ECG CLASSIFICATION USING THE CLONAL SELECTION ALGORITHM: AN ARTIFICIAL IMMUNE SYSTEM APPROACH

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Abstract

Electrocardiogram (ECG) classification plays a critical role in diagnosing cardiac abnormalities such as arrhythmias. Traditional machine learning and deep learning approaches have demonstrated effectiveness in ECG classification but often require large datasets and significant computational resources. In this study, we explore the Clonal Selection Algorithm (CSA), a bio-inspired artificial immune system (AIS) model, for classifying ECG signals from the PTB Diagnostic ECG Database. The CSA is designed to evolve a population of antibodies to recognize and classify normal and abnormal ECG patterns. We formulate the problem by representing each ECG segment as an antigen, while the antibodies evolve through cloning, mutation, and selection based on an affinity measure reflecting the similarity between normal ECG patterns. The antibodies then work as a classifier which classify unseen ECG segments as abnormal if they have a low affinity, and normal otherwise. Through this approach, an accuracy of 74.8% has been obtained.

1 Introduction

ECG data refers to the data which has been collated by measuring the electrical signals that are produced by the heart as it beats. Irregularities in these signals can indicate arrhythmia, characterized by abnormally fast, slow, or irregular heartbeats. Given this, numerous studies have used ECG classification to detect arrhythmia, applying methods like logistic regression, random forests, and neural networks[1]. Beyond arrhythmia detection, ECG classification can also identify conditions like Chagas disease[2]. The PTB Diagnostic ECG database[3], with its normal and abnormal (arrhythmic) signals, serves as a valuable benchmark for testing classification methods. While different traditional machine learning techniques and neural network architectures have been explored for ECG classification tasks, the use of methods belonging to, or inspired from artificial immune systems for the same remains underexplored.

In this report, we describe a binary classification system that has been implemented by using the clonal selection algorithm. This classification system hypothesizes that all of the 'normal ECG signals' collectively differ from the 'abnormal ECG signals' at a feature level, and the CSA during the binary classification task classifies unseen ECG signals as normal if they have a high affinity to the 'antibodies' generated through the algorithm, or abnormal otherwise. Figure 1 shows an overview of this system.

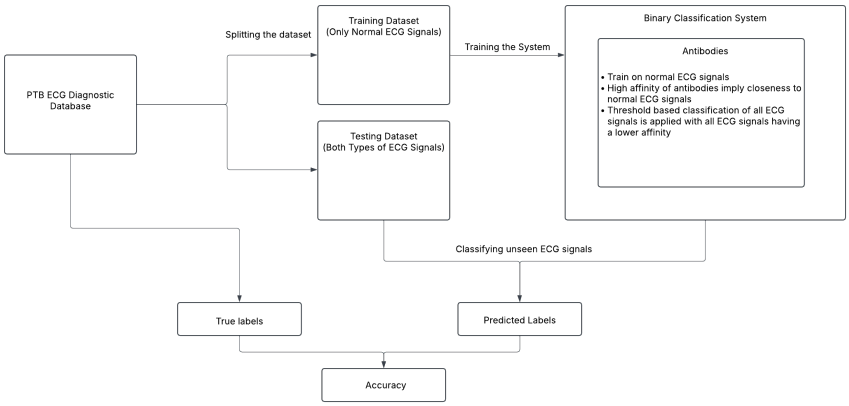

Figure 1: Overview of the ECG Binary Classification System

In this report, we aim to explore the following research questions:-

1. How accurately is the clonal selection algorithm able to perform the task of ECG classification?
2. What is the impact of changing the hyperparameters of the clonal selection algorithm on the accuracy?
3. How does the clonal selection algorithm compare against other traditional machine learning methods for ECG classification?

