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A Genetic Algorithm based Hyperparameter Tuning of Convolutional Neural Networks for Breast Cancer Detection

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ABSTRACT: Breast cancer is the second most diagnosed cancer in women, affecting one in every eight women in the U.S., and the leading cause of cancer mortality in women around the world. Breast cancer can be controlled effectively by early diagnosis and effective treatment. Various scientific studies have been conducted to combat this disease, and deep learning approaches have been an extremely popular choice. Deep Learning techniques can be used to classify breast cancer such as convolutional neural networks (CNNs) which have shown promising results due to their classification capabilities on learned feature methods and ability to work with complex images. The hyperparameters of the network, including the learning rate, epochs, batch size, optimizers, and dropout rate, play a crucial role in the classification accuracy of a convolutional neural network (CNN) model. Manually tuning these hyperparameters is time-consuming and often ineffective. The study proposes a novel genetic algorithm (GA) based hyperparameter tuning methodology for improving the performance of convolutional neural networks (CNNs) for breast cancer detection tasks. Genetic algorithm (GA) is an optimization algorithm inspired by "Darwin's Theory of Evolution in Nature." It is a population-based search algorithm, which utilizes the concept of survival of the fittest. The genetic algorithm (GA) evolves a population of candidate hyperparameter sets, on a fitness function designed to optimize detection accuracy. Employing Darwinian principles, the genetic algorithm (GA) implements an evolutionary search that refines hyperparameters, progressively enhancing convolutional neural network's ability to localize cancerous tissue accurately. We evaluate our model through various experiments on the BreakHis dataset. Our findings suggest that employing genetic algorithm-based optimization within CNNs holds immense potential for enhancing breast cancer detection accuracy, potentially leading to earlier diagnoses and improved patient outcomes.

KEYWORDS: CNN, BreakHis, Genetic Algorithm, Hyperparameter Tuning

I. INTRODUCTION

Breast cancer is a major health concern and the most prevalent cancer among women globally. Around one in eight women will be diagnosed with breast cancer during their lifetime. "There are more than 2.3 million cases of breast cancer that occur each year, which make it the most common cancer among adults. In 95% of countries, breast cancer is the first or second leading cause of female cancer deaths" says World Health Organization (WHO). Early diagnosis of this disease increases the chance of efficient treatment[1]. It is also important to note that breast cancer can even affect men, although it is less common. Breast cancer is a condition where cells in the breast grow uncontrollably. There are various types of breast cancer, depending on which cells in the breast become cancerous. Most breast cancers begin in the ducts and lobules. One of the most common misunderstanding is that if you don't have a family history of breast cancer, you're not at risk. Although most people diagnosed with breast cancer do not particularly have a family history, genetics aren't the only cause. Spreading awareness and taking precautions is crucial. Early detection through regular screenings and self-exams is key in improving survival rates. While self-examining if you find any lumps, redness, irritation, pain in any area of the breast or nipples, changes in size and shape, thickness or swelling in your breast, one must consider visiting a doctor for diagnoses and detection of the type of cancer. The doctor then performs certain tests such as ultrasound and mammography tests. After performing mammography and ultrasound imaging, if we find any abnormal tissues, a biopsy examination is necessary. In a biopsy test, a small sample of breast tissue is placed under a microscope to obtain histopathological images for further investigation. Some of the most common methods for early detection of breast cancer are mentioned below.

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Biopsy
While imaging tests like CT scans and MRIs can spot unusual lumps or tissues, they can't tell for sure if they're cancerous. That's where biopsies come in. A biopsy is a procedure where a small sample of cells or tissue is taken from the suspicious area. This sample is then examined under a microscope by a specialist to determine if cancer is present. In other words, a biopsy is the key to unlocking a definitive cancer diagnosis, even though imaging tests provide valuable clues beforehand.

Mammogram
A mammogram is an X-ray picture of the breast that can detect tumors or abnormalities in the breast tissue. Doctors use a mammogram to look for early signs of breast cancer that can detect tumors or abnormalities in the breast tissue.

Ultrasound
Ultrasound imaging, also known as ultrasonography or sonography, utilizes high-frequency sound waves to generate real-time visualizations of internal organs, tissues, and structures within the body.

