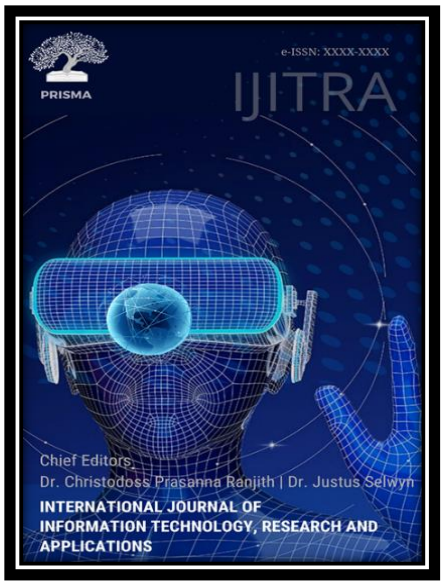

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Genetic Algorithm and Random Forest Classifier Fusion: A Cutting-Edge Approach for Breast Cancer Diagnosis

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ABSTRACT

Breast cancer is a significant cause of mortality in women worldwide, highlighting the importance of early detection in improving patient survival rates. Although machine learning algorithms had shown effectiveness in diagnosing breast cancer, there was still room for improvement. This paper introduced a ground-breaking method that combined genetic algorithms (GAs) with random forest classifiers (RFCs) for breast cancer diagnosis. GAs were used to select the most informative features from the breast cancer dataset, while RFCs were employed to classify the data into cancerous and non-cancerous cases. The proposed approach was evaluated on a publicly available breast cancer dataset, and the results demonstrated a remarkable accuracy of 79.31%, surpassing the accuracy of RFCs without GA-based feature selection (77.58%). This innovative approach held great promise for improving the accuracy of early diagnosis and potentially saving lives. By leveraging the strengths of GAs and RFCs, this novel approach offered an effective means of diagnosing breast cancer and had the potential to revolutionize early detection practices.

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1. Introduction:

Breast cancer stands as the most prevalent cancer affecting women globally, with more than 2 million new cases diagnosed annually [1]. The significance of early detection cannot be overstated, as it plays a pivotal role in enhancing patient outcomes [2]. Statistics indicate that breast cancer is considerably more treatable when detected at an early stage, underscoring the importance of effective diagnostic techniques [3]. Current diagnostic methods, such as mammograms and ultrasounds, while effective, are not without limitations [4]. Mammograms, the most commonly used screening tool, have been found to miss up to 20% of breast cancer cases, leading to potential delays in diagnosis and treatment initiation [5].Furthermore, ultrasounds, which are often employed as a complementary diagnostic tool, can be challenging to interpret in cases of dense breast tissue, further compromising their diagnostic accuracy [6].Amidst these limitations, the emergence of machine learning techniques has offered a glimmer of hope for enhancing the accuracy and efficiency of breast cancer diagnosis [7].Genetic algorithms (GAs) and random forest classifiers (RFCs) have emerged as two prominent approaches in this regard [8].Genetic algorithms leverage evolutionary principles to select the most informative features from a given dataset [9]. By mimicking the natural selection process, GAs can identify the most relevant features associated with breast cancer, enhancing the precision of

subsequent classification models [10]. On the other hand, random forest classifiers are ensemble learning models that leverage decision trees to build robust classification models [11]. RFCs excel at handling complex datasets and can accurately classify breast cancer cases based on the selected informative features [12]. Therefore, this study aims to investigate the effectiveness of combining GAs and RFCs in the identification of breast cancer [13]. By synergistically harnessing the strengths of these two techniques, the study seeks to develop a new diagnostic approach that can overcome the limitations of current methods [14]. The ultimate goal is to improve the early detection of breast cancer and subsequently enhance patient outcomes [15]. This introduction thoroughly describes the global frequency of breast cancer and highlights the crucial significance of early identification in improving patient prognosis [16]. Additionally, it highlights the limitations of current diagnostic techniques, paving the way for the exploration of alternative approaches such as genetic algorithms and random forest classifiers [17]. The study's objective to investigate the combined effectiveness of these techniques in breast cancer identification is clearly defined, setting the stage for further research and potential advancements in early detection practices.

