A Hybrid Genetic Algorithm Model for Early Detection and Classification of Breast Tumours.

ABEBE ALEMU BALCHA

A PhD Dissertation submitted to the Department of Computer Science and Engineering. School of Electrical Engineering and Computing.

Presented in Fulfilment of the Requirement for the Degree of Doctor of Philosophy in Computer Science and Software Engineering,
(Specialization in Artificial Intelligence and Machine Learning).

Office of Graduate Studies
Adama Science and Technology University.

May, 2025.
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ABEBE ALEMU BALCHA

SUPERVISOR: - ANTENEH GIRMA, (PhD)
Prof., Computer Science/Cyber-
Security, University of the District of
Columbia.

CO-SUPERVISOR: MESFIN ABEBE, (PhD)
Associate Prof., Computer Science and
Engineering, Adama Science and
Technology University.

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DECLARATION AND RECOMMENDATION

Declaration

I hereby declare that this Dissertation entitled **"A Hybrid Genetic Algorithm Model for Early Detection and Classification of Breast Tumour**" is my original work. That is, it has not been submitted for the award of any academic degree, diploma, or certificate in any other university. All sources of materials used for this thesis have been duly acknowledged through appropriate citations.

Abebe Alemu Balcha	_____	_____
Name of student	**Signature**	**Date**

Recommendation

I/we, the supervisor(s) of this dissertation, hereby certify that I/we have read and revised the dissertation entitled "**A Hybrid Genetic Algorithm Model for Early Detection and Classification of Breast Tumours**" prepared under my/our guidance by **Abebe Alemu Balcha** submitted in partial fulfilment of the requirements for the degree of Doctor of Philosophy in Computer Science and Software Engineering. Therefore, I/we recommend the submission of the dissertation to the department for further review and defense.

Anteneh Girma	_____	_____
Major Supervisor	Signature	Date
Mesfin Abebe	_____	_____
Co-supervisor	Signature	Date

Approval Page of Ph.D. Dissertation

I/we hereby certify that the recommendations and suggestions made by the board of examiners are appropriately incorporated into the last version of the dissertation entitled "**A Hybrid Genetic Algorithm Model for Early Detection and Classification of Breast Tumour**" by **Abebe Alemu Balcha**.

Anteneh Girma	_____	_____
Major Supervisor	Signature	Date
Mesfin Abebe	_____	_____
Co-supervisor	Signature	Date

We, the undersigned, members of the Board of Examiners of the dissertation open defence by Abebe Alemu Balcha, have read and evaluated the dissertation entitled "A Hybrid Genetic Algorithm Model for Early Detection and Classification of Breast Tumour" and examined the candidate during the open defence. This is, therefore, to certify that the dissertation is accepted for partial fulfilment of the requirements of the degree of Doctor of Philosophy in Computer Science and Software Engineering.

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Thanks to God!!!

Table of Contents

LIST OF TABLES

LIST OF FIGURES

LIST OF ACRONYMS AND ABBREVIATIONS

AB	Ada Boost
ACS	American Cancer Society
AI	Artificial Intelligence
ANN	Artificial Neural Network
AUC	Area Under Curve
BC	Breast Cancer
BI-RADS	Breast Imaging Reporting and Data Systems
CI	Computational Intelligence
CNN	Convolutional Neural Network
CRNN	Convolutional Recurrent Neural Network
DCE-MRI	Dynamic Contrast-Enhanced Magnetic Resonance Imaging
DL	Deep Learning
DT	Decision Tree
EC	Evolutionary Computation
FC-CSO	Firefly Algorithm and Chicken Swarm Optimization
FN	False Negative
FP	False Positive
GA	Genetics Algorithm
GB	Gradient Boost
GCO	Global Cancer Observatory
GLOBOCAN	Global Cancer Incidence, Mortality and Prevalence
IARC	International Agency for Research on Cancer (WHO)
IRB	Institutional Review Board
KNN	K Nearest Neighbors
K-SVM	Support Vector Machine (based on K-means)
LMBCDS	Local Mammography Breast Cancer Data Sets
LR	Logistic Regression
MCS	Monte Carlo Simulations
ML	Machine Learning
MLP	Multi-Layer Perceptron
NCI	National Cancer Institute
NSVM	Neural Support Vector Machine
ODE	Ordinary Differential Equation
PMP	Pontryagin's Minimum Principle
RF	Random Forest
SVM	Support Vector Machine
TN	True Negative
TP	True Positive
WBCD	Wisconsin Breast Cancer Dataset
WHO	World Health Organization

ABSTRACT

The severity and fatality prevalence of breast cancer remain a global issue. The existing diagnosis and treatment are not efficient enough to successfully detect breast cancer tumours at an early stage. According to recent studies, breast cancer causes 25.84% of all cancer-related fatalities. New breast cancer cases account for 29.46% and 31.85% of all new cancer cases in Africa and Ethiopia, respectively. In Ethiopia, 72.56% of breast cancer diagnoses are in advanced stages (95% CI: 68.46-76.65%), emphasizing the critical need for early detection.

Furthermore, a lack of radiologists causes delays in the annual reading and classification of Breast Imaging Reporting and Data Systems (BI-RADS). To address the problem areas of early detection, false positives and false negatives, research efforts continue to present different solutions using different advanced techniques. The techniques used are artificial intelligence (AI), machine learning (ML), and Genetic Algorithms (GA). Artificial intelligence and Machine learning are crucial in improving breast cancer diagnosis to reduce late discovery, which significantly affects survival chances.

In this study, we collected 4092 mammographic image data from the diagnosis center with the radiologist's recommendation for the diagnosis and future patient steps. In addition to this, we use the Wisconsin breast cancer public image data for training, validation, and testing of the model. We work on a hybrid model using genetic algorithms and machine learning for early detection and classification of the stage and type of breast cancer tumours to reduce the outliers for false-positive and false-negative results. The implemented models are hybridizing Genetic Algorithms with K-Nearest Neighbour (K-NN) and Support Vector Machine (SVM), (GA-KNN-SVM), a modified GA with Pontraygin Minimum Principles (PMP), and a hybrid GA model with K-Means++.

The GAKNN-SVM model achieves superior performance in breast tumour detection, utilizing the Wisconsin Breast Cancer Diagnostic Dataset. The results show significant improvements, with accuracy, sensitivity, and specificity rates reaching 98.25%, 98.15%, and 98.41%, respectively, of the test sample data. At last, we have outperformed results in detecting breast tumours and classified mammography image data by BI-RADS scoring.

Keywords: *Breast Cancer, Mammography, Genetic Algorithm, Pontryagin Minimum Principles, GA-KNN-SVM, Wisconsin Breast cancer.*

CHAPTER ONE

1 INTRODUCTION

In the opening chapter of this research report, provide a background on the study and discuss breast cancer's rising prevalence and impact on public health. This study highlights the progress in survival rates and emphasize the ongoing need for research and innovation. The research examines the latest technologies used for diagnosing breast cancer, focusing on methods that improve detection efficiency and the scientific advancements in early diagnosis. It also addresses the challenges healthcare professionals face in diagnosing breast cancer and the barriers to timely and accurate detection. This chapter outlines the report's goals, specific aims, research questions, and proposed solutions. This report defines the scope of our study, noting its limitations and the ethical guidelines that guide our research. In summary, this chapter offers a clear overview of key themes and findings related to breast cancer, guiding future work in this important field.

1.1 BACKGROUND OF THE STUDY

1.1.1 Breast Cancer. –

Cancer is a group of more than one hundred diseases that begin when genetic changes interfere with the orderly process of cells to grow uncontrollably (Debi, 2018). When mutations or genetic changes disrupt the normal process of cell growth, it leads to proliferation and the formation of a mass or tumour. Breast cancer is the most common type of cancer and is the second leading cause of death worldwide (Farahnaz, 2018; Sanchez, 2020), (T.G., Debelee 2019), (V. R. Gurudas, 2022). According to GLOBOCAN (WHO, 2022), it is a major public health issue that affects women around the world (J. Seladi-Schulman, 2022).

The breast consists of three main components: Lobules are glands that produce milk. Second, Ducts: Tubes that carry milk. Third, connective tissue: Fibrous and fatty tissue surrounds and supports these structures (Farahnaz, 2018). Breast cancer begins in the lining of the ducts 85% or lobules 15% in the glandular tissues of the breast and spreads beyond the breast through blood vessels and lymphatic vessels (Sanchez, 2020; Seladi-Schulman, 2022).

Initially confined to the lining of the ducts or lobes, it affects about 85% of cases without causing any symptoms. Over time, stage 0 invades the surrounding area of the breast. Invasive breast cancer spreads to the nearby lymph node, and it goes to the

regional metastasis or other organs of the body, which is called distant metastasis. Lastly, it causes the women to die.

For the best results and health preservation, prompt action is essential (GLOBOCAN, (Sung et al., 2021). Early detection is crucial for successful treatment, as noted by (T.G., Debelee, 2019) and (V. R. Gurudas, 2022). The survival rate for early-stage breast cancer is 100%, while the survival rate drops to 28% for stage IV breast cancer.

The term "ductal carcinoma in situ" (DCIS) describes the existence of aberrant cells in a breast milk duct. The initial type of breast cancer, DCIS, is thought to be noninvasive, which means it has not moved outside of the milk duct and has little chance of developing into an invasive variety.

Early identification and treatment of breast cancer depend on the ability to recognize its signs. One of the most important symptoms to look for is a significant breast thickening or lump, which may not hurt any modifications to the breast's dimensions form or general look uneven skin tone, including pitting redness or dimpling changes that seem out of the ordinary in the nipple or the areola any unusual or crimson nipple discharge. If the patient encounters these symptoms, remain alert and seek medical advice. Early intervention can have a significant impact.

Early breast cancer is classified as zero to three, while late-stage or progressed breast cancer is classified as four or metastatic breast cancer. TNM (tumour, Node, and Metastasis) is the most often used staging method for breast cancer. TNM enables medical professionals to communicate in the same language. tumour size measured in centimeters. N- the number of positive lymph nodes. M - indicates whether the malignancy has spread to the distant (T.G., Debelee, 2019; V. R. Gurudas, 2022).

The tumour can be classified as benign, pre-malignant, or malignant (WHO, 2022). Benign tumour can be recognized by their extremely sluggish development or inability to spread. Although pre-malignant cells are not yet cancerous, they can develop into malignant cells if left untreated. However, malignant cells are carcinogenic and can spread to other regions of the body through aggressive growth. Malignant tumour are cancerous, and the uncertainty surrounding the diagnosis eventually spreads beyond the initial tumour to different parts of the body. The breast cancer spreads to the nearby lymph node and goes to regional metastasis or distant metastasis (V. R. Gurudas, 2022; WHO, 2022). It is important to understand that breast cancer may be effectively treated, especially if the illness is discovered early.

Calcifications are tiny calcium deposits that appear as dazzling white spots or specks

on the breast's soft tissue backdrop during mammography. The X-rays from mammography are easily absorbed by the calcium. Calcifications seldom appear on breast magnetic resonance imaging and rarely do so on ultrasounds. Mammograms frequently show calcified tissue, which is more prevalent after menopause (breastcancer.org, 2024).

A fibroadenoma is a solid, painless, non-cancerous (benign) breast tumour. It is the most common type of non-cancerous breast tumour and usually does not increase the risk of breast cancer. Fibroadenomas can be divided into four categories based on their size and development. Simple fibroadenoma is the most common type. It tends to be smaller, and the cells look the same throughout the tissue. Complex fibroadenoma is the second category, more common in people older than 35 years. It tends to be larger and may have calcifications or cysts in it. Finding any kind of lump in the breast tends to set off alarm bells. But if there is a painful lump in the breast, there may be a breast cyst, which can result from normal hormonal changes. Although breast cysts can develop at any age, women in their 30s and 40s are more likely to get them.

Globally, 19.3 million new instances of cancer and about 10.0 million cancer-related deaths occurred in 2020 (Sung et al., 2021; Bray, F. et al., 2024).

Table 1-1: Cancer distribution

Type	Worldwide			Africa			Ethiopia		
	All types of cancer	Breast cancer	Ratio %	All types of Cancer	Breast Cancer	Ratio %	All types of Cancer	Breast Cancer	Ratio %
New Cases	8,751,759	2,261,419	25.84	633,456	186,598	29.46	50,598	16,133	31.88
Death	4,403,488	684,996	15.56	387,546	85,787	22.14	32,970	9,061	27.48
Prevalence	23,087,599	7,790,717	33.74	1,298,101	429,220	33.07	87,153	27,872	31.98

The global cancer burden is expected to be 28.4 million cases in 2040, a 47% rise from 2020. Around 685,000 women are victimized by breast cancer globally. Projections indicate that around 12.9 million people will die due to cancer by 2030, and around 857,000 will die of breast cancer (Sung et al., 2021). These high mortality rates are associated with late diagnosis of the disease (Freeman, K. et al., 2021). In 2020, the estimated females of all ages, new cases, deaths, and prevalence of breast cancer are shown in Table 1.1 (Sung et al., 2021; and WHO, 2022).

Mammogram screening is the gold standard worldwide because it effectively lowers the

death rate from cancer of breast cancer in women over 40 years of age. Nonetheless, it is a sophisticated public health approach that necessitates infrastructure and coordinating resources. The WHO advises against implementing screening programs unless their efficacy has been shown in the local setting and there are enough resources to provide a population-based service. Due to the disease's high prevalence, this expenditure is justified.

1.1.2 Artificial Intelligence for the diagnosis of breast cancer. –

Breast cancer detection involves analyzing medical data to determine whether tumours are malignant or benign. The revolution in artificial intelligence has enabled the automation of breast cancer detection using digital mammography and digital breast tomosynthesis, facilitated by AI, ML, DL, CNN, and other intelligent technologies (Geras et al., 2019). However, AI has limitations in certain areas that require the development of a large set of rules, and it faces challenges due to increasing demands in learning and search optimization (Farahnaz, 2018). To overcome these challenges, statistical methods and AI techniques play a vital role (Farahnaz, 2018). Even though AI has a gap in the early detection of BC (computersciencewiki.org, 2024), it has a positive impact on enhancing performance in the diagnosis of BC with data-intensive methods.

The use of artificial intelligence (AI) technology holds great promise for improving the early detection and diagnosis of breast cancer, increasing women's chances of survival (Sanchez, 2020), (T.G., Debelee, 2019), (V. R. Gurudas, 2022). AI is essential for feature selection and classification. According to J. Seladi-Schulman (2022), efficient feature selection is essential for enhancing model correctness and scalability as well as identifying the optimal solutions within acceptable computing time limits (computersciencewiki.org, 2024). However, a substantial amount of computer power is needed for this activity. This study uses a genetic algorithm, a kind of evolutionary algorithm, by integrating it into artificial intelligence, to optimize hyperparameters to tackle this problem.

Machine learning and deep learning are being used to detect breast cancer in medical imaging. Machine learning has a trade-off between accuracy and intelligibility (Freeman et al., 2021). More accurate models are usually not intelligible; in contrast, more intelligible models offer significantly worse accuracy (stackoverflow.com, 2024). DL has the downside of overfitting the training data, leading to reduced performance. Research shows that deep learning models for early breast cancer detection are not optimal due to a lack of large data sets and require high-quality

images as input.

According to the research (J.Seladi-Schulman, 2022), computer algorithms can identify cancer just as accurately as doctors. This means there is no evident advantage or disadvantage in their diagnostic abilities. Overall, these algorithms function similarly to human specialists. Research studies demonstrate that diagnosis performance depends on data quality and feature selection. The current data analysis and study show that radiologists miss 15% to 35% of breast cancers using mammography data.

The study paper by Bhushan A. et al. (2021) offers chances to employ other deep learning mechanisms, such as LSTM, GAN, and RNN, to predict the breast tumour status. On the other hand, research ignores the confusion matrix and AUC factors in favour of concentrating solely on the accuracy measure for performance evaluation. Since the accuracy metric does not differentiate between false positives and false negatives, it is inadequate. Future studies should include at least AUC and F-scores to assess the performance of each model. These can improve sensitivity and ensure fewer false positives than radiologists. However, it may have the risk of overfitting the training data, resulting in a breakable, degraded performance in certain settings.

To ensure AI technology applies to cancer diagnosis and prognosis successfully, first, resolve the challenges that AI faces. For example, input data cannot be used directly from the medical imaging technology; this is a crucial step to extract features from the imaging data and process. (stackoverflow.com, 2024), emphasize the development and popularization of technology. In addition, the weight coefficient in the neural network models is evaluated and calculated, and the confidence interval is reasonable, so medical interpretation needs further research. Screening another patient from the positive is a time-consuming task. Countries like Ethiopia have limited radiologists for screening the images, and the calcification process takes time. For this reason, such a study has a solution to easily screen the image by BI-RADS scoring (Bhushan A. et al., 2021). According to the researchers, the screening is good for age groups of 40 to 45 years. In our country, these age groups are around 23%.

AI-based image classification delivers useful findings for radiologists when deciding on follow-up visits or further imaging. The radiologist focuses on the patients having breast images at the highest levels, to reduce false positives and false negatives and improve the screening procedure for breast mammography images.

1.1.3 Computational Intelligence. –

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 with bioinspired computing techniques, such as evolutionary and genetic algorithms. Computational intelligence uses computer science and technology known as the Intelligence optimization approach to emulate human behaviour and the natural world. It falls into three primary categories: fuzzy computing, evolutionary algorithms (EAs), and neural computation. In the past few decades, computational intelligence techniques have received more attention. Different novel computational intelligence approaches, including fuzzy neural networks, deep learning networks, and extreme learning machines (ELM), have been proposed to address the practical challenge, despite the significant accomplishments that have been made (Zhang, 2017, and R. Manikandan et al., 2020).

A number of studies have demonstrated the effectiveness of CI-based techniques, including genetics and an evolutionary approach, in various applications (R. Manikandan et al., 2020; breastcancer.org, 2024; and Balcha, A., Woldie, S., 2023). Scientific research and engineering practice extensively use CI. The continuous increase of computational resources and the size decrease of computing architectures make use of CI (Antonio E Ruano et al., 2014, and R. Manikandan, et al., 2020).

AI and CI are two research categories for working on similar problems, having different methodologies, histories, and tools. CI resembles using bio-inspired computing, like evolutionary and genetic algorithms, whereas AI uses powerful theoretical techniques, and it is community-focused with deductive reasoning. Both AI and CI studies involve Machine learning, especially studies in NN. Logical and expert systems and statistical approaches to machine learning, like regression, are in AI but not in CI. Genetic programming, fuzzy logic and ant colony optimization are solidly in CI, but possibly not in AI (Antonio E Ruano, et al., 2014). CI-rooted techniques, Genetics and an evolutionary approach have major performance in specific problems (Zhang, W. J., 2017).

Different novel computational intelligence approaches, including fuzzy neural networks, deep learning networks, and extreme learning machines (ELM), have been proposed to address the practical challenge, despite the significant accomplishments that have been made (Shuzhi Sam et al., 201; Zhang, 2017, and R. Manikandan et al., 2020).

1.1.4 Genetic Algorithm. –

Genetic Algorithm (GA) is a heuristic search algorithm inspired by natural selection and genetics principles. 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 a binary search space over successive generations, using principles such as selection, crossover, and mutation to improve the solutions' fitness iteratively (Katoch et al., 2020). Features such as parallelism, global optimization, a larger set of solution space, requiring less information (Tomasz Tarkowski, 2022), 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 (Tomasz Tarkowski, 2022).

1.1.5 Support Vector Machine. –

One of the most often used methods for supervised learning is the Support Vector Machine (SVM). Classification is the main use of SVM. The goal of the SVM method is to find the optimal line or decision boundary that can divide an n-dimensional space into classes, allowing it to conveniently place new data points in the proper category in the future. We refer to this optimal decision boundary as a hyperplane.

When a data set can be divided into two classes using a single straight line, it is said to be linearly separable. In this case, the classifier is called a Linear SVM classifier (Resmini et al., 2021). When a data set cannot be classified using a straight line, it is referred to as non-linear data, and the classifier employed is known as a non-linear SVM classifier. Non-linear SVM is used for non-linearly separated data.

SVM outperforms other classifications by comparing the SVM-based classifier with ANN and Bayesian classifier. First, it is used for identification of the lesion and, second, for classification as malignant or benign. The proper use of SVM identifies solid breast nodules at exceedingly high accuracy. The approach used for the SVM-based ensemble learning algorithm increases the diagnosis accuracy and reduces the diagnosis variance (Savita Ahlawat, 2020).

The concept of risk reduction is the primary distinction between ANNs and SVMs. An SVM uses the principle of structural risk minimization instead of practical risk minimization, which gives it superior generalization ability in situations with small numbers of samples. Conversely, an ANN uses empirical risk minimization to reduce the error in the training data.

1.2 MOTIVATION OF THE STUDY

The prevalence of breast cancer has become an increasingly pressing concern. Reports indicate that the rates of new cases, deaths, and overall prevalence of breast cancer stand at 25.84%, 15.56%, and 33.74%, respectively, across various cancer types worldwide. According to Yunmeng Zhang et al. (2025), in 2022, there were approximately 2.3 million new cases of breast cancer and 666,000 related deaths globally. If national rates remain stable, new cases and deaths are projected to rise by 54.7% and 70.9%, respectively, by 2050. Despite advancements in technology that facilitate the diagnosis of breast cancer, its incidence continues to climb. The global burden of breast cancer is escalating at an alarming rate, with significant disparities observed among different countries. In China and South Korea, both the incidence and mortality rates of breast cancer have increased dramatically (Lei et al., 2021).

There was not enough awareness about cancer before hospital visits, particularly breast cancer, which is serious if not diagnosed early. This became personal when the family faced a terrible situation. The patient received a definitive diagnosis, including a mammogram and ultrasound, and the doctor advised the patient to begin chemotherapy, as the cancer had progressed to stage four. Tragically, despite five rounds of chemotherapy, the patient did not survive. The lack of accurate diagnoses and the inability to distinguish between benign and malignant tumours early on were critical issues.

This research underscores the urgent need for early detection and prevention strategies to improve survival rates. To address this critical issue, the study integrates genetic algorithms with machine learning technologies in healthcare diagnostic methods, aiming to detect and predict breast cancer as early as possible. The goal is to enhance early detection by reducing the rates of false positives and negatives through advanced computing techniques.

1.3 STATEMENT OF THE PROBLEM

Misdiagnosed Breast cancer leads to the delayed detection of breast cancer (Seladi-

Schulman, J. 2022). About 31% of individuals with breast cancer are overdiagnosed. Thus, for no apparent reason, healthy people receive severe cancer therapies. About 16% of instances of breast cancer are missed by mammograms. The survival rate for breast cancer in its initial stages is about 100%. Nonetheless, 28% of people who have stage IV breast cancer survive for five years or more. Delays in the diagnosis and treatment of breast cancer will result in the death of many people.

In the case of Ethiopia, because of breast cancer, 9,061 women died, which is 27.48% of other cancers. The prevalence of BC is 31.98%, according to GLOBOCAN. Though the causes of death due to breast cancer are not yet known, early breast cancer detection would result in better treatment and enhanced recovery (R. Manikandan et al., 2020). The revolution in artificial intelligence (AI) has profoundly changed the landscape of automated breast cancer detection, digital mammography, and digital breast tomosynthesis, primarily through the use of deep learning and convolutional neural networks (Geras et al., 2019).

While AI technologies are increasingly employed to identify tumours, they encounter challenges in areas that require extensive rule-based processing and feature complex datasets. These challenges stem from the growing demands for learning and optimization in search (F. Sadoughi et al., 2018; Sechopoulos et al., 2021).

Consequently, delays in the early detection and prediction of breast tumour can result in the progression to invasive cancer before a diagnosis is made. This issue is critical, as breast cancer has emerged as the leading cause of death among women (Bichen et al., 2014).

There is currently insufficient research on the hybrid Genetic Algorithm (GA) model that combines K-Nearest Neighbours (KNN) and Support Vector Machines (SVM) to improve the training of breast images for the early detection and classification of tumours as benign or malignant. Additionally, there is a notable lack of models that integrate a modified genetic algorithm with Pontryagin's minimum principles. This integration aims to enhance the validation process of feature selection, specifically for breast cancer detection. Furthermore, there is a significant scarcity of BI-RADS scoring, which supports decision-making regarding the stage of breast tumours and allows radiologists to assess a patient's condition without requiring further diagnosis.

1.4 RESEARCH QUESTION OF THE STUDY

This study has the following research questions:

1. What models improve the accuracy and reliability of classifying breast tumours as benign or malignant?
2. What models can be employed to improve the accuracy of early breast tumours detection?
3. What systems can be effectively utilized to automatically assess the level of breast tumours?
4. What methods can be followed to create a digital data set suitable for analysis by technology-enabled Systems?

1.5 GENERAL AND SPECIFIC OBJECTIVES OF THE STUDY

1.5.1 General objective. -

The general goal of this study is to enhance the accuracy and efficiency of identifying breast abnormalities, classifying whether malignant or benign, and preparing an applicable breast image dataset.

1.5.2 Specific Objectives of the Study. - The specific objectives of the study are to

- Design a hybridized GA model with ML to improve the early detection and classification of breast tumours.
- Model a modified genetic algorithm with the optimized fitness function by applying PMP.
- Implement a BI-RADS scoring. to categorize and assess the stage of the tumours.
- Prepare public and locally organized breast mammography image data sets.
- Do the process of training and tuning of the model until it improves the precision of breast cancer detection and prognosis.

1.6 SIGNIFICANCE OF THE STUDY

Oncologists, radiologists, and pathologists are increasingly relying on advanced technical support systems to enhance early tumour detection and improve the accuracy of predictive diagnostics. This collaboration is crucial not only for identifying malignancies at their earliest stages, when treatment options are most effective, but also for integrating diverse data sources such as imaging studies, biomarker analysis, and genetic profiling. By harnessing cutting-edge technologies like artificial intelligence and machine learning algorithms, these specialists can elevate diagnostic precision and reduce the occurrence of false positives and negatives. Ultimately, this

synergy among medical professionals aims to improve patient outcomes, streamline treatment approaches, and significantly contribute to the overarching goal of saving lives.

This research plays a crucial role in identifying tumour at an early stage and determining their type using minimal image data. The focus of this work is on computational intelligence, specifically an evolutionary computation algorithm known as Genetic Algorithms (GA), which is integrated with machine learning concepts. The process also aims to optimize the usage of computational resources. This study will produce a locally trained breast mammography image dataset and contribute valuable insights to the research community. We have developed a computational intelligence model designed to screen, analyze, and interpret mammography images to detect potential breast abnormalities. Our curated BI-RADS dataset offers a comprehensive and standardized collection of mammography images for training and testing the model. The research approach seeks to enhance the accuracy and efficiency of breast cancer screening by leveraging advanced computational methods to assist radiologists in the early detection and diagnosis of breast abnormalities. One of the objectives of this study is to assess the stage of breast images based on the BI-RADS scoring system, thereby streamlining the screening process, and reducing the need for specialized resources and time. Additionally, we aim to provide patients with prompt information about the results.

Integration of Computational Intelligence technology: This study has an integration of computational intelligence (CI) technology; with advanced computational techniques, specifically genetic algorithms, and Pontryagin's Minimum Principle (PMP), into the domain of breast cancer detection. This integration highlights the potential of these technologies to enhance medical diagnostics, particularly in the early and accurate identification of breast cancer.

Enhancement of Feature Selection Processes: The research improves feature selection processes, which are critical for optimizing model accuracy and scalability. By refining these processes, the study addresses a significant challenge in machine learning-based medical diagnosis. This enhancement not only boosts accuracy but also lowers the computational burden, rendering the approach more efficient and practical for real-world applications. Overall, we anticipate the following outcomes:

- Mathematical Model: Modified Mathematical Model of GA with PMP.
- Detection: Breast abnormality and tumour detection

- Prediction: Is the tumour going to be cancerous or not?
- tumour Stage: Identify the stage of the tumour and the type of tumour.
- Optimally: Process with optimal computational resources.
- Construct further Research area: locally trained breast cancer data.

1.7 SCOPE AND LIMITATIONS OF THE RESEARCH

1.7.1 Scope. - The scope of the study includes the following.

- Study and explain the benefits of genetic algorithms with optimization.
- Collect digital breast mammography image data from the diagnosis center.
- Extract, preprocess, and make ready of the data as a breast image dataset.
- Prepare models to answer the research question based on the problem.
- Train the data using SVM and KNN by hybridizing with Genetic Algorithms
- Test the performance of the result, by Confusion matrix, Accuracy, Precision, Recall, and Specificity, and find the F1 score.
- Study and analyze the results from the model.
- Write the study result and prepare the research document.
- Breast cancer can be initiated and varies by the patient's geographic location, blood type, genetics, economic background, and social interaction. Data collection not from various locations, and focuses on the collected mammography data.

1.7.2 Limitation. –

The primary limitation of this study lies in the constrained budget and resources available. The funding allocated for this research is limited, allowing for expenses related only to printing copies and data collection. To gain a more comprehensive understanding of the factors affecting patients, additional expertise and participation are necessary to categorize data by geographical location, economic background, and literacy levels. The objective does not include investigating the social factors that lead to patients arriving late at the diagnosis center, particularly when they are often at an advanced stage of cancer. Even though we have collected data from a single diagnosis center, we faced challenges due to the lack of access to a high-performance computing machine, which hampers our ability to obtain accurate results and analyze data using various parameters and algorithms. Furthermore, certain medical centers have shown reluctance to collaborate on this study, making it difficult to secure participation from senior radiologists.