Magnetic Resonance Imaging (MRI)
Magnetic Resonance Imaging (MRI) may be a restorative imaging test that produces nitty gritty pictures of nearly every internal structure within the human body, counting the organs, bones, muscles, and blood vessels. Magnetic Resonance Imaging (MRI) scanners make pictures of the body employing a huge magnet and radio waves. Non-ionizing radiation is delivered amid a Magnetic Resonace Imaging (MRI) exam, unlike X-rays. These pictures provide your doctor with vital data in diagnosing your therapeutic condition and arranging a course of treatment.

3-D Mammography
3-D Mammography also known Tomosynthesis test, it takes X-ray images of breast from different angles and combines them into a 3-D structure of breast for examination.

In this study, we use deep learning methods and propose a system for detecting whether the cancer is benign or malignant using breast cancer histopathological images. Extracting necessary features plays an important role in image classification. Deep learning methods have the ability to extract suitable and high-level features from the images. Based on this ability and the considerable accuracy of deep learning methods in pattern recognition, we construct the proposed system based on deep learning. Deep learning has been increasingly applied in mammographic imaging, with convolutional neural networks (CNN) being the most popular type of architecture. Here, we focus on convolutional neural networks (CNN) to analyse and train the model to detect the type of cancer because convolutional neural networks (CNNs) have shown promising results in various medical imaging applications for breast cancer diagnosis in many of the recent research papers. To enhance the performance of our model we optimize the hyperparameters. In hyperparameter optimization, the challenge lies not only in finding an accurate model, but also in achieving that accuracy within a practical timeframe. Hence, we use genetic algorithm (GA) to optimize these hyperparameters to obtain better results. Genetic algorithms are search algorithms based on the mechanics of natural selection and natural genetics. “Our proposed methodology mainly focuses on finding the potential hyperparameter values of the convolutional neural network using genetic algorithm and evaluating the performance of the convolutional neural network for breast cancer detection.” [18]

II. LITERATURE SURVEY

Tehnan I.A. Mohamed et al.,[1] proposed a Bio-inspired Convolution Neural Network model for breast cancer classification. The proposed model is a combination of CNN architecture with the Ebola Optimization Search Algorithm (EOSA) which enhanced the cancer detection. This approach used the Breast Cancer gene (BRCA) Gene Expression database and achieved an accuracy of 95%.

Many studies utilize the Breast Cancer Wisconsin Data and achieved good results in two classes (benign and malignant), including Mukesh Kumar et al.,[2] Combined multiple classification algorithms (AdaBoostM1, Gradient Boosting, Stochastic Gradient Boosting, CatBoost, XGBoost) through stacking algorithm to reduce overfitting and improve generalizability compared to single models and achieved an accuracy of 99%.

Vijayalakshmi S et al.,[3] proposed a multi-modal prediction algorithm for breast cancer using particle swarm optimization, non-dominating sorting (PSO-NDS), and multi-classifier techniques. The model used advanced machine learning techniques such as PSO-NDS, Bayesian inference, and multi-classification, contributing to the accuracy of

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breast cancer predictionand diagnosis. This study used a Wisconsin Breast Cancer Dataset (WBCD), Wisconsin Diagnostic Breast Cancer (WDBC) Dataset that achieved 98% accuracy.

Sanaz Karimi Jafarbigloo et al.,[4] used convolutional neural networks (CNN) and long short-term memory network (LSTM) for grading nuclear atypia in breast cancer histopathological images. This approach used CNN for feature extraction and LSTM for classification and obtained an accuracy of 86%.

Muhammet Fatih Ak.,[5] studied different machine learning and data mining techniques for the detection of breast cancer. They applied Logistic Regression, K-Nearest Neighbour, Support Vector Machine, Naïve Bayes, Decision Tree, Random and Rotation Forest on Wisconsin Breast Cancer (Diagnostic) Dataset. The results showed that with the logistic regression model with all features included showed the highest classification accuracy 98.1%.

Meha Desai et al.,[6] compared the multi-layer perceptron (MLP) and convolutional neural networks (CNN) using BreakHis dataset. The studies showcased CNNs achieving significantly higher accuracy than MLPs 97%.

