection method and the retained feature subset [20,22].

In this context, adaptive approaches based on evolutionary optimization are particularly attractive. For instance, genetic algorithms have already been used to select HRV-derived features in arrhythmia classification problems using support vector machines (SVMs), enabling the identification of feature subsets with high discriminative power [24]. They have also been proposed as wrapper methods for gene or variable selection in biomedical applications, where they have shown the ability to produce compact subsets [25]. Similarly, in high-dimensional biomedical problems, genetic optimization has been combined with nonlinear learning strategies to select a reduced number of relevant variables [26]. Recent studies on electroencephalographic (EEG) biosignals have also documented the use of evolutionary algorithms for channel selection, feature extraction, feature selection, and classification [27], while ECG-based studies have shown that metaheuristic optimization can mitigate the effect of irrelevant attributes and improve classification performance [28]. Taken together, this evidence supports the use of an adaptive genetic strategy when multiple potentially redundant physiological descriptors are available and an appropriate balance among parsimony, discriminative ability, and robustness is required.

Another key aspect of this work was the validation of the selected feature subset across multiple classifiers. This decision was motivated by the fact that the literature on physiological signal-based stress detection remains methodologically heterogeneous, with differences in the analyzed signals, acquisition protocols, feature selection strategies, and classification algorithms [1,5]. In this regard, published results have been distributed across different models, including SVMs [17,29], random forests [30,31], decision trees [15,30,31], and k-nearest neighbors (KNN) [14,30]. Under these conditions, validating a genetic algorithm with only one classifier could bias the selection process toward a single decision rule, particularly because feature selection itself may be affected by classifier dependency [26]. Therefore, in this study each candidate subset was evaluated using logistic regression, linear SVM, SVM-RBF, KNN, and decision tree classifiers in order to determine whether the retained features preserved their discriminative ability under linear, nonlinear, neighborhood-based, and rule-based decision schemes. From this perspective, the multi-classifier evaluation strengthened the validation of the genetic algorithm by reducing dependence on a single model and favoring more robust, parsimonious, and potentially generalizable feature subsets.

Although previous studies have explored ECG- and HRV-based stress detection using physiological descriptors and feature selection strategies [1,5,17,20,22], there remains a need for interpretable optimization-based frameworks that combine explicit HRV and ECG morphology descriptors from multichannel ECG recordings. In particular, ECG-based stress detection still faces challenges related to high dimensionality, redundancy between physiological descriptors, and the need to balance discriminative performance, parsimony, and robustness across classifiers. To address this problem, the present study aimed to develop and evaluate a cognitive stress classification framework based on a standardized ECG acquisition protocol, in which cognitive stress was induced through a structured task based on the Factor R subtest of the Primary Mental Abilities Revised test (PMA-R) [32]. The proposed framework integrated HRV and morphological features extracted from 12 ECG leads (I, II, III, aVR, aVL, aVF, and V1–V6), together with an adaptive feature selection strategy using a genetic algorithm with explicit dimensionality penalization regulated by the parameter λ in the fitness function. The proposed approach was compared with two reference schemes: the original feature set without dimensionality reduction and a conventional PCA-based reduction using a 99% cumulative explained variance threshold. The central hypothesis was that combining controlled physiological acquisition, a complementary multichannel representation, and a parsimonious evolutionary search strategy would enable the identification of compact, informative, and stable feature subsets with consistent discriminative capacity across different decision models. Accordingly, the main contributions of this study can be summarized as follows:

- A standardized experimental framework for 12-lead ECG acquisition under baseline and cognitive stress conditions.
- A multichannel representation integrating complementary HRV and morphological descriptors.
- An adaptive penalized genetic algorithm for identifying compact and discriminative feature subsets.
- A comparative evaluation against conventional dimensionality reduction strategies, including the unreduced feature space and PCA.
- A multi-classifier validation scheme aimed at improving the interpretability, robustness, and generalization potential of ECG-based cognitive stress classification.

The remainder of this article is structured as follows: Section 2 describes the methodology, including the study population, the ECG acquisition protocol, preprocessing, feature construction, adaptive selection of genetic features, PCA-based dimensionality reduction, and classifier configuration. Section 3 presents the experimental results. Section 4 discusses the study's main findings, methodological implications, and limitations. Finally, Section 5 presents the conclusions and future perspectives.

2. Materials and Methods

The methodological procedure followed in this study is described in this section. It comprises the study population and experimental acquisition protocol, ECG preprocessing, construction of the multichannel feature space, adaptive and PCA-based dimensionality reduction, and classifier configuration. The description begins with the participants and the ECG acquisition protocol.

2.1. Population and Data Acquisition Protocol

The study included 70 healthy Biomedical Engineering students aged between 18 and 25 years. The experimental protocol was previously approved by the Ethics Committee of the Faculty of Engineering of the Autonomous University of Querétaro under approval number CEAIFI-183-2021-PI. Before participation, all subjects provided written informed consent in accordance with the ethical principles of the Declaration of Helsinki.

Data acquisition was conducted using a standardized protocol designed to minimize variability from external sources. Figure 1 illustrates the experimental setup and acquisition protocol. Figure 1a shows the 12-lead ECG electrode placement and TLC 5000 Holter monitor (CONTEC Medical Systems Co., Ltd., Qinhuangdao, Hebei Province, China), while Figure 1b summarizes the temporal organization of the baseline relaxation and cognitive stress recordings. The protocol began with a 5 min pre-rest phase, followed by a 7 min baseline relaxation condition, during which ECG signals were continuously recorded at a sampling frequency of 200 Hz. From this stage, 300 s of ECG signal were extracted from the central portion and considered as the physiological reference under non-stress conditions.