2 Methodology

2.1 The PTB Diagnostic ECG Database

This subsection is going to describe the dataset which has been used for experimentation in ECG binary classification tasks, and the different methodologies and techniques associated with the experiments. The PTB Diagnostic ECG Database is a publicly available dataset from the Physikalisch-Technische Bundesanstalt (PTB) in Germany[3]. It is part of the PhysioNet platform, a resource that provides access to complex physiological data for biomedical research. Below are a few features of the dataset:-

1. Number of Rows - The entire dataset consists of 14552 rows, with each row representing a single ECG reading. The last column of each row represents the category that the ECG signal belongs to (normal, or arrhythmic). The dataset is imbalanced, with around 27.8% of the rows (4046) being in the normal category, and the remaining belonging to ECG signals associated with arrhythmia.
2. Number of Columns - Each row consists of 188 columns, with the last column denoting the class of the ECG signal (0 for normal, 1 for arrhythmic). The first 187 values correspond to the signal values at equidistant time steps. All of the values have been preprocessed and are standardized to have a value between 0 and 1. In case an ECG signal occurs for a smaller time than desired, the rest of the columns have been padded with zeros with the signal taking up less number of columns for representation.

2.2 Generation of Training and Testing Datasets

For working on binary classification tasks on this dataset, the below approaches have been followed for splitting the dataset into training and testing datasets for evaluating model performances:-

1. For the clonal selection algorithm - Our clonal selection approach to classifying ECG signals (described below) requires only one class of ECG signals for training. Thus, out of 4046 values of the 'normal' ECG signals available, the decision to sample 3500 random values out of these 4046 values for the training dataset was taken. Another unique 500 ECG signal values were taken for adding to the testing dataset. Another 500 values were implemented to be randomly sampled from the 10506 abnormal ECG signals available to us, to create a full testing dataset of 1000 values. The training and testing datasets are always generated from scratch before running our classification experiments to ensure that the analysis of the different experiments collectively can remove any bias that might occur in the results due to bias in the training or testing data. This method of data selection also ensures that the testing dataset is completely balanced, removing the need for looking at different metrics such as precision, recall, and f1-score for accurately determining the performance of a model, with just accuracy serving as a good metric.

2. For the traditional machine learning classification techniques - Since the traditional machine learning techniques require the presence of both types of categories in the training dataset for the desired results, the entire database of 14552 rows was split in the ratio of 80:20 with the larger amount of data present in the training dataset.

2.3 Clonal Selection Algorithm

This subsection describes the clonal selection algorithm in great detail, with the subsequent subsection focusing on the methodological details that are specific to the application of this algorithm for ECG classification. Clonal selection algorithms are a set of algorithms that have been inspired by Burnet's clonal selection theory, which posits that lymphocytes (B and T cells, similar to antibodies in the clonal selection algorithm) with specific antigen receptors are chosen and cloned for mounting an immune response (the antibody being chosen depends on its affinity with the antigen encountered)[4]. The differentiation of the lymphocyte into effector cells and memory cells has been the basis for the "hypermutation" aspect of the clonal selection algorithm.
Clonal selection algorithms are often implemented as a feature of artificial immune systems, which are a class of rule-based machine learning systems inspired by the principles and processes of the vertebrate immune system. Clonal selection algorithms have been applied for solving a lot of different problems in the past, some of them include:-

1. Fault Diagnosis and Virus Detection - CSA has been used for identifying system faults and detecting viruses. Its immune-based pattern matching capabilities make it effective for anomaly detection and cybersecurity[5].

2. Pattern Recognition - Digits can be recognized with the antigen representing a single digit, let's say 8 in the form of a 11x11 pixel with binary values, with antibodies trying to achieve the highest affinity by having the closest 11x11 pixel values to the antigen[5].

3. Optimization of mathematical functions - CSA has been applied to multi-modal and continuous function optimization problems, helping to find optimal solutions in complex and dynamic search spaces[5].

Figure 2 provides an overview of the clonal selection algorithm with its different steps.

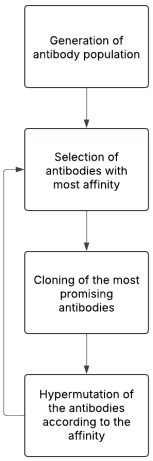

Figure 2: Overview of the Clonal Selection Algorithm

The below figure provides more context to the algorithm with the pseudocode.

GENERAL STRUCTURE OF THE ALGORITHM

1. Generation of the antibody population
2. Set the fitness function
3. for every i from 1 to n:
    a. for each antibody:
        i. Calculate fitness for each antibody
    b. Select the n best antibodies
    c. for each antibody selected:
        i. Perform cloning proportional to affinity.
        ii. Perform hypermutation inversely proportional to affinity.