1.8 Ethical Consideration

The prepared data set for the research is human-related data, which is planned to be collected from the medical diagnosis center. All ethical standards will be considered according to the rules and regulations set by the university IRB (Institutional Review Board). These ensure that the researcher will not apply the research data for any purpose other than this research. All the data is reported to and reviewed by the IRB. Furthermore, the individual's name will not be identified in all collected images. Encrypt and create a unique identifier for each image. In this regard, for any other organizations, educational institutes, or research centers that align to work with this research or in any way, all the rules and compliance will be applied. This research bind the rules and regulations of the Ethiopian Personal Data Protection Proclamation No. 1321/2024.

1.9 Disclamation

This research dataset consists of a curated collection of breast mammography images and is intended solely for academic and scientific research purposes. It is essential to recognize that any conclusions drawn from this dataset should not be applied directly to diagnostic practices. All findings must undergo thorough clinical evaluations to ensure compliance with established medical standards and protocols. The researcher accepts no responsibility for the interpretation of these results, including decisions regarding the classification of images as malignant or benign, or the assignment of a BI-RADS score. It is critical that healthcare professionals conduct comprehensive assessments using clinically validated methods before reaching any conclusions based on this research dataset and its results.

1.10 Chapter organization of the study

- Chapter Two: Literature Review and Related Works. In this chapter of the study, we delve into an extensive review of existing literature and related scholarly works concerning breast cancer. We highlight the intricate nature of breast cancer as it affects diverse populations around the globe, exploring the strategies implemented by the World Health Organization (WHO) and various researchers to combat this formidable disease. We analyze the implications of breast cancer within the community, discussing the reasons behind the lower survival rates associated with this condition. Additionally, we investigate the technological advancements that facilitate the accurate diagnosis of breast cancer, including

insights drawn from studies utilizing artificial intelligence (AI), machine learning (ML), deep learning (DL), computational intelligence (CI), and hybrid technologies integrated with genetic algorithms (GA) for effective diagnosis, detection, and prediction.

- Chapter Three: Methodology outlines the comprehensive methodology employed in this study. Here, we detail the study's design framework and the systematic processes we followed to reach our conclusions. We discuss the various methods of data collection, specifying which data were gathered and how these data were processed and analyzed for our research. Furthermore, we elaborate on the tools implemented during the study and provide a thorough description of the training and testing methods used to evaluate the models developed.
- Chapter Four: In Proposed Solutions, we present a critical examination of the proposed solutions derived from our literature review. We reflect on the extent of the literature analyzed, elucidating our selection criteria for including certain studies while excluding others. We describe the specific models proposed, detailing their design and the methodology employed to process data through these models, providing a clear understanding of the rationale behind our choices and approach.
- Chapter Five: Results and Discussion focuses on presenting the outcomes of our analysis through the three models proposed in the previous chapter. We offer a detailed description of our dataset, outlining its characteristics and the design framework involved. Results are illustrated through both tabular and graphical representations, allowing for a comprehensive comparison of our findings with those from prior research in the field. This juxtaposition serves to underscore the advancements made by our model relative to existing studies.
- Chapter Six: Conclusion and Future work of the study. In the concluding chapter, we synthesize our findings, summarizing the key insights garnered from the study and their implications for medical centers and practitioners. Our recommendations emphasize enhanced approaches to BC detection and classification, advocating for the integration of technology and healthcare facilities. We highlight the potential to reduce both FP and FN through the application of AI and CI alongside dedicated researchers. Additionally, we discuss the strengths and limitations identified throughout the research, providing a balanced view of our findings.

CHAPTER TWO

2 LITERATURE REVIEW AND RELATED WORKS

2.1 Literature Review

In this study, we explore the use of genetic algorithms for the selection of optimal features based on sample data. Throughout the literature review, we assess the advantages of genetic algorithms and identify which ones are most effective in delivering optimal solutions for breast cancer detection and prediction. Additionally, we discuss the benefits and drawbacks of machine learning in this field. We examine the challenges that arise in this type of AI research and consider how these applications are implemented in cancer diagnosis.

Many other research papers have also explored the use of genetic algorithms for classification by combining them with machine learning algorithms. The primary focus of these studies is to enhance the accuracy of early breast cancer detection by integrating genetic algorithms with ML and PMP to select the best-fit score. Our literature review and related works discuss the findings of various research results related to genetic algorithms, enabling us to compare the outcomes of our model.

2.1.1 Breast Cancer and Diagnosis. -

Breast cancer is the most common cancer among women around the world. Despite enormous medical progress, breast cancer has remained the second leading cause of death globally (F., Sadoughi et al., 2018). Breast cancer occurs when the cell tissues of the breast become abnormal and uncontrollably divide. These abnormal cells form a large lump of tissue. This consequently becomes a tumour. Taye Girma Debelee, F. S. (2019) noted that if breast cancer is detected early, the treatment becomes successful. Thus, there is a need to have appropriate methods for screening the earliest signs of breast cancer.

Breast cancer is a disease in which abnormal breast cells grow out of control and form tumour. If left unchecked, the tumour can spread throughout the body and become fatal. Breast cancer cells begin inside the milk ducts, the breast's milk-producing lobules. The earliest form (in situ) is not life-threatening and can be detected in the initial stages. Cancer cells can spread to nearby breast tissue (invasion). This creates tumour that cause lumps or thickening. Invasive cancers can spread to nearby lymph

nodes or other organs (metastasize). Metastasis can be life-threatening and fatal (Mojtaba Sepandi et al., 2018; Chun-jiang Tian et al., 2021). Cancer is the second leading cause of death in the United States, exceeded only by heart disease. One in every four deaths in the United States is due to cancer. In 2019, (R. Manikandan et al., 2020), in the United States, 264,121 new cases of Female Breast cancer were reported among women, and 42,280 women died from this cancer. For every 100,000 women, 130 new Female Breast cancer cases were reported, and nineteen women died of this cancer. Breast cancer was the most prevalent cancer among women in 157 out of 185 countries in 2022, with 0.5–1% of cases occurring in men. According to the World Health Organization (WHO), as reported on March 13, 2024, breast cancer accounted for 670,000 deaths worldwide in 2022. Notably, half of all breast cancer cases arise in women with no specific risk factors aside from their sex and age. Global estimations show glaring disparities in the incidence of breast cancer based on human development. For instance, 1 in 12 women may receive a breast cancer diagnosis throughout their lifetime, and 1 in 71 will pass away from the disease in nations with extremely high Human Development Indexes (HDI). In comparison, 1 in 48 women will die from breast cancer in nations with a low HDI, and only 1 in 27 women will receive a breast cancer diagnosis throughout their lifetime.

A recent study in four countries in Sub-Saharan Africa revealed that the overall prevalence of breast cancer screening was only 12.9% during the study period. According to a document by the EMoH, initiatives outlined in the national guide aim to enhance the survival rate of breast cancer by prioritizing early detection at stages I and II. The goal is to achieve a diagnosis of invasive cancer in over 60% of cases by the year 2030. Screening women within the defined eligible age group allows for early diagnosis and swift treatment, improving the prognosis and outcomes by addressing the disease early. In 2020, the estimated number of new cases in Ethiopia is rising, and breast cancer became the most common cancer.

According to GLOBOCAN, NCI, and WHO (2022), women misdiagnosed as not cancerous result loss of critical treatment time. If the woman has frequent mammograms, then the more likely to see a false-positive result. The diagnosis of breast cancer using mammography has resulted in a "false negative".

From **Table 2-1** the distance classifies the distribution of new breast cancer as

localized, regional, distant, and unstaged (NIH, 2022). Most of the data is localized. From the data, distant distribution is, on average, 6.5% of the data categorized by race.

Table 2-1: New cancer distance distribution,

Measure from	Percent	Count
Localized	66.00%	832,142
Regional	25.80%	325,488
Distant	5.80%	73,054
Unstaged	2.40%	30,785

In

Table 2-2, the survival rate of distant distribution of breast cancer is around 30%, whereas localized is 99.1% (NIH, 2022). The prevalence of counts is 1,093,984 with a rate of 65.58% of the 5-year USA on January 1, 2019. The 5-year relative survival rate is 90.6% for all races, while whites 91%, Black people 82.6%, and other races 91.2% have a relative survival rate. U.S. 5-Year Age-Adjusted Mortality Rates, 2016-2020, 19.6% (210,505) all races, 26.6% (32,478) Black, including Hispanic and 19.1% (170,082).

Table 2-2: 5-Year relative survival rates, 2012-2018.

Measure from	5-Year Relative Survival (%)	Lower 95% C.I.	Upper 95% C.I.
Localized	99.1%	98.9	99.2
Regional	86.1%	85.8	86.4
Distant	30%	29.1	30.8
Unstaged	60%	58.3	61.7

There are various imaging methods available for the screening and diagnosis of breast cancer, the most important of which are mammography, ultrasound, and thermography. Of these, mammography is not remarkably successful for dense breasts, the recommended techniques are Ultrasound or diagnostic sonography. Image-based diagnosis can be affected by distinct factors (K., Dembrower et al., 2020), including the presence of noise in images, the radiologist's visual perception ability, inadequate clarity, poor contrast, and the less experienced radiologist. The current mammography radiologist has a 15% to 35 % missing breast cancer rate.

Even though mammography is the standard method to detect early-stage breast cancer before the lesions become clinically palpable, it has its disadvantages (Riccardo et al., 2021; Taye Girma Debelee and F. S., 2019; Inoa, A. L., 2021).

- Risk of false alarm

- It is difficult for the radiologist to interpret the results from mammograms as mammogram images have low contrast (Samraj, D. et al., 2023)
- Double reading of mammograms leads to an increase in the cost of detection.
- Mammography alone misses many cancers in dense-breasted women.

Tomosynthesis or "3D" mammography is a new type of digital X-ray mammogram that creates 2D and 3D-like pictures of the breasts. This tool improves the ability of mammography to detect early breast cancers and decreases the number of women "called back" for additional tests for findings that are not cancers (Katoch et al., 2020). Ultrasound is Suitable for dense and soft tissues, but the quality and interpretation of the image depend highly on the skill of the person doing the scan. From this, one can conclude that the treatment of using only such technology for breast cancer is prone to error, so there must be another mechanism here that becomes artificial intelligence. Tomosynthesis demonstrated excellent sensitivity and specificity, but the technique did not meet the expectations, given the risk of overdiagnosis and the lack of reduction in the number of breast cancer intervals (Riccardo et al., 2021).

The radiologist must properly locate the region where the tumour is to define the stage of the tumour (Sechopoulos et al., 2021). There are various stages of the tumour,

- Localized: when cancer has not spread outside of the breast
- Regional: spread outside the breast to nearby structures or lymph nodes
- Distant: spread to other parts of the body, such as to the liver, lungs, or bones

Breast cancer is a complex disease, and its stages help determine how extensively it has spread. To properly classify the tumour stage, first, clearly define the characteristics. Here in the table, researchers define the behaviours of the tumour by the stage.

- Stage 0 (in situ): Abnormal cells are confined to the milk ducts or lobules. It is non-invasive and highly treatable. This is a precancerous stage with no invasive cancer cells.
- Stage 1 (localized): The tumour is small and localized to the breast (less than 2 cm) and has not spread beyond the breast. There may be a small amount of cancer in nearby lymph nodes.
- Stage 2 (localized): The tumour is still localized to the breast but is larger and may have spread to several nearby lymph nodes (2cm - 5cm) or those with limited lymph node involvement.

- Stage 3 (regional): This stage includes cancers that have spread to the skin, chest wall, or multiple lymph nodes in or near the breast, or locally advanced cancer with significant lymph node involvement.
- Stage 4 (distant): Metastatic cancer that has spread to distant organs. It is spread to one or more distant parts of the body, most commonly to the bones, lungs, or liver.

The stages of the breast tumour help the radiologist to determine the status and give recommendations for the patient.

The diagnosis of breast cancer is too challenging; statistical methods and artificial intelligence (AI) techniques are especially important to minimize these challenges. AI is said to be an artificially intelligent machine in various situations. In other words, these are systems that can respond to similar conditions, such as an intelligent human, including understanding complex situations, simulating thinking processes and human reasoning methods, and demonstrating accurate responding, learning and ability to acquire knowledge, and reasoning for solving problems, (F., Sadoughi et al., 2018).

Medical image processing is one of the fastest-growing areas in the healthcare sector, to make proper images of the human body, which are reliable for use in the diagnosis and treatment processes. In the early 1980s, there was an increase in the use of neural networks in image and signal processing.

It is important to note that no matter how well-constructed the algorithm is, its diagnostic performance depends on the volume of raw data and the quality of training. AI-based algorithms are data-intensive, and the performance of the result is affected by the quality of the data sets (Bhushan A. et al., 2021; stackoverflow.com, 2024). Similarly, DL algorithms require reliable, high-quality image inputs to have better results (Freeman et al., 2021). Peng Xue et al. (2022) suggest that deep learning algorithms are not yet superior or inferior in terms of performance compared to clinicians. An acceptable diagnostic performance with analogous deep-learning algorithms was observed in the breast.

2.1.2 Feature Extraction, Selection and Classification. -

Feature Extraction: Image features refer to the information collected from images that can uniquely identify the image or be used for further processing (Na Xu, and C. L., 2020). The extraction process aims to reduce the number of features in a dataset by creating new features from the existing ones. The techniques can also lead to other types of

advantages, such as:

- Accuracy improvements.
- Overfitting risk reduction.
- Speed up training.
- Improved data visualisation.
- Increase in explainability of the model.

Feature selection or variable selection is a process that reduces the number of attributes and selects a subset of original features. It plays a significant role in intelligent diagnosis, often used in data pre-processing to identify relevant features by removing irrelevant or redundant features which do not have significance in the classification task. It aims to improve classification accuracy. It identifies a subset of features or weighs the relative importance of features in target representation. This enables a computer-aided diagnosis model that is cost-effective, easy to interpret, and generalizable. So far, Feature selection methods have been explored in target recognition, logistic regression, disease detection and diagnosis, bioinformatics, and many industrial applications. Generally, Feature selection is for filtering irrelevant or redundant features from the dataset. Science, E. D. (2022) stated that feature extraction is for creating a new, smaller set of features that still capture most of the useful information.

Table *2-3* gives a briefing on the strengths and weaknesses of the methods of feature extraction and selection. Feature selection keeps a subset of the original features, while feature extraction creates new ones (Chun-jiang TianImage, and J. L.-f., 2021). We understand that methods for feature selection and extraction have their strength and weaknesses. We have taken into consideration the dataset and objectives of the task (Noor Ahmad et al., 2022).

Table 2-3: Feature selection and extraction algorithms, Bell, S. (2019).

No	Methods for Dimensional reduction	Strength	Weakens
1	Variance Thresholds	Applying variance thresholds is based on solid intuition: features that do not change much also do not add much information. This is an easy and safe way to reduce dimensionality at the start of the modelling process.	If the problem does require dimensionality reduction, applying variance thresholds is rarely sufficient. Furthermore, one must manually set or tune a variance threshold, which could be tricky. Recommended to start with a conservative (i.e., lower) threshold.
2	Correlation Thresholds	Applying correlation thresholds is also based on solid intuition: similar features provide redundant information. Some algorithms are not robust to correlated features, so removing them can boost performance.	We can manually tune a correlation threshold, which can be tricky to do. If the threshold is too low, then risk of dropping useful information. Whenever possible, prefer algorithms with built-in feature selection over correlation thresholds.
3	Genetic Algorithms (GA)	Genetic algorithms can efficiently select features from exceedingly high dimensional datasets, where an exhaustive search is unfeasible. When need to preprocess data for an algorithm that does not have built-in feature	GA add a higher level of complexity to the implementation, and they are not worth the hassle in most cases. If possible, it is faster and simpler to use PCA or to directly use an algorithm with built-in feature selection.

		selection (e.g., nearest neighbours) and when it is necessary to preserve the original features (i.e., no PCA allowed), GA is the best.	
5	Linear Discriminant Analysis (LDA)	LDA is supervised, which can (but does not always) improve the predictive performance of the extracted features. Furthermore, LDA offers variations (i.e., quadratic LDA) to tackle specific roadblocks.	As with PCA, the new features are not easily interpretable, and one must still manually set or tune the number of components to keep. LDA also requires labelled data, which makes it more situational.
6	Autoencoders	Autoencoders are neural networks, which means they perform well for certain types of data, such as image and audio data.	Autoencoders are neural networks, which means they require more data to train. They are not used as general-purpose dimensionality reduction algorithms.

2.1.3 Genetic Algorithm and Optimization with Hybrid GA. -

Dimensional reduction techniques are valuable tools for feature selection, extraction, and classification. Evolutionary Algorithms (EAs) excel in simultaneously exploring multiple regions of the solution space. These algorithms incorporate mechanisms for parallel processing and are characterized by self-organization and self-learning capabilities. EAs are frequently leveraged to optimize the structural parameters of machine learning algorithms (Zhang, W. J., 2017).

Among these, the Genetic Algorithm (GA) has found applications in medical imaging, such as in MRI for edge detection and in CT scans for identifying pulmonary nodules. In the context of CT image analysis, a template-matching technique that integrates GA is employed. GAs can function in parallel to discover patterns in biological datasets (Silva, T. et al., 2020). Furthermore, a sequential GA utilizing cellular automata has been applied to model COVID-19 data, breaking down the process into smaller sub-generations and concurrently assessing the fitness of each solution (Ghosh, S., B. S., 2020).

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 (Katoch et al., 2020).

Among the metaheuristic algorithms, the Genetic algorithm (GA) is a well-known algorithm, which is inspired by the biological evolution process. The GA is an optimization procedure that operates in binary search spaces and manipulates a population of potential solutions. A point in the search space is represented by a finite sequence of 0s and 1s, called a chromosome (R., Resmini et al., 2021). It can perform image processing tasks such as pre-processing, segmentation, object detection, denoising, and recognition. 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 (liquisearch.com, 2024).

GA passes through initialization, evaluation, selection, mutation, and cross-over and terminates the process to minimize multi-objective functions. 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. The selection operator selects elites to transfer directly to the next generation. Selected chromosomes undergo genetic operations such as crossover and mutation to generate offspring for the next generation. The crossover operator randomly swaps a portion of chromosomes between two chosen parents to produce offspring chromosomes. Crossover involves combining genetic information from two parent chromosomes, while mutation introduces random changes to maintain genetic diversity within the population. The mutation operator randomly alerts a bit in chromosomes, (Katoch et al., 2020). 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.

The quality of workable solutions is evaluated by a fitness function. The probability of survival is proportional to the chromosome's fitness value.

Advantages of Genetic Algorithms

- Parallelism.
- Global optimization
- A larger set of solution space
- Requires less information.
- Provides multiple optimal solutions.
- Probabilistic in nature
- Genetic representations using chromosomes.

GAs have also been instrumental in tackling various challenges in biomechanics, supporting predictive pathological treatments during examinations. Specifically, a GA-based region-growing method has been developed for brain tumour detection. In addition, GAs have been utilized for medical predictions, such as assessing the adverse effects of specific drugs (Katoch et al., 2020). They have also been employed to optimize Artificial Neural Networks (ANN), yielding significant enhancements in classification performance. Support Vector Machines (SVM) are often used in

conjunction with GAs for feature selection, thereby improving classification outcomes. As illustrated in

Figure 2-1, a Genetic Algorithm is proposed for a collection of models and feature selection, particularly in scenarios where data availability is limited. For instance, visual analysis in mammography achieves an accuracy of no more than 80% in breast cancer classification, underscoring the subjective nature of image analysis.

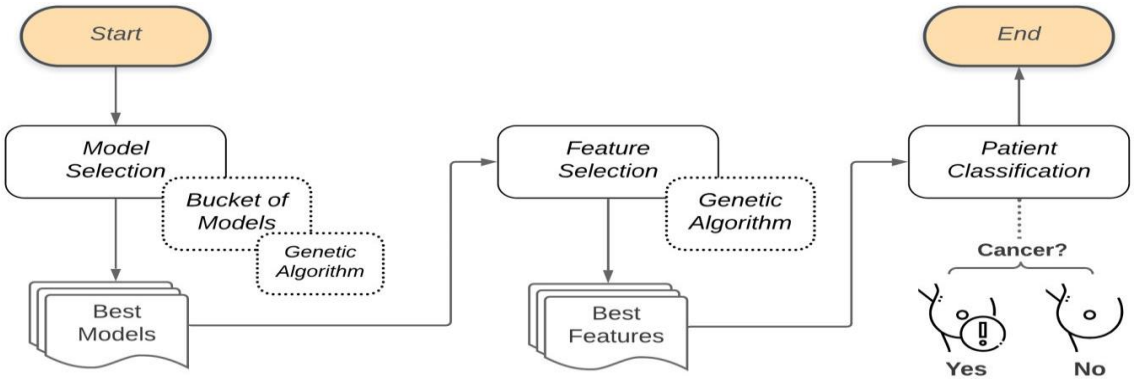


Figure 2-1: Process of GA for feature selection (R., Resmini, et al., 2021)

The ideal scenario for applying GA is if there is not enough data available and the theory on the problem is not remarkably high, as shown in **Figure 2-2** of intelligent systems.

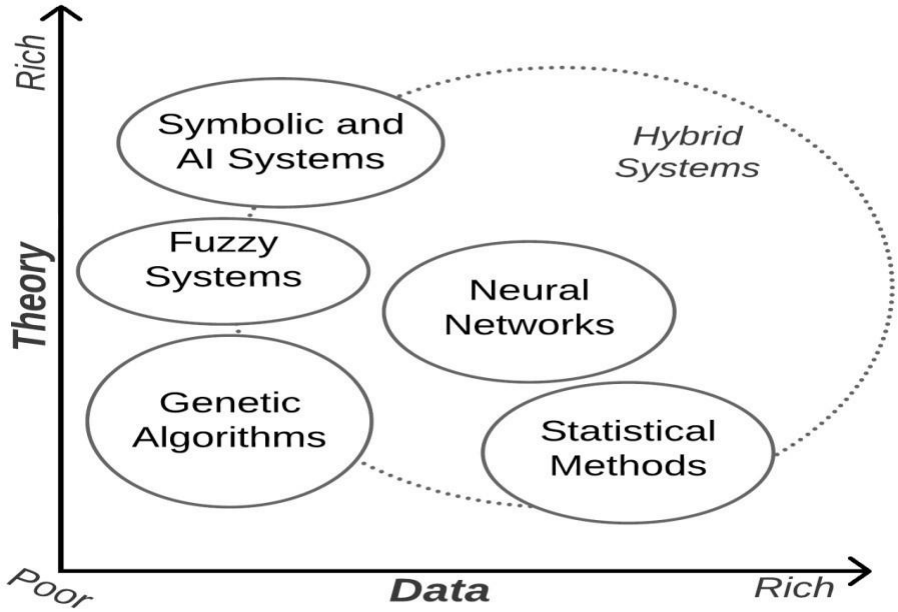


Figure 2-2: Methods for problem-solving depending on the availability of data.

On the other side, CNN and DL could perform better when working with a large amount of data (Science, E. D., 2022). Using the global search capability of the GA to evolve the CNN weights for the histopathological breast image classification problem,

Mishra, et al. (2020) train the CNN model using the BreakHis dataset images as input and three different optimization approaches.

The GA-based classifier performs as powerfully as the Adam optimizer, with a negligible difference. When the batch size is equal to 32, the CNN and DL algorithms have the best accuracy, but when the batch size is equal to 128, GA scores the best accuracy, using the technique Bucket of Models. The paper, Diyar Qader et al. (2017), uses a search method based on the principles of natural selection and genetics.

A hybrid computational method combining Dynamic Infrared Thermography and Static Infrared Thermography (SIT) has been proposed for the screening and diagnosis of malignant tumour. This approach utilizes both supervised and unsupervised machine learning techniques. An SVM (Support Vector Machine) classifier applied to SIT achieved an impressive accuracy of 95% in the diagnostic center. the The combination of a Genetic Algorithm and SVM demonstrated high performance, effectively selecting the best features in just a few generations (R. Resmini et al., 2021). This method identifies a small set of features that is optimal for classifying data related to breast cancer diagnosis. In summary, when comparing the proposed algorithm with related works, it outperforms others with impressive metrics: an F1 score of 97.29%, accuracy (ACC) of 97.18%, sensitivity (SENS) of 97.18%, specificity (SPEC) of 94.79%, and an area under the curve (AUC) of 97.91%.

The usability of different methods for problem-solving depends on the availability of data and expertise (theories) on a problem; the process of the Genetic Algorithm flow is shown in (R., Resmini et al., 2021).

In the summary of Diyar Qader et al. (2017), Sari et al. (2018), an overview of combining K-Means and GA, in all the cases, the K-Means algorithm with GA has more efficiency. Performance is more effective and efficient in converging complexity to the global optimum. It showed that Hybrid models have better performance accuracy. In addition, using GA as a combination of other algorithms enhances the accuracy of results in the case of a small data set. The main advantages of hybridized GA with other methods are better solution quality, better efficiency, a guarantee of feasible solutions, and optimized control parameters. As concluded in the paper, the Hybridization of intelligent techniques for an effective predictive model is essential.

As reported by Dinesh K. Sharma, H. H. (2021), the accuracy of the GA and ANN

hybrid model is greater than a single backpropagation neural network (BPANN). Using principles of global optimization, GANN performed well.

In the paper of Katoch et al. (2020), P. Chauhan and A. Swami. (2018), Samraj, D. et al., (2023), the genetic algorithm-based weighted average method implemented in the prediction of multiple models. The comparison has been done between Particle swarm optimization (PSO), Differential evolution (DE) and Genetic algorithm (GA). The genetic algorithm outperforms by using weighted average methods. The other comparison has been made between the classical ensemble and the GA-based weighted average methods, which suggests that the GA-based weighted average method outperforms.

Natural selection and genetic concepts underpin search-based and adaptive heuristic algorithms (Balcha, A. and Woldie, S., 2023), (Hari Mohan Pandey, 2016), and (Alison Jenkins et al., 2019). These algorithms are a subset of a much larger domain of evolutionary computation. They can be used in optimization, artificial neural networks, image processing, and machine learning (Denny Hermawanto, 2013).

Although the fitness function is sufficiently fast to compute, considering its representation in phenotype and genotype spaces, an improper representation leads to deficient performance. The function must quantitatively measure how fit a given solution is. How much do individuals produce from the given solution?

Pre-processing, segmentation, object detection, denoising, and recognition are the primary activities of image processing. Segmentation is the initial stage in addressing image processing challenges. It demands significant computational resources for image decomposition or partitioning. A genetic algorithm is one of the methods for optimizing computational resources. GA finds to minimize multi-objective functions:

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

$$J = (1 + \lambda S^*).J^* - - - - - - - - - - - - - - - (2.1)$$

where J, J^*, λ objective function, cost function and Lagrange multiplier, respectively. The cost function is equivalent to the mean square error, which is computed as,

$$J^* = MSE = \frac{1}{n}\sum_{i=0}^{n}(y_i - y_i^*)^2 - - - - - - - - - - - (2.2)$$

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.

$$J^* = \frac{1}{n}\left(\sum_{i=1}^{n}(y_n - y_i^*)^2 + \sigma\sum_{i=1}^{n}(C_i - C_i^*)\right) - - - - - - - - -(2.3)$$

where the classification error is included, with C as the actual class, C* as the predicted class, and σ as a weight factor. The objective function J can be obtained from Equations (2.1,2.2, and 2.3).

Genetic algorithms (GAs) are heavily based on the values of their control parameters. The control factors for GA are the starting population's size, the crossover rate, and the mutation rate (Mustafa Abbas Albadr et al., 2020). The crossover ratio determines the frequency of the crossover operator's usage. According to Allison et al. (2019), a high crossover rate rapidly reveals the variety of the community, while a low frequency makes the search more time-consuming. In the case of genetic algorithms, a high mutation rate makes the search process unpredictable (Mustafa Abbas Albadr et al., 2020); hence, a low mutation rate is preferable. Unlike traditional search methods, genetic algorithms can discover unique combinations with higher fitness values in each generation by applying the best objective and optimal fitness function values (M García et al., 2020). Furthermore, genetic algorithms can solve nonconvex design spaces with mixed, continuous, and discontinuous design variables (Kaya, M., 2023). Some termination scenarios include reaching the maximum number of permitted iterations, reaching the plateau of the fitness function, and achieving a previously specified fitness function value by any genotype (Tomasz Tarkowski, 2022).

A genetic algorithm is highly parallelizable, allowing it to effectively leverage multiple processors. Optimization problems typically require significant computational resources, as evaluating each potential solution can be resource-intensive. By evaluating multiple solutions concurrently, a genetic algorithm capitalizes on the benefits of parallel computing. This parallelization significantly decreases the time required to identify an optimal solution, rendering genetic algorithms a more efficient optimization approach.

2.1.4 Fitness Function. -

A chromosomal representation can be transformed into a scalar value or real number that assesses the quality of the solution. This transformation is known as a fitness

function (Saturncloud.io, July 18, 2023), denoted as $f: \Gamma \rightarrow R$, where Γ represents the space of chromosomes. The objective function comprises a final state function Φ [x(T)] and a cost function (or loss function) $J = \phi [x(T)] + \int x(T_0)(u, x)dt$, which is integrated over time. These terms constitute the fitness function:

- Unconstrained: the most basic example where the fitness function satisfies the objective function.
- Constrained: consisting of terms of the original goal and a penalty term that penalizes solutions that do not adhere to the constraints that may make up the fitness function.
- Multiple objectives: Each goal has a different fitness function, and the combined fitness functions yield the final fitness function. Phrases like Pareto-optimal will frequently come up in this situation.
- Dynamicity or Noise Fitness for where solutions may change over time or depend on noise, such as Gaussian noise.