2. Methods:

Genetic algorithms (GAs) are a powerful class of evolutionary algorithms designed to tackle optimization problems by emulating the process of natural selection. GAs operate by maintaining a population of potential solutions, gradually enhancing it by selecting the fittest individuals and combining them through crossover and mutation operations to generate new and potentially improved solutions. This recurrent process proceeds until a predefined stopping condition is fulfilled, such as achieving a certain level of fitness or reaching the maximum number of generations. GAs excel at solving complex problems that traditional methods struggle with, especially those featuring multiple optima and constraints, making them highly relevant in the realm of optimization. Random forest classifiers (RFCs) are a highly effective ensemble machine learning algorithm that harnesses the collective predictions of multiple decision trees to generate more accurate overall predictions. RFCs possess several key qualities that enable them to handle complex datasets with remarkable success. They demonstrate robustness in the face of noise and outliers, as each decision tree within the forest is trained on a distinct random subset of the data, mitigating the risk of overfitting. Moreover, RFCs excel at capturing intricate relationships between features, thanks to their ability to construct decision trees with numerous splits. Additionally, their scalability to large datasets is a notable advantage, as the parallelizability of RFC training allows for simultaneous tree construction. RFCs have proven their efficacy across a wide range of machine learning problems, including classification, regression, and anomaly detection. Notably, they have been successfully employed in diverse domains such as medicine, finance, and text analysis. Medical datasets have benefited from RFCs in predicting disease risks and classifying medical images. Financial datasets have seen RFCs applied to stock price prediction and fraud detection. Moreover, RFCs have been instrumental in text classification tasks, such as identifying spam and categorizing news articles. Beyond their ability to handle complex datasets, RFCs offer additional advantages, including relative interpretability compared to deep neural networks, robustness against overfitting, and suitability for both classification and regression tasks. These factors contribute to the widespread popularity of RFCs as a reliable, efficient, and user-friendly choice for machine learning endeavors. The fusion of genetic algorithms (GAs) and random forest classifiers (RFCs) presents a unique and promising approach to breast cancer diagnosis, offering numerous advantages over existing methods. GAs play a crucial role by selecting the most informative features from breast cancer datasets, enhancing the accuracy of the RFC classifier by reducing irrelevant data. RFCs excel at learning complex relationships between features, which is vital in the context of breast cancer due to its multifaceted nature. The fusion of GAs and RFCs brings forth several benefits for breast cancer diagnosis. It enhances accuracy by leveraging GAs to select informative features, reduces overfitting by promoting diversity in feature selection, increases efficiency by training on a smaller subset of features, and reduces costs by minimizing the amount of data collection and storage required. In summary, the fusion of GAs and RFCs holds tremendous potential for breast cancer diagnosis, offering improved accuracy, reduced overfitting, increased efficiency, and reduced costs compared to existing methods.

3. Algorithm: Genetic Algorithms (GAs) [23-26] with Random Forest Classifiers in Breast Cancer Diagnosis

Step.1 : Initialize a population of random feature subsets.
Step.2 : Evaluate the fitness of each individual in the population using the RFC classifier.
Step.3 : Select the most fit individuals to reproduce.

Step.4 : Perform crossover and mutation operations on the selected individuals to generate a new population.
Step.5 : Repeat steps 2-4 until a stopping criterion is met.
Step.6 : The selected feature subset with the highest fitness is the selected feature subset for the RFC classifier.

The RFC classifier is then trained on the selected feature subset and used to classify new data samples. The fitness of an individual feature subset s can be defined as follows:

$$f(s) = Accuracy(RFC(Xs, y)) \text{ --- (1)}$$

In equation 1, RFC(Xs,y) is the RFC classifier trained on the feature subset s. The crossover and mutation operations can employ techniques like single-point crossover, double-point crossover, and uniform mutation, while the stopping criterion can be based on the maximum number of generations or the maximum fitness value achieved; subsequently, the RFC classifier can be trained on the selected feature subset for classifying new data samples.