Subsequently, a brief pause was introduced to explain the cognitive stress task to the participants. Stress was induced using a structured task based on the Factor R subtest of the PMA-R battery, which was used as a standardized stimulus to elicit cognitive demand during signal recording. A 7 min cognitive stress phase was then recorded. For this condition, the central 300 s segment was also selected, while the initial and final 60 s were discarded because these intervals may be influenced by transient adaptation, anticipation, attentional shifts, and post-task relaxation processes, thereby introducing variability that is not representative of the stable physiological state of interest. Finally, a recovery period was considered after task completion.

Before data collection, participants were required to have slept adequately, to have avoided physical exercise during the previous 12 h, to have reported no history of cardiac problems, and to have refrained from consuming coffee or energy drinks. They were also instructed to hydrate at least 30 min before acquisition. All measurements were performed in a controlled environment at 21 ± 4 °C. In addition, participants presenting stress-related headache, influenza, common cold symptoms, or any other relevant physical discomfort at the time of the experiment were excluded from the acquisition process.

The coded raw ECG recordings from both experimental states are openly available in Zenodo [33]. These acquisition-stage 12-lead ECG signals were used as the source recordings for the subsequent HRV and ECG morphology feature extraction.

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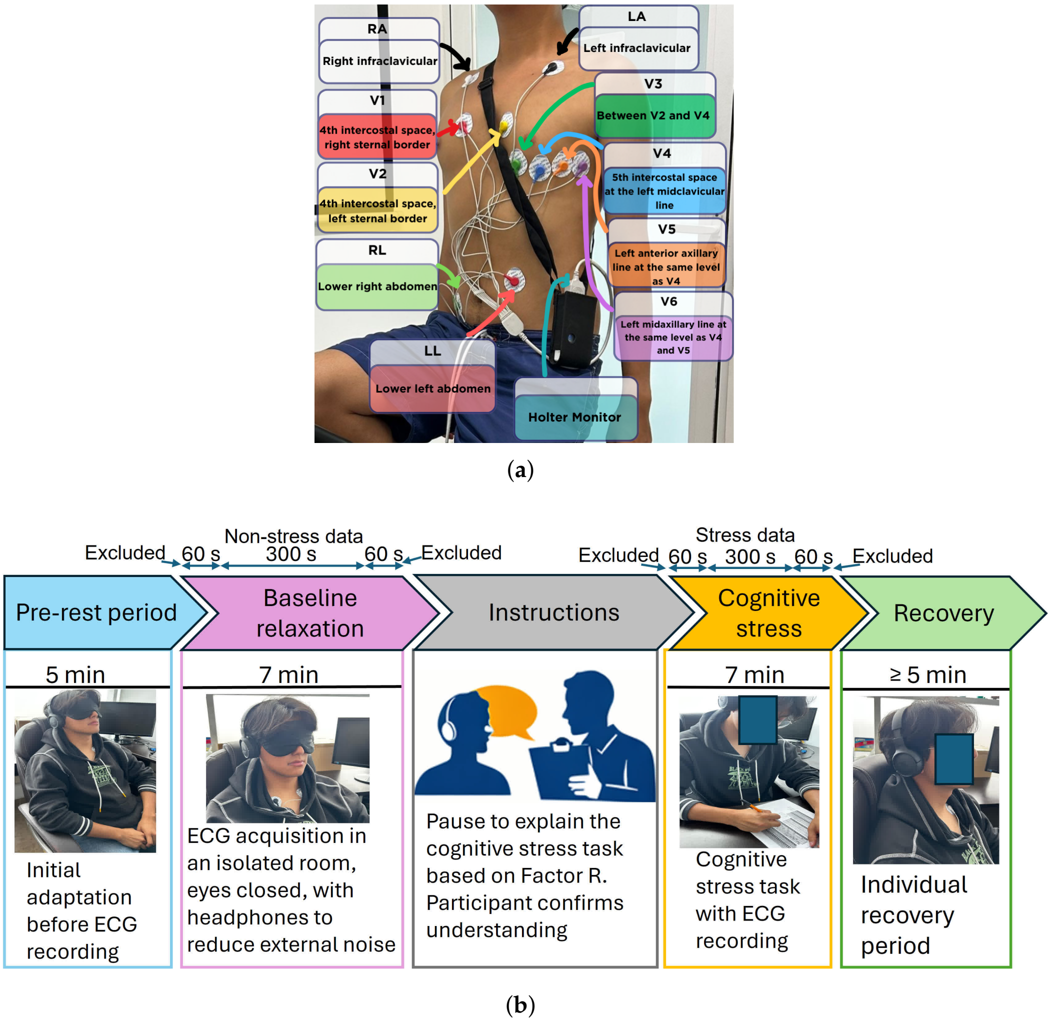

Figure 1. Experimental setup and acquisition protocol. setup and acquisition protocol. (**a**) The 12-lead ECG electrode placement and Holter monitor. (**b**) Baseline relaxation and cognitive stress protocol.

2.2. Preprocessing of ECG Recordings

The preprocessing steps described below were applied only to the ECG signals analyzed in this study; the public Zenodo dataset contains the original raw ECG recordings before preprocessing.

The ECG signals were preprocessed to reduce noise, attenuate unwanted components, and preserve physiologically relevant information. First, each recording was robustly centered by subtracting its median. Next, robust outlier clipping was applied using limits of ± 5 times the median absolute deviation (MAD) relative to the median to attenuate non-physiological peaks and other sources of distortion. The signals were then filtered using a 0.5 Hz high-pass filter and a 20 Hz low-pass filter in order to reduce baseline wander and high-frequency noise while preserving the ECG frequency band of interest [14,34–36]. Finally, the mean of the filtered signal was subtracted to obtain the centered signal.