The fitness function evaluates the quality of a potential solution and assigns a score based on predefined criteria (Jean-Baptiste Caillau et al., 2022). The fitness function defines the objectives or goals of the problem, and the fitness score indicates the quality of a candidate's solution. It is used to guide the evolution process towards optimal solutions and the selection, crossover, and mutation operations of the genetic algorithm. Individuals with higher fitness scores have a greater chance of survival and passing on their genetic material to future generations (Saturncloud.io, July 18, 2023). The calculation of the fitness score is specific to the problem at hand. The general process for calculating the fitness score is as follows:

- Evaluate everyone in the population using the fitness function.
- Apply the fitness function to everyone,
- Assign a fitness score to everyone based on the fitness function evaluation.
- Normalize the fitness scores if necessary to ensure that they are within a specific range, between 0 and 1.

An algorithm designer can use a different fitness function for more intricate situations that involve numerous objectives and restrictions, as noted by Jean-Baptiste Caillau et al. (2022). Proportionate fitness selection, or the roulette wheel, is one of the genetic operators used for selecting potentially useful solutions for recombination in genetic

algorithms (Balcha, A. and Woldie, S., 2023). The fitness function assigns a fitness value to viable solutions or chromosomes in any selection method, including fitness-proportionate selection. This fitness level was used to associate a probability of selection with each chromosome. Combines the objective function and the state equations, multipliers λ(t), and costate variables. We need to compute the objective function let us call as ObjF value, of each of the chromosomes to produce initialization (Denny Hermawanto, 2013, and M García et al., 2020).

$$ObjF(i) = |f(x_i)| - - - - - - - - - - - - - - - - - (2.4)$$

The fittest chromosomes have a higher probability of being selected for the next generation. To compute the fitness probability, first compute the fitness of each chromosome. From Equation (2.4), the fitness function is calculated as:

$$Fittnes[i] = \frac{1}{1 + ObjeF[i]} - - - - - - - - - - - - - (2.5)$$

The probability for each chromosome is formulated by probability calculation, for the population of N individuals and the fitness of an individual in the population is denoted as f_i , and then its probability of being selected, from Equations (2.5, 2.6), is given by Equation (2.7):

$$P[i] = \frac{Fittness[i]}{\sum_{i=0}^{n} Fittnes[i]} \quad - - - - - - - - - - - - - - - - - (2.6)$$

$$\frac{p_i}{\sum_{i=0}^{n} p_i} \quad , where\ p_i = \min_i \frac{(J_i)}{J_i} \ , i \in 1, \dots, L - - - - - - - - - - - - (2.7)$$

The issue's objective function implies evaluating the problem with genetic algorithms. In some cases, however, design variables may limit goal functions. The restricted objective function f(s) transforms into the unconstrained objective function ϕ(s). In the first transformation, which is not dependent on design variables using two different methods, the transformation uses error functions.

$$\phi(s) = [\, f(s) + R. \sum_{i=0}^{n} \sigma(Z)] \ - - - - - - - - - - - - - (2.8)$$

if $Z \geq o$ then $\sigma(Z) = Z_2$ and if $Z \leq 0$ then $\sigma(Z) = 0$. The unconstrained objective function $\phi(s)$ is transformed into the fitness function F(s) via the second transformation.

$$F(s) = \phi \max - [f(s) + R.\sum_{i=0}^{n} \sigma(Z)] \quad ---------(2.9)$$

Thus, Equation (2.9) can be rewritten as,

$$F(s) = \phi \max - \phi(s) \quad ----------(2.10)$$

- Constrained objective function represented by f(s).
- R denotes the predefined error coefficient (R = 2, 5, 10).
- σ (Z): Loss function.
- ϕ (s) denotes an uncontrolled function of objectives.
- ϕ max refers to the unconstrained maximum result function of the objective.
- F(s): denotes the functions of the fitness (G., Vaira Suganthi, et al. 2023)

Equation (2.10) converts the unconstrained objective function ϕ(s) into a fitness function F(s) by subtracting it from the maximum possible value ϕmax. This ensures that higher fitness values correspond to better solutions.

2.1.5 Controlled System. -

In Optimal Control Problem: Consider a continuous-time system described by the dynamics: $\dot{x}(t) = f(x(t), u(t))$ where x(t) represents the state, u(t) is the control input, and f is a continuously differentiable function. We work to find an optimal control trajectory u(t) that minimizes a cost function over a given time interval [0, T]. In the dynamic system of ODE.

$$X^*(t) = f(X(t), \quad X(0) = x^0, t > 0, ----------(2.11)$$

f: R⋉ → R⋉ and initial point x0∈R, X: [0, ∞] → R⋉ is the unknown curve; it interprets the dynamic change of the system's condition (Jean-Baptiste Caillau et al., 2022). As a change of time t_1, t_2, t_3, ... changing the parameters a ∈ A as a_1, a_2, a_3, ... function can be defined as

$$\propto (t) = \begin{cases} a_1, 0 \leq t \leq t_1 \\ a_2, t_1 \leq t \leq t_2 \\ etc \end{cases} ----------(2.12)$$

$$\begin{cases} X^*(t) = f(X(t), \propto (t) \\ X(0) = X^*, t > 0 \end{cases} ----------(2.13)$$

Simply, X (·), the solution of the ODE, depends on the control α(.) and x_0, the initial condition, but in a more complicated way, written as X (.) = X (., α(.), X_0). The overall task of the mathematical formulation here is to find which one is the best condition, "Optimal". Let us define the reward or reward as

$$P[\propto(.)] = \int_0^T g\big(X(T)\big) + r\big(X(t), \propto(t)\big)dt \; ----------(2.14)$$

where for the control α (·), the ODE is solved by X (·). Equation r: $\mathbb{R}^{\propto} X A \rightarrow \mathbb{R}$ is the running payoff, and g: R∝ → R, T > 0 is the terminal payoff. Generally, the optimal solution is given by.

$$P[\alpha*(\cdot)] \leq P[\alpha(\cdot)] \; \forall \alpha(\cdot) \in A, \alpha*(\cdot) \; ----------(2.15)$$

2.1.6 Hamiltonian dynamics. -

Hamiltonian and Cost Function:

1. The Hamiltonian function H (x, u, λ) is defined as:

$$H(x, u, \lambda) = F(x, u) + \lambda^T f(x, u) \; ---------- (2.16)$$

where F (x, u) is the cost function and λ is the vector of Lagrange multipliers. According to Lawrence C, the Hamiltonian equation is defined as

$$H(X, P) = -L(X, V(X, P)) + P.V(X, P).$$

The Hamiltonian dynamics is given by.

$$\begin{cases} X^*(t) = \nabla_p H(X(t), P(t)) \\ P^*(t) = -\nabla_p H(X(t), P(t) \end{cases} ----------(2.17)$$

where X(.) solve the Euler-Lagrange equation. The Hamiltonian is solved by a combination of (X(.), P(.)) and mapping of t → H(X(t), P(t)) remains constant. For a given curve, ∃P. [34; 35]

$$P(t) \coloneqq \nabla_u L\big(X(t), X^*(t)\big), 0 \leq t \leq T, (ADJ) ----------(2.18)$$

2. The cost function is typically of the form:

$$J(u) = h\big(x(T)\big) + \int_0^T g(x(t), u(t)dt \; ----------(2.19)$$

where h (x (T)) represents the terminal cost.

The Hamiltonian H (x, u, λ) combines the objective function F (x, u) and the system dynamics f (x, u), weighted by the co-state variables p(t). Equation (2.16) is a function that is central to Pontryagin's Minimum Principle and is used to derive the necessary conditions for optimal control.

2.1.7 Pontryagin Minimum Principles (PMP). -

Minimum Principle: Pontryagin's minimum principle states that the optimal state trajectory, optimal control, and corresponding Lagrange multiplier vector must minimize the Hamiltonian (Zak, S.H., 2013).

$$H(x^*, u^*, \lambda^*) = \min_u H(x^*, u, \lambda^*)$$

For all time and all permissible control inputs, there must be an extremal control that satisfies these necessary conditions.

Extremal Control: An extremal control $u^*(t)$ is the one that achieves the minimum Hamiltonian. The optimal control trajectory can be inferred from the policy $\lambda^*(t)$ and the system dynamics: $\dot{x}(t) = f(x(t), u^*(t))$.

For an optimal control $\alpha(.)$ there exist , a costate function $P^*(.)$ Lagrange Multiplier, the optimal curve $X(.)$ satisfies the ODE.PMP $\alpha(.)$ for optimal ODE let corresponding trajectory $X(.)$ and P, then there exist P function as of $P^* : [0, T] \to \mathbb{R}^{\propto} \ni \mathbb{R}$ (Zak, S.H., 2013, and Onori, S., et al., 2016).

$$\begin{cases} P^*(t) = -\nabla_x H\big(X^*(t), P^*(t), \propto^*(t)\big), (ADJ) \\ X^*(t) = -\nabla_p H\big(X^*(t), P^*(t), \propto^*(t)\big), (ODE) \\ H\big(X^*(t), P^*(t), \propto^*(t)\big) = \max_{a \ni A} H(X^*(t), P^*(t), a), (0 \le t \le T^*), (M) \end{cases} --(2.20)$$

$H(X^*(t), P^*(t), \alpha^*(t)) \equiv 0$ $(0 \le t \le T^*)$, target point x^1 state of optimal controlled system hits by, the first time the trajectory $x^*(.)$ denoted by T^* and $P^*(.)$ is the costate [33; 35] In a given system and a given optimal criterion, let $U^* \in U$ be an optimal control, then $\exists$ a variable called costate which together with the state satisfies the Hamiltonian canonical equation, (Erdal Aydin et al., 2018)

$$X^* = \nabla_\lambda H; State ---------- (2.21)$$

$$\lambda = -\nabla_x H; Cotate\ or\ multiplier ---------- (2.22)$$

from the equation

$$H(t, x, u, \lambda) = \lambda^T(t) \cdot f(x, u, t) - L(t, x, u) \text{ ------- ---------- } (2.23)$$

and from the Hamiltonian definition,

$$H = \lambda^T f + L, \text{ ---------- } (2.24)$$

Then the minimum Hamiltonian w.r.t. u is given by

$$H(t, x^*, u^*, \lambda^*) \le H(t, x^*, u, \lambda^*), u \in U \text{ ---------- } (2.25)$$

Based on Equations (2.2, 2.9, and 2.19), we combine and substitute them to determine the costate and state functions as shown in Equations (2.22, 2.23). In this scenario, we make use of Pontryagin's Minimum Principle (PMP) to calculate the fitness. PMP is a foundational concept in optimal control theory (blogs. cuit. columbia.edu, 2019), offering valuable insights into the structure of optimal control problems (Erdal Aydin et al., 2018). It enables us to identify optimal control strategies considering both the

system dynamics and the cost function (breastcancer.org, 2024).

2.2 Related works

Breast cancer is the most common cancer and remains the second leading cause of death globally. Although mammography has its drawbacks, it is the standard method for detecting early-stage breast cancer before the lesions become clinically important.

To ensure AI technology is applied to cancer diagnosis and prognosis successfully, first, resolve the challenges that AI faces. For example, input data cannot be used directly from the medical imaging technology, this is a crucial step to extract features from the imaging data and process. (Shigao Huang, J. Y., 2019), Emphasize the development and popularization of technology. In addition, the weight coefficient in the neural network models is tested and calculated, and the confidence interval is reasonable, so medical interpretation needs further research.

Deep Learning techniques are transforming our ability to interpret imaging data. These results may improve sensitivity and ensure fewer false positives than radiologists. However, they run the risk of overfitting the training data, resulting in a brittle, degraded performance in certain settings. Machine learning has a tradeoff between accuracy and intelligibility. More accurate models are usually not intelligible; on the contrary, more intelligible models offer significantly worse accuracy (Shigao Huang, J.Y., 2019).

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 (Katoch et al., 2020), (Tomasz Tarkowski, 2022), (Denny Hermawanto, 2013), and (Ghosh, S., B. S., 2020). Furthermore, a genetic algorithm has been applied to optimize machine learning algorithms.

The genetic algorithm has been shown to impact 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. On the other hand, convolutional neural networks (CNN) and deep learning are more effective when dealing with large amounts of data, as reported in articles such as (M García et al., 2020) and (Kaya, M., 2023).

According to Noor Salah et al., (2021), in medical imaging and Diyar Zeebaree et al. (2017), the combination of K-Means and GA has shown higher efficiency and performance in converging and complexity to the global optimum. A paper by Dinesh K. Sharma and H. H. (2021) highlights the essentiality of hybridizing intelligent techniques for an effective predictive model.

A researcher, Gousia et al. (2022), has pointed out that CNN is a resource-intensive processing technique that requires a large amount of data to achieve better precision in detecting breast cancer. Due to this, the researcher is focusing on optimization solutions for diagnosing and predicting breast cancer. The study by Mojtaba Sepandi et al., (2018), focuses on optimizing CNN to detect and predict breast cancer.

Machine learning algorithms such as KNN and SVM are commonly used for detection tasks due to their effectiveness in classification (Bichen Zheng et al., 2020; and S. Chidambaranathan, 2016). However, the accuracy of these algorithms depends heavily on the selection of relevant features and the selection of optimal parameters (Chun-jiang Tian et al., 2021).

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. There are also false positives, which means that a patient has no cancer, but the result reports that the patient has cancer (Amin Zadeh Shirazi et al., 2017). To be sure the patient has cancer, a biopsy diagnosis must be taken. A biopsy is taking a sample of breast tissue from the suspicious area for further observation under a microscope (Amin Zadeh Shirazi et al., 2017; Ali et al., 2018; Ioannis Sechopoulos et al., 2021).

In a paper by G. Vaira Suganthi et al. (2023), the researchers categorize breast mass mammography images from the DDSM database, feature selection is performed using three methods, namely the GA, the t-test, and PSO. Image classification uses three machine learning algorithms: KNN, multi-SVM, and Naive Bayes. The AUC result from the training shows that GA+KNN outperforms the other methods.

The paper G., Meenalochini, S., Ramkumar, (2023) discusses the GA-CNN model, which reduces the error rate and achieves an accuracy of 98.5%, a sensitivity of 99.38%, and a specificity of 98.4%. The model uses Gaussian and adaptive histograms 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.

In the research paper by S.R., Kebede et al. (2024), an ensemble-efficient classifier with the YOLOv5 suspicious mass detection model was proposed to assist radiologists. The model achieves an F1-score of 0.87 and a sensitivity of 0.82.

A., Lashkari, et al. (2016) use 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.

The authors B., Krawczyk, et al. (2020) applied 150 thermograms and achieves a sensitivity of 83.10% while maintaining a high specificity of 89.44%.

The authors Debelee et al. (2018) categorizes mammography image data into two datasets: local hospital data and public data from MIAS. Using an equal number of datasets for both, SVM scores an accuracy of 99% and 97.46%, a sensitivity of 99.48% and 96.26%, and a specificity of 98.16% and 100%, respectively. MLP achieves an accuracy of 97% and 87.64%, a sensitivity of 97.40% and 96.65%, and a specificity of 96.26% and 75.73%, respectively. From the result, we see that SVM outperforms the MLP.

According to Gastounioti et al. (2022), the rise and dissemination of AI in breast cancer screening are poised to improve breast cancer risk assessment and enable personalized screening recommendations. However, many technical challenges related to the inherent properties of mammographic imaging have yet to be addressed, especially as AI developments transition to digital breast tomosynthesis. Furthermore, to accelerate the validation of AI breast cancer risk models and their transition to clinical implementation, it is paramount to enhance their reproducibility, interpretability, and robustness using large and heterogeneous datasets. With creative AI solutions to improve accuracy, validate performance, and cultivate trust in decision-making, AI will transform the way breast cancer screening is performed (Gastounioti et al.,2022).

In the research paper by Freeman K. (2021), twelve studies on AI mammography systems for routine breast screening were reviewed. It was discovered that in six smaller studies, AI outperformed individual radiologists in accuracy. However, it

remained uncertain whether the lower accuracy in other cases was attributed to variations in the case mix or the expertise of the radiologists. The two largest retrospective cohort studies in Europe revealed that all AI systems were less accurate than the consensus of two radiologists, and thirty-four out of thirty-six AI systems were less precise than a single reader. Furthermore, a separate large retrospective study indicated that while AI exhibited higher sensitivity compared to the original first reader decision, it showed lower specificity and was less accurate than a consensus reading.

Table 2-4: Breast Cancer diagnosis results (Y., Kumar et al., 2021),

Training Data	Technique	Challenge	Result
Mammogram images	CRNN CSO FC-	Bluer images work; need a filter, not	Accuracy = 98.4% Specificity = 99.9% F1-score = 74.5%
Wisconsin BC Datasets	KNN	Failed to work with a large data set	Accuracy= 97.51%
Mammogram images	CNN | Logistic Regression	To improve, need a large dataset	precision= 98.5%
DCE-MR Image	Multi-variant ML Model	need uniform scanning and contrast protocol	AUC= 77.1%
Mammogram images	Segmentation	need to scale to improve accuracy	Matching ratio 96.3%
mammogram images	KNN	need enhancement for classification	Accuracy= 94.44%
Digital mammogram	SVM	A challenge to interpret for high-dimensional data. matrix	Accuracy= 96.55, Sensitivity= 96.97%, Specificity= 96.20%
mammography images	SVM	need to improve accuracy with a large data set	Accuracy = 87.2% AUC= 94%

According to Y. Kumar et al. (2021) research, mammogram image classification using CRNN techniques achieves an accuracy rate of 98.4%, a specificity of 99.9%, and F1 scores of 74.5%. However, CRNN techniques struggle to classify blurred images and require additional filtration. It is observed that using the WBCD, the KNN model demonstrates an accuracy of 97.51%. In contrast, when applied to a mammogram dataset, KNN exhibits an accuracy of 94.44%, but further improvements are needed

for better classification. SVM techniques for digital mammogram images have 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. Large data sets are required to improve the accuracy of SVM for mammography image datasets, as the current accuracy rate is 87.2% with an AUC of 94%.

In summary, the highest precision in breast cancer diagnosis using mammography image data is approximately 98.4%, with a specificity rate of 99.9% in CRNN and a sensitivity rate of 96.97% in SVM, as shown in **Table 2-4**.

According to the research paper Ruban, S et al. (2024), the experimental investigation employed 1646 mammography pictures from four subjects. The radiologist can follow this model when analyzing mammogram images. The prediction model provides results registered with a precision of 75%, 96%, and 60% for BI-RADS-0, BI-RADS-1, and BI-RADS-2, respectively.

Table 2-5: Classification accuracy results from different datasets with different methods, Fuat Türk et al. (2024).

Task	Dataset	methods	Accuracy %
BI-RADS Classification	DDSM	MLP	88.02
Mass Malignancy Classification			83.85
BI-RADS Classification	DDSM	BPNN	84.50
BI-RADS Classification	a public dataset	DNN	94.22
BI-RADS Classification	InBreast	CNN	83.40
Mass Malignancy Classification	DDSM	FFnn	98.10 (Sens)
Mass Malignancy Classification	a public dataset	CNN	90.50
Mass malignancy Classification	DDSM	SVM	80.00
Microcalcification Classification	a public dataset	SVM	80.00
Microcalcification Classification	a public dataset	MLP	82.00
BI-RADS Classification	a public dataset	SVM	86.42
Mass malignancy classification	a public dataset	SVM	92.59

From (Fuat Türk et al., 2024), the SVM-based model could classify BI-RADS categories as malignant and benign with an accuracy rate of 86.42% and 92.59%, respectively. The CNN-based model showed a precision of 79.01% and 83.95% for the BI-RADS categories as malignant and benign discrimination, respectively. These results showed

that a well-designed machine learning-based classification model could give better results than a deep learning model.

The system demonstrated by Boumaraf, S, et al. (2020) achieves classification accuracy, positive predictive value, negative predictive value, and a Matthews correlation coefficient of 84.5%, 84.4%, 94.8% and 79.3%, respectively. According to the paper by S.R., Kebede et al. (2024), the classifier model achieves an F1 score of 87% and a sensitivity of 82%. With the addition of suspicious mass detection, sensitivity increases to 89%, though at the expense of a slightly lower F1-score of 79%.

From the paper, Chokri, F. et al., (2017), the performance of the work is demonstrated by an overall accuracy of 94.22%, an average sensitivity of 95.31%, an average specificity of 99.15% and an area under curve (AUC) of 0.9723.

When applied to the screening for breast cancer for Asian women who are more likely to have dense breasts, this model is expected to give a higher accuracy than others in the literature since it was trained using mammograms taken from Taiwanese women.

In the research paper, Wisaeng K. (2022), a BI-RADS category was predicted as the output of block-based images segmented from mammogram datasets. The research achieved an accuracy of 94.22%, an average sensitivity of 95.31%, and an average specificity of 99.15%.

According to the paper by Fuat Türk et al. (2024), Classification has been done using a multi-layer perceptron with separate schemes; first, classify masses to distinguish the BI-RADS 2 to 5 and second, classify the abnormalities as benign or malignant. The results were encouraging, evaluated on 480 mammographic masses extracted from the digital database for screening mammography. From this research paper, the confusion matrix has been classified as malignant, which is positive as BC, and benign, negative as BC. There are 121 TN and 13 FP, with 90.30% accuracy in classifying, whereas, from the classes of malignant, there are 10 FN and 48 TP, which have 82.76% accuracy from the actual malignant. The accuracy of well classified is 88.02%.

According to the paper, Karmilasari et al. (2014), BC detection methods with KM++SCO have an accuracy of 96.42% with the data sets Mini-MIAS, with DDSA 96.45% and 96.92% with the dataset of BCDR. Generally, KM++CS has an average of 96.27% accuracy in the detection of BC. It uses k-means clustering for the determination of stages of BC based on the size of the cancerous cells in different steps

of the process.

In Noor Salah et al. (2021), also used K-means for the diagnosis of BC, and it is reliable to identify a malignant from a benign tumour. In the context of breast cancer diagnosis, the use of genetic algorithms can significantly improve the selection of specific features. This approach helps to identify the most optimal fitness value, as detailed in Kumar et al. (2021). When coupled with the C4.5 algorithm, genetic algorithms exhibit greater accuracy in diagnosing breast cancer compared to when combined with K-means (Samuel R. et al., 2024). The integration of genetic algorithms improves the accuracy of feature selection by 3.6%.

Research suggests that rank-based selection techniques, as discussed in Pontryagin's work (Martin Bohner et al., 2017), are highly effective for complex tasks but may not be ideal for simpler problems. It is also important to note that the computational costs associated with derivative information and recurrent fitness value computation (Vandana Rawat et al., 2022; Lawrence C., 2024; Kalyanmoy Deb, 2011) can be substantial.

Table 2-6: Breast Cancer diagnosis result with GA.

Method	Accuracy	Sensitivity	Specificity	F1-Score	AUC
Feature Extraction GA with SVM Ensemble	97.18	N/A	94.79	97.29	97.91
EG2 MCS with GA	91.09	80.60	94.82	N/A	N/A
GA with AdaBoost Selection	85	N/A	N/A	N/A	N/A
GA Classifier	98	97	100	N/A	N/A

In a study on feature extraction **Table *2-6***, the use of genetic algorithms within the SVM ensemble produced outstanding results, achieving an impressive F1 score of 97.29%, accuracy of 97.18%, specificity of 94.79%, and an AUC of 97.91%.

However, it is worth mentioning that the accuracy of genetic algorithm classification alone achieved an even higher percentage at 98%. It is essential to emphasize that performance is heavily influenced by the data pre-processing methods and the quality.

Extracted a series of image features from 146 images of these twenty-nine malignant and 117 cases were benign (Krawczyk et al., 2012). The decision tree-based EG2 algorithm was used for classification. GA is used to select the best Multi Classifier System (MCS), which the author used to create multiple random subsets of attributes (ensemble), which consists of a set of independently trained classifiers. In this work,

the ensemble has several sets ranging from 1-, 3-, 5- and 7-fold cross-validation, the crossover performed at two points. The GA iteration stops when the criterion was the moment when one hundred new populations are generated without increasing. The paperwork registered an accuracy of 91.09%, a sensitivity of 80.60%, and a specificity of 94.82%, with Ensemble V = 7.

Extracted twenty-three features from cancer images for the proposed algorithm for cancer classification (Lashkari et al., 2016). The features include statistical, morphological, frequency domain, histogram, and Gray Level Co-Occurrence Matrix (GLCM) from the segmented right and left breast. The Author reduces the numbers using minimum redundancy, Maximum Relevance Sequential Forward Selection, Sequential Backwards Selection, and includes GA to select the Best Feature. AdaBoost, SVM, and K-Nearest Neighbors (KNN) were used as classifiers. The best result was obtained for the frontal images with the reduction by GA combined with the AdaBoost classifier, which generated a mean accuracy of 85% and 87% for the left and right breast, respectively.

Support-Vector Machine (SVM) is used to classify patients as healthy or with breast abnormalities (Silva et al., 2020). The first step is the definition of a Region of Interest (ROI) of each sequence of images. From the ROI, a temperature time series was built, and several features were calculated. The major features were automatically selected in the WEKA (Waikato Environment for Knowledge Analysis) tool using the Cfs Subset Eva attribute evaluator and the Best First Search method, and then classified by SVM. The authors achieved 100% accuracy and used the DMR-IR database.

Reviewed around forty articles, each of which used image processing (F., Sadoughi et al., 2018). The result showed that SVM had the highest accuracy percentage for different images (Ultrasound 95.85%, Mammography 93.068%, and thermography 100%). The writer of the paper recommended that computerized diagnosis of breast cancer contributes to the development of medicine, and that computer-assisted methods increase diagnosis accuracy by reducing false negatives and false positives.

Propose a methodology for classifying the breast as normal and abnormal (Sánchez-Ruiz et al., 2020). It contributes to the development of automatic segmentation of RoI. To reduce the number of features and increase the performance classifier, the Authors used GA. The results obtained were: 98% accuracy, 97% sensitivity, and 100% specificity using the Artificial Neural Networks (ANN) classifier.

In the paper of Mojtaba Sepandi et al. (2018), its result demonstrated that the ANN could perform well in estimating the probability of malignancy and improve the positive predictive value (PPV) of the decision to perform a biopsy. In the conclusion of Mojtaba Sepandi et al. (2018), ANN could effectively discriminate benign masses from malignant ones.

The Performance of existing research works, according to the study (Fuat Türk et al., 2024), uses two machine learning models. The first SVM-based model classifies BI-RADS categories and malignant-benign discrimination, with an overall accuracy rate of 86.42% and 92.59%, respectively. Whereas using the CNN-based model gets an accuracy of 79.01% and 83.95%, respectively. The research was done on 264 mammogram images of 139 patients after working on the data augmentation.

Table 2-7: Benign and Malignant performance metrics (Fuat Türk et al., 2024)

Algorithm	class	Accuracy	Precision	Recall	F1-score
SVM	Benign	92.59	90.60	90.60	90.60
	Malignant	92.59	93.90	93.90	93.90
CNN	Benign	83.95	78.80	81.30	80.00
	Malignant	83.95	87.50	85.70	86.60

The results shown in

Table 2-7, based on the research work (Fuat Türk et al., 2024), the malignant-benign discrimination SVM is outperformed in the listed performance measurements.

According to (Fuat Türk et al, 2024), the highest accuracy is registered in the BI-RADS-2 and 5, 95.06 with the SVM algorithm, and the highest F1-score is registered in the BI-RADS 5, as described in **Table 2-8**.

Table 2-8: BI-RADS classification metrics using SVM (Fuat Türk et al., 2024).

class	Accuracy	Precision	Recall	F1-score
BI-RADS-2	95.06	83.30	83.30	83.30
BI-RADS-3	91.36	70.00	63.60	66.70
BI-RADS-4	91.36	85.30	93.50	89.20
BI-RADS-5	95.06	96.00	88.90	92.30

In the case of CNN, the highest accuracy is registered in BI-RADS 3, 91.36 and F1-score in BI-RADS 5, as described in **Table 2-9**. From the algorithms, SVM and CNN, the overall accuracy has been registered as 86.42% and 79.01%, respectively.

Table 2-9: BI-RADS performance metrics using CNN (Fuat Türk et al., 2024).

class	Accuracy	Precision	Recall	F1-score
BI-RADS-2	88.90	66.70	61.50	64.00
BI-RADS-3	91.36	70.00	63.60	66.70
BI-RADS-4	84.00	79.40	81.80	80.60
BI-RADS-5	93.80	88.00	91.70	89.80

2.3 Gap analysis from the reviewed literature and related works:

The reviewed document highlights breast cancer as the leading cause of cancer-related deaths, underscoring the importance of early detection supported by technology. However, there are challenges with artificial intelligence (AI) in handling complex data sets during feature selection and extraction. Deep learning (DL) methods require large datasets to yield accurate results and often struggle with issues like overfitting and underfitting, as well as getting stuck in local minima. Hybrid approaches that incorporate Genetic Algorithms (GA) demonstrate superior performance, achieving 98% accuracy and 100% specificity based on the BI-RADS system. Additionally, a combination of Ensemble Support Vector Machine (SVM) with GA results in 97.18% accuracy and an area under the curve (AUC) of 97.91%. Overall, hybrid methods that utilize GA, particularly when combined with SVM and K-Nearest Neighbors (KNN), deliver the best performance. The Pontryagin Minimum Principle effectively optimizes GA during fitness evaluations while minimizing computational resources.

