Genetic Algorithm-optimized k-nearest Neighbors and Support Vector Machines for Breast Cancer Detection in Resource-constrained Environments

Abebe Alemu, Anteneh Girma, Mesfin Abebe, Ramasamy Srinivasagan

***Abstract*—Breast cancer poses a significant global threat, highlighting the urgent need for early detection to reduce mortality rates. Researchers are working to minimize the occurrence of false positives and false negatives, thereby improving the efficiency of breast cancer detection models. To achieve this, they employ advanced techniques such as artificial intelligence, machine learning, deep learning, and computational intelligence. Support vector machines (SVM) and k-nearest neighbors (KNN) are two popular lightweight machine-learning techniques.; however, their effectiveness depends on proper feature selection and parameter tuning. Genetic algorithm optimization provides a solution by intelligently selecting relevant features and fine-tuning parameters, which enhances classification accuracy for early diagnosis. This study demonstrates the effectiveness of a hybrid computational intelligence model that utilizes genetic algorithms for feature selection. The proposed GAKNN-SVM model shows superior performance in detecting breast tumors, utilizing the Wisconsin Breast Cancer Diagnostic Dataset. The results indicate significant improvements, with accuracy, sensitivity, and specificity rates reaching 98.25%, 98.15%, and 98.41%, respectively, based on 171 test samples. Overall, genetic algorithms and machine learning approaches hold great promise for improving breast cancer detection accuracy, ultimately leading to better diagnostic outcomes and reduced mortality rates, especially in resource-constrained environments.**

***Index Terms*—GAKNN-SVM, Breast Cancer, Hybrid, Computational Intelligence, Genetic Algorithms.**

TABLE I
ACRONYMS

Short form	Description
AI	Artificial Intelligence
ANN	Artificial Neural Network
BC	Breast Cancer
CI	Computational Intelligence
CNN	Convolutional Neural Network
CT	Computed Tomography
DE	Differential Evolution
DL	Deep Learning
FP	False Positives
FN	False Negatives
GA	Genetic Algorithm
IDC	Invasive ductal carcinoma
ILC	Invasive lobular carcinoma
KNN	K nearest neighbors
LR	Logistic Regression
MCC	Matthews correlation coefficient
MIAS	Mammographic Image Analysis Society
ML	Machine Learning
PSO	Particle swarm optimization
RF	Random Forest
SVM	Support Vector Machine
TP	True Positives
TN	True Negatives
WDBC	Wisconsin diagnosis of BC

I. INTRODUCTION

A. Background

CANCER encompasses more than 100 diseases caused by genetic changes, disrupting normal cell growth and leading to uncontrolled proliferation. As a result, a mass called a tumor forms [1]. Breast cancer is the most common type of cancer and is the second leading cause of death worldwide [2], [3]. Early detection is crucial for successful treatment, as noted by [4] and [5]. The survival rate for early-stage breast cancer is 100%, while the survival rate drops to 28% for stage IV breast cancer. Breast tumors can be malignant (cancerous) or benign. According to GLOBOCAN [6], breast cancer is a major public health issue that affects women around the world [7].

Breast composition, mass, density, shape, margin, size, and architectural distortion are some of the factors used to diagnose breast cancer. Identification as malignant or benign depends on the characteristic extraction process [8]. Once the features are extracted, the next step is to segment the image and obtain important properties such as depth, coarseness, smoothness, and regularity. These properties are crucial in accurately differentiating between the two types of cancer. Those are invasive ductal carcinoma, which starts in the milk ducts and spreads to nearby breast tissue, and invasive lobular carcinoma, which starts in the milk-producing glands (lobules) in the breast and often spreads to nearby breast tissue. Evaluating and choosing the best image extraction algorithms is important to ensure the accuracy of the results [9].

Breast cancer detection involves analyzing medical data to determine whether tumors are malignant or benign. The revolution in artificial intelligence has made it possible to automate breast cancer detection with digital mammography and digital breast tomosynthesis using AI, ML, DL, and CNN. However, AI has limitations in certain areas that

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Abebe Alemu is a PhD candidate at Adama Science and Technology University, Adama, Ethiopia. (corresponding author to provide phone:+251-911-180703; e-mail: abebe.alemu@research.astu.edu.et).

Anteneh Girma is a professor of Computer Science /Cyber-Security department, University of the District of Columbia, Washington D.C. USA. (e-mail: anteneh.girma@udc.edu).

Mesfin Abebe is a professor of Computer Science and Engineering department, Adama Science and Technology University, Adama, Ethiopia. (e-mail: mesfin.abebe@astu.edu.et).

Ramasamy Srinivasagan is a professor of the Computer Engineering department, CCSIT, King Faisal University, Al Hufuf, Saudi Arabia. (e-mail: rsamy@kfu.edu.sa).

require the development of a large set of rules, and it faces challenges due to increasing demands in learning and search optimization [2], [10]. To overcome these challenges, statistical methods and AI techniques play a vital role [2]. DL has the downside of overfitting the training data, leading to reduced performance in some scenarios. Research shows that deep learning models for early breast cancer detection are not optimal due to a lack of large data sets [11], and require high-quality images as input [12].

CNN is a resource-intensive processing method that needs a lot of data to gain improved precision in breast cancer detection, according to a researcher [13]. Due to this, the researcher is focusing on optimization solutions for diagnosing and predicting breast cancer. The researcher is working on optimizing CNN to detect and predict breast cancer, [14]. Machine learning algorithms such as KNN and SVM are commonly used for this task due to their effectiveness in classification [10]. However, the accuracy of these algorithms depends heavily on the selection of relevant features and the optimization of optimal parameters [15].

Evolutionary and genetic algorithmic computing techniques aid in the diagnosis of breast cancer [16]. Among the metaheuristic algorithms, genetic algorithms are commonly used.

In summary, the accuracy of diagnosis depends mainly on the amount and quality of the training data, and therefore, high-quality image data is crucial for deep learning. According to current data analysis and research, radiologists miss 15% to 35% of breast cancer cases from mammography image data. Furthermore, most research papers focus primarily on the accuracy metrics to evaluate the performance of detecting breast cancer rather than the confusion matrix and other metrics.

B. Genetic algorithm

Computational Intelligence: is a distinct branch of Artificial Intelligence (AI). It is widely used in scientific research and engineering practice. Although both AI and CI are used to address similar problems, they have different methodologies, histories, and tools. CI often involves enhancing performance bioinspired computing techniques, such as evolutionary and genetic algorithms. Several studies have demonstrated the effectiveness of CI-based techniques, including genetics and an evolutionary approach, in various applications [16], [17], [18].

Genetic Algorithm (GA): is a heuristic search method that draws inspiration from genetics and natural selection. It is useful for optimization problems in large and complex search spaces. Its adaptability makes it a valuable tool for solving complex problems across different domains. It works by evolving a population of potential candidate solutions in binary search space over successive generations, using principles such as selection, crossover, and mutation to improve the solutions' fitness iteratively [19].

The features such as parallelism, global optimization, a larger set of solution space, requiring less information [22], providing multiple optimal solutions, probabilistic in nature, and genetic representations using chromosomes make it selective. Its easy customization capability makes it suitable for multi-objective problems such as specialized fitness functions and solution diversity, and it optimizes objectives to minimize cost and maximize performance. Based on this, GA can help the Breast Imaging Reporting and Data System for better decision-making. Striking a balance between conflicting objectives and providing satisfactory performance for all objectives [22].

GA is a versatile optimization method that can be applied in various contexts, including both supervised and unsupervised scenarios. It can also identify informative and relevant features from high-dimensional data, improve the efficiency and accuracy of classification algorithms, and escape local optima due to its population-based approach, which makes it robust. Decomposing or partitioning an image can take a long computational time. However, genetic algorithms can help solve this issue due to their superior search capability [19].

It can perform image processing tasks such as preprocessing, segmentation, object detection, denoising, and recognition. However, decomposing/partitioning an image requires high computational time. By intelligently selecting features and fine-tuning parameters, GA improves classification accuracy, which facilitates breast cancer diagnosis early and accurately. This approach highlights the potential of combining evolutionary computation with lightweight machine-learning techniques to address challenging medical diagnostic tasks, [20].