2.3. Feature Extraction and Feature Set

The initial dataset comprised 324 features derived from the 12 ECG leads, including heart rate variability (HRV) descriptors from the time, frequency, and nonlinear domains, as well as ECG morphology descriptors. Feature extraction was performed using custom MATLAB R2025b (The MathWorks, Inc., Natick, MA, USA) scripts developed for this study, supported by the Signal Processing Toolbox. For each lead, R peaks were detected using a derivative-based energy envelope, moving-average smoothing, `findpeaks`, and local maximum refinement. RR intervals were then used to compute HRV descriptors, with spectral features estimated using `pwelch`, whereas window-based ECG morphology descriptors were extracted around each R peak to characterize amplitude, QRS complex shape, slope, energy, and ST–T segment characteristics.

Figure 2 shows the general feature extraction procedure and the methodological workflow of the proposed model. Figure 2a shows the detection of R peaks and RR intervals used to compute the HRV descriptors. Figure 2b shows the morphology descriptors extracted around each R peak. Figure 2c summarizes the five-step workflow, including ECG acquisition, preprocessing, feature extraction, feature selection or dimensionality reduction, and multi-classifier evaluation.

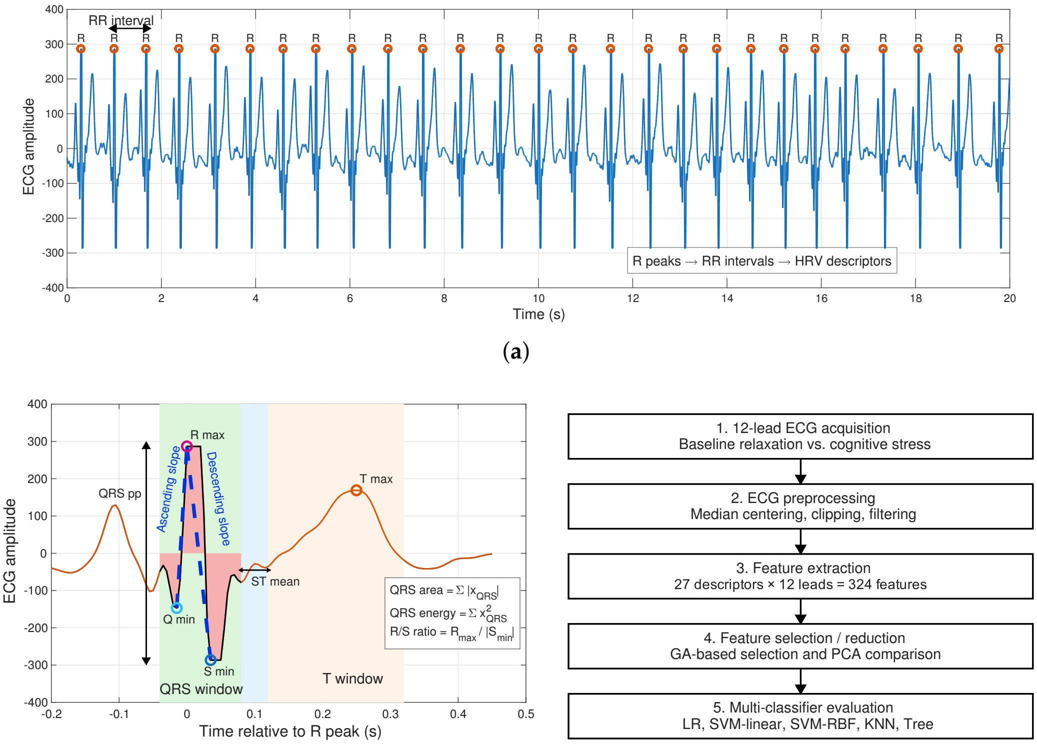

Figure 2. ECG-derived feature extraction procedure and workflow of the proposed model. (**a**) R-peak detection and RR intervals for HRV analysis. (**b**) Extraction of morphology descriptors. (**c**) Five-step methodological workflow used for classification.

The complete feature set is summarized in Table 1. This high-dimensional representation was used as the input space for classification, which justified the subsequent stages of PCA-based dimensionality reduction and adaptive genetic feature selection.

Table 1. Composition of the initial feature set by physiological domain.

Group	Features	Total	Main Reference
Time-domain HRV	HR mean, RR mean, SDNN, RMSSD, pNN50	60	[3,13,28,30,37]
Frequency-domain HRV	VLF, LF, HF, LF/HF, Total Power	60	[15,29,30,38]
Nonlinear HRV	SD1, SD2, Approximate Entropy (ApEn), DFA α_1, DFA α_2	60	[3,12,30]

Table 1. *Cont.*

Group	Features	Total	Main Reference
Morphology	Number of peaks, Q minimum, R maximum, S minimum, QRS peak-to-peak amplitude, QRS area, QRS energy, ascending slope, descending slope, R/S ratio, T maximum, ST mean	144	[6,39]
Total	27 features	324	–

2.4. Automatic Feature Selection Using a Genetic Algorithm

Feature selection was formulated as a combinatorial optimization problem to identify compact subsets of ECG features with high discriminative ability for stress classification. For this purpose, a binary genetic algorithm was adopted, since it enables efficient exploration of high-dimensional discrete search spaces without requiring exhaustive search [26,27,40,41]. The proposed strategy was designed to balance predictive performance and parsimony by incorporating an explicit penalty on subset size, together with an evaluation scheme using multiple classifiers.

2.4.1. Subset Encoding and Population Initialization

Let p denote the total number of candidate features. Each individual was represented by a binary vector:

$$\mathbf{z} = [z_1, z_2, \ldots, z_p], \quad z_i \in \{0,1\},$$

where $z_i = 1$ indicates that the i-th feature was selected, and $z_i = 0$ otherwise. The number of active features in each individual was defined as

$$|\mathbf{z}| = \sum_{i=1}^{p} z_i$$

Each individual was constrained to satisfy

$$m_{\min} \leq |\mathbf{z}| \leq m_{\max}$$

where $m_{\min}$ and $m_{\max}$ denote the minimum and maximum number of allowed features, respectively. The initial population was randomly generated from valid individuals satisfying these constraints.