CHAPTER THREE

3 RESEARCH DESIGN AND METHODS

The study has a detailed literature review on the research area and had an extensive discussion with the domain experts about breast tumour. What is breast cancer? How could we determine the tumour stage? What are the specific features of the tumour?

3.1 Research Design

This study follows an experimental research design. The research design process in experimental research, particularly within the framework of randomized controlled trials (RCTs), intricately involves the critical methodology of cross-validation. A foundational element of RCTs is randomization, which plays a pivotal role in minimizing bias and bolstering the internal validity of the study.

By assigning participants to different intervention groups through a random selection process, researchers ensure that each participant has an equal opportunity to be placed in any group. This strategy significantly mitigates the risk of confounding variables that could skew the study outcomes, leading to more equitable and comparable groups, and ultimately enhancing the reliability of the findings. In addition to randomization, crossover designs are employed, wherein participants receive multiple interventions in a predetermined sequence, interspersed with appropriate washout periods. These washout periods are vital as they allow for the elimination of residual effects from previous interventions before introducing the next one.

This design is particularly advantageous because it enables researchers to assess the effects of various interventions within the same cohort of individuals, thus minimizing interpersonal variability and providing a clearer understanding of the efficacy of each treatment.

In the context of genetic algorithms applied to feature extraction, selection of partners for creating offspring is conducted through a process of random pairing. This random selection is critical for generating diverse offspring, which can potentially exhibit improved characteristics. The population undergoes a systematic selection process that incorporates crossover techniques, allowing for the combination and recombination of features. This not only enhances the potential for discovering optimal attribute sets for training and testing but also reinforces the overall robustness of the feature extraction

process in machine learning applications. The overall process of the research is shown in **Figure 3-1.**

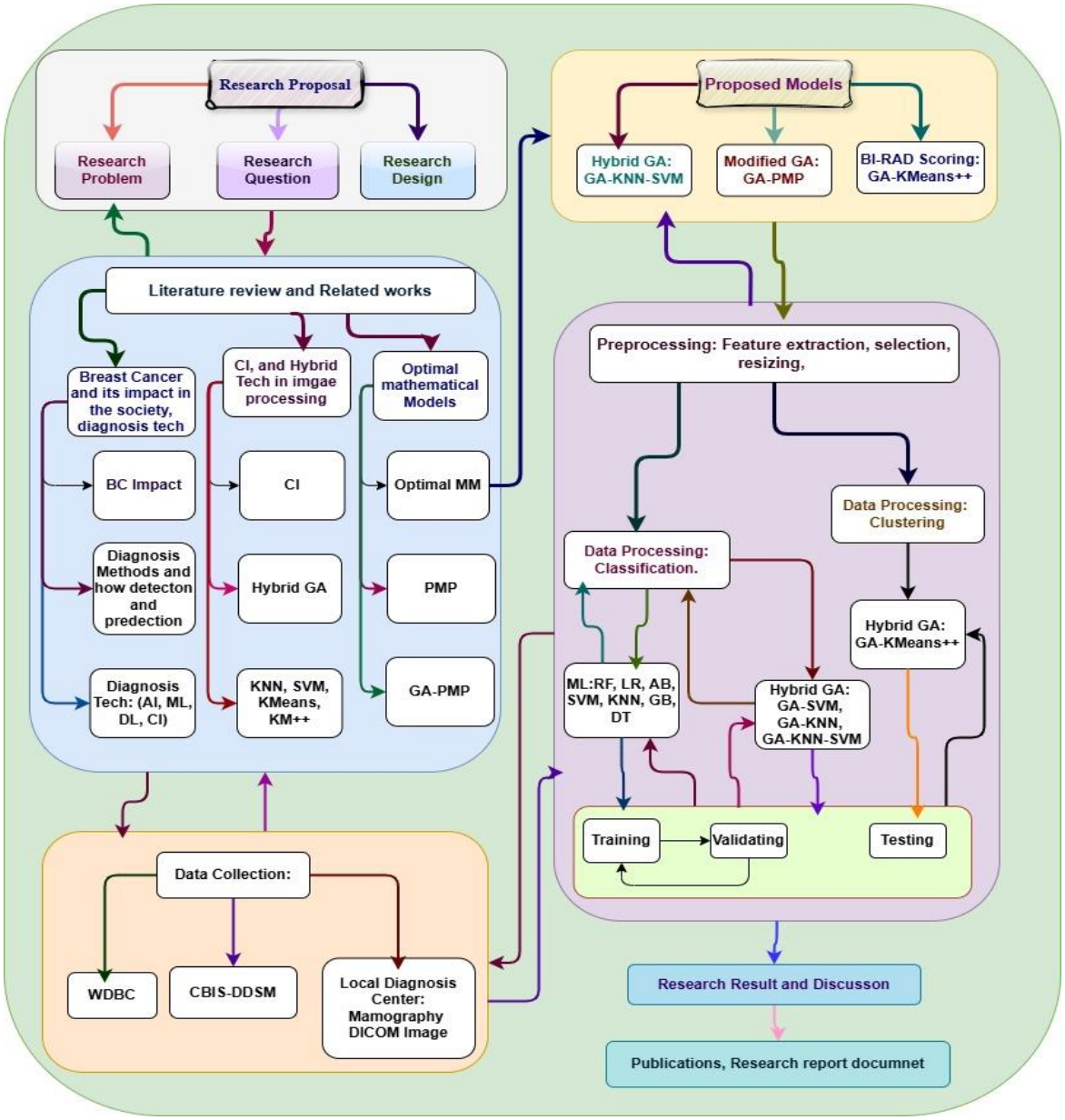


Figure 3-1Research Design Framework

3.2 Methods of the study

It has a systematic literature review that encompasses the collection of approximately 989 research papers from reputable databases, including PubMed, Elsevier, Springer, IEEE, and Science Journals. All selected papers are published in peer-reviewed journals, ensuring the reliability of the research. Databases including Medline (Ovid), Embase (Ovid), Web of Science, and the Cochrane Database of Systematic Reviews (CENTRAL) were utilized.

3.2.1 Data collection. -

Journal Type and Publication Date: The review focused on papers published from 2018 to the present in peer-reviewed journals, ensuring both the recency and credibility of findings.

- Domain Areas: The research is centered specifically on breast cancer.
- Research Analysis Technology: Studies incorporating artificial intelligence, machine learning, deep learning, computational intelligence, genetic algorithms, and hybrid technologies utilizing genetic algorithms were included.
- Breast Image Sources: The focus was on mammography imaging as the primary source for diagnosing breast cancer.

A particularly notable contribution identified in the reviewed literature published in the paper titled "Impact of Genetic Algorithm for the Diagnosis of Breast Cancer, " which synthesizes findings from forty-five published studies, showcasing the potential of genetic algorithms to enhance diagnostic accuracy.

Public Dataset: we used a public dataset, the Wisconsin Breast Cancer Database (WBD), the datasets MIAS and DDSM suggested by Taye Girma Debelee, M.A. (2018), to describe the datasets for learning the model with accuracy in image processing, artificial intelligence, and CNN.

The Breast Cancer Wisconsin (Diagnostic) dataset is a well-known collection frequently used in machine learning and medical research. It consists of digitized images of fine needle aspirates (FNA) obtained from breast masses. The dataset includes 569 instances and 30 numerical attributes used for predictive analysis. The class distribution is comprised of 212 instances classified as malignant and 357 instances classified as benign. It provides an excellent foundation for exploring the accuracy variance between existing machine learning algorithms and our proposed model. This well-organized dataset is sourced from reputable platforms, UC Irvine Machine Learning Repository (Wolberg, W., et al., 1993), including a dedicated website and Kaggle (Kaggle, 2025).

The research had effectively incorporated the Curated Breast Imaging Subset of the Digital Database for Screening Mammography (CBIS-DDSM), which encompasses approximately 6.3 GB of data and includes 6,674 JPEG-formatted breast images along with a comprehensive labelled dataset (Sawyer-Lee, R., et al, 2016), (Lee, R., Gimenez, F., Hoogi, A. et al., 2017).

The scientific data processing conducted as part of this research was essential, involving the segmentation of the region of interest (ROI), careful selection and extraction of features, and systematic organization of these features in databases. This structured approach enhances our ability to analyze the data effectively and draw meaningful insights.

Locally, Mammography breast image data was collected in DICOM format from the Pioneer Diagnostic Center, Addis Ababa, in 2021. In a simple random sampling method, a total of 4,092 images were obtained from 376 patients. All data are female images and vary in age from 30 to 75. The information was registered on the summary page in parallel with the BI-RADS score and the senior radiologist's recommendation summary. The domain expert participated in annotating the image data for describe the region of selection, stage and type of tumour, calcification, Image view (CC, MLO).

We organized the data by the BI-RADS scores into six classes from 0 to 5 and others, see **Table *3-1***. Regarding a mammography image view, there were 1249 CC views and 1109 MLO; the remaining 1734 were categorized as other views. Out of the total dataset, 2062 images lacked clear BI-RADS scores, however, they had feature density, mammography view, and sizes.

Table 3-1: Local datasets classified by BI-RADS

No	BI-RADS	Number	Remark
1	BI-RADS-0	382	
2	BI-RADS-1	367	
3	BI-RADS-2	314	
4	BI-RADS-3	740	
5	BI-RADS-4	189	
6	BI-RADS-5	77	
7	Other	2023	Not identified with BI-RADS

Mammography images typically include bilateral craniocaudal (CC) and mediolateral oblique (MLO) views, which are standard for routine screening. The CC view entails the X-ray beam travelling from the head toward the feet, whereas the MLO view involves the X-ray beam moving from the inside to the outside. We have received approval from the diagnostic center to use these data for research purposes. All patient identification names, IDs, and image numbers are removed and changed anonymously.

3.2.2 Data Processing and Presentation. -

The process of the research work included setting up and configuring the computer

with Python libraries, which enable the processing of the data. Study breast cancer images from locally collected and publicly available online data sets. Our reference was the University of California, Irvine Machine Learning Repository, the data set Breast Cancer Wisconsin (Diagnostic) also published and available on Kaggle,

- Work on the Pre-processing of the image data.
- Feature extraction, feature selection and classification have been done.
- Modelling, training, validating, and testing, take part in the research, with different parameters and performance testing criteria.

The final output of the research enables the detection of the breast tumour, classifying the stages of the tumour, and the breast cancer as benign or malignant. **Data Processing Tools**: RadiAnt DICOM Viewer is an application that processes and displays medical images in DICOM format. We used the RadiAnt DICOM viewer to read the DICOM format breast images, annotate, archive, export to other formats, and synchronize. In addition to this, we utilized Sante DICOM Editor Tools for the locally collected breast mammography image data. DICOM is the international standard for medical images and related information. It defines the formats for medical images that can be exchanged with the data and quality necessary for clinical use.

For preprocessing, training, and testing, we utilized the Python programming language and libraries, using the Jupyter Notebook framework and different libraries such as

- TensorFlow: for learning
- Scikit-learn for feature extraction and selection.
- Pandas for programming, script writing, analysis, and simulation.
- PyGAD: Python tool for Genetic Algorithm (pygal. nn for implementing neural network)
- PyGAD.gadnn: for training a neural network using GA.

For training purposes, we used Kaggle and Colab Google Cloud services in addition to the local PC. Colab is a hosted Jupyter Notebook service that offers free access to computing resources like GPUs and Tensor Processing Units (TPUs), making it ideal for machine learning, data science, and education. Python 3 Google Compute Engine backend, RAM 12.67 GB, Disk 107.72 GB, TensorFlow,

We used the local PC to organize and prepare the model and test with limited data. Once we had the model, we imported it into the online system to have accurate results.

Data Processing: We implemented hybrid models, GAKNN-SVM, GA with PMP, and GA with K-Means++. These models have been validated with different selected ML

algorithms to compare their performance. For training the model, 70% of the dataset is used for training, 20% for testing and 10% for validation from a total of mammography image data. To solve the challenge of overfitting, we use the cross-validation technique.

Our basic Hybrid genetic algorithm model incorporates and implements GA, SVM, and KNN. The method employs optimization, feature selection and comparison of the result implemented in different ML algorithms. With locally organized data implemented a model GA-K-Means++ was implemented, GA for data classification and training, K-Means++ clustering.

The hyperparameterization process has been done by the Python library Sklearn's preprocessing function for the feature encoding to binary, using Label Encoding.

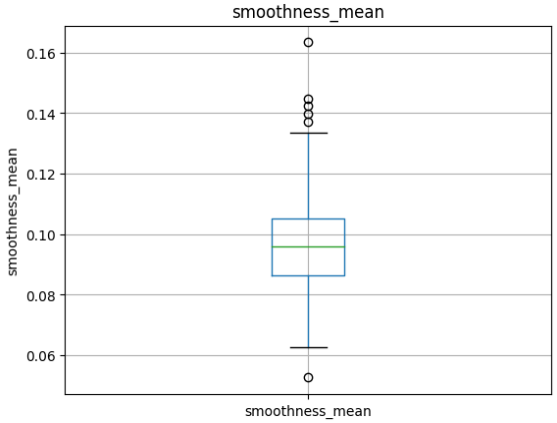


Figure 3-2: Preprocessing of WBCD dataset.

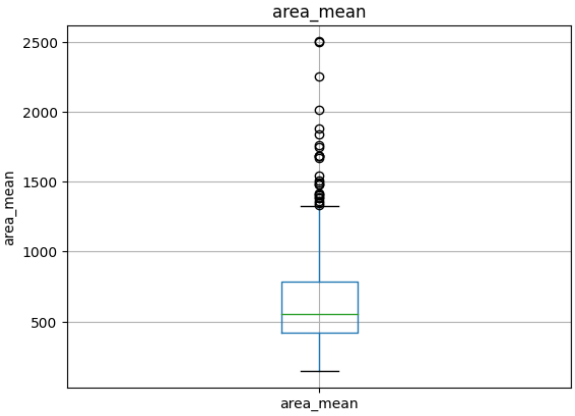


Figure 3-3: Preprocessing of WBCD dataset.

Preprocessing of images involves size, scaling, grayscale conversion, and noise reduction, as well as normalization, filtering, and region of interest selection. This visual representation offers a clear and organized method for data analysis, making it easier to derive meaningful insights from the results.

The report that is collected from the domain expert includes breast composition, mass (density, shape, margin, size), architectural distortion, and other associated formations. This information is used to make the decision based on the BI-RADS. BI-RADS is a standardized assessment system developed by the American College of Radiology (ACR). Radiologists use it to categorize their findings from the mammogram. Scientific data processing will be done in the process of the research work (Aigerim Mashekova et al., 2022). The data mining of the image data is as follows:

- Image acquisition and elimination of noise without losing vital details.
- Segmentation of the region of interest (ROI)

- Selection and extraction of the features
- Organization of selected features in databases
- Implements Hybrid learning technologies, KNN, Support Vector Machine (SVM)
- Characterization and classification of tumour according to the probability of malignancy and any abnormalities

```
In [14]: sns.pairplot(df, hue="diagnosis", vars=["radius_mean", "texture_mean", "perimeter_mean", "area_mean", "smoothness_mean"])
         plt.show()
```

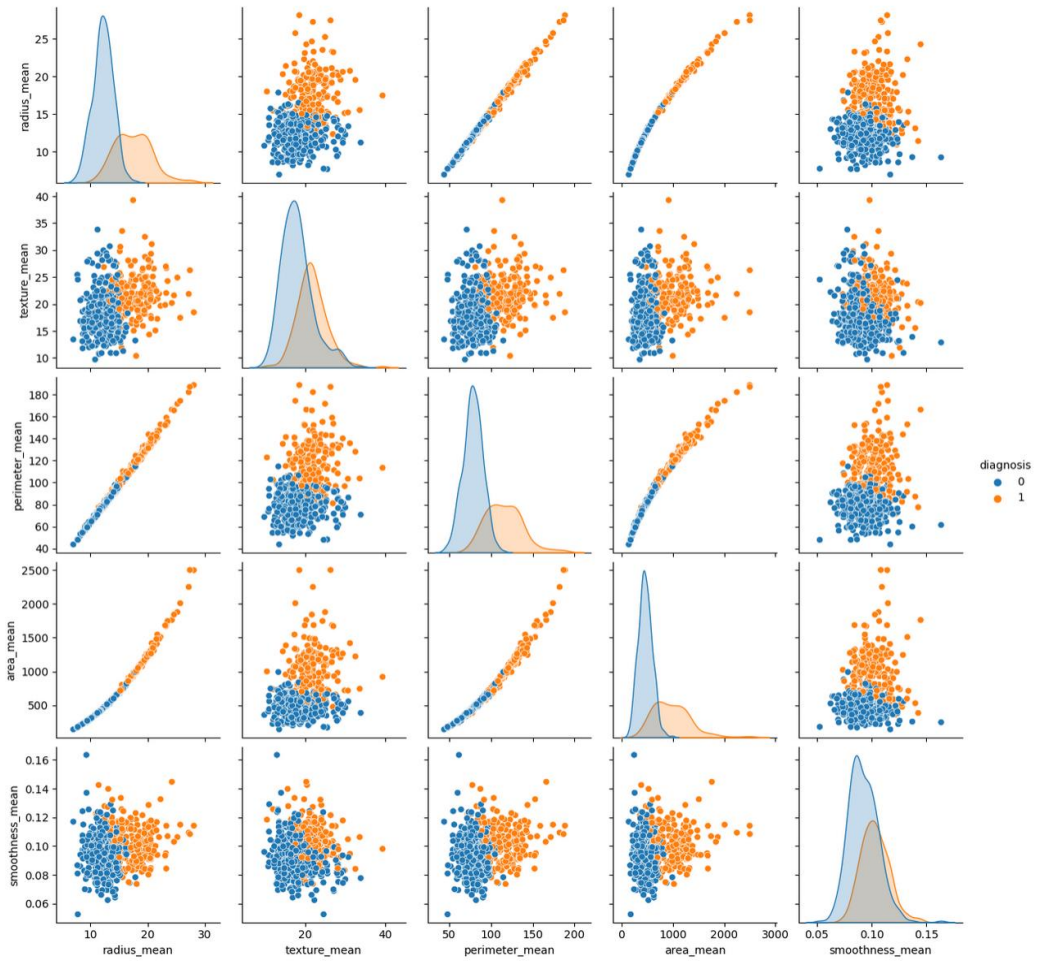


Figure 3-4: WBCD dataset preprocessing of the features with the two classes as M and B.

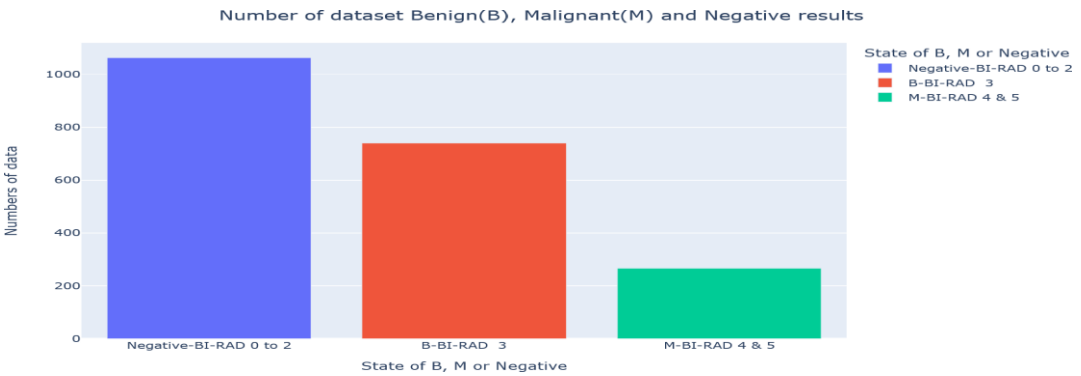


Figure 3-5: Mammography Breast Image categorized by BI-RADS.

For searching and optimization, use GA during the classification and clustering process. It goes back to the learning algorithm until it reaches the best fit

In **Figure 3-5,** most of the sample data lies in the categories from 0 to 2 which does not need a further diagnosis, whereas 3, 4, and 5 are very small to the total dataset as shown in **Figure 3-6**, **Figure 3-7** processed data by the views of the image as CC, MLO and others.

```
print(" Total number of CC    " + str(VCC))
print(" Total number of MLO   " + str(VMLO))
print(" Total number of Other View   " + str(otherV))
print(" Total number of High density   " + str(DH))
print(" Total number of Hetrogenous Density " + str(DHT))
print(" Total number of Scattered density   " + str(DSC))
print(" Total number of Extrem " + str(DEX))
print(" Total number of Fatty   " + str(DFT))
print(" Total number of other " + str(otherD))
total_Mammo_View_Data = VCC + VMLO + otherV
total_MassDensity_data = DH + DHT + DSC + DEX + DFT + otherD
print(" Total number of mammography view " + str(total_Mammo_View_Data))
print(" Total number of density data " + str(total_MassDensity_data))
```

```
Total number of CC    1249
Total number of MLO   1109
Total number of Other View   1734
Total number of High density   85
Total number of Hetrogenous Density 4
Total number of Scattered density   499
Total number of Extrem 8
Total number of Fatty   68
Total number of other 3428
Total number of mammography view 4092
Total number of density data 4092
```

Figure 3-6: Breast Image Pre-Processing.

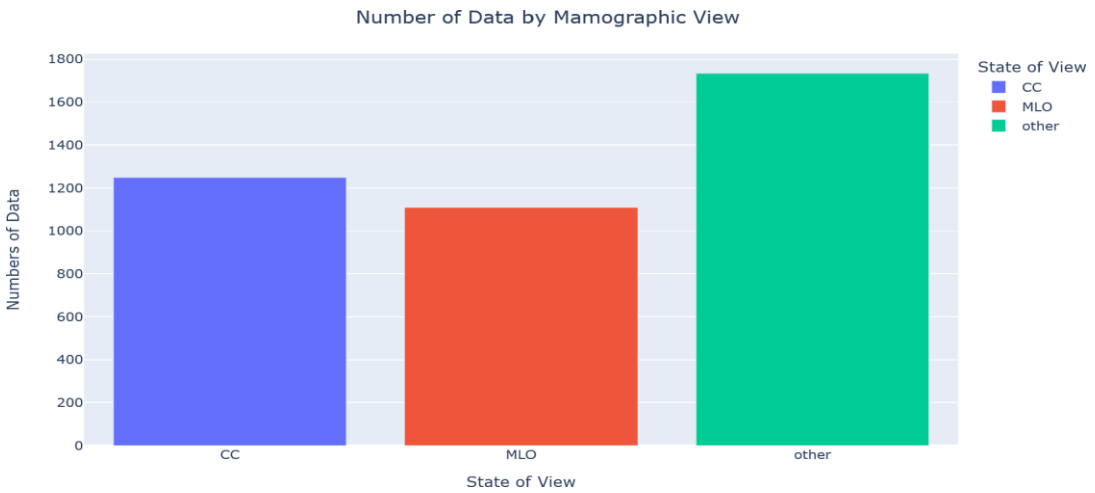


Figure 3-7: Mammography image data categorized by image view.

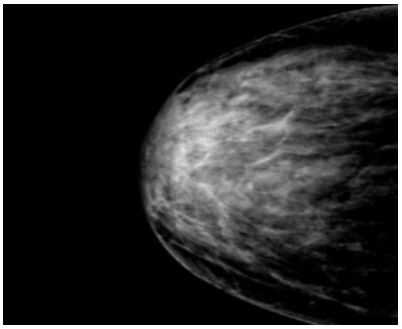
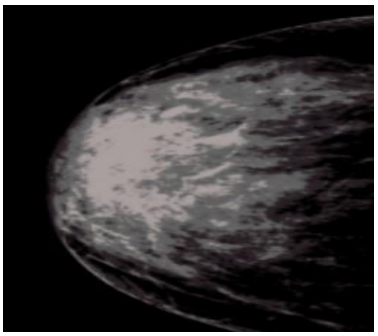



Figure 3-8: Pre-processing: Converting the image into grayscale.