Figure 3: Pseudocode of the Clonal Selection Algorithm

Below is an overview of the different steps of the clonal selection algorithm:-

1. Generation of the antibody population - Since the final aim of the algorithm is to produce a set of antibodies which have the maximum possible affinity with the potential antigens, an initial random population of antibodies is generated as the first step of the algorithm.

2. Selection of antibodies with the most affinity - Depending on the task, such as digit recognition, a fitness function is selected which can calculate the affinity of the generated antibodies in comparison with the required antigen. Proper metrics include the mean squared error, and metrics such as accuracy, precision, recall, or the F1-score. N-antibodies (with N varying between different applications and instances) having the best affinity scores are selected for the next steps in the algorithm.

3. Cloning of the most promising antibodies - The N-best antibodies selected are cloned in proportion to their affinity. The total number of clones depends on the cloning factor, which is a hyperparameter of

the clonal selection algorithm and represents the total number of clones which are generated during the cloning process. The total number of clones for each individual 'antibody' are calculated according to the below formula:-

$$QC_k^i = \left(\frac{af_k^i}{\sum_{k=1}^{n} af_k^i} \right) * Cl$$

where:-

QC_k^i = number of clones generated for each antibody k in iteration i.

af_k^i = affinity of antibody k in iteration i.

n = number of best antibodies selected for cloning in previous and next iterations.

Cl = Total number of clones to be generated from the antibody population.

4. Diversity Mechanisms - Aside from selecting the best N-antibodies and generating their clones which shall be used in the next iteration of the algorithm according to the cloning factor value, an arbitrary amount of antibodies are randomly generated at each step as well in some CSA implementations for ensuring that the population remains diverse enough to encourage broad explorations of the entire range of potential values.

5. Hypermutation of the antibodies according to the affinity - In each iteration, the entire 'newly formed' generation of antibodies goes through mutations according to the below formula for each of the feature of the antibodies:-

$$\text{hypermutation rate}_k^i = \left(1 - \frac{\text{affinity}_k^i}{\text{maximum affinity}} \right) * \beta$$

where:-

β is the hypermutation factor, a hyperparameter

affinity is a measure which directly corresponds to how good an antibody is.

6. Improvement Over Iterations - Steps 2 to 5 count as one iteration of the algorithm. The algorithm can be run for as many iterations as possible until convergence or desirable results are achieved (best antibodies are found).

2.4 Clonal Selection Algorithm for ECG Classification

For performing the task of binary classification on our dataset (described in section 2.1), after generating the training and testing datasets (as described in section 2.2), we make use of the clonal selection algorithm (described in section 2.3) with the following implementations of the different aspects of the algorithm:-

1. Antibody - An antibody consists of 187 values, with each value being a number between 0 and 1, similar to the ECG database (removing the last column, which is the label).

2. Initial Population Generation - An initial population of 100 antibodies is generated in the first step of our algorithm.

3. Manhattan distance- The Manhattan distance is a metric for calculating the similarity between two different entities, and has been incorporated in the choice of our fitness function for calculating affinities. The Manhattan distance between one antibody, and one antigen (normal ECG signal) is calculated as the sum of the magnitude of difference between each of the 187 values. In mathematical terms:-

$$d(x, y) = \sum_{i=1}^{n} \|x_i - y_i\|$$

where:-

x_i is the i^{th} feature of the antibody.

y_i is the i^{th} feature of the antigen.

n is the total number of features in both the antibody and the antigen.

4. Affinity / Choice of fitness function - Since we want each antibody to be representative of 'normal ECG signals', we want them to have the minimum manhattan distance value for all of the ECG signals in the training dataset collectively. Thus, our choice of fitness function is the collective Manhattan distance or the sum of all Manhattan distances between the antibody and all of the antigens in the training dataset. A lower Manhattan distance or 'affinity' corresponds to higher chances of being cloned.