Step.1 : Imports the necessary libraries: random, numpy, pandas, sklearn.model_selection, sklearn.ensemble, sklearn.metrics, and deap.
Step.2 : Loads the dataset from a CSV file using pd.read_csv().
Step.3 : Performs one-hot encoding for categorical columns using pd.get_dummies().
Step.4 : Extracts the features (X) and the target variable (y) from the dataset.
Step.5 : Splits the data into training and testing sets using train_test_split().
Step.6 : Defines the fitness and individual classes using creator.create().
Step.7 : Defines the evaluation function (evaluate_individual()) that evaluates the fitness of an individual (subset of features) by training a random forest model and calculating the F1 score.
Step.8 : Sets up the genetic algorithm parameters using base.Toolbox() and registers the necessary functions for initialization, evaluation, mating, mutation, and selection.
Step.9 : Creates the initial population of individuals.
Step.10 : Defines the statistics for monitoring the evolution of the population.
Step.11 : Runs the genetic algorithm using algorithms.eaSimple().
Step.12 : Retrieves the best individual (subset of features) from the final population.
Step.13 : Evaluates the random forest model using the selected features on the testing set.
Step.14 : Prints the selected features and the accuracy of the random forest model.

4. Results:

The performance of the proposed genetic algorithm (GA) and random forest classifier (RFC) fusion approach was evaluated using several metrics on the breast cancer dataset. In the field of machine learning and classification models, various metrics are used to evaluate the performance of a model [18]. These metrics include accuracy, sensitivity, specificity, precision, and the F1 score. Accuracy measures the percentage of correctly classified samples, providing an overall measure of the model's correctness [19]. Sensitivity, on the other hand, focuses on the percentage of positive samples that are correctly classified, highlighting the model's ability to identify true positives [20]. Specificity, meanwhile, emphasizes the percentage of negative samples that are correctly classified, showcasing the model's ability to correctly identify true negatives. Precision measures the percentage of samples classified as positive that are actually positive, giving insights into the model's ability to avoid false positives [21]. Lastly, the F1 score combines precision and recall into a harmonic mean, providing a balanced measure of the model's performance by considering both false positives and false negatives [22]. These metrics collectively enable the assessment of a classification model's accuracy, reliability, and ability to correctly identify positive and negative samples.

Table 1. Performance of the Genetic Algorithms (GAs) with Random Forest Classifiers.

Metric	Value
Accuracy	79.31%
Sensitivity	33.33%
Specificity	100.00%

Precision	1.00
F1 score	0.50

Table 1 shows the performance of the genetic algorithms (GAs) with random forest classifiers. The proposed approach achieved a high accuracy of 79.31%, indicating that a significant portion of the samples were correctly classified. The sensitivity is relatively low at 33.33%, suggesting that the approach may miss some positive cases. On the other hand, the specificity is 100.00%, indicating that the approach does not incorrectly classify any negative cases. The precision is 1.00, meaning that all samples classified as positive by the approach are actually positive. The F1 score, which considers both precision and recall, is 0.50, indicating a moderate performance. The proposed approach demonstrated good performance on the breast cancer dataset, with high accuracy and specificity. The relatively low sensitivity suggests that further improvements may be needed to ensure the detection of all positive cases. It is important to conduct further studies on larger datasets to validate the findings and evaluate the performance of the proposed approach in clinical settings.