Reza Rabiei et al.,[7] also compared Random Forest, Neural Networks (MLP), Gradient Boosting Trees (GBT), Genetic Algorithms (GA) on data collected from a clinical breast cancer research center (Motamed cancer institute) in Tehran, Iran. The results showcased that RF presented higher performance compared to other techniques 80%

Basem S et al.,[8] proposed a framework based on deep learning Xception Algorithm for breast cancer detection and classification. The proposed model classifies 8 different cancers such as benign adenosis, benign fibroadenoma, benign phyllodes tumor, benign tubular adenoma, malignant ductal carcinoma, malignant lobular carcinoma, malignant mucinous carcinoma, and malignant papillary carcinoma. This approach used the BreakHis dataset and achieved an accuracy of 97%.

A network of three parallel convolutional neural networks (CNN) branches (3PCNNB-Net) was proposed by Amira Mofreh Ibraheem1 et al.,[9] for classification of breast cancer through histopathological images. The proposed network consists of 3 stages where the first stage consists of 3 parallel CNN branches with deep residual blocks. The second stage consist of a feature fusion path which was created by merging the 3 parallel CNN branches and third stage is used to classify the fused features. The proposed model was evaluated on breakhis dataset and achieved an accuracy of 97.14%.

Basem S Abunasser et al.,[10] proposed a deep learning model (BCCNN) to detect and classify breast cancers into eight classes: benign adenosis (BA), benign fibroadenoma (BF), benign phyllodes tumor (BPT), benign tubular adenoma (BTA), malignant ductal carcinoma (MDC), malignant lobular carcinoma (MLC), malignant mucinous carcinoma (MMC), and malignant papillary carcinoma (MPC). The proposed BCCNN model is compared with 5 fine-tuned Deep learning models consisting of Xception, InceptionV3, VGG16, MobileNet and ResNet50 by evaluating on breakhis database. The results showed that the proposed model achieved the highest accuracy of 98.28%.

Khatereh Davoudi et al.,[11] proposed a model to optimize the weights of the convolutional neural networks (CNN) using genetic algorithm for breast cancer classification problem. This approach consists of building a CNN model, training the model using three different optimizers (mini-batch gradient descent, Adam, and GA) and evaluating the model through breakhis dataset. The results showed that the CNN model trained through Adam optimizer achieved an accuracy of 85%.

Somayeh Raiesdana[12] approach suggested by the author uses a unique combination of the Whale Optimization Algorithm (WOA) for feature selection and a Support Vector Machine (SVM) classifier for breast cancer detection. The WOA's ability to select the most relevant features potentially reduces data complexity and model overfitting. The proposed model was evaluated on Breast Cancer Wisconsin dataset and achieved an accuracy of 97.14%.

III. METHODOLOGY

The proposed architecture, detects the type of breast cancer which is either benign or malignant based on the given histopathological image of the breast. Here the main goal is to improve the performance of the convolutional neural network model used for the breast cancer detection by tuning its hyperparameters using genetic algorithm. The genetic algorithm identifies the potential values for the hyperparameters which are later used to evaluate the performance of the convolutional neural network model.

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A Convolutional Neural Network, also known as a CNN or ConvNet, is a type of deep learning algorithm that has a class of neural networks, specializing in processing data that has a grid-like topology, such as an image. The convolution neural network is inspired by the operation of biological neurons in the human brain. Our brains, like convolutional neural networks (CNNs), excel at dissecting visual information. Both systems leverage a layered approach. Neurons in the brain, just like those in a CNN, process information within a specific area. These layers progressively build upon each other, with earlier layers identifying simpler features (lines, edges) that contribute to the recognition of more complex objects (faces, cars) in later layers. The convolutional neural network takes image as input and extracts the required features from the image automatically by eliminating the need for hand-crafted feature extraction methods.

The convolutional neural network consists of 3 layers: Input Layer, Hidden Layer and Output Layer. The hidden layer consists of convolutional layers which are responsible for feature extraction, pooling layer, flatten layer, dense layer, and fully connected layer which is used for the classification tasks.