5. Reasoning for three fitness functions - Since most of the ECG signals in the dataset have been padded with 0s after 100 columns, or even after points between the 50th and 75th columns, all of the experiments have been conducted three times, with 'fitness function 1' calculating Manhattan distance for only the first 50 columns or time samples, 'fitness function 2' calculating Manhattan distance for the first 75 columns, and 'fitness function 3' calculating Manhattan distance for the first 100 columns. The usage of Manhattan distance only till a certain column helps in preventing the training of the model on useless features such as the padded zeros.

6. Cloning - The 10-best antibodies are selected for future cloning in each iteration. Apart from these 10 selected antibodies, the next generation of antibodies consists of the clones of the antibodies which are generated in proportion to their affinities, with antibodies having lesser 'collective Manhattan distance' values having more clones. A cloning factor of 90 has been selected to generate a total of 100 new antibodies (combined with the 10-best antibodies) in all of the experiments, except the experiment where the cloning factor was varied to observe the impacts.

7. Hypermutation - After cloning, each of the 100 antibodies present in the new generation are hypermutated as expected in direct proportion with the hypermutation factor, and in inverse proportion to how close they are to representing 'normal ECG signals'. Thus, each feature of the antibody is randomly mutated according to the formula given for hypermutation in section 2.3, and on hypermutation, the value gets changed to a different random value between 0 and 1.

8. Reasoning for a lack of diversity mechanism - Clonal selection algorithms, apart from selection of n-best antibodies and cloning, often also involve the introduction of random new antibodies to introduce diversity to the search space and ensure that the algorithm does not end up conducting limited exploration of the possible search space. However, in this case, since the initial population of antibodies is already sufficiently diverse, along with the hypermutation mechanism effectively maintaining exploration, sufficient diversity is achieved without even adding any more diverse antibodies. Thus, our implementation does not introduce random antibodies in each generation.

As we have generated balanced testing datasets, a threshold measure of taking the median of all the affinities has been the basis for the classification of the different ECG signals. Other approaches include taking the mean of the entire training dataset's best antibodies, or the i^{th} samples (e.g. 70% of the dataset has 'Manhattan Distance' value below threshold).
As mentioned earlier, as the dataset is completely balanced and keeps changing over different iterations of the algorithm being run, the accuracy metric alone has been determined to be a good choice of metric for evaluating model performance on the testing dataset. An enhancement that was given thought was running the algorithm multiple times to take an average over multiple runs, however, since not much variability was observed among multiple runs, that enhancement was not implemented.
In the below sections, the results (and discussions) of performing binary ECG classification using our described clonal selection algorithm methodology have been displayed. Our proposed classification methodology differs from the traditional machine learning techniques in the sense that the other techniques such as logistic regression and random forest classification are focused on determining the distinguishable factors of all the categories, but our approach hypothesizes that all of the ECG signals belonging to one class of signals have some inherent features, the identification of which, in the form of antibodies, can result in accurately identifying that particular class with a greater affinity than other classes.

3 Results

The below subsections contain a few figures that represent the different experiments which were conducted. Using three different fitness functions has given rise to more data points for further discussion. Unless specified, all of the figures are using the fitness function considering 50 time samples.

3.1 Sample Iterations of Clonal Selection Algorithm and Highest Accuracy Obtained

Figure 4 represents a sample run of the clonal selection algorithm with a low hypermutation factor value over 100 iterations. In contrast to figure 4, figure 5 represents a sample run with a high hypermutation factor over 100 iterations. Figure 6 represents the clonal selection algorithm run which resulted in the highest accuracy of 74.8% being obtained.