The GA process begins by initializing a population of chromosomes, each representing a potential solution. Each chromosome in the population is evaluated using a fitness function that measures its performance in terms of classification precision. Chromosomes with higher fitness values are more likely to be selected for the next generation. Selected chromosomes undergo genetic operations such as crossover and mutation to generate offspring for the next generation. Crossover involves combining genetic information from two parent chromosomes, while mutation introduces random changes to maintain genetic diversity within the population. The GA process continues for a predefined number of generations or until a termination criterion is met, such as reaching a satisfactory level of classification accuracy or stagnation in fitness improvement. GA passes through initialization, evaluation, selection, mutation, and cross-over and terminating the process. GA finds to minimize multi-objective functions as:

$$ObjF(i) = |f(x_i)|$$

$$J = (1 + \lambda S^*) \cdot J^* \tag{1}$$

According to [21], *where, J, J^*, λ objective function, cost function, and Lagrang multiplier, respectively.* The mean square error, which is calculated using the cost function, is equal to

$$J^* = MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - y_i^*)^2 \tag{2}$$

where y is the true output (actual), y^* is the model output (forecast) and n is the total number of observations.
For classification problems, the cost function is identified by the mean square error and the classification error.

$$J^* = \frac{1}{n}(\sum_{i=1}^{n}(y_n - y_i^*)^2 + \sigma \sum_{i=1}^{n}(C_i - C_i^*)) \quad (3)$$

where C, the actual class, C^*, the projected class, and σ, a weight factor, are used to identify the classification error. One may derive the objective function J by combining (1,2, and 3).

The probability of selecting the next population is given by (4) and the selection function is derived from (1 and 3): $\mathrm{p}_i / \sum_i P_i, where P_i = \frac{min_i(J_i)}{(J_i)}$
$, 1, l" \ell 1, ..., L$

$$\dot{X}(t) = f(X(t), u(t), t), \quad (4)$$

where X(t) = $[x_1(t), ..., x_n(t)]^T$ denotes a vector state, $u(t)$ is a vector control variable. Equation (4), leads to the solution of the differential equation trajectory $X(t, x_0, t_0)$ described as in (5).

$$max_{u(t)}J = \int_{t_0}^{t_1} I(X(t), u(t), t)dt \quad (5)$$

H(x(t),u(t),$\lambda(t), t) = I(x(t), u(t), t) +$
$\lambda^T(t) f(X(t), u(t), t)$ Equation (7), combines the objective function and the state equations, multipliers $\lambda(t)$, and co-state variables. The steps of the algorithm for feature extraction are represented by the pseudo-code to be implemented into the algorithm as 1, [21].

Algorithm 1 A genetic algorithm's generalized pseudo-code.

Require: t := 0;
Require: T :=N;
1: $start \leftarrow Genetice_Algo()$;
2: $init_{P \leftarrow P(t)}$;
individual population randomly initialized;
3: $eval_fit \leftarrow P(t)$; initial population fitness calculation;
4: **while** $t \leq T$ **do**
5: $t \leftarrow t + 1$;
6: $P \leftarrow selectparentsP(t)$; {select a sub-population for offspring production.}
7: $re_comb \leftarrow P(t)$; { reassemble the "genes" of chosen parents, then cross across with probability.}
8: $mut \leftarrow P(t)$; {randomly alter the mated population, mutation with probability.}
9: $P \leftarrow survive_p(t)$; {select the survivors from actual fitness.}
10: **end while**
11: $ret \leftarrow bestFit$
12: end Genetic$_A lgo. = 0$

Methods: Integrating GA with kNN and SVM: To illustrate the effect of the genetic algorithms and how to enhance the other machine learning algorithms, we integrate KNN and SVM with GA here.

a. Feature Selection: One critical aspect of improving classification accuracy is selecting the most informative features from the dataset. GA can perform feature selection by evaluating the fitness of different feature subsets. The algorithm iteratively generates and evaluates candidate feature sets, selecting those that contribute most to accurate classification.

Algorithm 2 KNN algorithm

Require: d :=[i]
Require: n := 0; initial n;
Require: Dataset :=N;
1: $start \leftarrow KNN(Datasets, Sample, k)$:
2: **while** $n \leq Dataset$ **do**
3: $d \leftarrow calculate\_d(item, sample)$;
4: $distance(d(i)) \leftarrow d.append(item, distance)$;
5: $sorted\_d \leftarrow sort(distance, key = lambda)$;
6: $n \leftarrow (n + 1)$; {increase the counter};
7: $neighbors \leftarrow (sorted\_d(k))$;
8: **end while**neighbor in neighbors
9: $group\_label \leftarrow neighbor.class\_label$
10: $group\_count[class\_label] \leftarrow class\_counts.get((class\_label, 0) + 1)$;
11: $predicted\_group \leftarrow max(group\_counts, key = group\_counts.get)$;
12: $return \leftarrow predicted\_group$;
13: End(KNN); =0

Algorithm 3 SVM Pseudocode

Require: Input(x,y):= (X-train,y-train); Training data X (features), y (labels);
Require: Output(x-trained): = trained(model);
Require: W:= 0;
Require: b := 0; W weight and b bias;
Require: set(alpha) : = n ;
Require: set(C) := m; learning rate alpha and regularization parameter C;
Require: (X_new) := 0; New data point;
1: $convergence \leftarrow convergence(X)$;
2: **while** $convergence \neq 0$ **do**
2: **for** $iinrangedata(Xi, yi)$ **do**
3: $margin \leftarrow calculate_margin(yi * (w * xi + b))$;
4: **if** $margin < 1$ **then**
5: $updateweights :\leftarrow W = w + alpha * (yi * xi - 2 * C$;
6: $updatebias :\leftarrow b = b + alpha * yi$;
7: **else**
8: $updateweight :\leftarrow W = W + alpha * (-2 * C * W)$;
9: **end if**
9: **end for**
10: **end while**
11: $caldecisionf(X\_new) \leftarrow W * X\_new + b$;
12: **if** f(X_new) > 0: **then**
13: $predict\_class \leftarrow 1$;
14: **else**
15: $predict\_class \leftarrow -1$;
16: **end if**
16: $perfnc[i] \leftarrow perfnc(acrcy, prec, F1 - s)$;
16: $EndSVM$; =0

b. Parameter Optimization: Both kNN and SVM algorithms have parameters that significantly influence their performance. Through the evolution of a population of parameter configurations and the selection of those that have the maximum classification accuracy, GA may be used to improve these parameters. This process helps fine-tune the algorithms to suit the specific characteristics of the dataset. The pseudo-code for KNN and SVM is shown in 2 and 3.

Supremacy of Using GA with kNN and SVM:

a Feature Selection: GA helps identify the most relevant features, reducing dimensionality and computational complexity.
b Parameter Optimization: GA fine-tunes algorithm parameters to improve classification performance.
c Robustness: GA can handle non-linear and high-dimensional data effectively, making it suitable for complex datasets like those encountered in medical diagnosis.

Benefits of Hybrid Model in BC Detection: Combining GA with kNN and SVM in the context of BC detection has several advantages.:

a Improved Accuracy: By selecting optimal features and tuning parameters, the classification accuracy of kNN and SVM models can be significantly enhanced.
b Reduced Overfitting: Feature selection helps mitigate the risk of overfitting by focusing on the most informative features.
c Interpretability: The selected features and optimized parameters provide insights into the characteristics of malignant and benign tumors, aiding in quick and resilient medical decision-making for a resource-constrained environment.

Problem and hypothesis: Genetic algorithm is best suited for multiple constraint optimization problems with objective functions [23]. Although there are research papers on hybridizing in genetic algorithms the result shows it needs further improvement. False positive and false negative result during classification is a challenge in the diagnosis of breast cancer. This paper will improve the accuracy with the highest F1 scores compared to other machine learning algorithms. The major contributions of the paper:

- Model a hybrid computational intelligence GAKNN-SVM, which has the best performance in the classification of breast cancer
- It can be an input for the early detection of breast tumors
- It can be an input for further research of computational intelligence using Genetic algorithms in clinical study.

Result: This research paper focuses on the performance of feature selection from breast cancer mammography imaging to detect cancer. As a result, the genetic hybrid model increased its accuracy by two% from the existing result.

The outline for the manuscript: Section I: Introduction. This section overviews the problem, research hypotheses, researcher's interests, and detailed descriptions of key concepts. It also discusses the challenge of early breast cancer diagnosis and the benefits of AI technology, genetic algorithms, and hybrid models. Additionally, it includes brief descriptions of the methods, problems, results, and contributions.