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4092 entries, 0 to 4091
Data columns (total 9 columns):
 #   Column              Non-Null Count  Dtype
---  ------              --------------  -----
 0   No                  4092 non-null   int64
 1   PID                 4092 non-null   object
 2   ImageID             3260 non-null   object
 3   Mammographic_view   2389 non-null   object
 4   Mass_Density        1975 non-null   object
 5   Cal_MB              370 non-null    float64
 6   BI_RAD              2069 non-null   object
 7   Final-Assesment     371 non-null    object
 8   Recommondation      2187 non-null   object
dtypes: float64(1), int64(1), object(7)
memory usage: 287.8+ KB
```

Figure 3-9: Processed the dataset information.

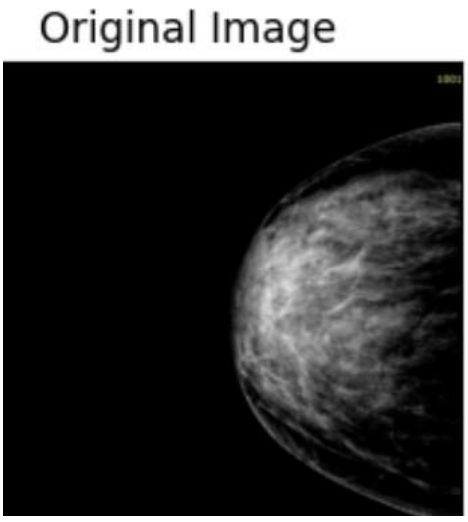


Figure 3-11: a. The original images.

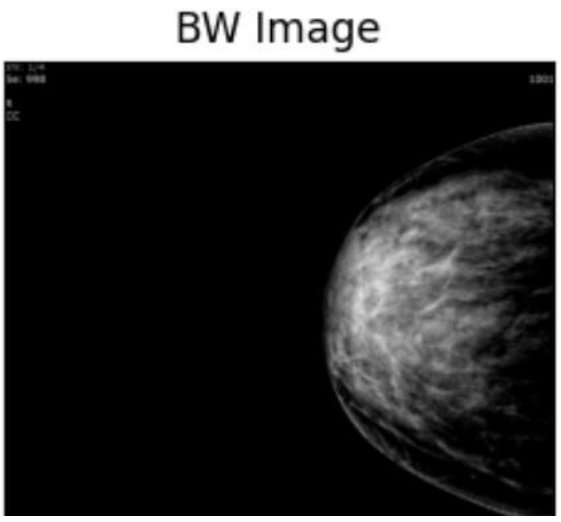


Figure 3-10: b. The result after preprocessing, original and black and white images.

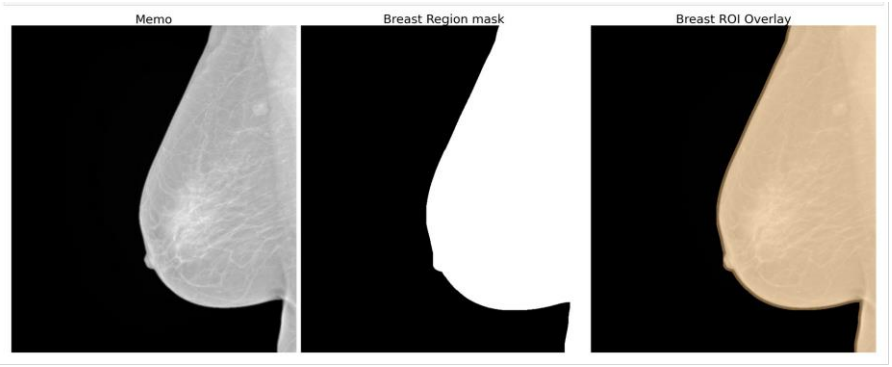


Figure 3-12: Result of the image after preprocessing of the Region of Interest (ROI)

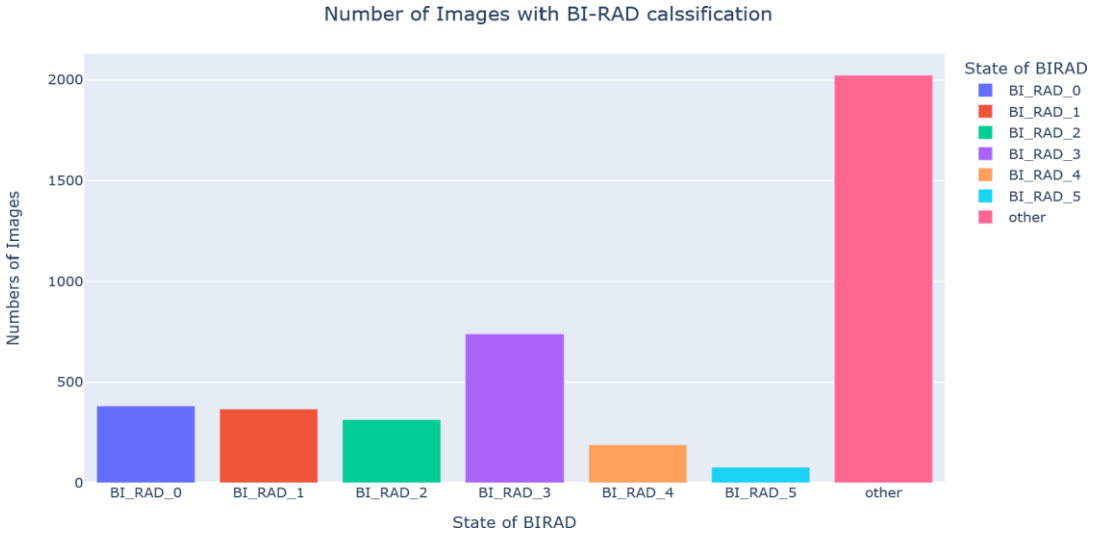


Figure 3-13: Number of the data by BI-RAD Scoring

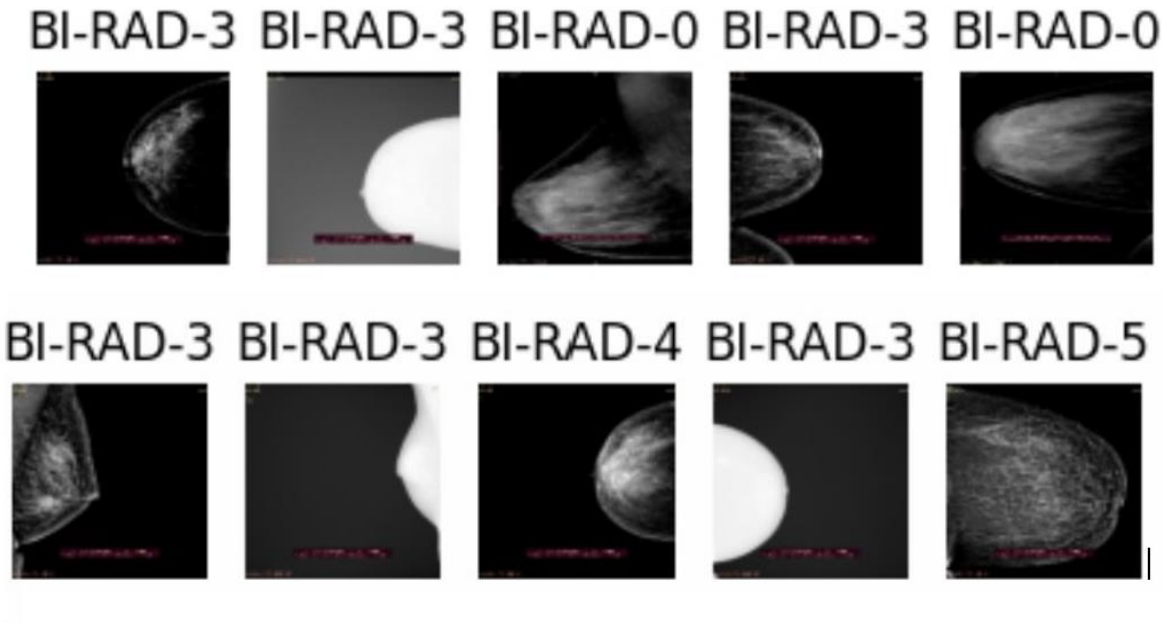


Figure 3-14: Breast Image visualizing during clustering.

The image, **Figure 3.8**, is compressed and processed into grayscale; this helps to minimize the complexity of the image and optimize the performance and computational resources. **Figure 3-9,** is the processed image data information. **Figure 3.10** compares the original image after the greyscale process. Next to this, in **Figure 3-12,** we did the process to identify the region of interest in the image data by removing the noise. This helps to minimize the complexity and enhance the performance during the processing of the model. **Figure 3.12** shows the number of BI-RADS data ready for the training by the proposed algorithm and lists the number of image data by BI-RADS classification. **Figure 3-14**, illustrates the image, which is ready for training after preprocessing, and describes the mammography breast image data after classification by the BI-RADS. These data were used for data training to screen the patient using BI-RADS scoring.

Inclusion and Exclusion Criteria from Locally Collected Mammography Image Data: We include all data with suggestions and recommendations from senior radiologists as a summary. BI-RADS is a scoring system used by radiologists to describe mammogram findings.

- BI-RADS-0: Incomplete. If the findings are unclear, more tests are needed. Additional mammograms or ultrasounds may be recommended to get a clearer picture of breast tissue.
- BI-RADS-1: Negative. The breast tissue appears normal, with no masses, calcifications, or abnormalities. Regular monitoring with mammograms is recommended.
- BI-RADS-2: Benign. Although an abnormality (such as scar tissue) can be detected, it is non-cancerous. Continued monitoring with regular mammograms is recommended.
- BI-RADS-3, probably benign. An abnormality is likely noncancerous, but follow-up is needed. Another mammogram in six months checks for changes. Fewer than 2% of category three findings develop into cancer.
- BI-RADS-4, Suspicious for malignancy, (2% - 95%), with 4a being low level (2% -9%), 4b intermediate (10% - 49%), and 4c highly suspicious,
- BI-RADS-5, highly suggestive of malignancy
- BI-RADS-6, Known biopsy-proven malignancy.

3.2.3 Performance measurement. -

Performance measures include accuracy, specificity, sensitivity, and the F1 score. Accuracy gauges how often the classifier is correct. We applied different tools for clustering and classification accuracy measures. Confusion Matrix, F1 score, and Mean Absolute Error will be used for validating the accuracy of the model. For each of the models, use performance measures. Noted from different literature that the hybrid model will have the best performance in learning data, and propose a hybrid model, will measure the performance, and put the result as Accuracy, Sensitivity, Specificity.

To evaluate the performance of a multi-class classification problem, we use the area under the curve (AUC) and the receiver operating characteristic (ROC) curve. The ROC curve shows the trade-off between the true positive rate (TPR) and the false positive rate (FPR). An AUC value close to one indicates an excellent model with good separability. We aim for high precision and accuracy to ensure better model performance. Low sensitivity and precision make analysis challenging, so we can use the F-1 score, which combines recall and precision into a single metric. Specificity and sensitivity are inversely related. In the breast cancer protection classification process, the quality of the result is measured using performance measurement tools. In this research, we work on:

A. Mean Absolute Error (MAE): MAE's strength against outliers ensures a more balanced training process. The process to work on the MAE is shown as in equation 3.1, whereas the mean square error is calculated as in equation 3.2. MSE can be particularly useful when we have continuous data or regression problems. This is more beneficial if there are no more outliers. To validate the performance of the process of GA process, we need to show the graph of the cost of training. The error should be minimal to be successful or have the best performance.

$$MAE = \frac{1}{n}\sum_{i=1}^{n}|y_i - x_i| \quad (3.1)$$

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - Y_i^*)^2 \quad (3.2)$$

Where y is the true output (actual) and y^* is the predicted result of the model output.

B. Performance measures have been performed with the confusion matrix, the F1 score, precision, sensitivity, and specificity. The confusion matrix is now simply a

matrix containing true positives, false positives, true negatives, and false negatives.

Based on the confusion matrix for binary classifiers, different rates are computed. Accuracy defines the Overall classification; it responds, how often the classifier is correct. The classification accuracy is the ratio of the number of correct predictions to the number of predictions made.

- True positives: - correct predictions of true events.
- False positives: - incorrect predictions of true events.
- True negatives — correct predictions of false events
- False negatives — incorrect predictions of false events.
- Accuracy $= \frac{TP+TN}{Tp+TN+FP+FN}$ - Assess the measurement to find the target value on average.
- Precision $= \frac{TP}{Tp+FP}$ - How close the measurements are to each other.
- Sensitivity $= (TPR\ or\ recall) = \frac{TP}{Tp+FN}$ - A test to correctly exclude individuals who do not have BC. The more specific a test, the fewer false positives.
- Specificity $= \frac{TN}{TN+FP}$ - A test to correctly identify people who have BC. The more sensitive a test, the fewer "False negatives".
- $\mathrm{F1-Score} = \frac{2TP}{2Tp+FP+FN}$ - Balanced measure of precision and recall
- $\mathrm{FPR} = 1 - Specificty = \frac{FP}{TN+FP}$ – Is the difference from the specificity
- $MCC = \frac{((TNxTP)-(FNxFP))}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}}$ – A Matthews Correlation Coefficient is a common measure for quality control in medical testing for disease. It is good for unbalancing datasets.

CHAPTER FOUR

4 PROPOSED MODELS FOR THE RESEARCH

In this chapter, we explore the innovative models we have thoroughly designed and developed. Our first model is a Hybrid Genetic Algorithm that seamlessly integrates K-Nearest Neighbors (KNN) and Support Vector Machine (SVM). This model excels in feature extraction and fitness selection, leveraging the capabilities of genetic algorithms. It efficiently selects the most likely chromosomes to advance to the next iteration, ensuring that only the fittest individuals are utilized for training, thus maximizing performance.

Next, we introduce a powerful modified genetic algorithm that incorporates Pontryagin's Minimum Principles. This advanced model significantly enhances the fitness selection process within the genetic algorithm, resulting in superior feature selection and extraction. The optimization provided by this approach leads to remarkably effective solutions.

Our third model, the Genetic Algorithm with K-Means++, is specifically tailored to classify breast images based on the BI-RADS score. This classification system empowers radiologists to make informed decisions regarding a patient's tumour risk level, streamlining their diagnostic process.

For the first two models, we utilized WBCD, whereas for the last model locally organized dataset and DDSM. Overall, this section highlights the strategic design of our models and articulates their key components, demonstrating their potential to transform current practices in medical imaging and analysis.

4.1 Hybrid Genetic Algorithm GA-KNN-SVM

The study titled "Hybrid Genetic Algorithm for Breast Cancer Detection and Prediction using KNN and SVM" investigates the use of genetic algorithms in conjunction with k-nearest neighbors (KNN) and support vector machines (SVM) for breast cancer detection in resource-limited settings. By implementing this hybrid genetic model, the accuracy of the detection method increased by two percent compared to previous outcomes.

The genetic algorithm processes selection, crossover, and mutation in the process of finding the best-fit population. In the model, we adopt a generational approach by generating 'n' offspring, where n is the size of the population. At the end of each iteration, we replace the entire population with the new one. The process of the genetic algorithm, shown in **Figure. 4.1**

- Problem Definition: Define the optimization problem and specify the objective

function to be maximized or minimized.

- Chromosome Representation: Choose an appropriate representation for potential solutions (chromosomes). Common representations include binary strings, vectors with real values, or permutations.
- Population Initialization: Create an initial population of chromosomes randomly or using domain-specific knowledge. Ensure diversity in the initial population to explore a wide solution space.

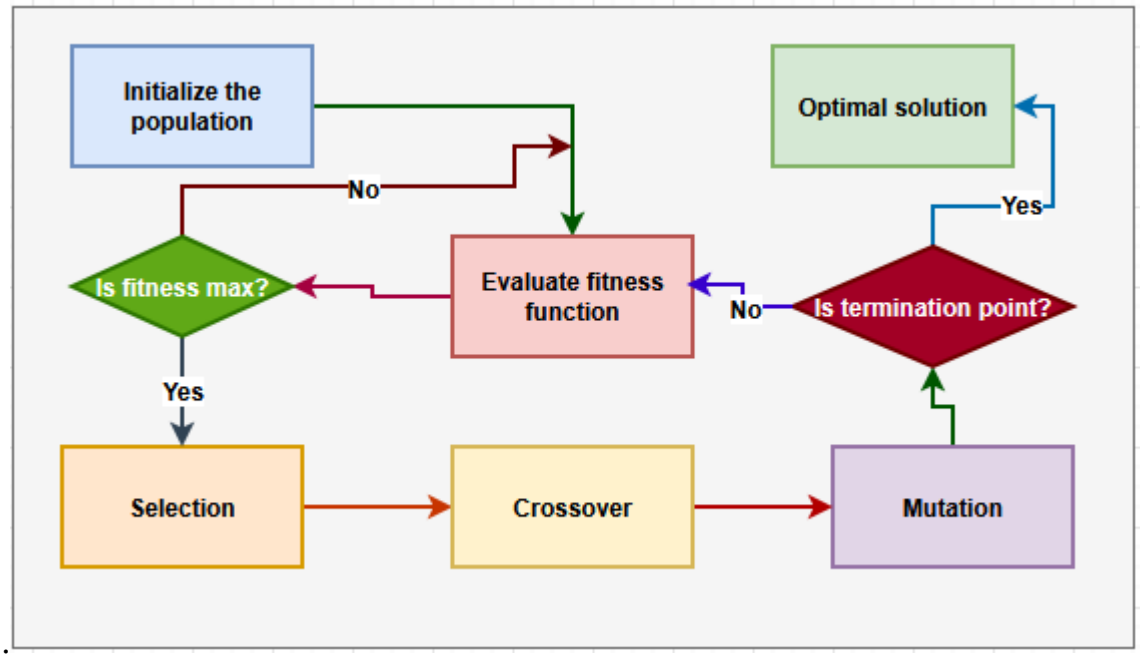


Figure 4-1 Process of the Genetic Algorithm in feature selection and fitness optimization.

- Fitness Evaluation: Evaluate the fitness of each chromosome using the objective function. Assign a fitness score to each chromosome based on its performance.
- Selection: Select individuals (chromosomes) from the population for reproduction. Here we utilized common selection methods, "roulette wheel selection" and Stochastic Universal Sampling (SUS), which is similar to Roulette wheel selection; however, instead of having just one fixed point, we have multiple fixed points. Therefore, all the parents are chosen in just one spin of the wheel. Also, such a setup encourages the highly fit individuals to be chosen at least once.
- Crossover (recombination): Apply crossover (recombination) to selected pairs of chromosomes. New offspring are created by combining genetic material from the parents. There are single-point, two-point, uniform, whole arithmetic recombination and Davis' order crossover. from these, we work on the whole arithmetic recombination.

- Mutation: Introduce small random changes (mutations) to the offspring. Mutation helps maintain diversity and prevents premature convergence.
- New Population Generation: Create a new population by combining parents and offspring. Apply elitism (keep the best individuals) if desired.
- Termination Criteria: Decide when to stop the algorithm (e.g., after a fixed number of generations or when a satisfactory solution is found).
- Repeat steps for multiple generations until the termination criteria are met.

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. This iterative process enables a genetic algorithm to navigate the solution space and converge toward optimal or near-optimal solutions for complex problems. The research also involved the characterization and classification of tumour based on the probability of malignancy and any abnormalities.

To illustrate the effect of the genetic algorithms and how to enhance 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.
b. Parameter Optimization: Both KNN and SVM algorithms have parameters that significantly influence their performance. GA can be utilized to optimize these parameters by evolving a population of parameter configurations and selecting those that result in the highest classification accuracy. 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 **Algorithm 2** and **Algorithm 3**.

The steps of the algorithm for feature extraction are represented by the pseudo-code to be implemented in the algorithms.

4.1.1 The Design of Proposed Framework. -

The GAKNN-SVM is a hybrid learning algorithm consisting of a genetic algorithm with K-nearest neighbours and support vector machines. Fitness optimization during feature selection, GA plays a role, and data classification is performed by the KNN algorithm, followed by SVM training. **Figure 4-2** illustrates the process of the model, at the beginning

the data is initialized by the GA, the main objective of the GA is feature extraction and fitness selection, by new generation and finding the optimal solutions.

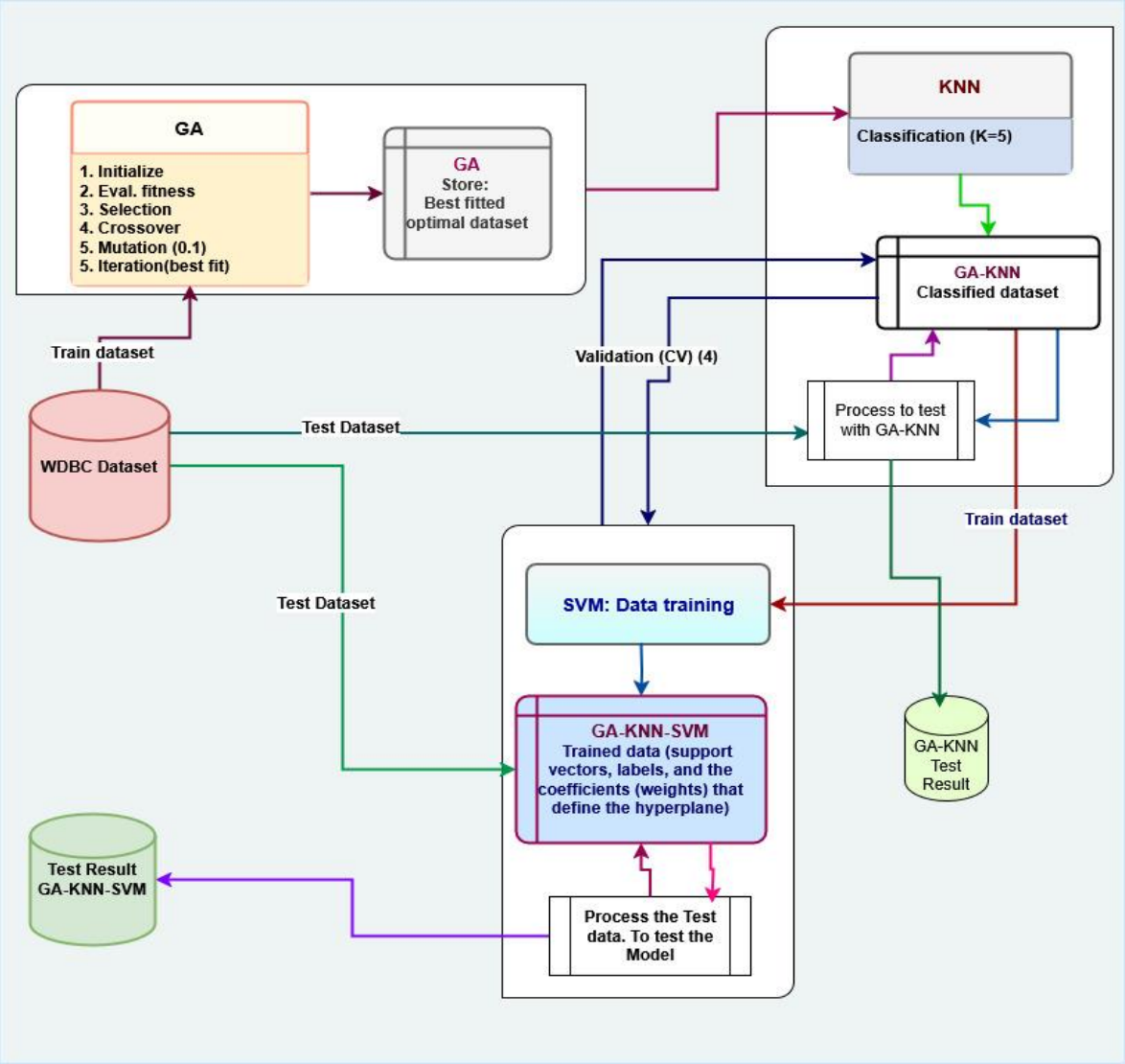


Figure 4-2: Proposed GAKNN-SVM model framework.

Next to this, KNN works on the classification of the data by K=5. The process of the KNN model with GA provides an opportunity to test separate test results to determine how accurate the classification is. The classified dataset is an input for the Support Vector Machine.

The choice of (k) in k-Nearest Neighbors (k-NN) serves as a crucial hyperparameter that defines the number of nearest neighbors considered when making predictions. This selection can significantly influence the algorithm's performance. A small value of (k) (e.g., (k = 1)) may render the model highly sensitive to noise within the data, leading to increased variance and a higher risk of overfitting to the training data. In contrast, choosing a larger (k) enhances model stability and reduces sensitivity to noise, but it may also cause

the model to become overly generalized, resulting in high bias and potential underfitting. Determining the optimal value of (k) typically involves experimentation and cross-validation. It is customary to evaluate a range of (k) values and choose the one that demonstrates the best performance on validation data. The appropriate value of (k) should not be fixed; instead, it should be tailored to the specific dataset and problem being addressed, often through a process of trial and error alongside validation.

Cross-validation is a technique employed to evaluate the performance of a machine learning model. For Support Vector Machines (SVM), K-Fold cross-validation is utilized to partition the data into four segments.

4.1.2 Solution Model Algorithm. -

To significantly enhance classification performance, the reserch exploit the power of a hybrid approach that synergistically combines the Genetic Algorithm (GA) with K-Nearest Neighbors (KNN) and Support Vector Machine (SVM) techniques successively.

In the initial phase, the Genetic Algorithm thoroughly processes the dataset to pinpoint the most impactful features based on their fitness values. The GAKNN-SVM model employs a strategic feature selection process that leverages GA alongside KNN classification.

The process begins with the Genetic Algorithm, which evaluates the data to classify features through rigorous fitness calculations. The optimal objective function identified during this phase serves as the critical input for KNN classification. Using the Euclidean distance metric, KNN effectively classifies these features.

K-Nearest Neighbors (KNN) stands out as an instance-based algorithm that operates without a formal training phase, maintaining the entire training dataset for predictions. In contrast, Support Vector Machines (SVM) engage in a structured training methodology, striving to identify the optimal hyperplane that distinguishes various data classes. One of the challenges with KNN is its susceptibility to outliers, especially those near the decision boundary. Since KNN relies heavily on distance metrics, an outlier can dramatically skew classification outcomes. On the other hand, Support Vector Machines demonstrate remarkable resilience to outliers, as they prioritize maximizing the margin between classes; outliers only influence this margin if they are designated as support vectors. By combining the robust capabilities of Support Vector Machines with K-Nearest Neighbors, the study creates a powerful hybrid model,

KNN-SVM, that addresses these limitations head-on. The data generated through the GA-KNN process is expertly trained using SVM, paving the way for superior classification outcomes. Algorithm 1 provides clear pseudocode for the Genetic Algorithm, detailing each step from initiation to completion.

Algorithm 1 A generalized pseudo-code for a genetic algorithm.

Require: t := 0;

Require: T :=N;

1: $start \leftarrow GA()$;
2: $initpopulation \leftarrow P(t)$; initialize random population of individuals;
3: $evaluate \leftarrow P(t)$; evaluate fitness of all initial population;
4: **while** $t \leq T$ **do**
5: $t \leftarrow t + 1$;
6: $P \leftarrow selectparentsP(t)$; select a sub-population for offspring production.
7: $recombine \leftarrow P(t)$; recombine the "genes" of selected parents, cross over with probability.
8: $mutate \leftarrow P(t)$; perturb the mated population stochastically, mutation with probability.
9: $P \leftarrow survive_p(t)$; select the survivors from actual fitness.
10: **end while**
11: $return \leftarrow bestFit$
12: End GA.

Algorithm 2 provides the pseudo-code for implementing the K-Nearest Neighbors (KNN) algorithm. It begins with N samples of data and a predefined value of k. The algorithm calculates the distance of each sample from a specified point, grouping the data according to these distances. By identifying the nearest neighbors, it can classify the data based on the chosen number of classifications (k = 1, 2, 3, etc.).

Algorithm 2 KNN algorithm

Require: d :=[i]

Require: n := 0; initial n;

Require: Dataset :=N;

$start \leftarrow KNN(Datasets, Sample, k)$:

while $n \leq Dataset$ **do**

    $d \leftarrow calculate\_d(item, sample)$;

    $distance(d(i)) \leftarrow d.append(item, distance)$;

    $sorted\_d \leftarrow sort(distance, key = lambda)$;

    $n \leftarrow (n + 1)$; ▷ increase the counter;

    $neighbors \leftarrow (sorted\_d(k))$;

end while

for neighbor in neighbors **do**

    $group\_label \leftarrow neighbor.class\_label$

    $group\_count[class\_label] \leftarrow class\_counts.get((class\_label, 0) + 1)$;

end for

$predicted\_group \leftarrow max(group\_counts, key = group\_counts.get)$;

$return \leftarrow predicted\_group$;

End(KNN);

Algorithm 3 presents the pseudo-code for a Support Vector Machine (SVM), which is designed to process input data, encompassing both the number of training and test samples. This algorithm takes into account weight and bias values and continues to train the model until it achieves convergence.

Algorithms 4 and 5 outline the processes for GA-KNN and GA-SVM, respectively. These pseudo-code examples represent a hybrid algorithm that integrates Genetic Algorithms (GA). A notable aspect of this approach is that feature selection is conducted using GA. This hybrid algorithm harnesses the optimization and search capabilities of GA to effectively manage complex datasets, even in cases where the data size is limited.

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;

$convergence \leftarrow convergence(X)$;
while $convergence \neq 0$ **do**
    for $iinrangedata(Xi, yi)$ **do**
        $margin \leftarrow calculate_margin(yi * (w * xi + b))$;
        if $margin < 1$ **then**
            $updateweights :\leftarrow W = w + alpha * (yi * xi - 2 * C$;
            $updatebias :\leftarrow b = b + alpha * yi$;
        else
            $updateweight :\leftarrow W = W + alpha * (-2 * C * W)$;
        end if
    end for
end while
$caldecisionf(X\_new) \leftarrow W * X\_new + b$;
if f(X_new) > 0: **then**
    $predict\_class \leftarrow 1$;
else
    $predict\_class \leftarrow -1$;
end if
$perfnc[i] \leftarrow perfnc(acrcy, prec, F1 - s)$;
End (SVM);

The innovative model is called GAKNN-SVM, highlighting a major advancement in classification techniques. Algorithm 6 presents the pseudo-code for the hybrid model combining GA with KNN and SVM. The GAKNN and SVM processes operate on the same sample data. The workflow follows a sequential order: feature selection is performed using Genetic Algorithms (GA), classification is carried out with K-Nearest Neighbors (KNN), and training is conducted using Support Vector Machines (SVM).

Algorithm 4 Algorithm: GA-KNN

Require: Start

Require: Initialize population P with random candidate solutions.

1: Evaluate the fitness of each candidate solution in P using the fitness function.
2: Repeat until termination criteria are met:
3: Select parents from P based on their fitness.
4: Apply crossover and mutation operators to create offspring.
5: Evaluate the fitness of the offspring.
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.
10: END (GA-KNN)

Algorithm 5 Algorithm: GA-SVM

Require: Start

Require: Initialize population P with random candidate solutions.

1: Evaluate the fitness of each candidate solution in P using the fitness function.
2: Repeat until termination criteria are met:
3: Select parents from P based on their fitness.
4: Apply crossover and mutation operators to create offspring.
5: Evaluate the fitness of the offspring using SVM.
6: Select individuals for the next generation based on some selection
7: strategy (e.g., tournament selection).
8: Replace the old population with the new generation.
9: Select the best solution from the final population as the output.
10: Training and testing by SVM.
11: END (GA-SVM)

Algorithm 6 GAKNN-SVM Pseudocode

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

Require: initialize := (p);

1: $KNN - Fit(P(i)) \leftarrow calculate - fitness(P(i));$

2: **for** i in range N **do**

3: **while** termination true **do**

4: $bestFitt(p(i)) \leftarrow compare - fitness(P(i)P(i-1);$

5: $selectparentsP(i) \leftarrow Fit(P(i));$

6: $cros(P) :\leftarrow crossover(p(i);$

7: $mut(P) :\leftarrow mutaion(p(i));$

8: $calfit(p - offspring) \leftarrow calculate(Fit(P - offspring));$

9: $select(p - offspring) \leftarrow select(P - offspring(i));$