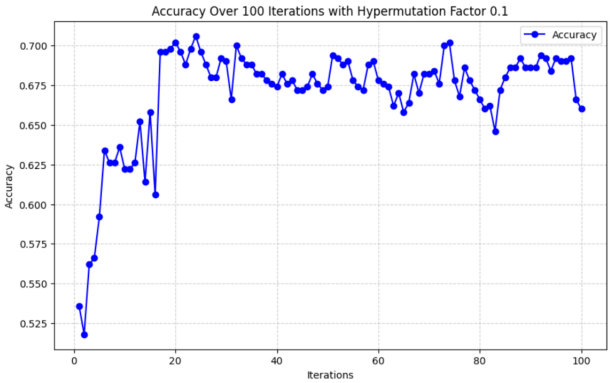

Figure 4: Running CSA and calculating accuracies on test set

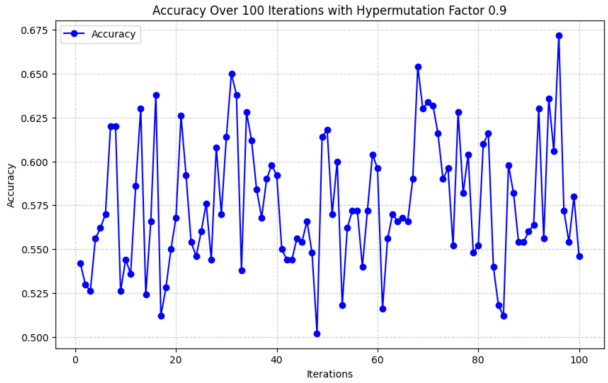

Figure 5: Running CSA with a high hypermutation factor

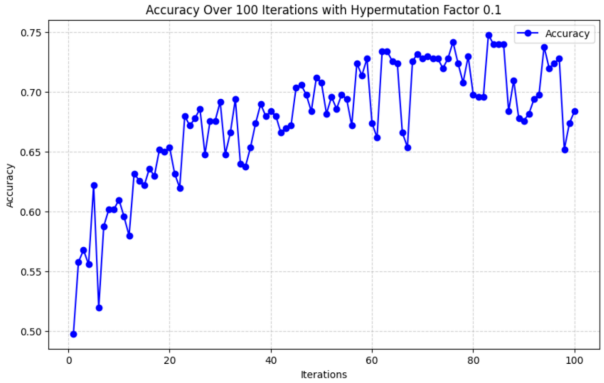

Figure 6: CSA run with highest accuracy (fitness function is considering 100 time samples)

The above sample runs demonstrate that the algorithm runs much more smoothly, without overshooting when the hypermutation factor is low (0.1, 0.2, etc.) rather than high (0.9).

3.2 Impact of varying the 'hypermutation factor'

The below 3 figures show how the 'maximum accuracy' obtained on running 100 iterations of the clonal selection algorithm vary with the hypermutation factor. The three figures correspond to three different fitness functions being used for calculating affinity (50, 75 and 100 time samples).

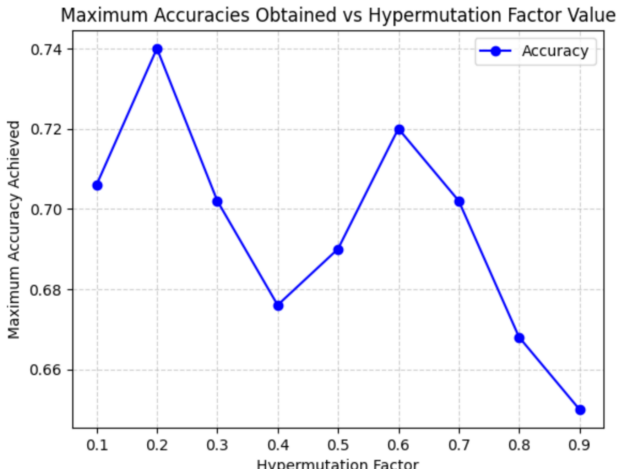

Figure 7: Varying Hypermutation Factors while considering 50 time samples for affinity

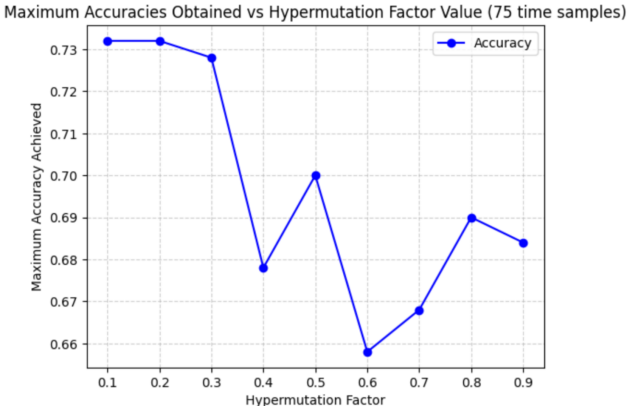

Figure 8: Varying Hypermutation Factors while considering 75 time samples for affinity