Section II: Literature Review. The literature review highlights research conducted by other scholars, focusing on scientific papers related to breast cancer detection and diagnosis, AI technology for classification and segmentation using various machine learning algorithms, and methods combining machine learning with genetic algorithms.

Section III: Dataset Collection and Data Processing Framework. This section presents the data collation process, including the processing of the data source and organization methods used for the research.

Section IV: Research Methodology. Here, we present our proposed models and provide algorithmic descriptions and pseudocode.

Section V: Results. This section focuses on presenting and analyzing the results, comparing the outcomes of our model with existing results in the same area, and using the same datasets.

Section VI: Discussion. This section provides a detailed research analysis, highlighting its pros and cons. Additionally, it discusses potential model enhancements for better algorithm performance and the importance of early breast cancer detection.

Section VII: Conclusion. This section provides a general overview of the research work, discusses its benefits, and identifies potential future work based on any existing gaps.

II. Related literature Review

The most prevalent cancer and the second greatest cause of mortality worldwide is breast cancer. Although mammography has its drawbacks, it is the standard method for detecting early-stage breast cancer before the lesions become clinically palpable.

A hybrid genetic algorithm has been developed to optimize the detection of nodules in computed tomography images. Additionally, a template-matching technique with a genetic algorithm applied in parallel mode has been used to find rules in biological datasets. These methods have been extensively studied and documented in various research papers, including [19], [22], [24], and [25]. Furthermore, a genetic algorithm has been applied to optimize machine learning algorithms.

The genetic algorithm has been shown to have a positive impact on classification performance. Support vector machine algorithms are often combined with GA for feature selection, resulting in optimal classification performance. GA is particularly useful when working with limited data. However, deep learning and convolutional neural networks (CNN) perform better when handling massive volumes of data, as reported in articles such as [26] and [27].

The Bucket of Models technique, combined with SVM, has performed well in GA model selection and has selected the best models in a few generations, according to [28]. Additionally, another GA has been used by the author to perform feature selection in the ensemble method, working in conjunction with SVM. This method has shown that a small set of features is best for classifying data related to breast cancer diagnosis.

In the summary of [29], the combination of K-Means and GA has shown higher efficiency and performance in converging and complexity to the global optimum. In a paper by Dinesh [30], it was reported that the accuracy of the GA and ANN hybrid model is greater than that of a single backpropagation neural network. The paper highlights the essentiality of hybridizing intelligent techniques for an effective predictive model.

The [31] discusses the weighted average method based on genetic algorithms implemented in the prediction of multiple models. Comparison of PSO, differential evolution, and GA, showing that the genetic algorithm outperforms weighted

average methods. The paper also compares the classical ensemble method and the GA-based weighted average method, deducing that the GA-based method outperforms.

The researcher utilizes the DDSM database to categorize breast mass mammography images in a publication by [32]. Three methods—the GA, the t-test, and the PSO—are used to choose features. Three machine learning algorithms—KNN, multi-SVM, and Naive Bayes—are used in image categorization. The AUC result from the training shows that GA+KNN outperforms the other methods.

[33] paper discusses the GA-CNN model, which reduces the error rate and achieves an accuracy of 98.5, sensitivity of 99.38, and specificity of 98.4. The model uses Gaussian and adaptive Histogram for preprocessing and Markov Random Adaptive segmentation for detecting boundary regions. A genetic algorithm is used for feature extraction and to obtain the global best fitness values. To help radiologists, a work by [34] models an ensemble efficient classifier using YOLOv5 suspicious mass detection. The model's sensitivity is 0.82 and its F1-Score is 0.87. [35] paper uses different thermogram image degrees. GA and other methods are used for feature extraction and selection. For image classification and labelling, different classifier algorithms are used. The result shows that GA with AdaBoost is the best combination for feature selection and classifiers for the evaluation of breast images. Using 150 thermograms, the [36] method maintains a high specificity of 89.44% while achieving a sensitivity of 83.10%.

Finally, [37] paper organizes mammography image data into two datasets: local hospital data and public data MIAS. With the same amount of datasets for each, SVM achieves 99% and 97.46% accuracy, 99.48% and 96.26% sensitivity, and 98.16% and 100% specificity. MLP attains 97% and 87.64% accuracy, 97.40% and 96.65% sensitivity, and 96.26% and 75.73% specificity, in that order.

III. Dataset Collection and Data Processing Framework

A. Dataset collection

The Wisconsin Breast Cancer Databases online data set comprises 569 records and 32 features [38], making it suitable for studying the accuracy variance between current machine learning algorithms and the proposed model. This structured sample dataset contains attributes related to breast cancer and is categorized as Malignant and Benign. The research utilized Python programming language along with libraries, the Jupyter Notebook framework, and modules such as TensorFlow, Scikit, Pandas, Numpy, and PyGAD.

B. Data Processing Framework

Based on data from the Breast Imaging Reporting and Data System (BI-RAD), the decision-making process included information on architectural distortion, breast composition, mass (density, shape, margin, and size), and other relevant parameters. Scientific data processing was integral to the research process [39]. The region of interest (ROI) was segmented, features were chosen and extracted, and the features were arranged in databases.

Data processing was carried out using a hybridization process, combining classifiers SVM and KNN with GA for feature selection. GA was employed to search for an optimal subset of features that significantly contribute to accurate predictions, thus improving computational efficiency by reducing noise and the number of features. The selected features were then classified by both SVM and KNN for prediction. Ensemble methods were used to leverage diverse models, often resulting in improved performance. The performance of trained SVM and kNN on the selected features was assessed using metrics such as accuracy, precision, recall, F1-score, and metrics. The hybrid approach was then compared to existing machine learning algorithms (without feature selection). It was emphasized that well-tuned GA parameters would lead to improved performance. The research also involved the characterization and classification of tumours based on the probability of malignancy and any abnormalities.

IV. Research Methodology

A. Proposed Solution Algorithm

The algorithm implemented for this research paper is a genetic algorithm for the selection and optimization of characteristics. To improve the performance of classification we use hybridization of the Genetic algorithm with KNN and SVM. In the first phase, the Genetic algorithm processes the dataset to select the best fitness. The process flow of a genetic algorithm typically involves the following stages:

- Initialization: Begin by generating an initial population comprising potential solutions.
- Evaluation: Assess the fitness of each member of the population using a fitness function to gauge its effectiveness in solving the problem.
- Selection: Choose certain individuals from the population according to their fitness to contribute their genetic information to the next generation.
- Crossover: Pair selected individuals to create new offspring through genetic recombination.
- Mutation: Introduce occasional random changes, or mutations, to some parts of the offspring.
- Replacement: Replace some or all of the old population with the new offspring.
- Termination: Until a stopping requirement is satisfied, such achieving a target level of fitness or generating a maximum number of generations, repeat this process for many generations.

A genetic algorithm may traverse the solution space and converge toward optimum or nearly optimal solutions for complicated problems thanks to this iterative process.

Fig. 1 illustrates the feature selection process using GA. In this process, an initial parent feature is selected from the population, its fitness is calculated, and the best feature with the highest fitness is selected from the population.

The GAKNN-SVM is a hybrid learning algorithm consisting of a genetic algorithm with K-nearest neighboring and support vector machines. For fitness optimization during feature selection, GA plays a role and for data training is by the KNN classification algorithm KNN. The output of the first training is going to be used as a feature input to SVM. SVM has classified the tumor as malignant and benign.