Accordingly, the mathematical model of the proposed feature selection strategy was defined as the following penalized optimization problem:

$$\mathbf{z}^* = \arg \max_{\mathbf{z} \in \{0,1\}^p} J(\mathbf{z}) \quad \text{s.t.} \quad m_{\min} \leq |\mathbf{z}| \leq m_{\max}.$$

In this formulation, $\mathbf{z}^*$ denotes the optimal binary vector that encodes the selected feature subset identified by the genetic algorithm, while the constraint ensures that the number of retained features remains between $m_{\min}$ and $m_{\max}$.

2.4.2. Fitness Evaluation

Each individual was decoded into its corresponding feature subset and evaluated using five supervised classifiers: logistic regression, linear SVM, SVM-RBF, KNN, and decision tree. The objective function balanced discriminative performance and parsimony through a fitness measure penalized by subset size:

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$$J(\mathbf{z}) = AUC(\mathbf{z}) - \lambda\left(\frac{|\mathbf{z}|}{m_{\max}}\right)$$

where $AUC(\mathbf{z})$ denotes the predictive performance associated with subset $\mathbf{z}$, and λ is a weighting parameter controlling the trade-off between predictive performance and subset compactness.

More specifically, $AUC(\mathbf{z})$ was defined as the highest mean area under the ROC curve (AUC) achieved by subset $\mathbf{z}$ across the evaluated classifiers:

$$AUC(\mathbf{z}) = \max_{m \in \mathcal{M}} \left(\frac{1}{R} \sum_{r=1}^{R} \mathrm{AUC}_m^{(r)}(\mathbf{z}) \right)$$

where $\mathcal{M}$ is the set of classifiers and R is the number of independent repetitions. This formulation enabled the genetic algorithm to favor subsets with high discriminative potential, thereby allowing the classifier structure to adapt to the most informative representation of the data.

2.4.3. Selection

Parent selection was performed using tournament selection, with preference given to individuals with higher fitness values. This mechanism maintained selective pressure while avoiding premature collapse of population diversity.

2.4.4. Crossover

Recombination was performed using one-point crossover. If $\mathbf{z}^{(1)}$ and $\mathbf{z}^{(2)}$ denote the parent individuals and q is the crossover point, the offspring were generated by exchanging the segments located after that point:

$$\mathbf{h}^{(1)} = [z_1^{(1)}, \ldots, z_c^{(1)}, z_{c+1}^{(2)}, \ldots, z_p^{(2)}]$$
$$\mathbf{h}^{(2)} = [z_1^{(2)}, \ldots, z_c^{(2)}, z_{c+1}^{(1)}, \ldots, z_p^{(1)}]$$

2.4.5. Mutation

After crossover, each gene was subjected to binary mutation with a predefined probability at each generation. This operation increased population diversity and promoted the exploration of new feature combinations, thereby reducing the likelihood of premature convergence to local optima. Formally, mutation of the i-th gene was defined as

$$z_i' = \begin{cases} 1 - z_i, & \text{with probability } p_m, \\ z_i, & \text{with probability } 1 - p_m, \end{cases}$$

where p_m denotes the mutation rate.

The main stages of the proposed adaptive genetic feature selection scheme are summarized in Algorithm 1.

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Algorithm 1 Adaptive genetic feature selection

Require: Candidate feature set $\mathcal{F}$, minimum subset size $m_{\min}$, maximum subset size $m_{\max}$, population size N, number of generations G, penalty coefficient λ, classifier set $\mathcal{M}$, number of repetitions R
Ensure: Best feature subset $\mathbf{z}^*$
Initialize a valid binary population $\mathcal{P} = \{\mathbf{z}_1, \mathbf{z}_2, \ldots, \mathbf{z}_N\}$
for $g = 1$ to G **do**
  for each individual $\mathbf{z}_i \in \mathcal{P}$ **do**
    Decode $\mathbf{z}_i$ into the selected feature subset $\mathcal{F}_i$
    for each classifier $m \in \mathcal{M}$ **do**
      Evaluate $\mathcal{F}_i$ over R independent repetitions
      Compute mean $\text{AUC}_m(\mathcal{F}_i)$
    end for
    Compute subset performance $A(\mathbf{z}_i) = \max_{m \in \mathcal{M}} \text{AUC}_m(\mathcal{F}_i)$
    Compute fitness $J(\mathbf{z}_i) = A(\mathbf{z}_i) - \lambda \left(\frac{|\mathbf{z}_i|}{m_{\max}} \right)$
  end for
  Rank the population according to fitness
  Preserve elite individuals
  Select parents by tournament selection
  Apply one-point crossover
  Apply bit-flip mutation
  Repair offspring to satisfy $m_{\min} \leq |\mathbf{z}| \leq m_{\max}$
  Build the next generation
end for
Return the individual with the highest historical fitness as $\mathbf{z}^*$

2.4.6. Algorithm Configuration and Output

At each generation, an elite fraction of the highest-fitness individuals was preserved to avoid the loss of high-quality solutions. The algorithm was executed for a fixed number of generations, and the final solution was defined as the individual with the highest historical fitness. This procedure enabled the identification of parsimonious subsets of ECG features with high discriminative ability. The algorithm configuration is summarized in Table 2.

Table 2. Parameters of the genetic algorithm used for automatic feature selection.