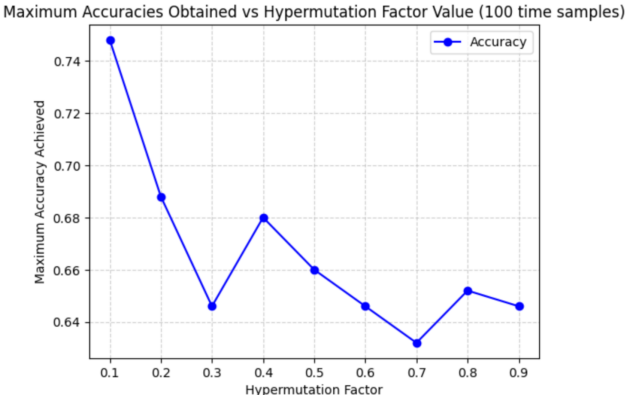

Figure 9: Varying Hypermutation Factors while considering 100 time samples for affinity

3.3 Impact of varying the 'cloning factor'

The total number of clones that generated after an initial population of 100 was initialized were varied from a minimum of 50 total clones to a maximum of 200 total clones with a step size of 50 clones. Below is the impact on the maximum accuracy being obtained which was observed. The hypermutation factor for all of the CSA iterations was 0.2.

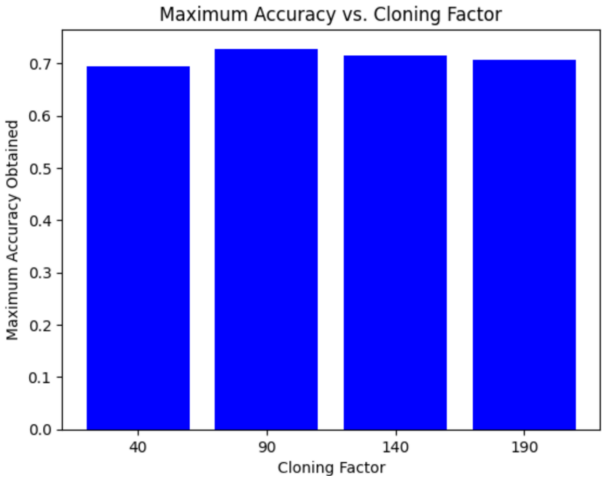

Figure 10: Comparison of accuracies while varying Cloning Factors with a fixed hypermutation factor of 0.2

3.4 Comparison against traditional machine learning techniques

The clonal selection algorithm (CSA) managed to achieve a highest accuracy of 74.8% in all of the experiments that were run. This accuracy was achieved with the fitness function considering 100 time samples, with a hypermutation factor of 0.1, and 100 clones being generated in each iteration. Figure 11 shows the

performance of our technique against other classification techniques (described in methodology). All of the other techniques outperform our proposed methodology.

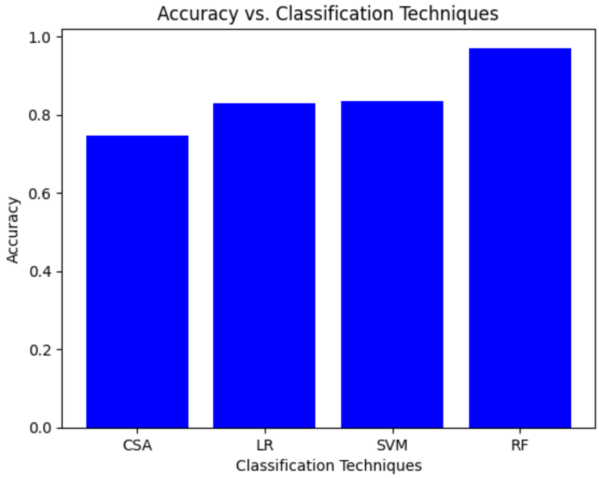

Figure 11: Comparison of the Clonal Selection Algorithm against other traditional Machine Learning Techniques for binary ECG classification