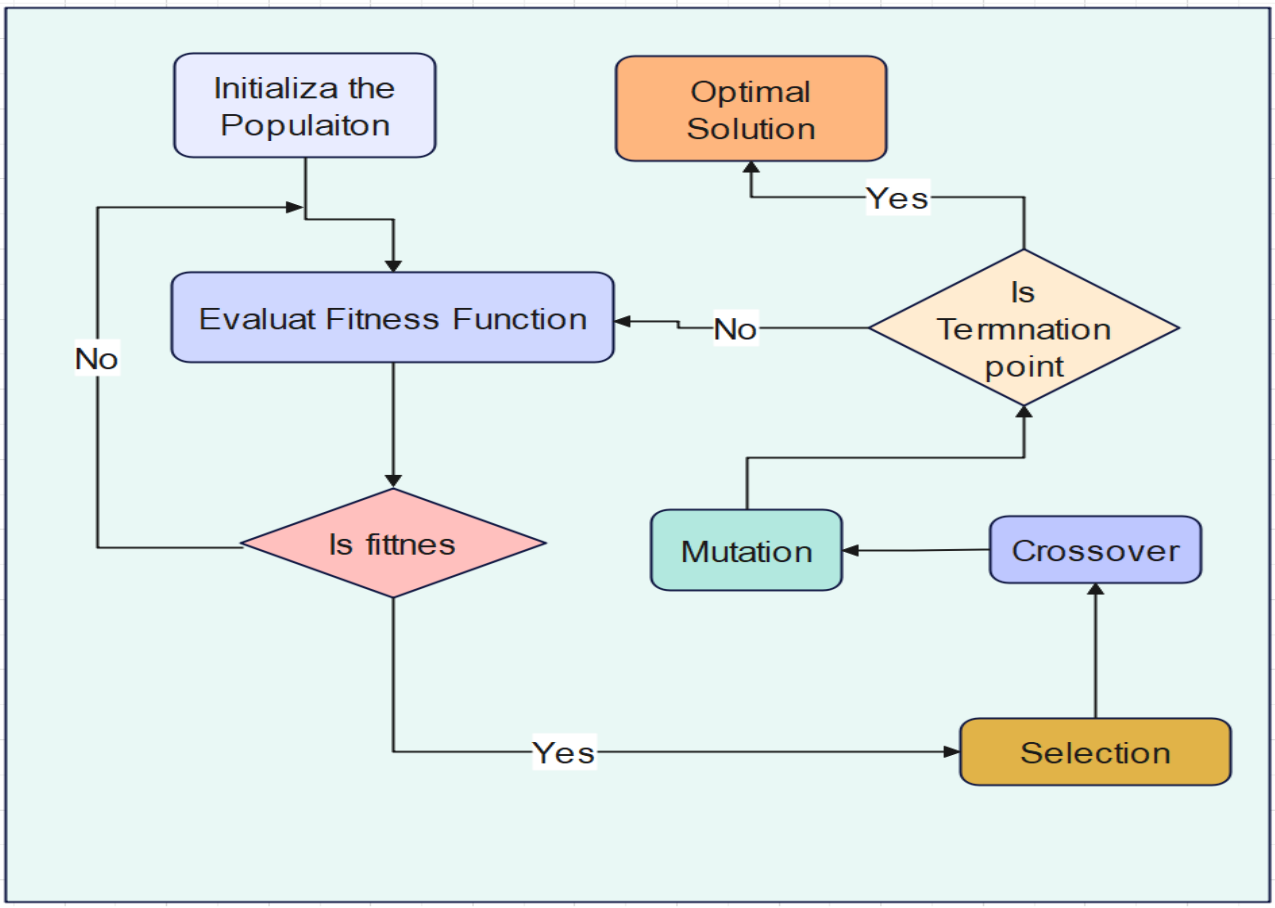

Fig. 1. Process of genetic algorithm flow diagram

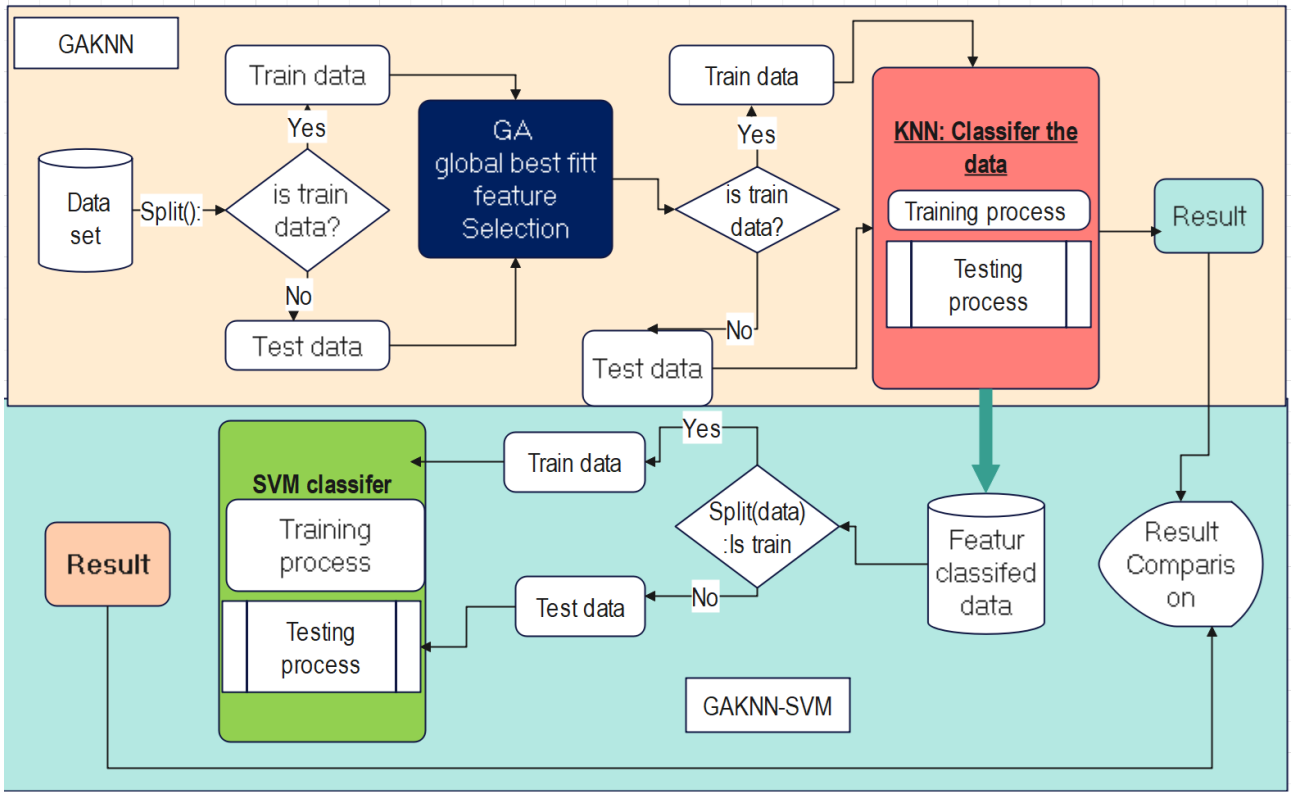

Fig. 2. Proposed GAKNN-SVM model framework

B. Proposed Design framework

In the process of classification for breast cancer protection, the quality of the result is measured by the minimum square (2) and other performance measurement tools expressed as:

$$\begin{aligned} Accuracy &= \frac{TN+TP}{FP+FN+TP+TN} \\ Precision &= \frac{TP}{FP+TP} \\ Sensitivity &= \frac{TP}{ActualPositive} \\ TotalActualPositive &= TP+FN \\ Specificity &= \frac{TN}{ActualNegative} \\ TotalActulaNegative &= TN+FP \\ F1score &= \frac{2TP}{2TP+FP+FN} \end{aligned}$$

Algorithm 4 Algorithm: GA-KNN

Require: Start

Require: Use random candidate solutions to initialize population P.

1: Use the fitness function to assess each candidate solution's fitness in P.
2: Continue until the requirements for termination are satisfied:
3: Choose parents from P according to their level of fitness.
4: To produce offspring, use crossover and mutation operators.
5: Assess the offspring's fitness.
6: Select individuals for the next generation based on some selection strategy (e.g., tournament selection).
7: Replace the old population with the new generation.
8: Select the best solution from the final population as the output.
9: Training and testing by KNN.
9: END =0

Algorithm 5 Algorithm: GA-SVM

Require: Start

Require: Use random candidate solutions to initialize population P..

1: Use the fitness function to assess each candidate solution's fitness in P.
2: Continue until the requirements for termination are satisfied:
3: Choose parents from P according to how fit they are.
4: To produce offspring, use crossover and mutation operators.
5: Use SVM to assess the offspring's fitness.
6: Choose members of the following generation based on a selection strategy (e.g., tournament selection).
7: Replace the old population with the new generation.
8: Select the best solution from the final population as the output.
9: Training and testing by SVM.
9: END =0

Based on the confusion matrix for a binary classifier different rates are computed. Accuracy defines the Overall classification, it responds, how often is the classifier correct? Fig. 2 presents the GAKNN-SVM model, which includes a feature selection process that uses GA with KNN classification. The GAKNN data obtained through this process is classified by using SVM. We use test data to evaluate the effectiveness of the model and determine how well it performed. The algorithms 4 and 5 demonstrate the selection optimization performed by GA. Subsequently, the machine learning algorithms KNN and SVM were utilized for classification and training, respectively.