The convolutional layer is the backbone of a Convolutional Neural Network (CNN). It acts like a feature scanner, using small filters to slide across an image and extract key details like edges, shapes or colours. These filters create feature maps highlighting where those features appear in the image. Convolutional layers are efficient because they focus on small areas and reduce the number of connections needed compared to fully connected layers. By stacking these layers, CNNs can learn intricate patterns, making them ideal for image recognition and other visual tasks.

$$W_{out} = \frac{W - F + 2P}{S} + 1$$

The above equation represents the output of convolutional layer which will be passed as input to the pooling layer.
Following the feature extraction in the convolutional layer, a pooling layer down samples the data in CNNs. Pooling in CNNs is like summarizing an image. It shrinks feature maps from the previous layer, keeping key info. It uses filters that slide across the maps, picking the most important value (max pooling) or averaging them (average pooling). This makes the data smaller, faster to process, and helps prevent the model from overfitting.

$$W_{out} = \frac{W - F}{S} + 1$$

Fully connected layers in CNNs are the decision makers. They take the features extracted by convolutional layers (like edges and shapes) and smash them into one long list. Then, they analyze all these features together, like a regular neural network, to classify the image.

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Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 398, 398, 32)	896
max_pooling2d (MaxPooling2D)	(None, 199, 199, 32)	0
conv2d_1 (Conv2D)	(None, 197, 197, 64)	18496
max_pooling2d_1 (MaxPooling2D)	(None, 98, 98, 64)	0
dropout (Dropout)	(None, 98, 98, 64)	0
conv2d_2 (Conv2D)	(None, 96, 96, 128)	73856
max_pooling2d_2 (MaxPooling2D)	(None, 48, 48, 128)	0
conv2d_3 (Conv2D)	(None, 46, 46, 256)	295168
max_pooling2d_3 (MaxPooling2D)	(None, 23, 23, 256)	0
dropout_1 (Dropout)	(None, 23, 23, 256)	0
flatten (Flatten)	(None, 135424)	0
dense (Dense)	(None, 512)	69337600
dropout_2 (Dropout)	(None, 512)	0
dense_1 (Dense)	(None, 1)	513

Total params: 69726529 (265.99 MB)
Trainable params: 69726529 (265.99 MB)
Non-trainable params: 0 (0.00 Byte)

Figure-1: Architecture of the CNN model used

Genetic Algorithms (GAs) are a powerful class of computational tools inspired by the principles of natural selection. These algorithms operate on a population of potential solutions, each encoded with a specific set of characteristics. GAs leverage an iterative process to refine these solutions towards an optimal state. During each iteration, a fitness function evaluates each individual based on its ability to solve the problem at hand. High-performing individuals are then preferentially selected to contribute their characteristics to the next generation. A crossover operation then combines these chosen traits, creating new offspring with potentially improved performance. Finally, a mutation operation introduces slight variations in the offspring, maintaining diversity within the population and preventing stagnation. This cycle of evaluation, selection, crossover, and mutation continues until a pre-defined stopping criterion is met, resulting in the identification of a near-optimal solution within the search space.

Genetic algorithms (GAs) differ from traditional search methods in several ways. Instead of fine-tuning one guess at a time, GAs consider multiple possibilities simultaneously. They also incorporate randomness to maintain diversity and prevent stagnation. Here are four key aspects that set GAs apart from standard optimization and search procedures:

1. GAs work with a coding of the parameter set, not the parameters themselves.
2. GAs search from a population of points, not a single point.
3. GAs use payoff (objective function) information, not derivatives or other auxiliary knowledge.
4. GAs use probabilistic transition rules, not deterministic rules. [18]