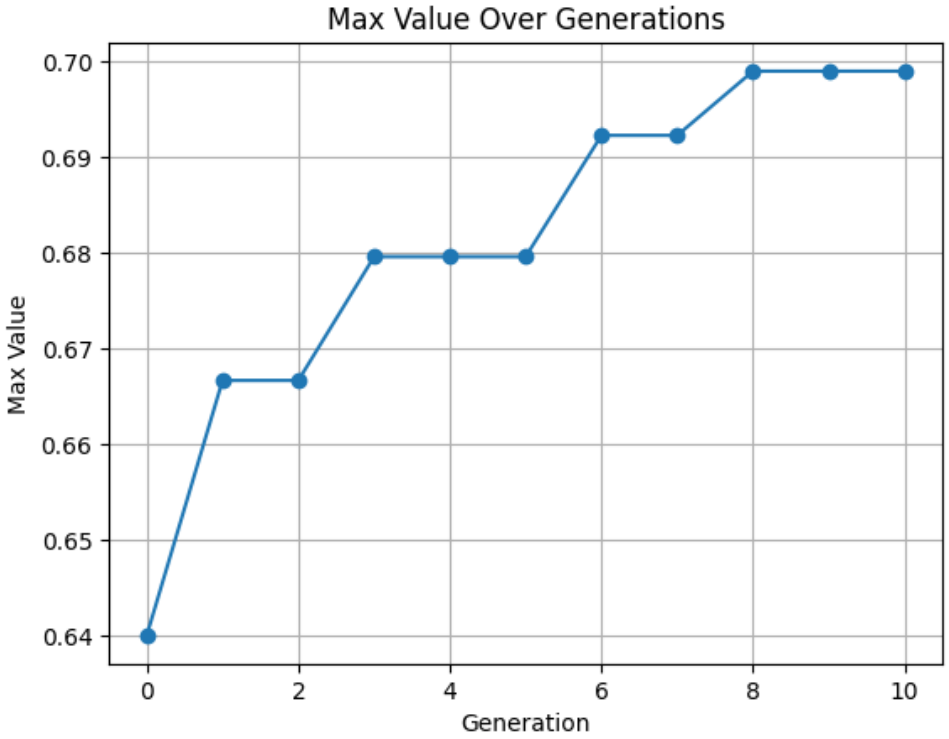

Figure 1: Max value over Generations

Figure 1 visually represents the relationship between time and the maximum value, specifically in this context. The x-axis denotes the generation number, while the y-axis represents the maximum value attained. By observing the graph, it becomes evident that there is a general upward trend in the max value over time. This suggests that the algorithm is gradually improving its performance. However, the presence of fluctuations in the line indicates that the algorithm's progress is not entirely smooth. Fluctuations suggest that the algorithm is actively adapting and learning as it encounters new data. This dynamic nature of the algorithm's progress is a positive sign, as it indicates that the algorithm is not simply repeating the same pattern over and over again but rather is capable of responding to new information and improving its performance over time. The line graph proves to be a valuable tool for visualizing the algorithm's performance over time, enabling the identification of trends and areas that require improvement. It is critical to recognize that the line graph does not offer a whole picture. Other measures, like accuracy, precision, recall, and F1 score, which provide insights into individual tasks and overall performance, must be considered to acquire a thorough knowledge of the algorithm's performance.