The algorithm 6, the ensemble process of GAKNN and SVM for the same sample data, after training the data with KNN, classification, and training has been done by SVM.

Algorithm 6 GAKNN-SVM Pseudocode

Require: i: =0, p(i), T: =N;

Require: initialize := (p);

1: $KNN-Fit(P(i)) \leftarrow calculate-fitness(P(i))$; i in range N
2: **while** termination true **do**
3: $bestFitt(p(i)) \leftarrow compare-fitness(P(i)P(i-1)$;
4: $selectparentsP(i) \leftarrow Fit(P(i))$;
5: $cros(P) :\leftarrow crossover(p(i)$;
6: $mut(P) :\leftarrow mutaion(p(i))$;
7: $calfit(p-offspring) \leftarrow calculate(Fit(P-offspring))$;
8: $select(p-offspring) \leftarrow select(P-offspring(i))$;
9: $replaceold \leftarrow new-generation(P)$;
10: **end while**
11: $classify(P-GAKNN) \leftarrow classify-KNN(P(i))$;
12: $selectbestsolution \leftarrow select(P-GAKNN)$;
13: $classify(P-SVM) \leftarrow classify(P-GAKNN)$;
14: $select-best(P-GAKNNSVM) \leftarrow select(P-SVM)$;
15: $End(GAKNN-SVM)$; =0

V. Result

Breast cancer detection, particularly in resource-constrained environments, presents unique challenges due to the complexity of interpreting digital mammograms and the necessity for high accuracy even with limited data. In this study, we proposed a novel approach utilizing Genetic Algorithm-optimized k-Nearest Neighbors and Support Vector Machines to address these challenges. In research paper [40], the results of invasive cancer prediction using machine learning classifiers, shown in Table II, present the highest level of accuracy in SVMs when compared to LR and k-NN. The algorithms K-NN and SVM without GA, have an accuracy of 71.86% and 78.56%.

TABLE II
Existing Machine Learning Classification, [40].

No	Classifier	Accuracy %
1	Logistic Regression	71.80
2	K-NN	71.86
3	SVM	78.56

The categorization of mammography images utilizing CRNN with FC-CSO methodologies yields an accuracy rate

of 98.4%, a specificity of 99.9%, and F1 scores of 74.5%, according to Kumar's research, [41]. However, CRNN techniques struggle to classify blurred images and require additional filtration. On the other hand, KNN techniques achieve an accuracy rate of 94.44%, but further improvements are needed for better classification. Using SVM techniques for digital mammogram images has an accuracy rate of 96.55%, a sensitivity of 96.97%, and a specificity of 96.20%. However, the challenge with digital mammograms lies in their high-dimensional matrix, which makes interpretation complex. To improve the accuracy in SVM for mammography image datasets, large datasets are required, as the current accuracy rate is 87. 2% with an AUC of 94%. Table III, it trains the model by the WDBC data set with K-fold cross-validation. In this case, SVM has the highest accuracy next to the AB. However, our model outperforms with an accuracy of 99.3%.

TABLE III
CLASSIFICATION PERFORMANCE IN OTHER WORK [42]

No	Algorithm	Accu %	Sens%	Spec%
1.	BAGGING	95.78	97.75	92.52
2.	RANDOM FOREST	97.72	98.59	96.26
3.	ADA BOOST	98.77	99.44	97.66
4.	SVM	98.59	99.44	97.20
5.	KNN (k=3)	97.72	98.59	96.26

TABLE IV
PERFORMANCE RESULT AFTER APPLYING GA WITH DIFFERENT CLASSIFICATION ALGORITHMS WITH 143 DATASETS.

Algorithm	Accuracy	Sensitivity	Specificity	Confusion matrix	F1-score
RF	95.10	93.25	98.14	[[83,6][1,53]]	96.0
DT	93.00	92.13	94.44	[[82,7][3,51]]	94.25
KNN	96.50	98.87	92.59	[[88,1][4,50]]	97.24
SVM	96.01	98.0	0.93.1	[[87,2][4,50]]	96.67
AB	95.10	93.25	98.14	[[83,6][1,53]]	95.95
GB	95.80	96.62	94.44	[[86,3][3,51]]	96.63

The performance results of applying genetic algorithm feature selection to different ML algorithms with 143 test datasets are presented in Table IV, and Table V with 171 test datasets, using the WDBC 569 sample dataset. The resulting confusion matrix for SVM showed a true positive count of 87, a true negative count of 50, a false positive count of 1, and a false negative count of 2. Based on these values, the F1-score was calculated to be 96.67.

The program ran a KNN classification on the test data from WDBC and produced a confusion matrix as shown in Fig. 3 showcase for the K-NN model, resulted an F1-score of 97.24.

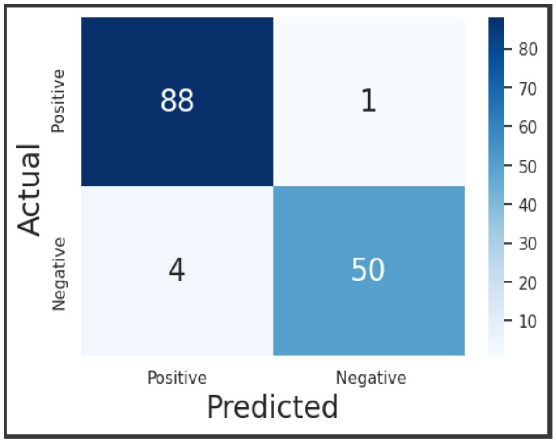

Fig. 3. Confusion Matrix for KNN with GA, in 143 sample test data

Table V shows that the accuracies rose to 95.91% and 96.49%, respectively, following the inclusion of GA. Nevertheless, the suggested model's accuracy outperformed all alternative techniques. These results show how effective GA is in enhancing classification models for breast cancer diagnosis. Furthermore, the use of our model showed how robust it is to different types of data. For example, Table V and comparison in Fig.4 demonstrate that our GAKNN-SVM model demonstrated exceptional accuracy, specificity, and sensitivity when tested on the Wisconsin Breast Cancer dataset, with an accuracy of 98.25%, a sensitivity of 98.15%, and a specificity of 98.41%.

The probability that a person with a negative test result does not have the illness, ailment, biomarker, or mutation (change) in the gene under investigation is known as the test's negative predictive value. The accuracy of a particular test may be gauged using the negative predictive value. From Fig.5 and Table VI, the NPV test value shows our model is very less value than the others. this determines that the number of false negatives is minimal which is 0.0185 or 1.85%. Moreover, the implementation of the genetic algorithm enabled us to optimize the parameters of our classifiers effectively. Through iterative refinement, we achieved the best fitness score of 0.993 in the second generation of the GA, demonstrating the efficacy of this approach in improving model performance. Generally, there is an improvement in the performance of classification to predict the benign or malignant using our model. From Table V, for comparison purposes we took accuracy and F1-scores, the outperformed difference of our model from others ranges from 1.19% to 5.95% in accuracy and 0.89% to 4.89% in F1-score, see Table VII.

TABLE V
PERFORMANCE COMPARISON OF OUR MODEL WITH OTHER ML ALGORITHMS, SUPPORTS 171 SAMPLE DATASET

Measurement	LR	RF	DT	KNN	SVM	GA-KNN-SVM
Accuracy	97.08%	97.08%	92.40%	95.91%	96.49%	98.25%
Sensitivity	98.15%	99.07%	90.74%	99.07%	98.15%	98.15%
Specificity	95.24%	93.65%	95.24%	90.48%	93.65%	98.41%
Precision	97.25%	96.40%	97.03%	94.69%	96.36%	99.07%
F1 Score	97.70%	97.72%	93.78%	96.83%	97.25%	98.60%
MCC (8)	93.70%	93.72%	84.35%	91.24%	92.44%	96.25%

TABLE VI
OUR MODEL NEGATIVE PREDICTED VALUE TEST RESULT IN COMPARISON WITH OTHER ML ALGORITHMS

Measurement	LR	RF	DT	KNN	SVM	GA-KNN-SVM
False Positive Rate	0.0476	0.0635	0.0476	0.0952	0.0635	0.0159
False Discovery Rate	0.0275	0.036	0.0297	0.0531	0.0364	0.0093
False Negative Rate	0.0185	0.0093	0.0926	0.0093	0.0185	0.0185