Parameter	Value
Population size	50
Number of generations	50
Crossover rate	0.80
Mutation rate	0.10
Number of elite individuals	4
Tournament size	3
Minimum number of features ($m_{\min}$)	2
Maximum number of features ($m_{\max}$)	15
Penalty coefficient (λ)	0.05
Fitness repetitions	30
Final evaluation repetitions	30
Hold-out split	70/30
Evaluated classifiers	KNN, linear SVM, SVM-RBF, logistic regression, decision tree

2.5. PCA-Based Dimensionality Reduction for Comparison

As a methodological reference, PCA was applied to compare the proposed method against a conventional dimensionality reduction strategy. PCA was used only as a benchmark method, whereas the proposed framework was based on genetic-algorithm feature selection as an optimization-based strategy. In each repetition, a hold-out partition was used, reserving 30% of the samples for testing.

PCA was fitted exclusively on the training set, and the number of retained components was chosen to explain 99% of the cumulative variance, with the aim of preserving as much discriminative information as possible. Subsequently, both the training and testing sets were projected onto the resulting subspace. The retained PCA components were then used as input variables for the same five classifiers evaluated in the proposed method, namely logistic regression, linear SVM, SVM-RBF, KNN, and decision tree. Performance was estimated over 30 independent repetitions and reported in terms of accuracy, sensitivity, specificity, and AUC [28,42,43].

2.6. Classifier Configuration

The configuration of the five classifiers was kept the same across all experiments. Features were standardized using z-score normalization, and classification was performed using binary class encoding. Table 3 summarizes the specific configuration of each model.

The five classifiers were selected to evaluate different classification strategies commonly used in ECG- and HRV-based stress classification. Logistic regression and linear SVM were included as linear reference models, SVM-RBF as a nonlinear kernel-based model, KNN as an instance-based classifier, and a decision tree as a rule-based classifier. This configuration allowed the same feature sets to be evaluated under models with different levels of complexity and nonlinear decision capability [1,5,17,24].

Table 3. Configuration of the classifiers used in all experiments.

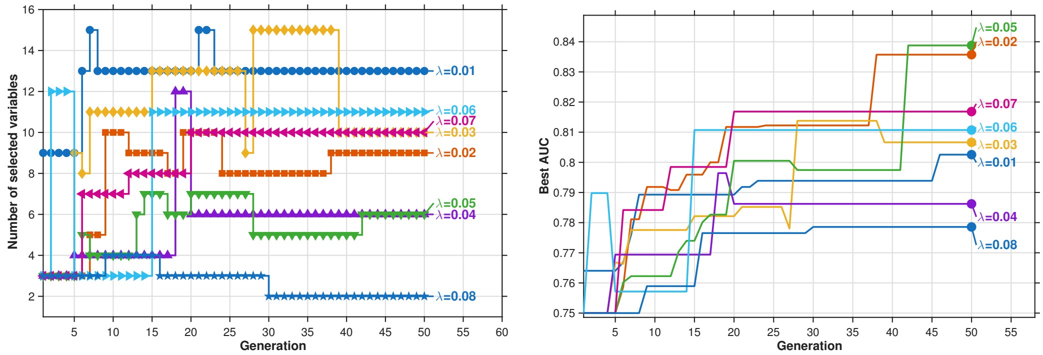
Classifier	MATLAB Function	Configuration
Logistic Regression	`fitclinear`	Learner = logistic
Linear SVM	`fitcsvm`	KernelFunction = linear
SVM-RBF	`fitcsvm`	KernelFunction = rbf
KNN	`fitcknn`	NumNeighbors = 5, Distance = euclidean
Decision Tree	`fitctree`	Default settings

3. Results

This section presents the main experimental findings obtained with the proposed framework. The results are organized as follows: first, to describe the behavior of the genetic optimization process; second, to present the characteristics of the selected trait subset; and finally, to report on the performance of the comparative classification.

3.1. Evolution of the Genetic Optimization Process

Figure 3a shows that the value of λ affected the size of the subset selected during the optimization process. Lower values of λ tended to retain a larger number of features, whereas higher values produced smaller subsets. At the end of the optimization, $\lambda = 0.01$ retained 13 features, while $\lambda = 0.08$ converged to only 2 features. The Figure 3b also shows the evolution of the highest AUC achieved during the optimization. The best result was obtained with $\lambda = 0.05$, yielding a mean AUC of 0.830 on a subset of 6 features. By comparison, $\lambda = 0.01$ achieved a mean AUC of 0.797 with a larger subset, whereas $\lambda = 0.058$ yielded a mean AUC of 0.786 with the most compact solution. Overall, these results demonstrate the effect of the penalization term on the trade-off between subset size and classification performance.



(**a**) (**b**)

Figure 3. Evolution of the genetic algorithm for different values of λ: (**a**) number of variables in the best individual; (**b**) best AUC per generation.

3.2. Optimal Feature Subset Identified by the Proposed Method

Figure 4 summarizes the feature reduction achieved by the proposed method and the variables retained in the final subset. Starting from an initial set of 27 feature types, the procedure reduced the representation to an average of 11 features, corresponding to an overall reduction of 59.26%. As shown in the figure, the largest relative reduction was observed in time-domain HRV features (80.00%), followed by morphological features (58.33%), whereas frequency-domain and nonlinear HRV features both showed reductions of 40.00%. Despite this reduction, the final subset preserved information from all analyzed physiological domains, retaining HR mean in the time domain; HF, LF/HF, and VLF in the frequency domain; ApEn, DFA α_1, and DFA α_2 in the nonlinear domain; and QRS area, number of peaks, Q minimum, S minimum, and T maximum in the morphological domain. Taken together, these results show that the proposed method produced a more compact representation without losing the physiological diversity of the selected features.