10: $replaceold \leftarrow new - generation(P);$

11: **end while**

12: **end for**

13: $classify(P - GAKNN) \leftarrow classify - KNN(P(i);$

14: $selectbestsolution \leftarrow select(P - GAKNN);$

15: $classify(P - SVM) \leftarrow classify(P - GAKNN);$

16: $select - best(P - GAKNNSVM) \leftarrow select(P - SVM);$

17: End (GAKNN-SVM);

4.2 Modified Genetic Algorithm with Pontryagin Minimum Principle (PMP)

4.2.1 Proposed Solution Design Framework. -

For utilizing the PMP fitness assessment process with GA, the research effectively processed the WBCD dataset for training and validation. It explores the Pontryagin Minimum Principle (PMP) in the genetic algorithm to optimize the selection process and identify the best-fit object more efficiently. Integrating PMP into the genetic algorithm helps minimize constrained objective functions and maximize the fitness function. The result shows the best-fit population for the next generation. The population selected undergoes a multi-objective function to improve efficiency and reduce computational time. This model explores the necessary conditions for

optimality, including the Hamiltonian system of equations and the transversality conditions. Research focuses primarily on optimizing the genetic algorithm selection process to achieve the highest fitness. This addresses the computational time required for the genetic algorithm to control the parameters, as tested with the Wisconsin Breast Cancer Binary Dataset. Researchers are using genetic algorithms for feature selection and machine learning. However, this study discusses how the integration of PMP enhances the accuracy of classification using machine learning algorithms.

The main differences between the proposed algorithm and other existing algorithms lie in its enhanced fitness evaluation through PMP, significant improvements in classification accuracy, optimized feature selection, and its robust performance across different machine learning models. These improvements collectively contribute to more reliable and efficient breast cancer detection, underscoring the potential to integrate advanced techniques like PMP with genetic algorithms in medical diagnostics.

To ensure the efficiency of our genetic algorithm (GA), the calculation of fitness values must be fast and accurate. If the computation of the fitness value is slow, then the GA's performance is severely affected. Thus, the study employs the Pontryagin's minimum principle (PMP). The probability of selecting the highest fitting value is given by.

$$p_i = \frac{f_i}{\Sigma_{j=1}^{N} f_j}, \tag{4.1}$$

$$\mathrm{ObjF}(i) = |f(x_i)|$$

$$J = (1 + \lambda S^*) \cdot J^* \tag{4.2}$$

where J, J^*, λ objective function, cost function and Lagrange multiplier, respectively. The cost function is equivalent to the mean square error, which is computed by:

$$J^* = MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - y_i^*)^2 \tag{4.3}$$

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.

$$J^* = \frac{1}{n}(\sum_{i=1}^{n}(y_n - y_i^*)^2 + \sigma \sum_{i=1}^{n}(C_i - C_i^*)) \tag{4.4}$$

where the classification error is identified by C, the actual class, C^* the predicted class and σ the weight factor. By combining (eq. 4.2,4.3, and 4.4), the objective function **J** can be obtained.

The probability of selecting the next population is given by (eq. 4.1), and the selection function derived from (eq. 4.2 and 4.4) is given by eq. 4.5.

$$p_i / \sum_i P_i, where P_i = \frac{min_i(J_i)}{(J_i)}$$
$$, 1, l"\ell 1, ..., L \tag{4.5}$$

$$\dot{X}(t) = f(X(t), u(t), t), \tag{4.6}$$

where $X(t) = [x_1(t), ..., x_n(t)]^T$ denotes a vector state, u(t) is a vector control variable. Equation (4.6) leads to the solution of the differential equation trajectory X (t, x_0, t_0), which is described as in (eq. 4.7).

$$max_{u(t)} J = \int_{t_o}^{t_1} I(X(t), u(t), t)dt \tag{4.7}$$

$$H(x(t), u(t), \lambda(t), t) = I(x(t), u(t), t) +$$
$$\lambda^T(t) f(X(t), u(t), t) \tag{4.8}$$

Equation (4.7) combines the objective function and the state equations, multipliers, λ(t), and co-state variables. The genetic algorithm fitness function evaluates potential solutions based on predefined criteria, assigning a fitness score that reflects the quality of the solution. The fitness function embodies the objectives of selecting the next generation in the genetic algorithm. Additionally, Pontryagin's Minimum Principle (PMP) provides an alternative approach for computationally efficient solutions in optimal control, specifying that certain conditions need to hold only over specific trajectories. The efficiency of a GA is often determined by its ability to balance exploration searching through the genetic space and exploitation refining the best solutions. Mathematically, a genetic algorithm can be represented by a set of equations that describe how the population evolves. This includes the probabilities of selection,

crossover, and mutation, as well as the expected distribution of fitness scores in the population.

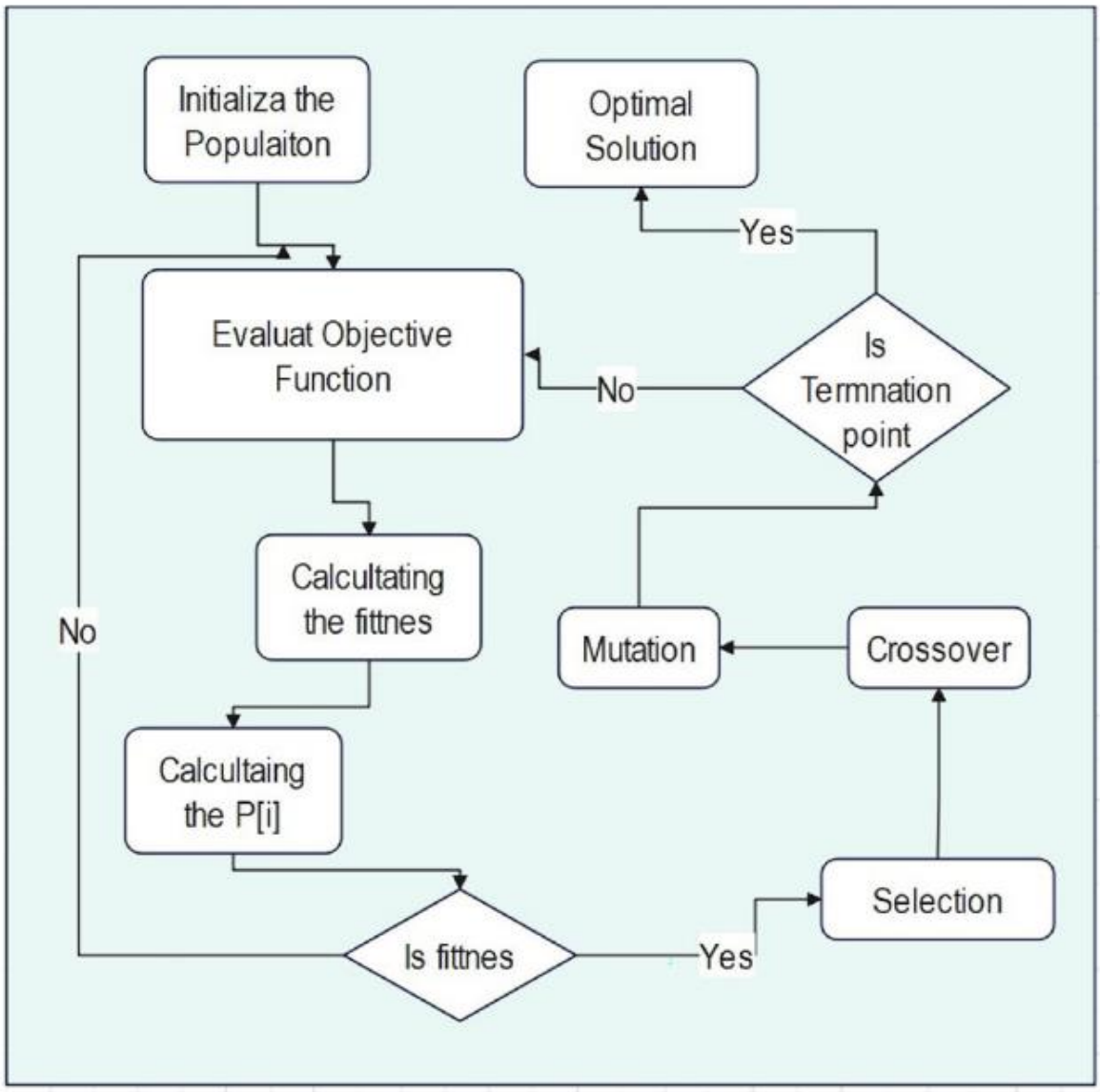


Figure 4-3: Genetic Algorithm process in the objective function fitting calculation.

The schema theorem for the genetic algorithm is given by.

$$f(H,t+1) \geq \frac{\left(f(H,t) \times \sigma(H,t)\right)}{f(t)} \times (1 - p_c \times \frac{\delta(H)}{l-1} - p_m \times o(H)) - - - (4.9)$$

Where:

- f (H, t) is the fitness of schema H at time t.
- $\sigma(H,t)$is the order of schema H (the number of fixed positions)
- f(t) is the population's average fitness at time t.
- pc is the probability of crossover.

- δ(H) is the defining length of schema H (the distance between the outermost fixed positions).
- l is the length of the chromosome.
- pm is the probability of mutation.
- o(H) is the order of schema H.

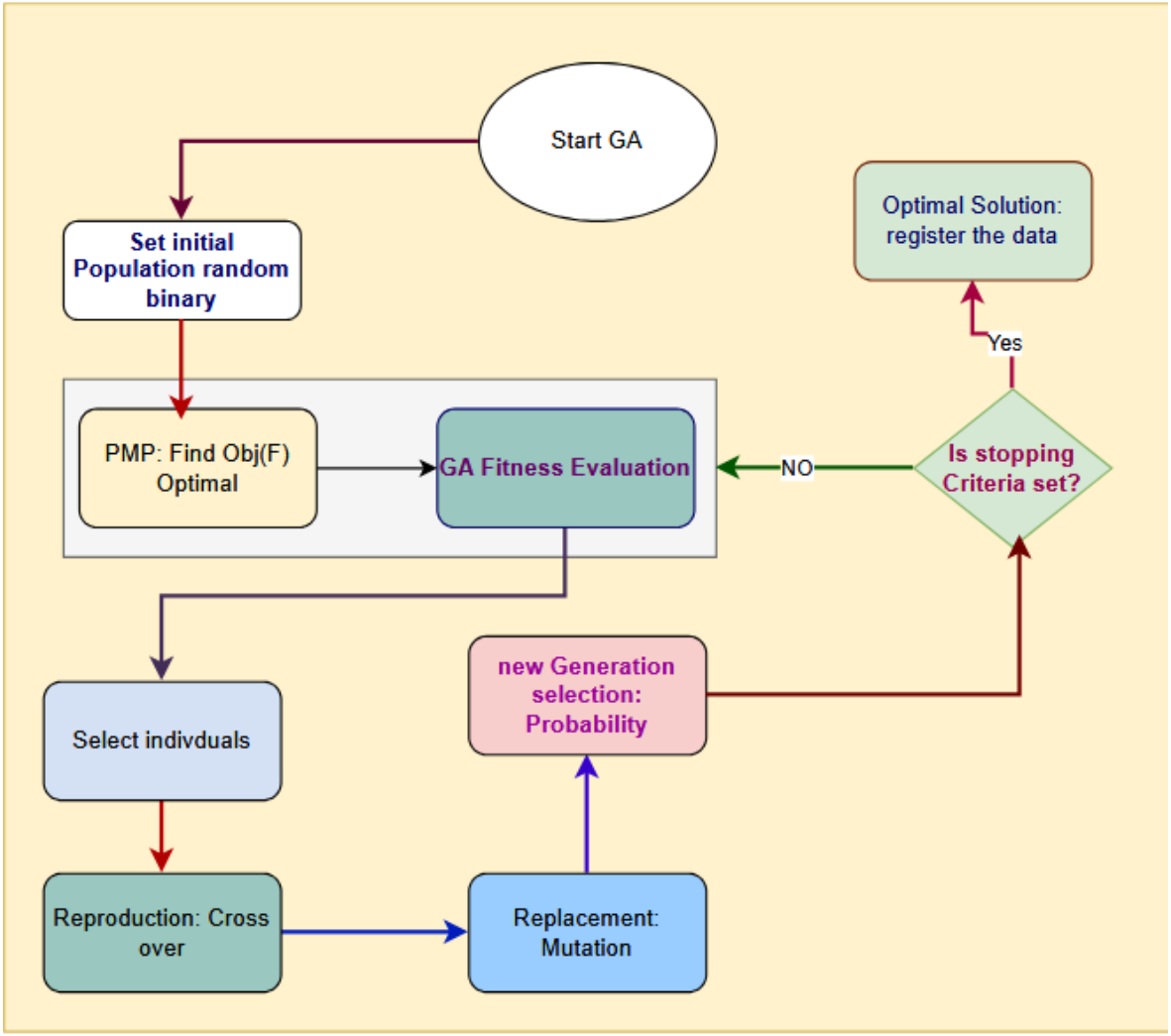


Figure 4-4 The proposed PMP Fitness valuation process.

Equation (4.9) evaluates the expected fitness of schema H at the next generation t + 1. It considers the schema's fitness at the current generation t, the order $\sigma(H,t)$and the defining length δ(H) of the schema, the probability of crossover P_c, and the probability of mutation P_m. This helps in predicting the propagation of schema through generations.

4.2.2 Solution Model Algorithm. -

The research method used in this study is experimental, and the goal is to show the effect of the PMP on the genetic algorithm for selection.

The dataset is Wisconsin's breast cancer binary data; 80 percent of the data is used for training, 10% of validation and the remaining is for testing. The pseudocode of the proposed model is described in **Algorithm 6**. The proposed method, differentiated from the existing genetic algorithms, is to add the PMP fitness function for better optimization. In Equation (2.8), $\phi(s) = [\, f(s) + R. \sum_{i=0}^{n} \sigma(Z)]$ the unconstrained objective function is denoted as ϕ max and is computed using the PMP. The coefficient of chromosomes corresponds to the column name of the data with the highest correlation. During the evaluation of the objective function, a value is obtained, and in the fitness function selection process, a score is acquired. To determine the likelihood of fitness, it seek the value closest to one, as it has the highest probability of being chosen for the next-generation chromosome. Machine learning algorithms are utilized for classifying and training the dataset.

4.3 Hybrid Genetic Algorithm with K- Means++

The study introduces an innovative hybrid genetic algorithm integrated with a K-Means++ clustering model, specifically designed to accurately classify BI-RADS scores for breast mammography screenings.

The BI-RADS (Breast Imaging Reporting and Data System) classification system is crucial for evaluating the severity of breast tumour, as it aids healthcare professionals in diagnosing patients effectively. This advanced model is intended to assist oncologists in the fine assessment of tumour characteristics and progression. Upon receiving a mammographic image from a radiologist, the model employs sophisticated algorithms to accurately determine the associated BI-RADS score. This classification not only enhances diagnostic precision but also empowers healthcare providers to engage in informed discussions with patients regarding their findings and potential treatment options.

The study utilises a comprehensive dataset comprised of well-annotated mammography images, precisely categorised by BI-RADS scores. The training of the model on this carefully structured data set is aimed at achieving optimal accuracy and reliability in score assignment. This approach not only enhances the model's predictive capabilities but also contributes to improved patient outcomes through timely and informed medical decision-making. By leveraging leading technology, our study addresses a critical need in breast cancer diagnostics, ultimately fostering a more

effective healthcare environment.

4.3.1 Data processing: Design framework. –

OpenCV is utilized for various tasks, including image detection, preprocessing, compression, selecting regions of interest (RoI), and data training. The Genetic Algorithm (GA) is used for feature extraction, while K-Means++ is applied for training, as illustrated in **Figure 4-5**.

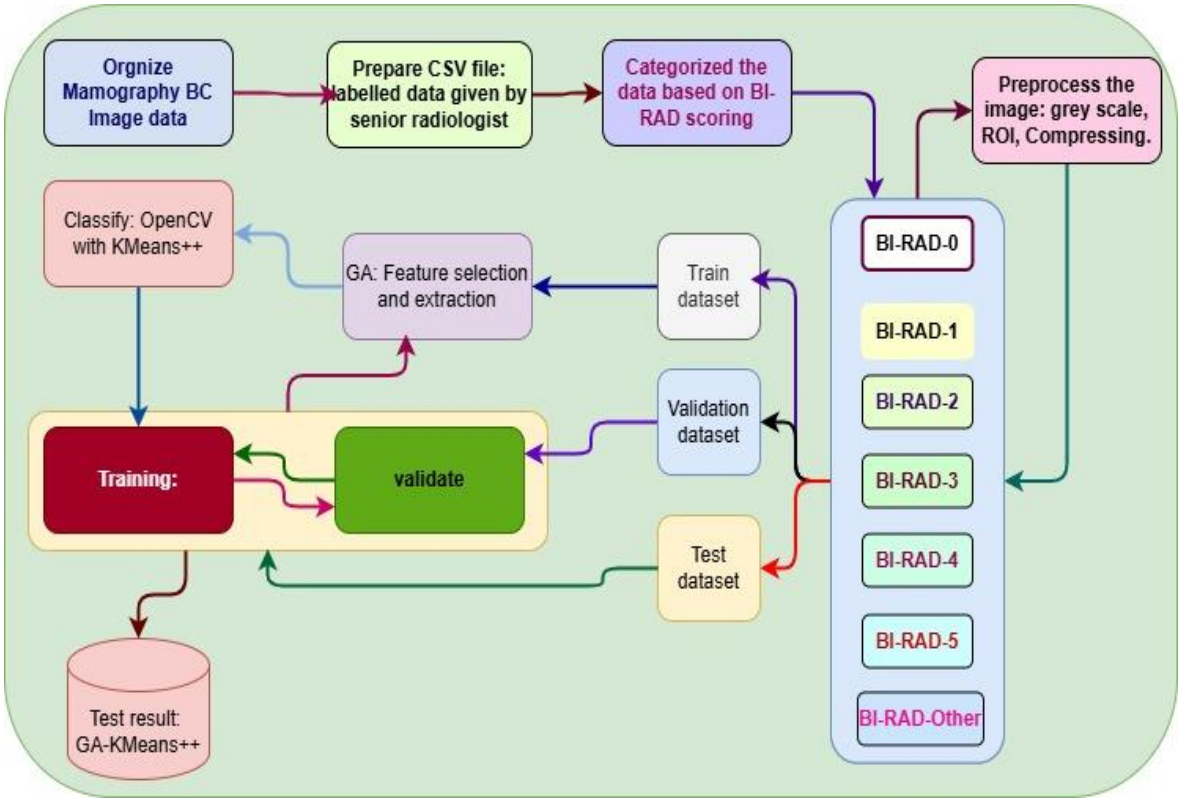


Figure 4-5 GA-Kmeans++ process framework.

The DICOM image dataset is initially processed to remove patient information, reduce noise, convert images to greyscale, and resize them to 224x224 pixels.

The data is categorized into six classes, ranging from BI-RADS-0 to BI-RADS-5, as defined by the radiologists. The training process is conducted based on these classes. The feature selection process employs a genetic algorithm that ensures optimal fitness validation. Subsequently, training is performed using K-Means++.

This technique addresses the limitations of standard K-Means by enhancing clustering quality. K-Means++ achieves this by ensuring that the initial centroids are well-distributed, which reduces the likelihood of poor clustering results that can stem from random initialization. After the training is completed with K-Means++, the trained data

is then validated.

4.3.2 Solution Model Algorithm. -

In the genetic algorithm, the research proposes Distance to Cluster Centers for clustering, and the fitness function is calculated according to Equation 4.17.

$$fitness = \frac{1}{\sum_{k=1}^{N_c}\sum_{j=1}^{N_k}\sqrt{\sum_{i=1}^{F}(C_k i - P_j j)^2}} \quad (4.17)$$

Where:

- N_c: is the number of clusters.
- N_k : is the number of samples within the cluster k.
- F is the number of features representing the sample.
- Ck is the center of the cluster k.
- C: the number of clusters

The following steps are followed to calculate the fitness,

- Loop through the cluster centers to calculate the Euclidean distance between all samples and all cluster centers.
- Assign each sample to the cluster with the least Euclidean distance.
- Another loop goes through the clusters to calculate the sum of all the differences in each cluster. If a cluster has zero samples, then its total distance is zero.
- Sum the distances in all clusters.
- Calculate the inverse of the sum of distances. This is the fitness value.

Algorithm 8 Algorithm for K-Means++ culstering

Require: Initialize:

1: Choose the number of clusters ← k.
2: Randomly initialize ← k centroids.
3: **while** convergence or n-number of iterations **do**
4: Assignment step:
5: **for** data point **do**
6: calculate the distance: ← each centroid;
7: Assign the data point: ← the nearest centroid;
8: **end for**
9: Update step:
10: **for** cluster **do**
11: calculate new centroid: ← assigned to that cluster; ▷ NOTE: calculate the new centroid by taking the mean of all data points;
12: Check for convergence:
13: **if** centroids not change significantly or converged **then**
14: stop the algorithm.
15: **else**
16: repeat steps ← 4 and 7.
17: **end if**
18: **end for**
19: **end while**

In the pseudocode, Algorithm 8 focuses on K-Means++ clustering, while Algorithm 9 describes the integration of a genetic algorithm with K-Means++ for the data training process. The genetic algorithm is responsible for feature selection with optimal solutions, while K-Means++ is used for image clustering and training.

Algorithm 9 Pseudo code for K-means++ with Genetic Algorithm: (GA-KMeans++)

Require: Initialize Population: Randomly generate an initial population of solutions;

Evaluate Fitness:
for solution in the population: **do**
    performs clustering;
    Calculate the fitness of each solution ← clustering quality
    sum of squared distances: ← from points to their cluster centers;
end for
while best **do**
    Selection: ← Select a subset of the population based on fitness;
    Crossover: ← Perform crossover; on the selected solutions to create new offspring.
    Mutation: ← Apply mutation; to the offspring to introduce variability.
    Evaluate Offspring: ← (Calculate the fitness of each offspring)
    Replacement: ← Replace the worst performing solutions in the population with the new offspring.
    Termination: ←
    if check termination condition is met **then**
        terminates the algorithm
    else
        repeat steps 8-14
    end if
end while
Output: ← Return the best solution found.

CHAPTER FIVE

5 RESULTS AND DISCUSSION

In this section, the study provides a detailed explanation of the models implemented in the study, each of which plays a crucial role in addressing the research questions. The first model, GA-KNN-SVM, demonstrates impressive performance in predicting breast cancer with a lower rate of false positives, paving the way for early tumour detection. The second model, GA with PMP, aims to improve accuracy while minimizing computational time for complex problems. The third model, GA-KMeans++, enhances the diagnostic process for radiologists by clustering BI-RADS scores. Here, the research will explore the results obtained from our processing of the datasets using these models.

5.1 Results of the models

5.1.1 Result on GAKNN-SVM. -

The intricacy of interpreting digital mammograms makes it difficult to diagnose breast cancer in settings with limited resources. According to Alanazi SA et al. (2021), SVMs had the highest accuracy at 78.56%, whereas K-NN's was 71.86%, **Table 5-1.** Kumar's research showed that mammogram classification using CRNN with FC-CSO techniques achieved an impressive 98.4% accuracy, 99.9% specificity, and 74.5% F1 scores (Kumar et al. 2021).

Table 5-1: Machine Learning Classification.

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

However, CRNN methods need further filtering and have trouble classifying blurry pictures. Conversely, KNN methods attain a 94.44% accuracy rate; nevertheless, more enhancements are required for improved categorization.

Support Vector Machine (SVM) approaches have demonstrated a high accuracy rate of 96.55%, with a sensitivity of 96.97% and specificity of 96.20% when applied to digital mammography images. However, the interpretation of digital mammograms presents a challenge due to their high-dimensional matrix. To improve the accuracy of SVM for mammography image collections, large datasets are essential, as the current accuracy rate stands at 87.2%, with an Area Under Curve (AUC) of 94%. Performance variations among different classifier methods are illustrated in Error! Reference source not found. **and Table**

5-2 of the study. **Table *5-2***The WBCD dataset is utilized to train the model using K-fold cross-validation, with k=4. In this scenario, SVM achieves the second-highest accuracy after the Adaboost (AB) method. Notably, this study model outperforms these methods with an impressive accuracy rate of 99.3%.

Table 5-2: Dataset classification performance with machine learning.

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	97.72	98.59	96.26
6	GAKNN-SVM	99.30	98.56	92.00

Using the WBCD dataset of 569 samples, the performance results of applying genetic algorithm feature selection to different machine learning methods across 143 test datasets are shown in **Table 5-3**, and for 171 test datasets shown in The negative predictive value of a test (NPV): The likelihood is that a person with a negative test result does not have the disease, condition, biomarker, or mutation (change) in the gene being tested. The negative predictive value is a way of measuring how accurate a specific test is. From **Figure 5-3** and **Table 5-5**, the NPV test value shows our model has a lower value than the others. This determines that the number of false negatives is very minimal, which is 0.0185 or 1.85%.

Table 5-4.

Table *5-3*, there are eighty-seven true positives, fifty true negatives, four false positives, and two false negatives in the confusion matrix that was produced for SVM. Using these data, 96.67 was determined to be the F1-score, in 143 sample test data.

Table 5-3: Performance result 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	98.00	93.10	[[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

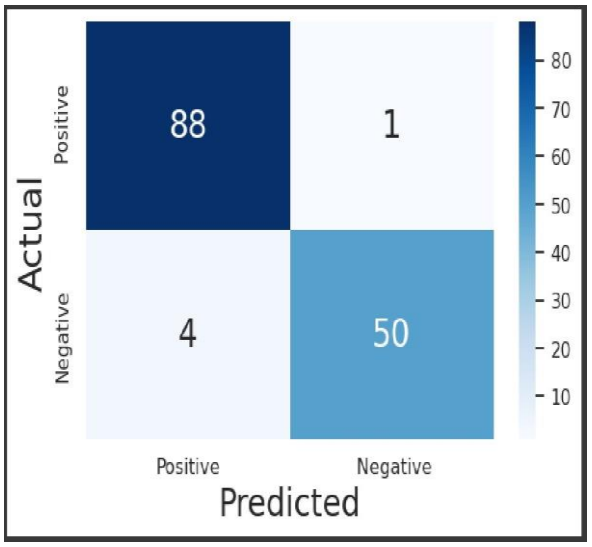


Figure 5-1 : Confusion Matrix for KNN

The application generated a confusion matrix after classifying the test data from WBCD using a KNN with an F1-score of 97.24, shown in **Figure 5.2**. When compared to the suggested model, the KNN and SVM models' performances showed notable gains. The negative predictive value of a test (NPV): The likelihood is that a person with a negative test result does not have the disease, condition, biomarker, or mutation (change) in the gene being tested. The negative predictive value is a way of measuring how accurate a specific test is. From **Figure 5-3** and **Table 5-5**, the NPV test value shows our model has a lower value than the others. This determines that the number of false negatives is very minimal, which is 0.0185 or 1.85%.

Table 5-4 The accuracy rose to 95.91% and 96.49% for KNN and SVM, respectively, following the incorporation of GA. On the other hand, the suggested model's accuracy was higher than any other approach. These findings demonstrate how well GA works to improve classification models for the diagnosis of breast cancer. Additionally, the use of the study model demonstrated how resilient it is to various kinds of data.

The negative predictive value of a test (NPV): The likelihood is that a person with a negative test result does not have the disease, condition, biomarker, or mutation (change) in the gene being tested. The negative predictive value is a way of measuring how accurate a specific test is. From **Figure 5-3** and **Table 5-5**, the NPV test value shows our model has a lower value than the others. This determines that the number of false negatives is very minimal, which is 0.0185 or 1.85%.

Table 5-4: Performance Comparison of our model with others, 171 sample datasets.

Measuremen	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	93.70%	93.72%	84.35%	91.24%	92.44%	96.25%

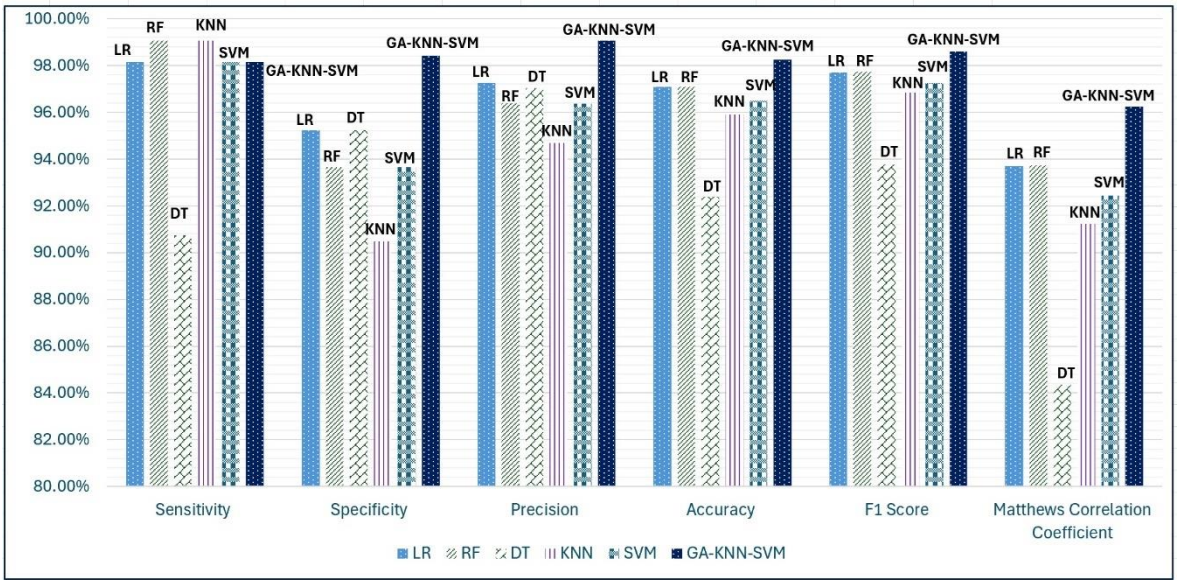


Figure 5-2: Performance comparison of the model GAKNN-SVM with other ML algorithms.

Table 5-5: Our model's Negative predicted value test result in comparison with other

Measurement	LR	RF	DT	KNN	SVM	GAKNN-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

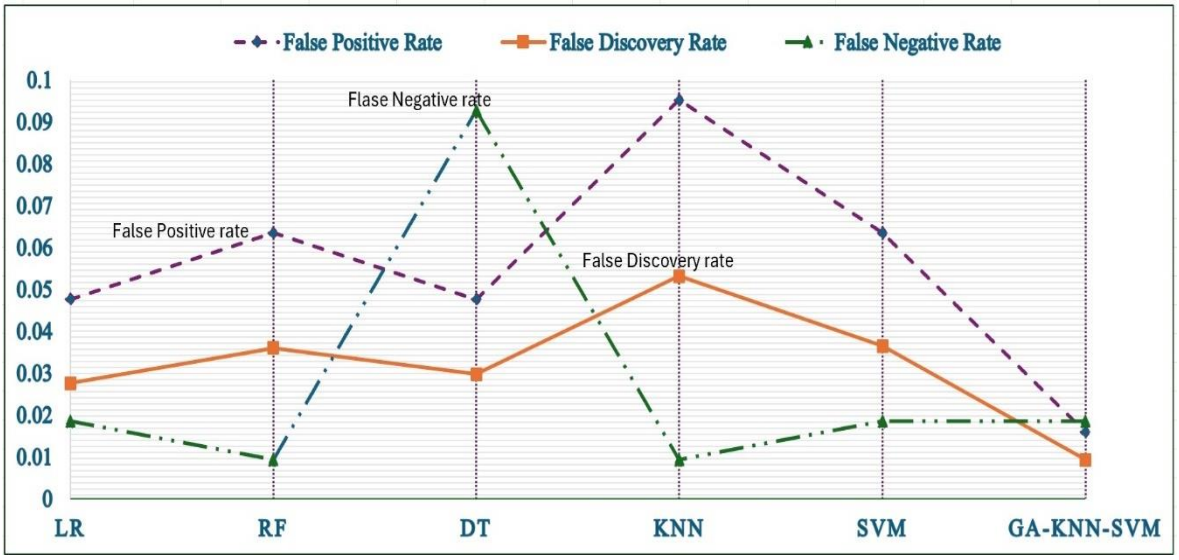


Figure 5-3: Graphical representation of our model, Negative predicted value test result in comparison with other ML algorithms.

For comparison purposes, it took the accuracy and F1-scores data from The negative predictive value of a test (NPV): The likelihood is that a person with a negative test result does not have the disease, condition, biomarker, or mutation (change) in the gene being tested. The negative predictive value is a way of measuring how accurate a specific test is. From **Figure 5-3** and **Table 5-5**, the NPV test value shows our model has a lower value than the others. This determines that the number of false negatives is very minimal, which is 0.0185 or 1.85%.

Table 5-4, the outperformed difference of our model result with others, ranging from 1.19% to 5.95% in accuracy and 0.89% to 4.89% in F1-score **Table 5-6**.

Table 5-6: Accuracy and F1-score difference from our model result to the ML .

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%	-

In the context of breast cancer classification, zero denotes benign, and one denotes malignant. From **Table 5-7**, KNN has an F1-score of 85% for benign and 93% for malignant protection. According to our process from the data set of WBCD with 171

sample tests, KNN has 97% and 94% F1-score in the prediction of benign and malignant, respectively. Whereas SVM has an F1-score of 97% and 95%, GAKNN has 97% and 95% for the prediction of benign and malignant, see **Table 5-8**.

Table 5-7: Precision, Recall and F1-Score of classifiers for malignant or benign with 114 test datasets.

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

Table 5-8: Precision, Recall and F1-Score of classifiers with 171 test datasets.

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

The proposed model demonstrates an F1 score of 99% for benign and 98% for malignant and a precision of 0.99 and 1.0.

Furthermore, the research analyzed the time complexity and identified the generation that exhibited the best fitness, as presented in Table 5-9. The highest

score, 0.993, was achieved in the second generation. Genetic Algorithms with different generations of iterations have better accuracy, with a 1% to 2% improvement.

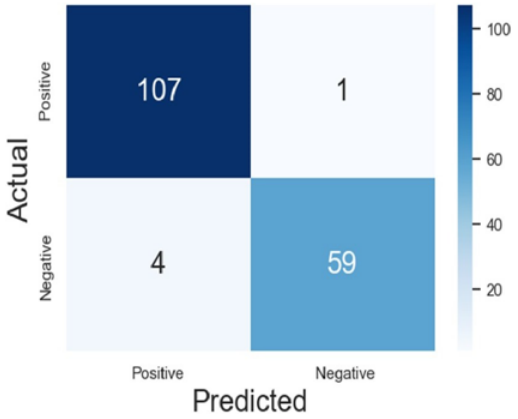


Figure 5-4: RF confusion matrix with 171 test data size.

Overall, the results indicate that the GA-KNN-SVM model demonstrates the best performance for classifying the dataset as either malignant or benign.

Table 5-9: The accuracy of different ML algorithms concerning GAKNN-SVM

No	Classifier	Accuracy
1	Random Forest	97.2028
2	Logistic	96.5035
3	K-Neighbors	96.5035
4	Linear SVM	95.8042
5	Gradient Boosting	95.8042
6	Radial SVM	95.1049
7	AdaBoost	95.1049
8	Decision Tree	93.0070
9	GAKNN-SVM	99.3000

Table 5-10: The Best score of GA with five iterations

Gen	Score
1	[0.986013986013986]
2	[0.993006993006993]
3	[0.993006993006993]
4	[0.993006993006993]
5	[0.993006993006993]

Additionally, it can effectively tune the parameters of our classifiers using a genetic algorithm. The effectiveness of this method in enhancing model performance was demonstrated when it obtained the greatest fitness score of 0.993 in the second generation of the GA through iterative refining. In general, our approach performs better in classification when it comes to predicting whether a tumour is benign or malignant.