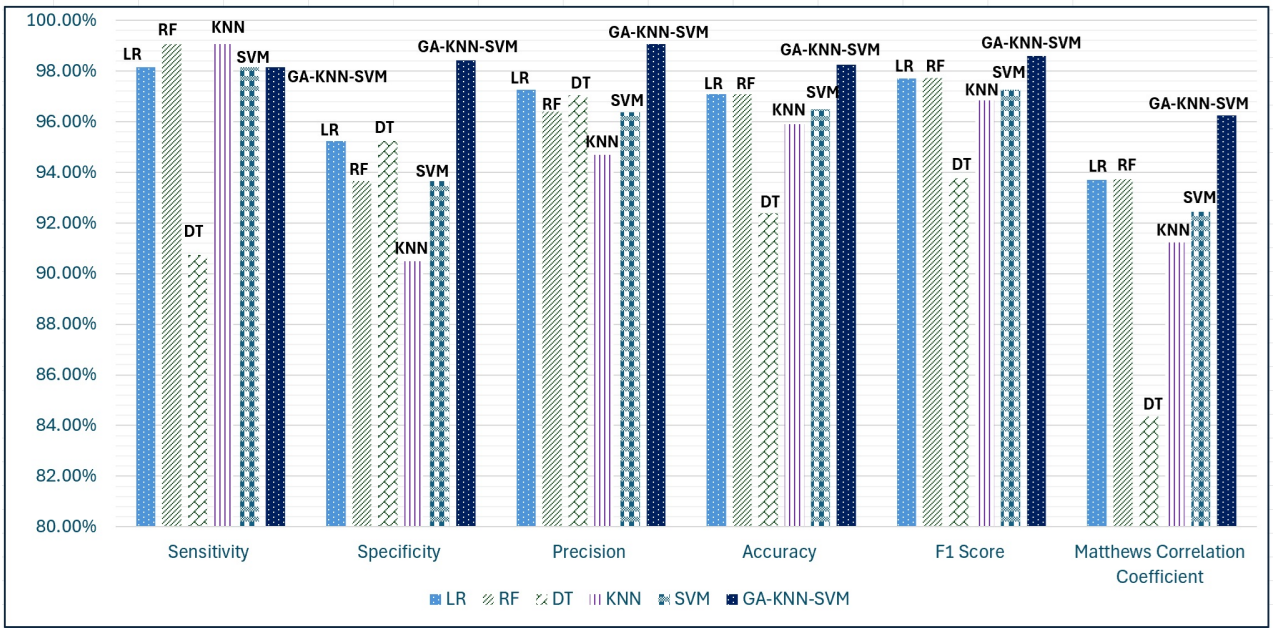

Fig. 4. Performance comparison of the model GAKNN-SVM with other ML algorithms

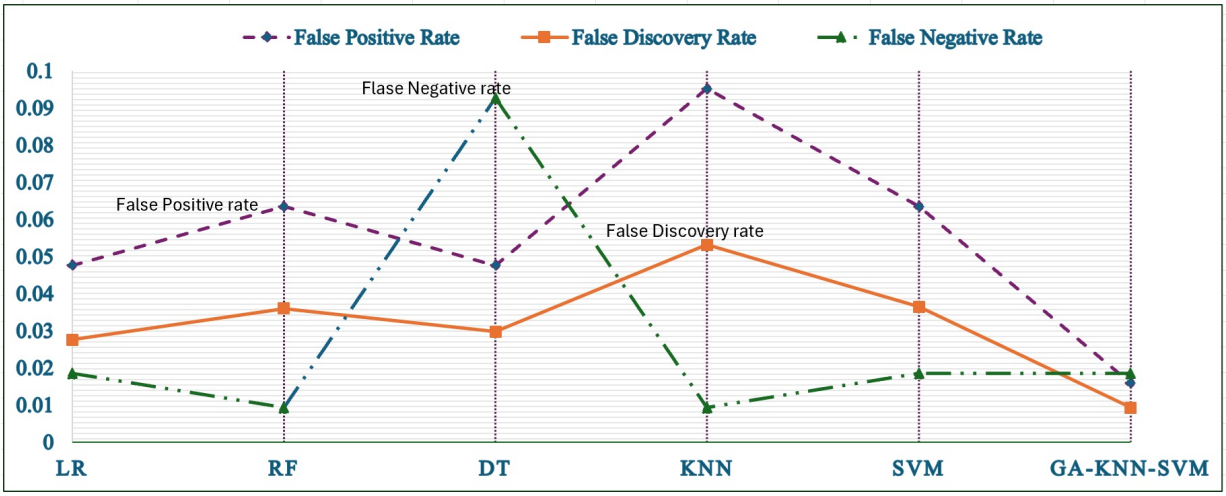

Fig. 5. Graphical representation of Our model Negative predicted value test result in comparison with other ML algorithms

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP + FN)(TP + FP)(TN + FN)(TN + FP)}} \tag{6}$$

TABLE VII
ACCURACY AND F1-SCORE DIFFERENCE IN PERCENT AS AN EXAMPLE FROM THE TABLE V.

Algorithm	Accuracy	Diff %	F1-Score	diff %
LR	97.08%	1.19%	97.70%	0.91%
RF	97.08%	1.19%	97.72%	0.89%
DT	92.40%	5.95%	93.78%	4.89%
KNN	95.91%	2.38%	96.83%	1.80%
SVM	96.49%	1.79%	97.25%	1.37%
GA-KNN-SVM	98.25%	-	98.60%	-

From the tables, we noticed that, when the ratio of the training with the test differs there is a change in the performance of prediction.

Here are the Fig. 6, 7, and 8 by changing the sample test data set size, 114,143 and 171, there are different results in the accuracy, sensitivity, specificity, F1-score, precession, and recall, see Fig. 10. We used the same classification algorithm RF, similarly for others too.

As shown in Table VIII, we use both KNN and SVM to

assess the F1 score, precision, and recall. When it comes to breast cancer categorization, benign instances are represented by a score of 0 and malignant cases by a score of 1. According to Table IX, KNN predicts benign tumors with an F1 score of 85% and malignant tumors with 93%.

```
Confusion Matrix :
 [[70  1]
 [ 3 40]]
Accuracy :  0.9649122807017544
Sensitivity :  0.9859154929577465
Specificity :  0.9302325581395349
```

```
from sklearn.metrics import classification_report
print(classification_report(Y_test, Y_pred))
```

	precision	recall	f1-score	support
0	0.96	0.99	0.97	71
1	0.98	0.93	0.95	43
accuracy			0.96	114
macro avg	0.97	0.96	0.96	114
weighted avg	0.97	0.96	0.96	114

Fig. 6. RF classification algorithm with 114 test data size

```
Confusion Matrix :
 [[88  1]
 [ 3 51]]
Accuracy :  0.972027972027972
Sensitivity :  0.9887640449438202
Specificity :  0.9444444444444444
```

```
from sklearn.metrics import classification_report
print(classification_report(Y_test, Y_pred))
```

	precision	recall	f1-score	support
0	0.96	0.99	0.97	89
1	0.98	0.93	0.95	54
accuracy			0.97	143
macro avg	0.97	0.96	0.96	143
weighted avg	0.97	0.97	0.96	143

Fig. 7. RF classification algorithm with 143 test data size

```
Accuracy :  0.9590643274853801
Sensitivity :  0.9907407407407407
Specificity :  0.9047619047619048
```

```
print(classification_report(Y_test, Y_pred))
```

	precision	recall	f1-score	support
0	0.95	0.99	0.97	108
1	0.98	0.90	0.94	63
accuracy			0.96	171
macro avg	0.96	0.95	0.96	171
weighted avg	0.96	0.96	0.96	171

Fig. 8. RF classification algorithm with 171 test data size

Our examination of the 171 sample tests in the WDBC dataset shows that KNN obtains an F1 score of 94% for malignant predictions and 97% for benign predictions. Similarly, F1 scores of 95% for malignant patients and 97% for benign cases are reflected in the SVM. Comparably, the GAKNN model achieves 95% for malignant predictions and 97% for benign ones. Notably, as shown in Table VIII, our suggested model exhibits an exceptional F1 score of 99% for benign and 98% for malignant classifications, with precisions of 0.98 and 1.0, respectively.