4 Discussion

4.1 Feasibility of using CSA for ECG Classification

CSA is able to achieve a maximum accuracy of 74.8%, and in general achieves maximum accuracies in the range of 60-75% for ECG binary classification tasks. While this is better than a random guessing model which would achieve accuracies closer to 50%, CSA alone does not seem to be a good alternative for achieving state of the art results. A few modifications such as using multiple antibodies (for classifying different classes separately, and combining these CSA approaches) might be explored for achieving further accuracy. Apart from this, further work includes applying this methodology on a different dataset. The MIT BIH arrhythmia database is a lucrative choice[6]. In contrast to our approach, CSA has also been used earlier for determining the 'most relevant' features of the ECG signals, and combined with other techniques for more deterministic classification[7]. More such hybrid techniques can be developed.

4.2 Impact of Hypermutation Factor

Figures 4 and 5 show that lower hypermutation factors lead to a faster convergence toward optimal accuracy compared to higher hypermutation factors. Higher hypermutation factors result in more noise due to increased mutations, causing the model to overshoot and deviate from the 'optimal antibody' characteristics. Although higher hypermutation factors may reach their own peak values faster, these peaks are often lower than those achieved with lower hypermutation factors, as can be seen from figures 7, 8, and 9. Thus, lower hypermutation factors are more effective for this task as they minimize overshooting and maintain stability. Even the highest accuracy value achieved involved a low hypermutation factor value, as can be seen in figure 6.

4.3 Impact of Cloning Factor

From figure 10, it can be seen that varying the cloning factor is resulting in minimal differences on the highest accuracy value being obtained. An argument for limited changes can be the lack of population diversity mechanisms which can result in a limited space exploration, however, as mentioned in the methodology, since each of the time sample has a lot of possible variations with a hypermutation factor of 0.2 having been used, lack of diversity mechanisms should not affect the results much for our task. The values not changing much with the different cloning factor values seems to suggest that for the ECG classification task, there is an inherent limit to the achievable accuracy based on the features and the data representation. If such a limit is approached, more clones cannot meaningfully increase accuracy, and a saturation point in learning has been reached while using the clonal selection algorithm.

4.4 Comparison with traditional machine learning classification techniques

Figure 11 shows a comparison of the accuracy being achieved while using CSA with three other classification techniques, logistic regression, support vector machines, and random forest classification. CSA seems to have the least impressive performance, with logistic regression and SVM performing marginally better. However, the random forest technique outperforms all of the other techniques, achieving a 97.08% accuracy. These findings indicate that even though CSA outperforms random guessing and is able to achieve better results, it is not feasible as an alternative to even the traditional classification methods, which have been outperformed by neural network architectures.

References

[1] Shalin Savalia and Vahid Emamian. "Cardiac arrhythmia classification by multi-layer perceptron and convolution neural networks". In: *Bioengineering* 5.2 (2018), p. 35.

[2] J. Marques et al. "ECG manifestations of the biggest outbreak of Chagas disease due to oral infection in Latin-America". In: *Arquivos Brasileiros de Cardiologia* 101 (2013), pp. 249–254.

[3] R. Bousseljot, D. Kreiseler, and A. Schnabel. "Nutzung der EKG-Signaldatenbank CARDIODAT der PTB über das Internet". In: *Biomedizinische Technik* (1995).

[4] F. M. Burnet. *The Clonal Selection Theory of Acquired Immunity*. Vol. 3. Nashville: Vanderbilt University Press, 1959.

[5] Berna Haktanirlar Ulutas and Sadan Kulturel-Konak. "A review of clonal selection algorithm and its applications". In: *Artificial Intelligence Review* 36 (2011), pp. 117–138.

[6] G. B. Moody and R. G. Mark. "The impact of the MIT-BIH arrhythmia database". In: *IEEE Engineering in Medicine and Biology Magazine* 20.3 (2001), pp. 45–50. DOI: 10.1109/51.932724.

[7] W. Rahman et al. "Cardiovascular disease prediction utilizing machine learning and feature selection with clonal selection algorithm". In: *2023 5th International Conference on Sustainable Technologies for Industry 5.0 (STI)*. IEEE, Dec. 2023, pp. 1–6. DOI: 10.1109/STI59929.2023.00006.