```
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
```

Figure 5-5:- RF classification algorithm with 114 test data points.

Figure 5-5,

Figure 5-7 the research used the same classification algorithm, RF, as others. The Classifier KNN model achieved a score of 0.9650, while the linear Support Vector Machine classifier achieved a score of 0.958. GASVM and GAKNN-SVM have comparatively better F1 scores, and RF surpasses GAKNN in precision for predicting benign and malignant cases.

```
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

Figure 5-7: RF classification algorithm with 143 test data points.

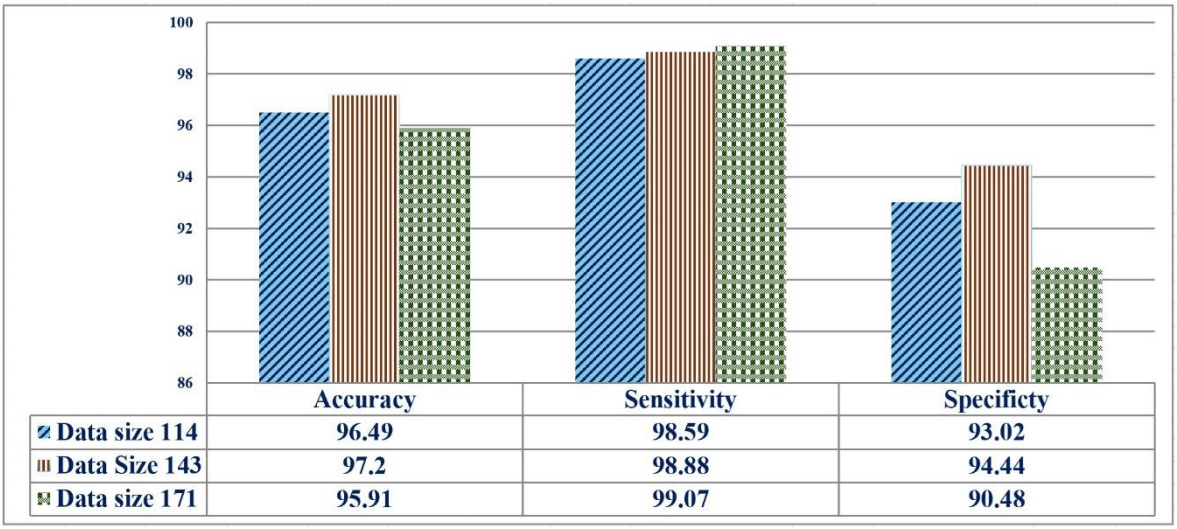
```
Accuracy :  0.9590643274853801
Sensitivity :  0.9907407407407407
Specificity :  0.9047619047619048
```

```
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

Figure 5-6: RF classification algorithm with 171 test data size.

From the **Figure 5-8,** the research explained that when the ratio of the training to the test differs by changing the sample test data set size, 114 (20%),143 (25%) and 171 (30%) of the total sample data size, there are different results in the F1-score, precision, and recall also.



	Accuracy	Sensitivity	Specificty
Data size 114	96.49	98.59	93.02
Data Size 143	97.2	98.88	94.44
Data size 171	95.91	99.07	90.48

Figure 5-8: Performance comparison with different sample data sizes.

5.1.2 Result Before Implementation of GA with PMP. -

Before incorporating the genetic algorithm into the dataset training procedure, 114 testing sample rows out of 569 were used to assess the classification performance. **Table *5-11*** shows the accuracy of the classification ML algorithms; from these, support vector machines and linear regression performed better in terms of accuracy. Both SVM and linear regression registered the highest accuracy of 97.37%, the best confusion matrices, and the best F1 scores of all the techniques that were assessed, **Figure *5-9***. These findings highlight how well-suited conventional classification techniques were for managing the dataset before the use of genetic algorithm optimization.

Table 5-11: The accuracy of the classification without implementing GA.

Algorithm	Accuracy%
LR	97.37
SVM	97.37
RF	95.01
K-SVM	92.98

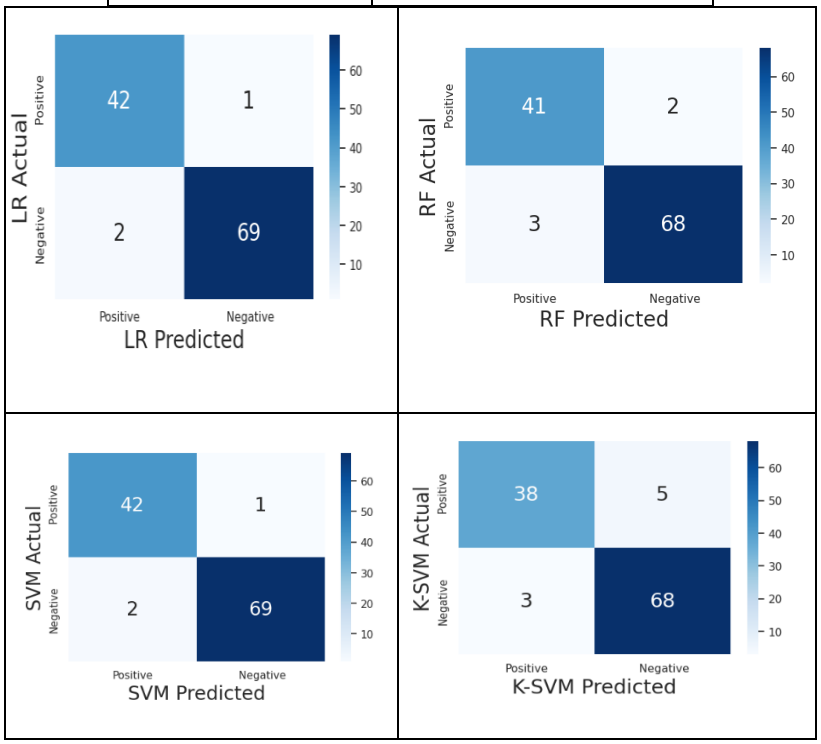


Figure 5-9 Confusion matrix for LR, SVM, RF and K-SVM

Machine learning models comprehensively examine the data collection, producing detailed performance measures. These include the F1 score, recall, specificity, accuracy, sensitivity, and precision. The categories benign(B) and malignant (M) were identified using

performance metrics. **Table 5-12** shows the performance results of the classification methods using the genetic algorithm (GA) before the implementation of the Pontryagin Minimum Principle (PMP). The displays calculate each algorithm's F1 scores across types 0 and 1, as well as its accuracy, sensitivity, and specificity. With the greatest accuracy and a confusion matrix of 106 TP, 2 TN, 2 FN and 61 FP, the Ada-Boost classifier was outperformed. For types 0 and 1, this matrix resulted in F1 scores of 0.98 and 0.97, respectively, and an accuracy score of 97.67%. Similarly, the classification tests using logistic regression yielded 106 True Positives and 60 True Negatives, respectively, yielding an accuracy score of 97.07% and F1 ratings of 0.98 and 0.96 for types 0 and 1. When compared to other methods, the Ada-Boost model fared better in terms of accuracy.

Table 5-12: The result of the performance with GA before applying PMP.

Algor	Acc.%	Sens.%	Spec.%	[B, M]	Prec.%	Recall	F1-Score
LR	97.07	98.15	95.24	0	0.97	0.98	0.98
				1	0.97	0.95	0.96
GB	95.91	97.2	93.65	0	0.96	0.97	0.97
				1	0.98	0.90	0.94
SVM	96.5	98.15	93.7	0	0.96	0.98	0.97
				1	0.97	0.94	0.95
DT	92.4	90.7	95.2	0	0.97	0.91	0.94
				1	0.86	0.95	0.90
KNN	95.91	99.1	90.5	0	0.95	0.99	0.97
				1	0.98	0.90	0.94
RF	97.08	99.1	93.65	0	0.96	0.99	0.98
				1	0.98	0.94	0.96
AB	97.67	98.15	96.83	0	0.98	0.98	0.98
				1	0.97	0.97	0.97

5.1.3 Result after implementation of PMP with GA. -

The classification and training process has been implemented using a Genetic Algorithm (GA) with a maximum limit of four generations due to computational resource limitations. The scores for each generation highlight the performance outcomes achieved by integrating Pontryagin's Minimum Principle (PMP) with Genetic Algorithms (GA) for classification and training, as displayed in **Table 5.13**. Each classifier's generation score is provided alongside the best-recorded score, as

well as metrics for precision, recall, and F1 score. The chromosome with the highest fitness is chosen from the population. This selection underscores the significance of reducing objective functions to enhance fitness. Interestingly, even though the generation scores for RF, AB, LR, and SVM are comparable, LR shows the highest precision and F1 score following the application of PMP with GA for fitness selection. According to Equation (4.3), the fittest chromosome within the population is more likely to be chosen.

$$\lim_{x \to \infty} F(x) \to 1$$

$\exists x \in \mathbb{R} \ni$. the most to minimize the objective functions.

$$\lim_{x \to \infty} Obj(x) \to 0$$

From Equation (4.4), the constrained objective functions f(s) should be minimal to maximize the fitness function F(s). Thus, Equation (2.9), F(s) = ϕ max −[f(s) + R. σ(Z)] is applicable here in the fitness calculation.

Table 5-13: Performance results with PMP

Classifier	Gen Score	Best Scor	B or M	Prec.	Recall	F1-Score
LR	0.9941	Starting from the 2nd iteration	0	0.99	1.0	1.0
			1	1.0	0.98	0.99
GB	0.9883	1st and 4th iteration	0	0.99	0.97	0.98
			1	0.95	0.98	0.97
SVM	0.9941	Starting from 1st	0	0.96	0.98	0.97
			1	0.97	0.94	0.95
DT	0.9766	At 1st iteration, then decrease	0	0.94	0.96	0.95
			1	0.93	0.89	0.91
KNN	0.9707	Same for all iterations	0	0.96	0.98	0.97
			1	0.97	0.94	0.95
RF	0.9941	At 2nd iteration	0	0.97	0.97	0.97
			1	0.95	0.95	0.95
AB	0.9941	At 2nd iteration	0	0.96	0.98	0.97
			1	0.97	0.94	0.95

From **Table 5-13** LR, SVM, RF, and AB have the same generation score with different numbers of iterations and times. LR has the best precision and F1 score after implementing PM with GA. The result of evaluating the fitness selection PMP and classification algorithms, SVM, has the best score of 0.9941 in a generation. However, SVM is expensive in terms of computational time.

Table 5-14, LR has the highest detection accuracy registered at 99.42%. This

table provides information on the accuracy of the generation score, the accuracy of detection, and the corresponding confusion matrix for each algorithm. Performance becomes highest for classification and training. Following the implementation of PMP in GA for fitness evaluation, LR's exceptional detection accuracy becomes 99.42%. These results underscore the efficacy of PMP in optimizing classification algorithms for enhanced breast cancer detection accuracy.

Table 5-14: Performance score GA with PMP

Algorithm	Accuracy Gen Score	Detection accuracy
LR	97.74	99.42
GB	1	97.66
SVM	98.24	98.24
DT	96.48	93.57
KNN	97.24	96.49
RF	99.5	96.5
AB	1	96.5

5.1.4 Results on the Model of GA-K-means++. -

In our research developed an innovative approach that integrates k-means++ clustering through a genetic algorithm (GA) to analyze datasets that are locally arranged. The primary goal of this study is to tackle the challenges associated with screening in breast cancer diagnosis. To validate our method, the study compared its findings with those of existing prominent research in the field. For our analysis, it utilized a comprehensively organized dataset of mammography breast images that had been curated and categorized by a radiologist. Specifically, the dataset was divided into five distinct BI-RADS (Breast Imaging Reporting and Data System) categories, while other potential classifications were excluded to ensure a focused analysis. Following this categorization, the study work consolidated all the data from the five BI-RADS groups into a unified dataset, which was subsequently fed into the k-means++ algorithm for clustering purposes. It applied three different models in our experiments: the standalone Genetic Algorithm model, the k-means++ algorithm, and a hybrid model that effectively combines the strengths of both GA and k-means++. The results indicated that the hybrid algorithm exhibited enhanced performance compared to the other methods utilized. This finding underlines the efficacy of our approach in

processing and analyzing mammography images.

Table 5-16, classified by KMeans++, and in **Table 5-17,** classified and trained by the model GA-Kmeans++.

Table 5-15, classified by only GA and the highest accuracy is registered in the BI-RADS-2. **Table 5-16**, classified by KMeans++, and in **Table 5-17**, classified and trained by the model GA-Kmeans++.

Table 5-15: GA for classifying BI-RADS with local data sets.

Class	Accuracy	Precision	Recall	F1-score
BI-RADS-0	92.70	86.65	85.60	86.12
BI-RADS-1	92.24	86.45	85.40	89.10
BI-RADS-2	94.28	90.40	84.65	88.45
BI-RADS-3	92.30	90.38	84.49	88.10
BI-RADS-4	90.50	83.54	85.90	85.60
BI-RADS-5	89.39	68.92	75.70	75.30

Table 5-16: KM++ for classifying as BI- RAD the local data set (LMBCDS)

Class	Accuracy	Precision	Recall	F1-score
BI-RADS-0	90.25	85.70	84.90	88.10
BI-RADS-1	89.90	85.70	84.90	88.70
BI-RADS-2	89.25	85.40	83.65	87.80
BI-RADS-3	89.25	85.40	83.60	87.50
BI-RADS-4	86.80	81.24	83.15	84.60
BI-RADS-5	77.10	70.12	78.30	77.00

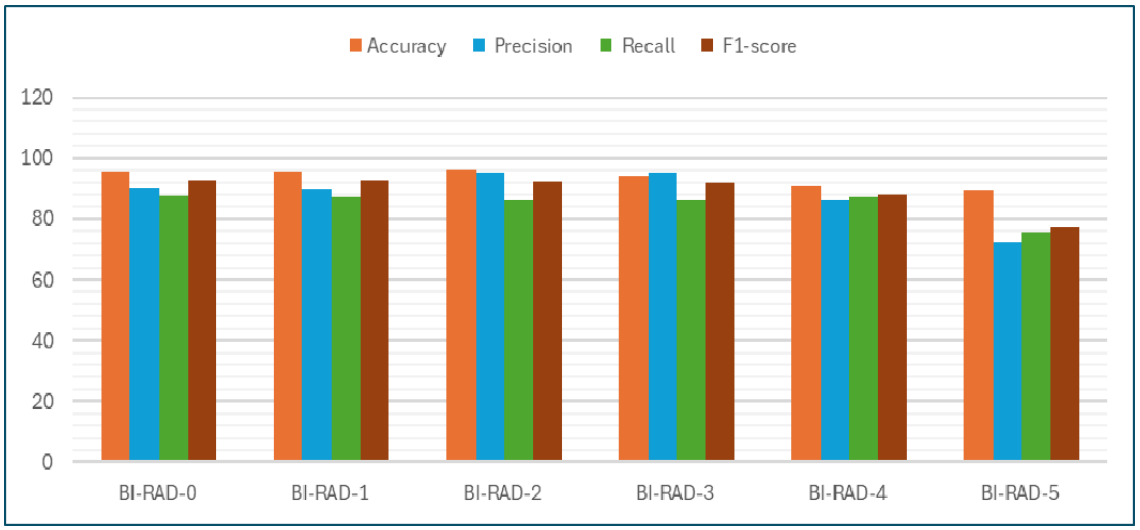


Figure 5-10: Screening performance from the classification based on BI-RADS scoring.

Table 5-17 and **Table 5-20** show the performance of the dataset with the BI-RADS screening with GA, KM++, and the hybrid model GA-KMeans++, respectively. The hybrid model has a significantly higher performance compared to the individual algorithms.

Table 5-17: GA-KM++ for classifying as BI-RADS from our local data set (LMBCDS)

class	Accuracy	Precision	Recall	F1-score
BI-RADS-0	95.67	89.95	87.40	92.80
BI-RADS-1	95.67	89.92	87.36	92.65
BI-RADS-2	96.02	95.34	86.45	92.10
BI-RADS-3	93.86	95.31	86.45	92.00
BI-RADS-4	90.80	86.29	87.00	87.90
BI-RADS-5	89.39	72.43	75.70	77.50

Furthermore, the research conducted a comparative analysis of our method against traditional machine learning approaches, specifically Support Vector Machine (SVM) and Convolutional Neural Networks (CNN). The comparative results, as elaborated in the review of literature (Fuat Türk et al., 2024) and displayed in **Table 2-8** and **Table *2-9***, showcased the commendable accuracy of our hybrid model.

Tables 5-18 and 5-19 describe the accuracy difference between the SVM, CNN, to our model with the locally collected dataset. The table shows that the hybrid model has better results in Accuracy and F1-score.

Table 5-18: Accuracy comparison with different datasets

BI-RADS Class	DDSM dataset		Local dataset		
	SVM	**CNN**	**GA**	**KMeans++**	**GA-KMeans++**
BI-RADS-2	95.06	88.90	94.28	89.25	96.02
BI-RADS-3	91.36	91.36	92.30	89.25	93.86
BI-RADS-4	91.36	84.00	90.50	86.80	90.80
BI-RADS-5	95.06	93.80	89.39	77.10	89.39

Although the research result acknowledges that the datasets and models are not entirely comparable due to differences in methodology and application contexts, the superior performance of our model suggests its potential as an effective tool for screening mammography images by BI-RADS scoring. This capability raises the exciting possibility of reducing reliance on radiologists for preliminary screenings, thereby streamlining the diagnostic process in clinical settings.

Table 5-19: F1-Score comparison

BI-RADS Class	F1-Score				
	SVM	**CNN**	**GA**	**KMeans++**	**GA-KMeans++**
BI-RADS-2	83.30	64.00	86.12	87.80	92.10
BI-RADS-3	66.70	66.70	89.10	87.50	92.00
BI-RADS-4	89.20	80.60	88.45	84.60	87.90
BI-RADS-5	92.30	89.80	88.10	77.00	77.50

Using the DDSM data set, our hybrid model has outperformed the KM++ CSO algorithm. However, using our dataset, the result is less accurate than the other dataset. This shows that the dataset may need further pre-processing or the quality of the data or the size of the data influences the outcome of the result.

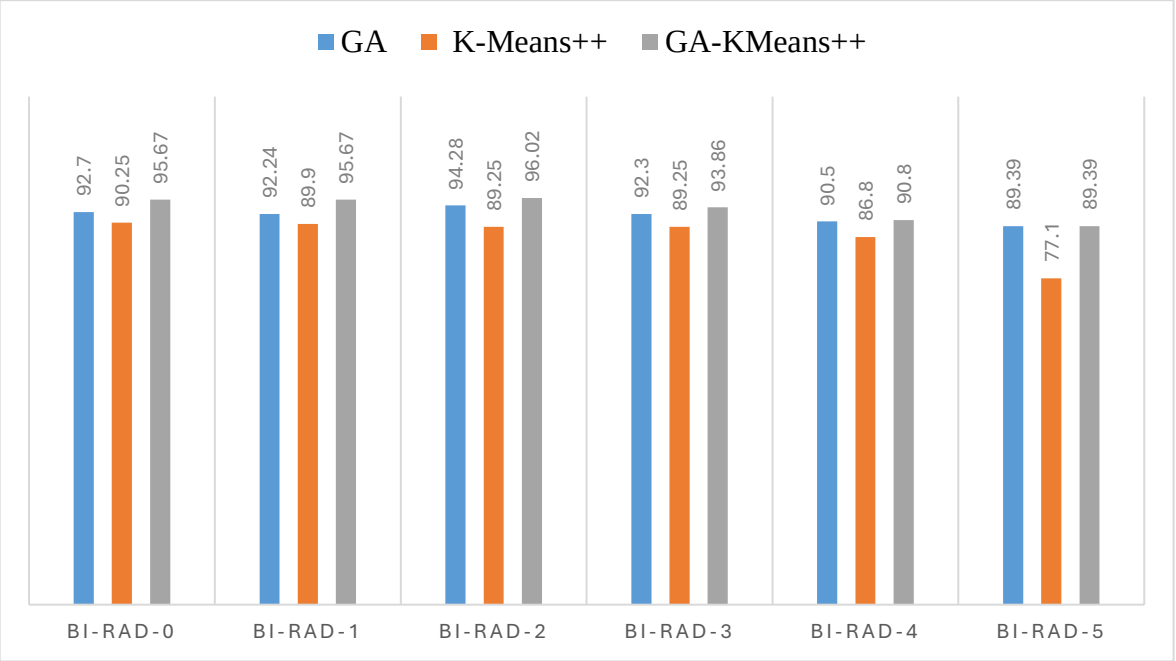


Figure 5-11: Accuracy comparison with GA, K-Means++ and GA-KMeans++

By applying datasets DDSM for the algorithms KM++CSO (Boumaraf, S, et al., 2020) and the algorithms GA, KM++, and GA-KM++ with our dataset and DDSM, the result is shown in **Table 5-20**. The model GA-KM++ has an accuracy of 95.88 and 96.05 with the local data and the DDSM dataset, respectively, which is the highest score from the other methods of classification.

Table 5-20: Performance Comparison of our model with other work.

Method	Dataset	ACC %	SEN %	SPEC %
KM++ CSO	DDSM	95.49	95.68	95.10
GA	DDSM	94.59	95.44	95.20
	Local MBIDS	93.90	94.60	94.90
KM++	DDSM	93.72	95.59	96.26
	Local MBIDS	93.05	94.95	95.02
GA-KM++	DDSM	96.05	96.13	95.94
	Local MBIDS	95.88	95.92	95.67

The **Table 5-21** illustrates the comparison of the result classification of BI-RADS as benign and malignant. As a result, our model has the best accuracy and F1-score from the SVM and CNN, see in **Table 5-22**.

Table 5-21: Benign to malignant classification from the local data with the algorithms

GA, KM++ and the hybrid one GA-KM++

Algorithm	BI-RADS Class	Accuracy	Precision	Recall	F1-Score
GA	Benign	93.92	92.55	92.55	93.00
	Malignant	93.90	94.50	94.50	94.00
KM++	Benign	93.00	87.60	89.94	91.00
	Malignant	93.00	93.50	93.50	93.50
GA-KM++	Benign	95.85	94.80	94.30	95.00
	Malignant	95.95	95.50	94.70	95.30

Table 5-22: Benign to malignant classification from the other data with the algorithms SVM and CNN

Algorithm	BI-RADS class	Accuracy	Precision	Recall	F1-score
SVM	Benign	92.59	90.60	90.60	90.60
	malignant	92.59	93.90	93.90	93.90
CNN	Benign	83.95	78.80	81.30	80.00
	malignant	83.95	87.50	85.70	86.60

5.2 Discussion of the results

5.2.1 Discussion on GAKNN-SVM. -

The above results recognized that the GAKNN-SVM model outperformed the existing KNN and SVM models in terms of accuracy. The results indicate the effectiveness of GA in refining classification models for breast cancer detection.

Our GAKNN-SVM model not only achieved higher accuracy but also exhibited significant improvements in precision, recall, and F1-score, especially in distinguishing between benign and malignant to diagnose breast images.

Table 5-23:Result comparison of machine learning with our model in classifying benign or malignant cases.

Accuracy					
Classification	**SVM**	**CNN**	**GA**	**KM++**	**GA-KM++**
Benign	92.59	83.95	93.92	93	95.85
Malignant	92.59	83.95	93.9	93	95.95

Precision					
Classification	**SVM**	**CNN**	**GA**	**KM++**	**GA-KM++**
Benign	90.6	78.8	92.55	87.6	94.8
Malignant	93.9	87.5	94.5	93.5	95.5

Recall					
Classification	**SVM**	**CNN**	**GA**	**KM++**	**GA-KM++**
Benign	90.6	81.3	92.55	89.94	94.3
Malignant	93.9	85.7	94.5	93.5	94.7

F1-Score					
Classification	**SVM**	**CNN**	**GA**	**KM++**	**GA-KM++**
Benign	90.6	80.0	93.0	91.0	95.0
Malignant	93.9	86.6	94.0	93.5.0	95.3

The model demonstrated enhanced capability in accurately identifying cancerous tissues, accuracy difference registered from 1.93% to 3.26% with our model to classify the image as benign or malignant **Table 5-23**, with a precision improvement ranging from 1.03% to 3.15%. Moreover, the evaluation of the time complexity showed that our GA-enhanced model significantly reduced the computational burden while maintaining high accuracy. By selecting the optimal parameters, it ensured efficient classification with minimal computational resources.

Table 5-24: The accuracy difference between GA-KNN-SVM and other machine learning methods for classifying benign and malignant cases.

Accuracy	**SVM**	**CNN**	**GA**	**KM++**
Benign	3.26%	11.90%	1.93%	2.85%
Malignant	3.36%	12.00%	2.05%	2.95%

The comprehensive analysis of our suggested GAKNN-SVM model shows that it is useful for identifying breast cancer, especially in environments with limited resources. From the **Table 5-24**, the difference between our model and CNN's is significant, but that does not imply that CNN performs poorly in classification. One factor affecting this is the small dataset.

By combining Genetic Algorithm with KNN and SVM classifiers, it offers a viable method to improve diagnostic precision, which may help with breast cancer early

detection and therapy. To sum up, it provides advantages like interpretability, computational efficiency, and appropriateness for smaller datasets, but other machine learning algorithms could be superior in areas like robustness, scalability, or user-friendliness. On the other hand, Deep Learning algorithms are excellent at handling big datasets, learning features automatically, and performing at the forefront of challenging tasks. The choice between these approaches depends on factors such as the nature of the problem, available data, computational resources, and the need for interpretability versus performance. The trade-off of the model with other ML techniques is described in **Table 5-25**.

Genetic Algorithms (GA) play a crucial role in pinpointing the most relevant features within a dataset. By leveraging refined evolutionary search techniques for feature selection and parameter optimization, GAs significantly enhance classification performance. This method not only improves accuracy but also streamlines the model-building process, making it an invaluable tool for data scientists striving to unlock the full potential of their data.

Table 5-25: Trade of ML with the GA-KNN-SVM

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 exceedingly difficult to acquire in the Ethiopian situation (privacy, rural nature, internet disruption, cloud facilities, economics).
Interpretability 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 often operate as "black boxes," making it challenging to interpret the learned representations and decision-making process.
Data Requirement and Performance:	Effective with smaller datasets and can achieve satisfactory 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 at the cost of accuracy.	Deep learning algorithms typically require substantial amounts of labeled data to train effectively, but they can achieve state-of-the-art performance on complex tasks given sufficient data.
Computational Efficiency	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	Robustness and generalization capabilities vary; some algorithms	Deep learning models have the potential for high generalization but can be prone to overfitting,

	optimized, but may suffer from over-fitting if not carefully tuned.	may be more robust to noise and outliers, while others may require careful regularization to avoid over-fitting.	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 were under- standing 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 behaviour 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.

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 exceedingly difficult to acquire in the Ethiopian situation (privacy, rural nature, internet disruption, cloud facilities, economics).

5.2.2 Discussion on PMP. -

The classification accuracy analysis has been performed before the implementation of the genetic algorithm with PMP. Machine learning algorithms such as linear regression and support vector machines exhibit superior accuracy, indicating better performance. After PMP implementation, logistic regression achieves the highest detection accuracy of 99.42%, a notable improvement. Ada-Boost emerges as the top post-preprocessing algorithm, achieving the highest F1 score. PMP results in substantial accuracy improvements across algorithms. In this case, highlight the effectiveness of PMP to optimize the genetic algorithm fitness evaluation. The findings underscore the potential of AI-driven approaches, particularly genetic algorithms with PMP, enhancing breast cancer detection accuracy. As shown in **Table 5-26** In the cases of the classification algorithms, working on GA with PMP has improved performance by up to 2.39%.

Table 5-26: Accuracy before and after the implementation of PMP

Algorithm	Accuracy before PMP	Accuracy after PMP	Difference
LR	97.07	99.42	2.392%
GB	95.91	97.66	1.808%
SVM	96.50	98.24	1.787%
DT	92.40	93.57	1.258%
KNN	95.91	96.49	0.603%
RF	97.08	96.50	-0.599%
AB	97.67	96.50	-1.205%

Despite the improvement of some classification algorithms, there is a degradation in performance. So, the researcher must be selective in using classification algorithms to implement PMP. For the sake of illustration and better insight, the accuracy of various ML classifiers before and after applying PMP is shown in **Figure 5-12.**

The F1 score and Precision before and after applying PMP are shown in **Figure 5-13**

after using our mathematical model to find the fitness LR that has the highest F1 score. The results underscore the potential of AI-driven methodologies, specifically the combination of GA with PMP, in improving breast cancer detection accuracy. This approach optimizes classification algorithms, yielding higher accuracy and better detection capabilities. In general, the study demonstrates the efficacy of integrating PMP with GA, significantly enhancing the performance of various machine learning algorithms in the detection of breast cancer, with logistic regression showing the most substantial improvement.

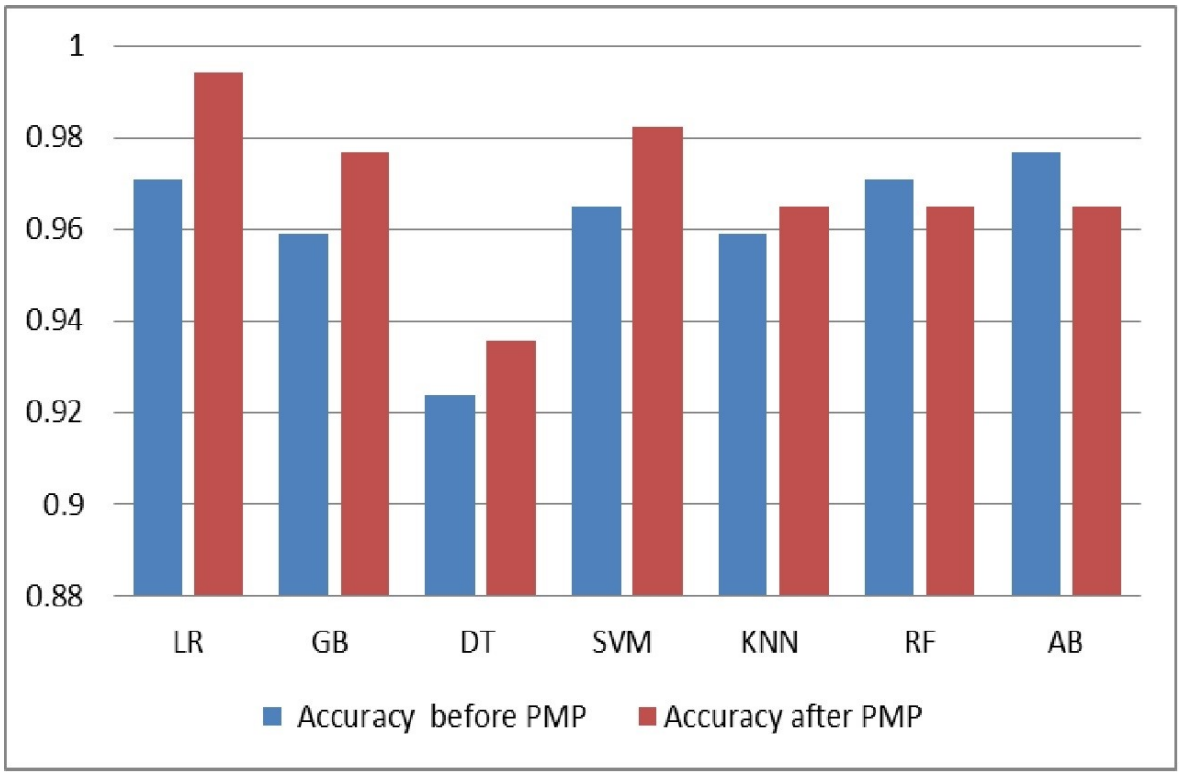


Figure 5-12: Before and after the implementation of PMP in GA fitness evaluation

The major findings from this model work are:

1. Substantial Accuracy Improvements: Logistic Regression (LR) achieved a remarkable detection accuracy of 99.42% post-PMP implementation, highlighting the effectiveness of the proposed method in optimizing classification algorithms.
2. Practical Implications for Clinical Settings: The improved accuracy and computational efficiency of the models can significantly impact clinical outcomes by enabling earlier and more precise breast cancer diagnoses, potentially leading to better patient care and prognosis.
3. Optimization of Feature Selection: The integration of PMP into GA helps in

enhancing the feature selection process, optimizing model accuracy, and scalability while reducing the computational burden, thus addressing critical challenges in machine learning-based medical diagnosis.

By demonstrating the effectiveness of AI-driven approaches, specifically the combination of GA and PMP, this research provides a promising avenue for enhancing the accuracy and reliability of breast cancer detection models. The findings have significant implications for clinical practices, offering a robust framework for integrating advanced computational techniques into medical diagnostics.

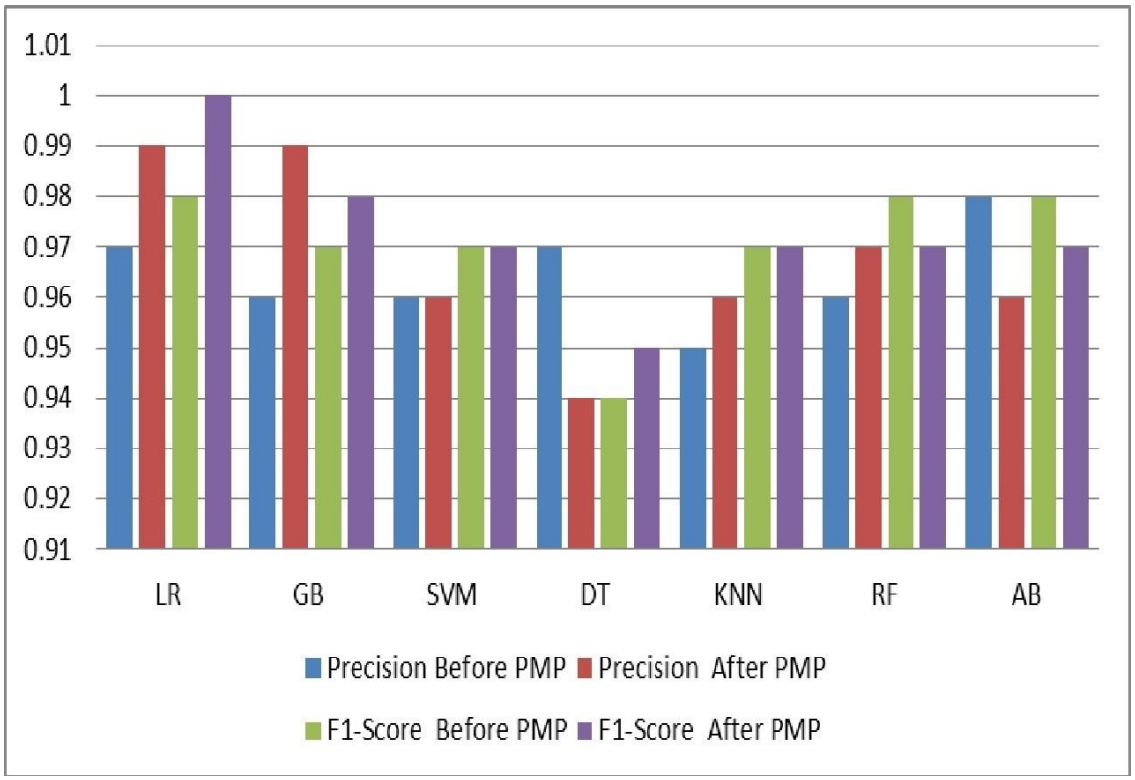


Figure 5-13: Before and after the implementation of PMP in GA fitness evaluation

Table 5-27: Comparison with ML, GA, GA-KNN-SVM and GA-PMP

Algorithm	Classification with ML	Accuracy before PMP with GA	Accuracy after PMP	Difference
LR	96.5035	97.07	99.42	2.392
GB	95.8042	95.91	97.66	1.808
SVM	95.8042	96.50	98.24	1.787
DT	93.0070	92.40	93.57	1.258
KNN	96.5035	95.91	96.49	0.603
RF	97.2028	97.08	96.50	-0.599
AB	95.1049	97.67	96.50	-1.205

Based on the information in **Table 5-27** most machine learning algorithms exhibit

lower performance when used to classify data in their standard form compared to when they are hybridized with Genetic Algorithms (GA) before the implementation of the Pontryagin Minimum Principles (PMP) method. In contrast, machine learning algorithms that have been combined with GA and modified using PMP demonstrate improved performance. The performance difference ranges from -1% to 2.39%.

5.2.3 Discussion on GA-K-Means++. -

The study has developed a computational intelligence model to screen, analyze, and interpret mammography images to detect potential breast abnormalities. Our prepared BI-RADS dataset provides a comprehensive and standardized collection of mammography images for training and testing the model. This model aims to enhance the accuracy and efficiency of breast cancer screening by utilizing computational methods to aid radiologists in the early detection and diagnosis of breast abnormalities. The goal of this research is to assess the stage of the breast image based on the BI-RADS scoring, thus streamlining the screening process and reducing the requirement for specialized resources and time. Additionally, it aims to provide patients with immediate information about their results.

Our study involved a comprehensive comparison of results obtained from various methods and models applied to the mammography image dataset. Through the analysis observed that the hybrid model developed exhibited superior performance in screening patients based on their BI-RADS images. However, the researchers believes that further optimization and data cleaning are necessary to enhance the efficacy of the approach. This is due to the varying performance levels observed in the accuracy of screening when employing algorithms such as GA and K-Means++.

GA-K-Means++ receiving an F1-Score of 92.10% and accuracy of 96.02% in BI-RADS-2 minimizes false negatives and false positives, empowering radiologists to accurately assess and categorize patients based on their criticality stages. The cases of BI-RADS-4 and 5 showed that the accuracy of the results decreased compared to BI-RADS-2, which is due to the data size. For such cases, it can use the balancing method to check the consistency of the accuracy. This remarkable precision not only enhances diagnostic confidence but also ensures timely and effective patient care.

CHAPTER SIX

6 CONCLUSION and FUTURE WORK

6.1 Conclusion

AI and deep learning technologies have had a significant impact on illness prediction and detection. Despite these advances, overall survival rates for breast cancer patients have not improved significantly. As a result, it becomes increasingly evident that early detection is crucial for reducing death rates. Previous research has shown that a hybridized model containing a genetic algorithm produces greater outcomes. However, it is important to emphasize that further study is needed to improve the early diagnosis of whether a tumour is malignant or benign. Notably, genetic algorithms outperform deep learning models because they may achieve satisfactory performance using fewer datasets and features and need fewer computer resources. The hybrid computational model, GAKNN-SVM, has been proven to deliver significantly enhanced accuracy, highlighting its potential to advance breast cancer research and diagnostic capabilities.
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 Breast Cancer Detection: In the context of breast cancer detection, integrating GA with KNN and SVM offers several benefits:

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 tumour, aiding in quick

and resilient medical decision-making for a resource-constrained environment.

The incorporation of Pontryagin's Minimum Principle (PMP) into Genetic algorithms (GA) resulted in a significant improvement in detection accuracy and the F1 scores matrix across multiple classification techniques. These factors contribute to a more accurate breast cancer diagnosis. The research process is adopted with practical consequences for clinical settings and the potential to improve patient outcomes by allowing for earlier and more accurate diagnosis.

GA with PMP significantly improves the computational efficiency of breast cancer detection models. In other words, make them appropriate for real-world clinical applications that need high accuracy within tolerable periods. This methodological innovation results in significant gains in the accuracy and F1-score of several classification algorithms, highlighting their ability to give more trustworthy breast cancer diagnoses.

Analyzing the algorithms of several genetic operators can produce the greatest results. The method might be tailored to handle the optimization issue effectively and efficiently by carefully choosing the values of the parameters. It is necessary to strike a balance between the necessity of a comprehensive search and realistic limitations on computing time and resources. The performance of machine learning models has been improved by the creative combination of PMP and GA. The results are promising, and this study has the potential to enhance medical diagnosis.

GA with the K-means++ model plays a crucial role in analyzing patients' breast mammography image data. This model assists radiologists in making informed decisions based on the image data. Most of the data observed at the diagnosis center are classified as BI-RADS 1 and 2, indicating no need for further diagnosis to allow patients to leave the center directly. Additionally, the research can determine whether the image is malignant or benign, providing valuable support to medical doctors in guiding patient consultation. While currently employing preprocessing tasks such as resizing, grayscale conversion, normalization, and noise reduction, the results suggest that further optimization processes and data cleaning could further enhance the work.

The study answers the first question by the model GA-KNN-SVM, strategically tackles the pivotal research question: "What models improve the accuracy and reliability of classifying breast tumours as benign or malignant?" It also delves into the crucial inquiry: "What models can be employed to improve the accuracy of early breast tumours detection?" The findings reveal that this innovative model outperforms other machine learning techniques and surpasses the current state of the art, showcasing its

effectiveness in the realm of breast cancer detection.

Building upon the foundation laid by the first model, the second approach, modified GA with PMP, refines and enhances the existing genetic algorithm (GA). This thoughtful modification empowers the first model to play a pivotal role in the fitness evaluation during the objective selection process. This strategic influence significantly improves feature selection for classifying breast images, offering a robust advantage in the early detection and classification of tumour. Consequently, this leads to a marked reduction in both false positives and false negatives, enhancing the reliability of diagnoses.

The third research question probes into the methodology of determining the level of breast tumour through the established BI-RADS scoring system. Complementing this inquiry, the fourth question explores the processes involved in preparing a digital dataset for analysis by advanced technology-driven systems. Addressing these essential queries is the final model, GA-Kmeans++, which exhibits an impressive ability to categorize images per the BI-RADS scoring criteria, offering substantial performance benefits. This capability proves to be invaluable for radiologists, as it supports them in making informed decisions regarding patient diagnoses while significantly curtailing unnecessary interventions and minimizing errors in positive diagnoses.

In summary, the suite of models developed in this study effectively and comprehensively addresses the salient research questions, paving the way for improved outcomes in breast cancer diagnosis and treatment.

6.1.1 Strengths of the Study. -

- Improved Accuracy and Efficiency: The proposed algorithm demonstrates substantial improvements in classification accuracy, achieving up to 99.42% with Logistic Regression and with others as well. This prominent level of accuracy is crucial for reliable breast cancer detection.
- Innovative Integration of PMP with GA: The study introduces a novel approach by integrating Pontryagin's Minimum Principle (PMP) with Genetic Algorithms (GA), significantly enhancing the performance of machine learning models, specifically tested in this study for breast cancer detection.
- Comprehensive Performance Evaluation: The study thoroughly evaluates the performance of multiple machine learning models before and after the

integration of PMP with GA, providing a clear comparison of the improvements achieved.

- Practical Implications for Clinical Settings: The enhanced accuracy and computational efficiency of the proposed method make it viable for real-world clinical applications, potentially improving early and accurate breast cancer diagnoses.
- The research presents a robust concept aimed at providing radiologists with the ability to effectively screen and categorize patients into BI-RADS groups 1 to 2, and so on, which represent the majority within this classification. It is important to highlight that BI-RADS-0, according to the senior radiologist's comments, was indicated to be incomplete or not easily interpretable.
- Consequently, this work encourages further exploration of the developed model and dataset to facilitate breast image screening, enabling the identification of image stages and the provision of information to patients before further diagnostic prescriptions are made.
- Robust Framework for Future Research: By laying the groundwork for further exploration of genetic algorithms by hybridizing with machine learning algorithms as KNN and SVM in our model and PMP in medical diagnostics, the study opens avenues for future research to optimize and refine these methods.

6.1.2 Weakness of the Work. -

The complexities of our research methodology, coupled with the inherent limitations related to the diversity of the dataset and the considerable computational demands, underscore crucial areas that merit further exploration and enhancement.

One of the most significant challenges in the study process faced was stemmed from budgetary constraints, which limited our capacity to involve a wider array of domain experts. Their specialized knowledge would have been instrumental in very carefully annotating the image data, offering professional insights, conducting evaluations in real-world contexts, demonstrating the practical implications of our findings, and identifying potential gaps within the research landscape.

Furthermore, expanding the diversity of our dataset by incorporating additional samples from various diagnostic centers is likely to yield more distinctive and comprehensive results.

While our application of genetic algorithms explored diverse methods of selection,

mutation, and crossover, these elements were not examined interchangeably in depth. Consequently, there may exist more effective strategies to address the complexities surrounding breast cancer diagnosis.

The k-fold cross-validation employed in our K-Nearest Neighbors (KNN) analysis proved insufficient for a thorough examination of overfitting and underfitting; illustrating this concept diagrammatically, leveraging advanced computational resources, would further clarify our findings.

Additionally, our attempts at DICOM image preprocessing did not achieve success through different methodologies, which should have undergone rigorous evaluation to identify the most effective approach. The authors only explored the imbalance scenario through correlation analysis; however, employing a range of methods could lead to more favorable outcomes.

Breast cancer detection can be approached through a myriad of methods, including calcification types such as diffuse, regional, grouped, linear, and segmental; mass characteristics related to shape, margin, and density; and additional considerations like breast size and asymmetry, both focal and global. Moreover, associated features including segmental characteristics, skin retraction, nipple retraction, skin thickening, and the various categories within BI-RADS classifications (A, B, C, D), further enrich the diagnostic landscape. Although the researcher organized the documents based on constructive discussions with domain experts, limitations in time and resources necessitated a narrower focus for this study, specifically centering on calcification and BI-RADS criteria.

However, the study predicts that by broadening the research to encompass additional identification types and processes, it to be possible to attain results that not only meet but exceed industry standards for accuracy and reliability. Each of these limitations in the study simultaneously represents opportunities for further inquiry within the field.

6.2 Future work

Future research could explore different genetic operators, selection algorithms, and crossover methods within GA to further optimize and enhance the results. This study did not delve into these areas, indicating potential for further improvements and refinements in the methodology. Due to the advantages of the GA, there is a strong recommendation to examine deeper into exploring genetic algorithms for optimizing classification and feature selection. Furthermore, the researcher suggests that

researchers consider our results as a baseline for future studies.

Access to robust computational resources is indispensable to effectively expanding the scope and applicability of this study. For our analytical processes, we utilized online platforms such as Kaggle and Google Colab, which were instrumental in allowing us to navigate various parameters and methodologies for result assessment without encountering significant constraints.

Nevertheless, for a research initiative of this scale that involves extensive image processing tasks, it is strongly recommended to establish a fully equipped computer laboratory; this is taken as a weakness for the study. This dedicated facility would not ensure that it has adequate resources available for the crucial phases of pre-processing, training, testing, and validation, as well as for the examination of real-world cases.

Future research should explore deeper into the roles of genetic algorithms (GA) and Pontryagin minimum principles (PMP) in the pursuit of computationally optimal solutions across various domains. While this study did not investigate the modification of selection algorithms within GA methods or assess the effectiveness of different crossover and mutation techniques, it is essential to recognize that optimizing these parameters could unlock new potentials in GA applications. By refining these key components, future investigations may uncover substantial advantages of using GA for the early detection and prediction of breast cancer, significantly enhancing diagnostic accuracy and patient outcomes. Moving forward, future efforts must prioritize the optimization of selection methods within GA to bolster performance in image processing tasks, particularly when computational resources are constrained.

Collaboration with domain experts is crucial not only for validating the results in real-world clinical environments but also for ensuring that the model can be effectively integrated with state-of-the-art imaging devices. This integration would enable real-time predictive outputs, providing significant support to healthcare professionals during diagnostic procedures.

In summary, future research should concentrate on refining locally organized datasets, rigorously testing the model through a systematic variation of GA selection, crossover, and mutation methods. Additionally, validating objective functions will be critical to effectively address fitness challenges during population selection, utilizing a diverse range of parameters. Finally, fostering collaborations with domain experts and integrating the model with advanced imaging systems will be vital steps toward translating these research findings into practical applications that improve breast cancer detection and treatment.

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Appendix: Publications

1. Genetic Algorithm-optimized k-nearest Neighbors and Support Vector Machines for Breast Cancer Detection in Resource-constrained Environments.
    a. Journal: International Journal of Computer Science (IJCS)
    b. Publisher: IAENG
    c. Date and Year: Volume 52, Issue 3, March 2025, Pages 848-861
2. Modified genetic algorithm using Pontryagin's minimum principle to optimize feature selection and classification for breast cancer detection.
    a. Journal: Iran Journal of Computer Science
    b. Publisher: Springer, Received: 25 April 2024 / Accepted: 6 August 2024 © The Author(s), under exclusive license to Springer Nature Switzerland AG 2024
    c. Published online 28 August 2024.
    d. https://doi.org/10.1007/s42044-024-00204-w
3. A Hybrid Genetic Algorithm with a K-Means++ Clustering Model to Accurately Determine BI-RADS Scoring for Breast Mammography Image Screening
    a. Journal
    b. Publisher: J. Electrical Systems 20-10s (2024): 7866-7884
    c. Date, November 2024.

Breast Image data screening as BI-RAD Project Using Local Breast Cancer Image Dataset.

This reseach is the part of PhD deseration work

Author, data collected by and analysi edby :

Abebe Alemu Adama Science and Technology University Ethiopia

First of Thank you for the Diagnosis center: Pinnoree Diagnosis Clincale center.

Jun 2024.