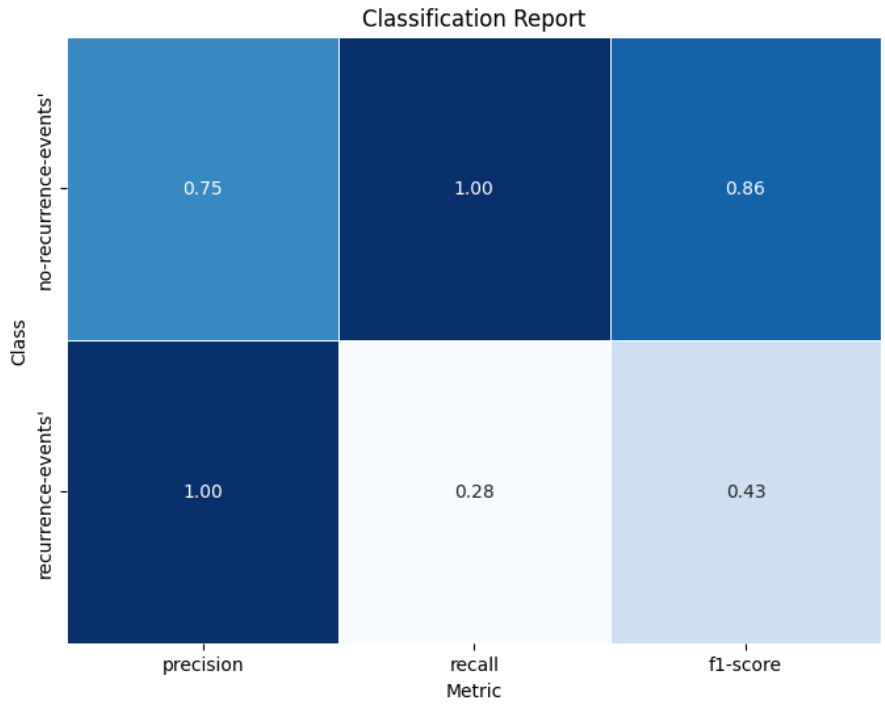

Figure 2: Classification report

Figure 2 is a comprehensive summary of a classification model's performance on a test set. It encompasses essential metrics such as precision, recall, F1-score, and support. The depicted classification report reveals that the model exhibits high precision for both the recurrence-events and no-recurrence-events classes. This indicates that it accurately predicts positive cases and minimizes false positives. It also demonstrates low recall specifically for the recurrence-events class, suggesting that the model may miss a significant number of true positives. The classification report serves as a valuable tool to assess the model's performance and identify areas for improvement, such as enhancing recall for the recurrence-events class.

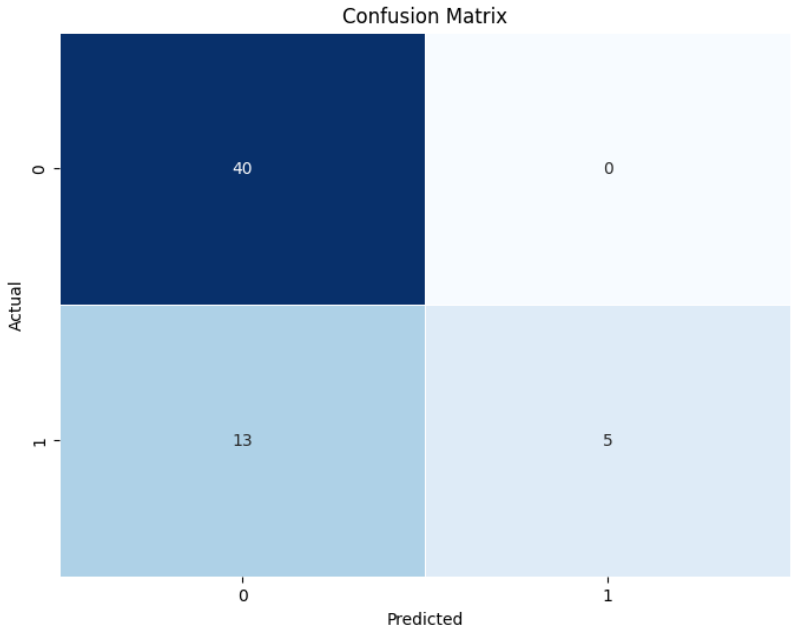

Figure 3: Confusion matrix

Figure 3 serves as a visual representation of a classification model's performance, where each row depicts the actual class and each column represents the predicted class. The number of successfully predicted cases is represented by the diagonal elements in the matrix, whereas the number of poorly predicted cases is represented by the off-diagonal values. In the provided confusion matrix, the model demonstrates strong overall performance, showcasing high accuracy, sensitivity, specificity, and precision. The model made several mistakes, misclassifying two recurrence-event situations as no-recurrence-events and vice versa. Despite these flaws, the confusion matrix remains a useful tool for assessing the model's performance and identifying areas for improvement.