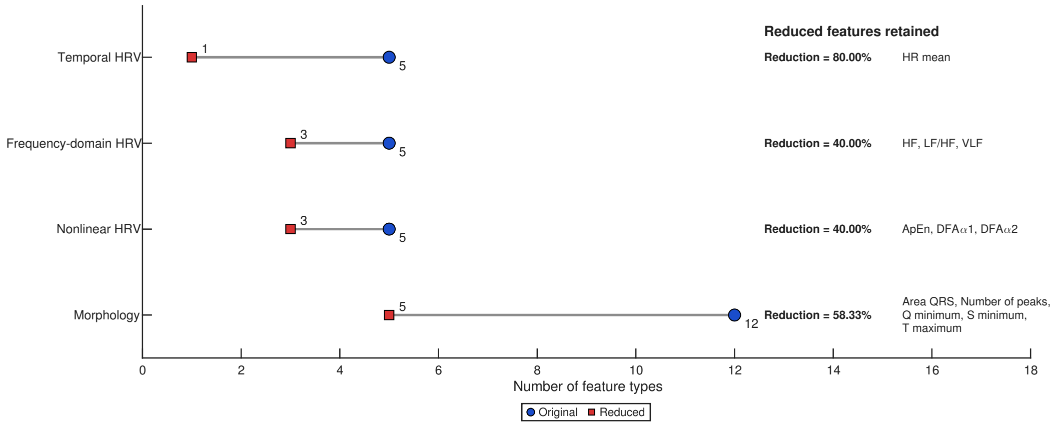


Figure 4. Reduction of feature types and retained variables in the final subset selected by the proposed method.

3.3. Comparative Performance of the Five Classifiers

Figure 5 shows the comparative performance of the five evaluated classifiers in terms of accuracy, sensitivity, specificity, and AUC. Overall, SVM-RBF exhibited the most favorable global discriminative performance, achieving the highest AUC (0.8304 ± 0.0465) and specificity (0.8143 ± 0.1150), albeit with a more moderate sensitivity (0.6643 ± 0.1218). These results indicate a stronger ability to correctly identify the negative class and the best overall discriminative performance among the evaluated models.

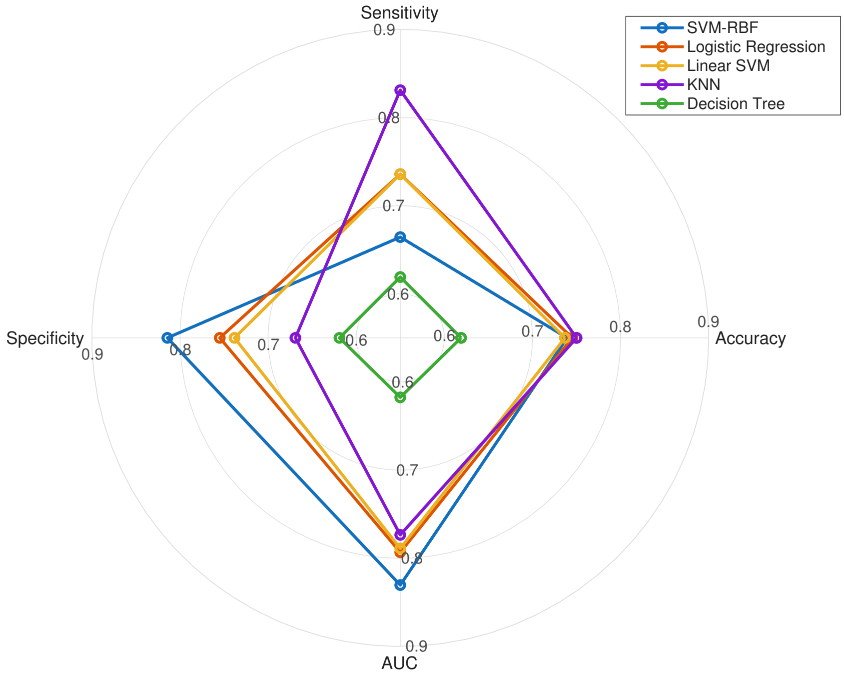


Figure 5. Comparison of the performance of the five evaluated classifiers in terms of accuracy, sensitivity, specificity, and area under the curve (AUC).

In contrast, KNN achieved the highest accuracy (0.7500 ± 0.0744) and the highest sensitivity (0.8310 ± 0.0947), indicating a greater ability to detect the positive class. However, this behavior was accompanied by lower specificity (0.6690 ± 0.0947) and AUC than SVM-RBF (0.7735 ± 0.0736), suggesting less balanced performance across both classes.

Logistic regression and linear SVM exhibited intermediate, relatively balanced profiles, with accuracy, sensitivity, specificity, and AUC values of 0.741 ± 0.070, 0.736 ± 0.012, 0.746 ± 0.095, and 0.791 ± 0.068, respectively. These results indicate competitive discriminative ability, although slightly below that of SVM-RBF. In contrast, the decision tree exhibited the lowest performance across all evaluated metrics, with an AUC of 0.6175 ± 0.0902, indicating a limited ability to separate the two classes under the conditions of the present study. Therefore, the results in Figure 5 show that the classifiers exhibited differentiated performance profiles and that SVM-RBF achieved the best overall discriminative performance on the analyzed dataset.

3.4. Comparison Among No Reduction, PCA, and Adaptive Genetic Algorithm

Figure 6 summarizes the performance of the five classifiers under three descriptor reduction or selection strategies: no dimensionality reduction, PCA with a 99% threshold, and the adaptive genetic algorithm. In general, the adaptive strategy yielded the best overall performance, with consistent improvements across most metrics and classifiers, particularly in AUC and specificity.