```
This breast cancer data set is collected from Pinor diagnosis center. Thank you Pinor. The process has bee done as
prepreoscssing feature extraction and selection. and then using K-means and GA train the data for predection. We have got a
total of 4890 mamography image data. The iamge view is CC and MLO both breast cancer. it has different density, size and BI-RAD
classificaion. The data has a senior radiologist sumamry report for each of the data. Here we categorized based on the BI-RAD
stage as 0-6. teh radiologis give the description of the Bi_RAD as follows
```

This project is only the image data set

Data Exploration

In [1]:
```
from tqdm import tqdm
```

In [2]:
```
#importing all the neccasry laibrary
import pandas as pd
import numpy as np
import cv2
import PIL
import matplotlib.pyplot as plt
import plotly.express as px
import seaborn as sns
import glob
import random
import os
from os import listdir
random.seed(100)
np.random.seed(100)
import PIL.Image
import tensorflow as tf
import tensorflow_datasets as tfds
```

Read the data from the file dicom_info, which has details of the data information.

Read csv data from the file

the collected raw data is put in Dicom image format. I am using the software RadiAnt Dicom Viewer 64 Bit windows versssion. The data This file is from the data annotated, sumarized and take sample 504 image data from 5276 image datas.

Export the Image description from teh RadiAnt database and saved as in CSV format, read from the file and here it is.

In [3]:
```
RadiAnt_info=pd.read_csv('C:/Users/Spectre/Documents/AbebePersonal/ASTU_PhD_Works/Experiment/BC_Exp_from_kaggle/BI_RAD/BC_loc
```

In [4]:
```
RadiAnt_info.head()
```

Out[4]:

	No	PID	ImageID	Mammographic_view	Mass_Density	Cal_MB	BI_RAD	Final-Assesment	Recommondation
0	1	98098ALEM2	IMG-0001-00001	CC	High	0.0	BI-RAD-2	Bilateral breast mammography	Annual screening mammography
1	2	98098ALEM2	IMG-0001-00002	CC	High	0.0	BI-RAD-2	Bilateral breast mammography	Annual screening mammography
2	3	98098ALEM2	IMG-0001-00003	MLO	High	0.0	BI-RAD-2	Bilateral breast mammography	Annual screening mammography
3	4	98098ALEM2	IMG-0001-00004	MLO	High	0.0	BI-RAD-2	Bilateral breast mammography	Annual screening mammography
4	5	98098ALEM2	IMG-0002-00001	CC	High	0.0	BI-RAD-2	Bilateral breast mammography	Annual screening mammography

In [5]:
```
RadiAnt_info.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4092 entries, 0 to 4091
Data columns (total 9 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   No                 4092 non-null   int64
 1   PID                4092 non-null   object
 2   ImageID            3260 non-null   object
 3   Mammographic_view  2389 non-null   object
 4   Mass_Density       1975 non-null   object
 5   Cal_MB             370 non-null    float64
 6   BI_RAD             2069 non-null   object
 7   Final-Assesment    371 non-null    object
 8   Recommondation     2187 non-null   object
dtypes: float64(1), int64(1), object(7)
memory usage: 287.8+ KB
```

In [5]:
```
RadiAnt_info.describe()
```

Out[5]:

	No	Cal_MB
count	4092.00000	370.000000
mean	2046.50000	0.251351
std	1181.40303	0.434377
min	1.00000	0.000000
25%	1023.75000	0.000000
50%	2046.50000	0.000000
75%	3069.25000	0.750000
max	4092.00000	1.000000

In [6]:
```
#Here it shows the total number of the Uniqe patcient image
no_class=len(RadiAnt_info)
print("The number of image data labled as BI-RAD 0 to 5 and other data",no_class)
```

```
The number of image data labled as BI-RAD 0 to 5 and other data 4092
```

Read the breast image data, classifed by BI-RAD including Other data

In [7]:
```
# The data set is Categories by BI-RAD
BIRAD0=0
BIRAD1=0
BIRAD2=0 # None cancer image data
BIRAD3=0  # cancer image data
BIRAD4 = 0 # Other data not 1 or 0
BIRAD5 = 0 # Other data not 1 or 0
other = 0
nodata= len(RadiAnt_info)
for img in range(0,nodata):
    if RadiAnt_info.BI_RAD[img] == 'BI-RAD-0' :
        BIRAD0 = BIRAD0 + 1
    elif RadiAnt_info.BI_RAD[img] == 'BI-RAD-1' :
        BIRAD1 = BIRAD1 + 1
    elif RadiAnt_info.BI_RAD[img] == 'BI-RAD-2' :
        BIRAD2 = BIRAD2 + 1
    elif RadiAnt_info.BI_RAD[img] == 'BI-RAD-3' :
        BIRAD3 = BIRAD3 + 1
    elif RadiAnt_info.BI_RAD[img] == 'BI-RAD-4' :
        BIRAD4 = BIRAD4 + 1
    elif RadiAnt_info.BI_RAD[img] == 'BI-RAD-5' :
        BIRAD5 = BIRAD5 + 1
    else: other = other + 1
img+= img
print(" Total number of BI-RAD 0  " + str(BIRAD0))
print(" Total number of BI-RAD 1  " + str(BIRAD1))
print(" Total number of BI-RAD 2  " + str(BIRAD2))
print(" Total number of BI-RAD 3 " + str(BIRAD3))
print(" Total number of BI-RAD 4  " + str(BIRAD4))
print(" Total number of BI-RAD 5  " + str(BIRAD5))
print(" Total number of other " + str(other))
total_BIRAD_data = BIRAD0 + BIRAD1 + BIRAD2 + BIRAD3 + BIRAD4 + BIRAD5 +  other
print(" Total number of data " + str(total_BIRAD_data))
```

```
 Total number of BI-RAD 0  382
 Total number of BI-RAD 1  367
 Total number of BI-RAD 2  314
 Total number of BI-RAD 3 740
 Total number of BI-RAD 4  189
 Total number of BI-RAD 5  77
 Total number of other 2023
 Total number of data 4092
```

In [8]:
```
data_BIRAD_1 = pd.DataFrame({'State of BIRAD' : ['BI_RAD_0','BI_RAD_1','BI_RAD_2','BI_RAD_3','BI_RAD_4','BI_RAD_5', 'other'],
```

In [9]:
```
bar = px.bar(data_frame=data_BIRAD_1, x = 'State of BIRAD', y='Numbers of Images', color='State of BIRAD')
bar.update_layout(title_text='Number of Images with BI-RAD calssification', title_x=0.5)
bar.show()
```