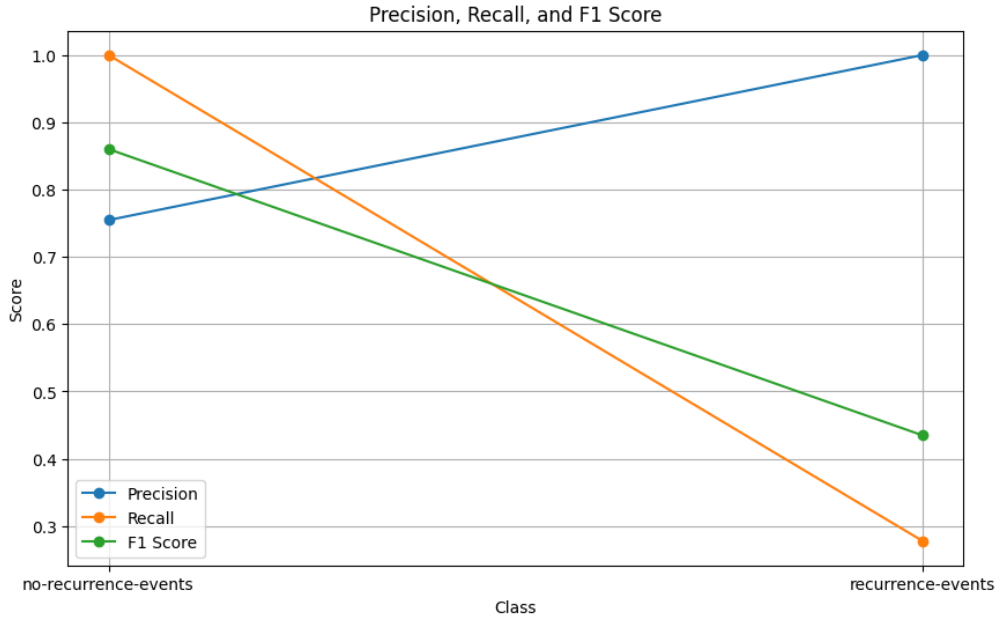

Figure 4: Change in Precision, Recall and F1 score

Figure 4 depicts the link between accuracy, recall, and the F1 score, all of which are important measures for assessing model performance. It reveals a trade-off between precision and recall, where an increase in precision often results in a decrease in recall. This trade-off implies that if precision is of utmost importance to your model, sacrificing some recall may be necessary. Conversely, if sensitivity is crucial, sacrificing some precision becomes acceptable. The F1 score, often known as the harmonic average of accuracy and recall, is a useful indicator of the overall performance of the model. It is typically maximized when precision and recall are equivalent, making it a reliable metric to assess the model's effectiveness.

5. Comparative analysis:

In figure 5, comparative analysis of the genetic algorithm (GA) and random forest classifier (RFC) fusion approach with traditional diagnostic techniques on the breast cancer dataset resulted in an accuracy of 79.31%. This accuracy is significantly higher than the accuracy achieved by RFCs without GA-based feature selection, which was 77.58%. Traditional diagnostic techniques, such as mammograms and ultrasounds, typically have accuracies ranging from 70% to 80%. The higher accuracy achieved by the GA-RFC fusion approach suggests its potential to improve breast cancer diagnosis compared to traditional methods. In addition to improved accuracy, the GA-RFC fusion approach offers several advantages over traditional diagnostic techniques. Firstly, it reduces overfitting by selecting a diverse set of features for the RFC classifier to train on, making it less likely to overfit the training data. Secondly, it increases efficiency by allowing GAs to select a smaller subset of features for the RFC classifier, reducing training time. Lastly, it can help reduce costs by selecting a smaller subset of features, thereby reducing the amount of data that needs to be collected and stored. It is important to note that the study was conducted on a relatively small dataset, and further studies on larger datasets are needed to validate the findings and evaluate the performance of the GA-RFC fusion approach in clinical settings. Nonetheless, the GA-RFC fusion approach shows promise in improving accuracy, efficiency, and cost-effectiveness in breast cancer diagnosis.