Without dimensionality reduction, performance was globally lower and more heterogeneous. Under this condition, logistic regression achieved the highest AUC (0.704 ± 0.080), followed by linear SVM (0.697 ± 0.083), whereas the decision tree showed the most limited performance (AUC $= 0.574 \pm 0.094$). Applying PCA with a 99% threshold led to an intermediate improvement, increasing the performance of several classifiers, with the best result obtained by logistic regression (AUC $= 0.763 \pm 0.067$). However, these values remained below those obtained with the proposed method.

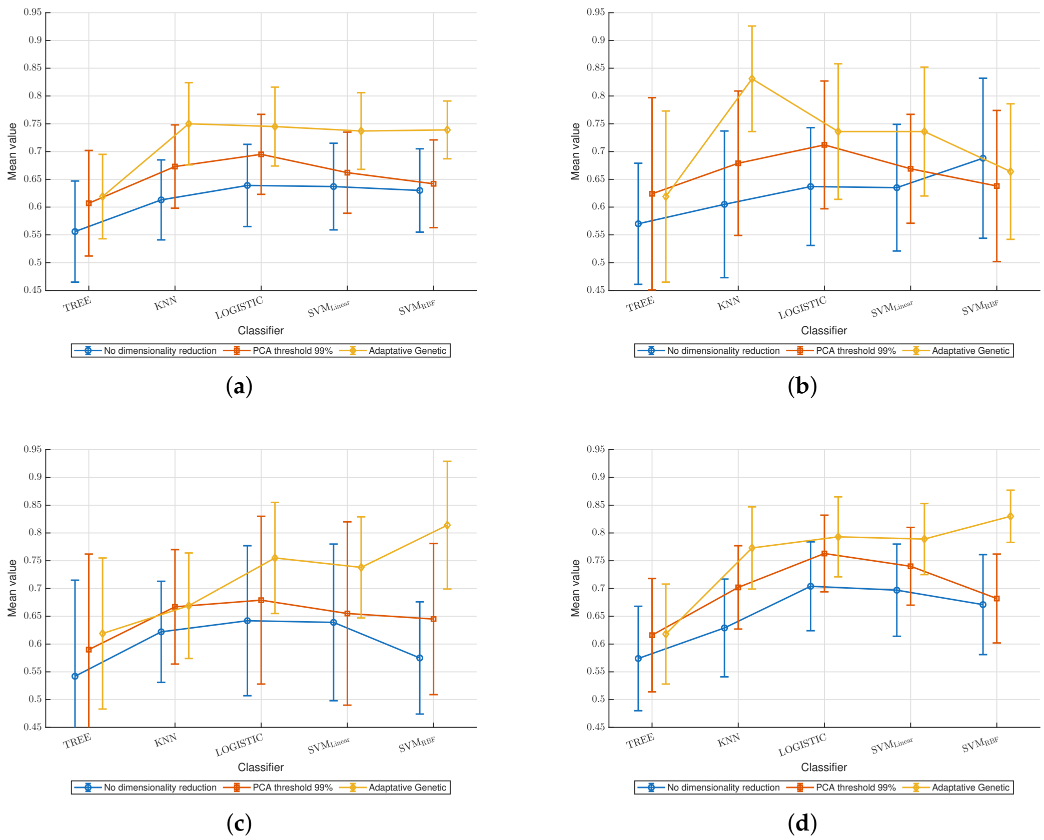


Figure 6. Comparison of classifier performance across dimensionality reduction methods in terms of (**a**) accuracy, (**b**) sensitivity, (**c**) specificity, and (**d**) AUC.

The adaptive strategy achieved the best results overall. In this case, SVM-RBF yielded the highest AUC (0.830 ± 0.047) and the highest specificity (0.814 ± 0.115), indicating the best overall discriminative ability and the best recognition of the negative class. In contrast, KNN achieved the highest accuracy (0.750 ± 0.074) and the highest sensitivity (0.831 ± 0.095), reflecting a greater ability to identify the positive class, although with lower specificity (0.669 ± 0.095) and a lower AUC than SVM-RBF (0.773 ± 0.074). Taken together, these findings support that the adaptive selection strategy preserved discriminative information more effectively than PCA and more effectively than the direct use of the full descriptor space.

Table 4 summarizes the comparison among the no-reduction condition, PCA-based reduction, and the proposed method. Both PCA and adaptive selection improved performance compared with using all descriptors directly. However, the best overall performance was achieved by the adaptive genetic algorithm combined with SVM-RBF, which achieved an AUC of 0.830 and higher accuracy and specificity. This improvement was achieved using a reduced subset of ECG-derived descriptors instead of the complete 324-feature space, indicating a compact representation for classification. Compared with conventional variance-based reduction, the adaptive strategy preserved the original physiological descriptors from the HRV and ECG morphology domains, resulting in an interpretable and discriminative representation for cognitive stress detection.

Overall, three main remarks can be drawn from the results. First, the penalty coefficient controlled the trade-off between subset size and classification performance, with $\lambda = 0.05$ providing the most favorable balance. Second, the selected subset preserved information from both HRV and ECG morphology domains, indicating that cognitive stress discrimination benefited from complementary physiological descriptors. Third, the adaptive genetic strategy achieved the highest AUC with SVM-RBF, whereas KNN favored sensitivity at the expense of specificity, showing that the selected features produced different classifier-dependent performance profiles.

Table 4. Comparison among no dimensionality reduction, PCA, and the proposed adaptive genetic method.