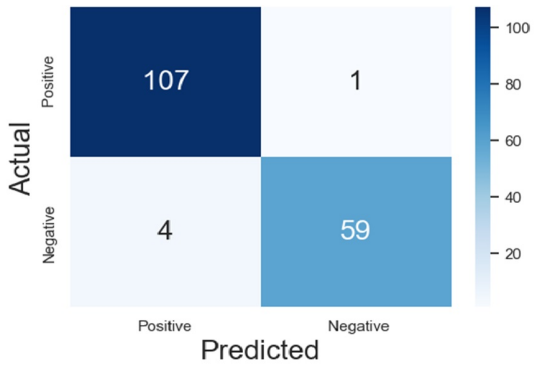

Fig. 9. RF confusion matrix with 171 test data size

TABLE VIII
PRECISION, RECALL AND F1-SCORE OF CLASSIFIERS WITH 171 TEST DATASETS.

Algorithm	M/B	Precision	Recall	F1-Score
RF	0	0.96	0.99	0.98
	1	0.98	0.94	0.96
LR	0	0.97	0.98	0.98
	1	0.97	0.95	0.96
DT	0	0.97	0.91	0.94
	1	0.86	0.95	0.90
AB	0	0.98	0.98	0.98
	1	0.97	0.97	0.97
GB	0	0.96	0.97	0.97
	1	0.98	0.90	0.94
KNN	0	0.95	0.99	0.97
	1	0.98	0.90	0.94
SVM	0	0.96	0.98	0.97
	1	0.97	0.94	0.95
GAKNN	0	0.95	1.00	0.97
	1	1.00	0.91	0.95
GASVM	0	0.97	1.00	0.99
	1	1.00	0.95	0.98
GAKNN - SVM	0	0.98	1.00	0.99
	1	1.00	0.96	0.98

TABLE IX
PRECISION, RECALL AND F1-SCORE OF CLASSIFIERS WITH 114 TEST DATASETS, [43].

Algorithm	M/B	Precision	Recall	F1-Score
RF	0	1.0	0.88	0.94
	1	0.94	1.0	0.97
LR	0	0.98	0.96	0.97
	1	0.98	0.99	0.98
DT	0	0.95	0.90	0.93
	1	0.95	0.97	0.96
KNN	0	0.97	0.96	0.85
	1	0.88	0.99	0.93

In Table X, we process ML algorithms by hybridizing the GA, to validate the score. The KNN classifier achieved an impressive score of 0.9650, while the linear Support Vector Machine (SVM) classifier attained a score of 0.958, and our model GAKNN-SVm has a score of 0.993.

TABLE X
THE ACCURACY OF OTHER ML CLASSIFICATION ALGORITHMS WITH GAKNN-SVM

No	Classifier	Accuracy
1	RandomForest	0.972028
2	Logistic	0.965035
3	KNeighbors	0.965035
4	LinearSVM	0.958042
5	GradientBoosting	0.958042
6	RadialSVM	0.951049
7	AdaBoost	0.951049
8	DecisionTree	0.930070
9	GAKNN-SVM	0.9930

A detailed examination of the GAKNN-SVM model's performance metrics is shown in Fig. 11. Table X demonstrates the model's remarkable 99.3% scoring accuracy. The GAKNN-SVM model stands out among the several machine learning classifier algorithms assessed in the research article [42] because of its accuracy rate. The comparison highlights the model's high accuracy and effectiveness in outperforming the other algorithms assessed in the study, reinforcing its robustness and reliability in practical applications. Overall, these findings underscore the GAKNN-SVM model's superiority in accuracy, making it a noteworthy option for consideration in the field.

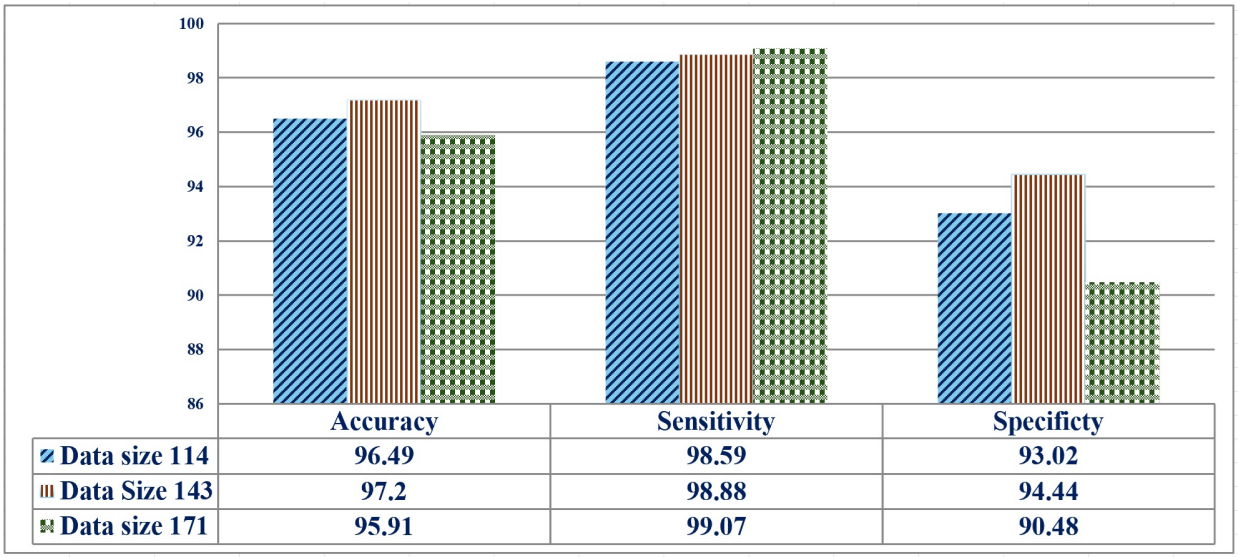

Fig. 10. Performacne with different sample data size

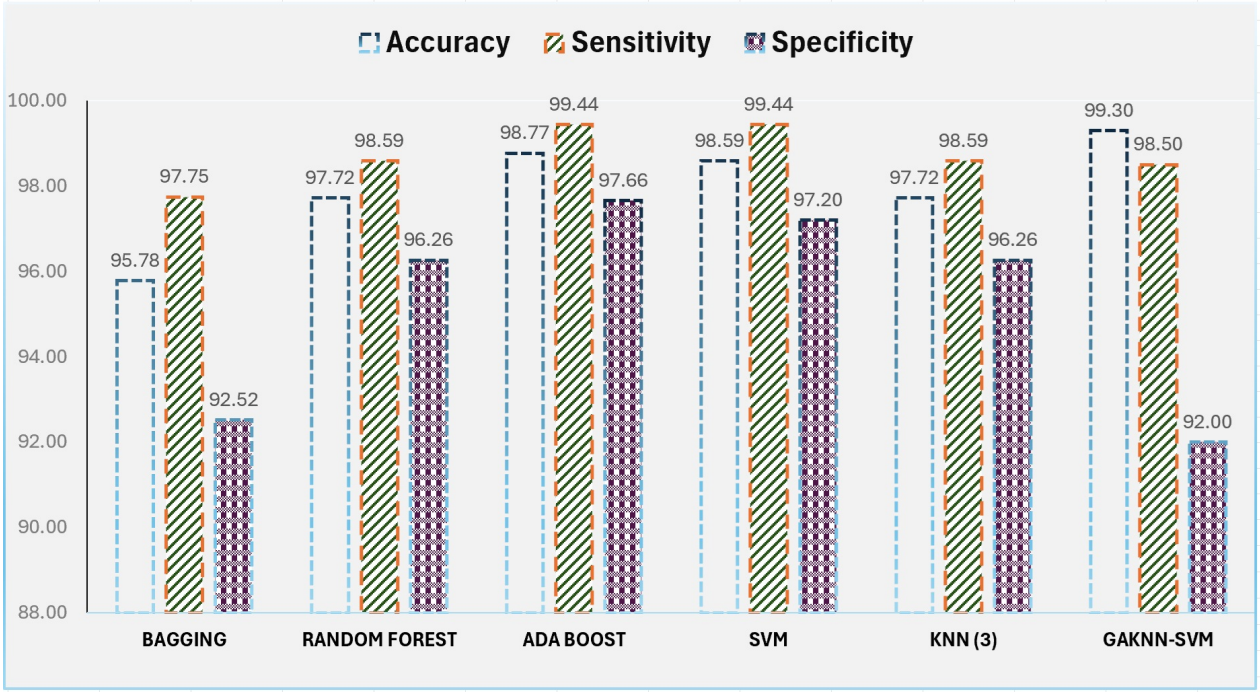

Fig. 11. Performance comparison of our model GAKNN-SVM with other research work [42]

Furthermore, we analyzed the complexity of time and identified the generation that exhibited the best fitness, as presented in Table XI. The highest score, which is 0.993, was achieved in the second generation.