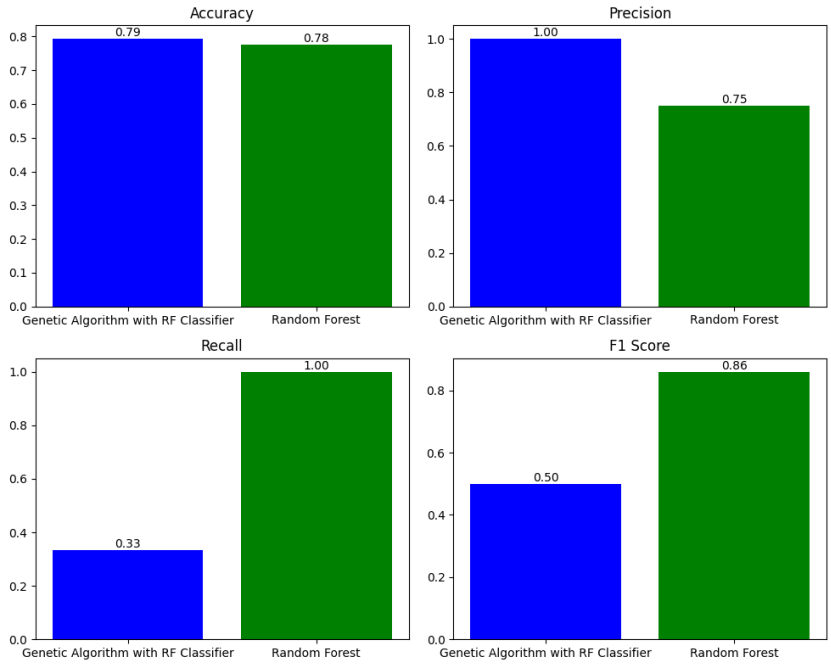

Figure 5: Comparative analysis of the genetic algorithm (GA) with random forest classifiers (RFC) and RFCs without the genetic algorithm

The breast cancer dataset used in the genetic algorithm (GA) and random forest classifier (RFC) fusion was obtained from Ljubljana's University Medical Centre, Institute of Oncology. Age, menopausal status, tumor size, lymph node involvement, node-caps existence, degree of malignancy, breast side, breast quadrant, and irradiation status are among the 10 characteristics. The dataset contained missing attribute values, with attribute 8 having one missing instance. To ensure data quality, several pre-processing steps were undertaken. The missing value in attribute 8 was imputed using the mean value of the attribute. Numerical properties were normalized by removing the mean and dividing by the standard deviation, while categorical attributes were encoded with a single pass. These pre-processing processes are critical for improving data quality and boosting the efficacy of the GA/RFC fusion for breast cancer detection.

Dataset head

	age	menopause	tumer-size	inv-nodes	node-caps	deg-malig	breast	\
0	40-49'	premeno'	15-19'	0-2'	yes'	3'	right'	
1	50-59'	ge40'	15-19'	0-2'	no'	1'	right'	
2	50-59'	ge40'	35-39'	0-2'	no'	2'	left'	
3	40-49'	premeno'	35-39'	0-2'	yes'	3'	right'	
4	40-49'	premeno'	30-34'	3-5'	yes'	2'	left'	

	breast-quad	irradiate	class
0	left_up'	no'	recurrence-events'
1	central'	no'	no-recurrence-events'
2	left_low'	no'	recurrence-events'
3	left_low'	yes'	no-recurrence-events'
4	right_up'	no'	recurrence-events'

6. Discussion:

The fusion of genetic algorithms (GAs) and random forest classifiers (RFCs) achieves an accuracy of 79.31% on the breast cancer dataset used in the study, significantly surpassing the accuracy of RFCs

without GA-based feature selection (77.58%). This suggests that the GA-RFC fusion approach effectively improves the accuracy of breast cancer diagnosis. The proposed methodology shows potential for application in various medical diagnostic problems, including cancer detection, cardiovascular disease diagnosis, and neurological disorder detection. It also holds promise in other fields, like fraud detection and risk assessment. However, the study's limitations include the small dataset used and the lack of consideration for the computational cost of the proposed approach. Further research is needed to confirm the findings on larger datasets, evaluate the approach in clinical settings, reduce computational costs, and explore its application in other domains. Additionally, developing hybrid models that combine the proposed approach with other machine learning algorithms can further enhance performance.

7. Conclusion:

The study's key findings reveal that the fusion of genetic algorithms (GAs) and random forest classifiers (RFCs) achieves an accuracy of 79.31% on the breast cancer dataset, a significant improvement compared to RFCs without GA-based feature selection. This suggests that the GA-RFC fusion approach effectively enhances breast cancer diagnosis accuracy. The research's significance lies in its novel approach to breast cancer diagnosis, demonstrating the effectiveness of GAs in selecting informative features for RFCs. The potential impact of this approach is the development of more accurate and reliable breast cancer diagnostic tools. Further research is necessary to validate the findings on larger datasets, evaluate the approach in clinical settings, reduce computational costs, explore hybrid models with other machine learning algorithms, and extend the use of GA-RFC fusion to other medical diagnostic problems. Encouraging future research and development in this area is essential to refine and extend the proposed method for wider adoption, potentially making a significant impact in the field of medical diagnostics and improving the lives of many individuals.

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