Method	Best Classifier	Accuracy (Mean ± SD)	Sensitivity (Mean ± SD)	Specificity (Mean ± SD)	AUC (Mean ± SD)
No dimensionality reduction	Logistic Regression	0.639 ± 0.074	0.637 ± 0.106	0.642 ± 0.135	0.704 ± 0.080
PCA threshold 99%	Logistic Regression	0.696 ± 0.072	0.712 ± 0.115	0.679 ± 0.151	0.763 ± 0.067
Adaptive Genetic	SVM-RBF	0.739 ± 0.052	0.664 ± 0.122	0.814 ± 0.115	0.830 ± 0.047

4. Discussion

The obtained results indicate that adaptive feature selection using a genetic algorithm improves cognitive stress classification compared with both the direct use of the full descriptor set and conventional PCA-based reduction. In particular, the value $\lambda = 0.05$ provides the best balance between parsimony and discriminative ability. These findings suggest that the subset-size penalty serves as an effective regularization mechanism, discouraging excessively large subsets and promoting more compact solutions without compromising predictive performance. This behavior is consistent with previous studies that have highlighted the usefulness of adaptive selection strategies in high-dimensional biomedical problems [24–28].

The superiority observed with respect to the two reference strategies supports this interpretation. Without dimensionality reduction, the best result was obtained by logistic regression with an AUC of 0.704 ± 0.080; with PCA at the 99% threshold, the best performance increased to an AUC of 0.763 ± 0.067; however, the adaptive strategy achieved the best overall result with SVM-RBF (AUC $= 0.830 \pm 0.047$; specificity $= 0.814 \pm 0.115$). These findings indicate that, in this problem, preserving total variance via PCA was insufficient to retain the information most relevant for discrimination, whereas penalized genetic selection favored features that were more informative for classification. This result is consistent with the literature recognizing PCA as a useful methodological benchmark, while also reporting advantages of more targeted selection methods over conventional compaction approaches [21–23].

Another relevant finding was that the final subset preserved information from all analyzed physiological domains, including time- and frequency-domain HRV features, as well as ECG morphological features. This suggests that discrimination between stress and non-stress conditions does not rely on a single feature set but rather on the complementary integration of autonomic and morphological changes. This observation is in agreement with previous studies that have emphasized the joint value of HRV and ECG morphology in stress assessment [5,6,17–20]. In addition, the multi-classifier evaluation revealed distinct performance profiles: SVM-RBF achieved the best overall discriminative performance, whereas KNN achieved the highest accuracy and sensitivity, albeit at the expense of lower specificity. This pattern supports the decision to validate the genetic algorithm across multiple classifiers, since it reduced the dependence of the selection process on a single model architecture and favored more robust feature subsets [1,5,26].

Based on the repeated holdout evaluation, SVM-RBF was selected as the base classifier because it achieved the highest AUC and the best balance between discriminative performance and specificity. This result is consistent with previous ECG- and HRV-based stress classification studies using SVM models and genetic algorithms [17,24] and suggests that nonlinear decision boundaries may be useful for modeling heterogeneous physiological descriptors [1,5].

Among the main strengths of this study are the standardized ECG acquisition protocol, the controlled induction of cognitive stress, the multichannel analysis using 12-lead ECG recordings, and the comparison of the proposed adaptive feature selection strategy against two reference approaches: the complete feature set and PCA-based dimensionality reduction. Nevertheless, the results should be interpreted considering several limitations. The sample consisted of 70 healthy students within a restricted age range and under an acute cognitive stress condition, which may limit the generalization of the findings to other age groups, clinical populations, and occupational settings. In addition, although repeated holdout partitions were used to evaluate model stability, the evaluation was performed on the same dataset and did not include external validation or a strictly subject-independent scheme. Therefore, the reported performance should be interpreted as a result of internal validation. Future validation should include larger and more heterogeneous populations, external datasets, and subject-wise validation protocols, such as subject-independent holdout or leave-one-subject-out, in order to better evaluate the generalization capacity.

Taken together, these limitations define several technical directions for future work. First, the robustness of the proposed genetic-algorithm-based feature selection and classification framework should be evaluated using wearable, flexible, or reduced-lead ECG systems, which have been previously explored for stress assessment and mental-stress detection [29,31]. This validation is necessary because motion artifacts, noise, variable skin–electrode contact, sweating, and electrode displacement may affect R-peak detection, RR interval estimation, and the stability of HRV and ECG morphology descriptors [6,12]. Second, the current binary formulation between baseline relaxation and cognitive stress should be extended to multiclass or continuous stress-level estimation, which could better represent stress dynamics under real-world conditions [3,10]. Finally, future studies should incorporate artifact-robust preprocessing strategies and evaluate the computational feasibility of the complete pipeline for real-time implementation in wearable or remote monitoring applications.

5. Conclusions

A multichannel ECG-based framework for cognitive stress classification is presented, integrating a standardized acquisition protocol, HRV and morphological features, and an adaptive feature selection strategy based on a genetic algorithm with explicit dimensionality penalization. The proposed method reduced the initial feature space to a compact representation while preserving information from all analyzed physiological domains. Compared with the direct use of the full feature set and conventional PCA-based reduction at the 99% threshold, the adaptive strategy achieved the best overall performance, with SVM-RBF emerging as the most competitive classifier in terms of AUC and specificity, whereas KNN yielded the highest accuracy and sensitivity. Overall, these findings indicate that penalized genetic selection validated across multiple classifiers constitutes an effective approach for identifying parsimonious, discriminative, and robust feature subsets for ECG-based cognitive stress detection. Nevertheless, additional studies involving larger and more heterogeneous populations, as well as external validation, are still required to confirm the generalizability and clinical applicability of the proposed framework.

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Data Availability Statement: The anonymized and coded raw ECG recordings from both experimental states are openly available in Zenodo [33].

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Abbreviations

The following abbreviations are used in this manuscript:

AUC	Area under the receiver operating characteristic curve
ECG	Electrocardiogram
GA	Genetic algorithm
HRV	Heart rate variability
KNN	k-nearest neighbors
PCA	Principal component analysis
PMA-R	Primary Mental Abilities Revised test
SVM	Support vector machine
SVM-RBF	Support vector machine with radial basis function kernel

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