TABLE XI
THE BEST SCORE OF GA WITH 5 ITERATIONS

Gen	Score
1	[0.9860139860139860]
2	[0.993006993006993]
3	[0.993006993006993]
4	[0.993006993006993]
5	[0.993006993006993]

Genetic Algorithm with different generations of iteration has a better accuracy from 1% to 2% improvement.

VI. DISCUSSION

The findings show that the accuracy of the GAKNN-SVM model is higher than that of the KNN and SVM models already in use. This demonstrates how well Genetic Algorithms (GA) work to improve classification models for the diagnosis of breast cancer. In addition to achieving greater accuracy, our GAKNN-SVM model demonstrated notable improvements in precision, recall, and F1-score, especially when it came to correctly differentiating between benign and cancerous breast images.

The model showed an improvement in precision ranging from 1.03% to 3.15% in identifying cancerous tissues. Furthermore, the assessment of time complexity revealed that our GA-enhanced model significantly alleviates computational burden while maintaining high levels of accuracy. By selecting optimal parameters, we ensured efficient classification with minimal resource utilization. A comprehensive evaluation of our proposed GAKNN-SVM model across various datasets underscores its effectiveness in breast cancer detection, particularly in resource-constrained environments. A potential strategy for improving diagnostic accuracy and enabling early breast cancer identification and therapy is the use of the Genetic Algorithm with KNN and SVM classifiers.

In summary, while Genetic Algorithms coupled with KNN/SVM provide advantages such as interpretability, suitability for smaller datasets, and computational efficiency, other machine learning algorithms may excel in different areas, including robustness, scalability, or user-friendliness. Deep Learning algorithms, in particular, thrive in automatic feature learning, managing large datasets, and achieving state-of-the-art performance on complex tasks. The decision between these approaches relies on several factors, including the nature of the issue at hand, the available data, computational resources, and the balance between interpretability and performance. A comparison of our proposed model with other machine learning techniques is outlined in Table XII.

TABLE XII
TRADEOFF OF PROPOSED ALGORITHM WITH OTHER MACHINE LEARNING AND DEEP LEARNING TECHNIQUES

Description	GA with kNN/SVM	Other ML Algorithms	Deep Learning
Feature Selection vs. Automatic Feature Learning:	GA aids in feature selection, helping identify the most relevant features from the dataset. Employs evolutionary search techniques for feature selection and parameter optimization, leading to improved classification performance	Different algorithms may use various approaches for feature selection and parameter tuning, such as greedy search, random search, or gradient-based optimization	Deep learning algorithms automatically learn features from raw data, potentially eliminating the need for manual feature selection. However, a huge data set is needed that is very difficult to acquire in the Ethiopian situation (privacy, rural nature, internet disruption, cloud facilities, economics).
Interpret ability vs. Complexity	Selected features and optimized parameters provide interpretable insights into the classification process.	Some algorithms like Decision Trees or Logistic Regression offer interpretable models, while others like Random Forests or Gradient Boosting Machines may provide less interpretability but higher accuracy.	Deep learning models frequently function as "black boxes," which makes it difficult to understand how they make decisions and interpret the learned representations.
Data Requirement and Performance:	Effective with smaller datasets and can achieve good performance with fewer data points, making them suitable for scenarios with sparse data availability.	Performance varies across algorithms; some may require large datasets to generalize well, while others, like Decision Trees or Naive Bayes, can perform adequately with smaller datasets but with sacrificed accuracy.	When given enough labeled data, deep learning algorithms may attain state-of-the-art performance on challenging problems, but they usually need a lot of data to train.
Computational Efficiency	Generally less computationally intensive compared to deep learning algorithms, making them suitable for resource-constrained environments.	Computational requirements vary; some algorithms may be computationally expensive during training and inference, requiring substantial computational resources.	Deep learning models, especially deep neural networks, require significant computational resources (e.g., GPUs or TPUs) for training, inference, and model optimization.
Generalization and Robustness:	May generalize well to new, unseen data if properly optimized, but may suffer from over-fitting if not carefully tuned.	Robustness and generalization capabilities vary; some algorithms may be more robust to noise and outliers, while others may require careful regularization to avoid overfitting.	Deep learning models have the potential for high generalization but can be prone to overfitting, especially with insufficient data or inadequate regularization.
Model Explainability	Provides transparent models with explicit feature importance, facilitating easier model interpretation and trust.	Model explainability varies across algorithms; some provide easily interpretable models, while others, like Neural Networks, may be less transparent.	Deep Learning: Deep learning models often lack explainability, which can be a concern, especially in critical domains where understanding model decisions is essential.
Domain Expertise and Parameter Tuning:	Requires domain expertise for defining fitness functions, selecting genetic operators, and fine-tuning parameters.	Varies in terms of tuning complexity; some algorithms may require less manual intervention for hyperparameter tuning, but understanding algorithm behavior and parameter selection is still crucial for optimal performance.	Deep learning models may require less manual intervention for hyperparameter tuning but demand expertise in architecture design and optimization strategies.

VII. Conclusion

In the field of breast cancer research, it is clear that AI and deep learning technologies have significantly improved the prediction and detection of the disease. However, despite these advancements, the overall survival rate for breast cancer patients has not shown substantial improvement. Therefore, it is increasingly evident that early diagnosis is critical for positively impacting mortality rates. Previous studies have indicated that a hybrid model incorporating a genetic algorithm has yielded superior results. It is important to note that further research is necessary to refine the early detection process to determine whether a tumor is cancerous or benign. Notably, genetic algorithms tend to outperform deep learning models because they can achieve high performance with smaller datasets and fewer features, thereby requiring less computational power. The hybrid computational model known as GAKNN-SVM has demonstrated significantly enhanced accuracy, underscoring its potential to advance breast cancer research and diagnostic capabilities. Given these advantages, there is a strong recommendation to explore genetic algorithms further for optimizing classification and feature selection. In future research, it has been observed that adjusting the parameters of the genetic algorithm's selection and hybrid ensemble models can yield even better results.

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BIOGRAPHY

Abebe Alemu (corresponding author) is currently a PhD student at Adama Science and Technology University, his area of study is computational intelligence modelling and simulation. He has earned an MSc in Computational Science and Computer Science, and his research interests lie in the fields of AI, ML, computational intelligence, and data analytics. His research papers have been published in international academic journals. Alongside his academic pursuits, he also serves as a lecturer at Kotebe University of Education, where he teaches computer science courses.

Anteneh Girma is an Associate Professor, in the Department of Computer Science and Information Technology. Areas of Expertise: Information Security and Assurance, CyberSecurity, CyberSecurity Intelligence, CyberSecurity Governance, Risk management, and Security Auditing, Cloud Computing and Security, Internet of Things and security, Artificial Intelligence, Machine Learning, Cryptography, and Data Science Building 42, Room 112 G. Tel: (202) 274-6548.

Mesfin Abebe is an Associate professor at the Department of Computer Science and Engineering at Adama Science and Technology University. His research areas are situated in the field of Smart and Autonomous Systems which includes Intelligent Systems, Software Engineering and Hardware. Dr. Mesfin Abebe has taught several courses for postgraduate students (MSc and PhD) since 2016 such as Advanced Machine Learning, NLP, AI, Image Processing, Big Data Analytics, Reinforcement Learning, Deep Learning, Semantic Web, Information Retrieval Storage, Application of IoT and several Software Engineering courses. He also supervised a number of MSc and PhD students with their research work.

Ramasamy S. completed his BE in Electrical and Electronics Engineering from Madurai Kamaraj University in the year 1991. He got his graduate and PhD degrees from the National Institute of Technology, Trichy, India in the field of VLSI systems in 2003 and 2010 respectively. He taped two-mixed signal ICs through Euro practice services under the India Chip Program. Since 2010, he has worked as an Electrical and Computer Engineering professor in India and overseas. He has executed several National and International Projects. He also serves as an NVIDIA Ambassador and Deep Learning Certified Instructor. Recently, he became coordinator for the TinyML academic community at King Faisal University, Saudi Arabia. He has established embedded systems, VLSI, and IoT labs with industry support. He has published more than 50 research articles in Journals and Proceedings. He supervised two PhD candidates and around 30 Graduate students.