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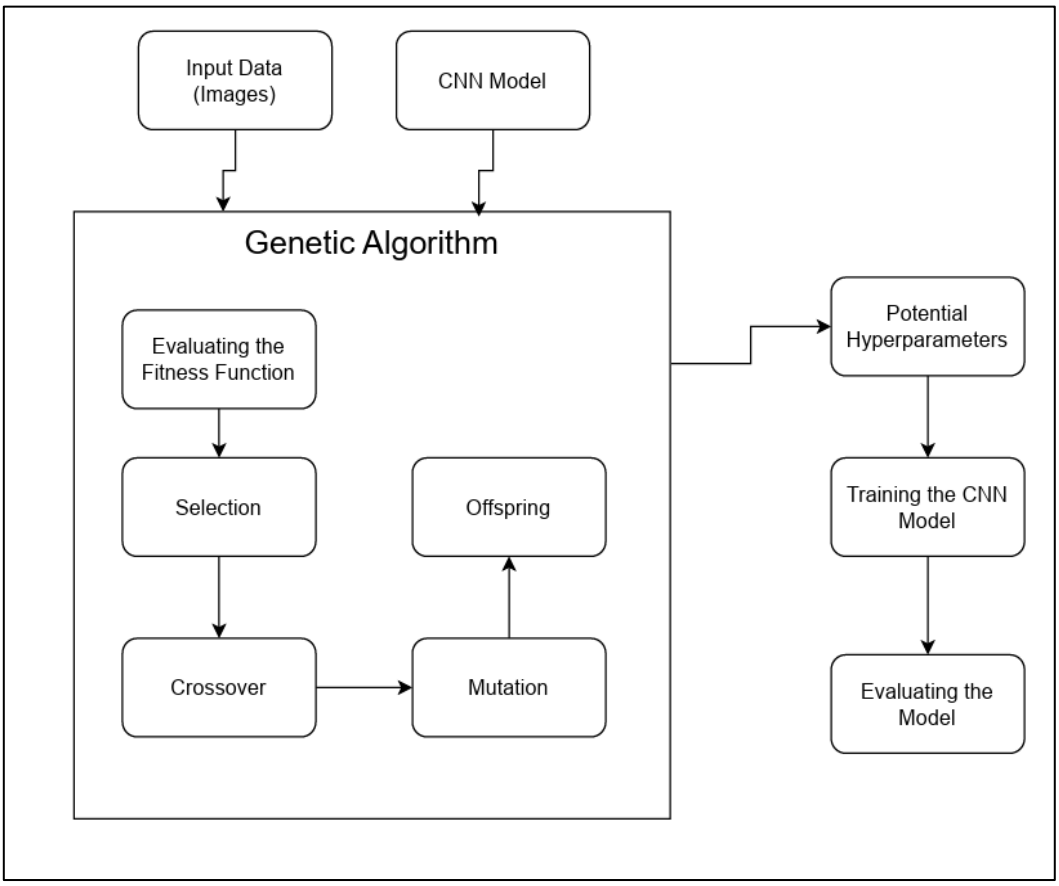

Figure-2: Architecture of the Proposed Method

Working of the proposed model:

1. **Population Initialization:** A set of individuals (candidate CNN configurations) is created. Each individual represents a unique combination of hyperparameters like learning rate, dropout rate, epochs, batch size, and optimizer (e.g., Adam, SGD).
2. **Fitness Evaluation:** Each CNN configuration in the population is trained on a subset of the data (training set). Then, a fitness function evaluates its performance, typically based on accuracy or loss on a validation set.
3. **Selection:** Individuals with higher fitness (better performance) are chosen to be parents for the next generation. This ensures promising hyperparameter combinations are carried forward.
4. **Crossover:** The genetic material (hyperparameter values) from two selected parents is exchanged at random crossover points. This creates new offspring with a blend of potentially good traits from both parents.
5. **Mutation:** With a small probability, random mutations are introduced in the offspring's hyperparameter values. This injects diversity and helps explore new areas of the search space, preventing the algorithm from getting stuck in local optima.
6. **Iteration:** Steps 2-5 are repeated for multiple generations. Over time, the population evolves towards hyperparameter combinations that lead to better performing CNNs.
7. **Selection of Best Model:** Finally, the individual (CNN configuration) with the highest fitness in the final generation is chosen as the solution with the near-optimal hyperparameters for the specific CNN architecture and dataset.

IV. RESULTS & DISCUSSIONS

We evaluated the performance of our proposed classifier on the Breast Cancer Histopathological Image Classification (BreakHis) dataset. The BreakHis, compiled in collaboration with the P&D Laboratory - Pathological Anatomy and Cytopathology, Parana, Brazil, is composed of 9,109 microscopic biopsies (700X460 pixels, 3-channel RGB, 8-bit depth in each channel, PNG format) of breast tumour tissue collected from 82 patients, captured at various

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magnifications (40X, 100X, 200X, and 400X). Each image is categorized as either benign (2,480 samples) or malignant (5,429 samples) facilitating researchers to train and assess their models by the development and evaluation of algorithms for distinguishing cancerous from healthy tissue.

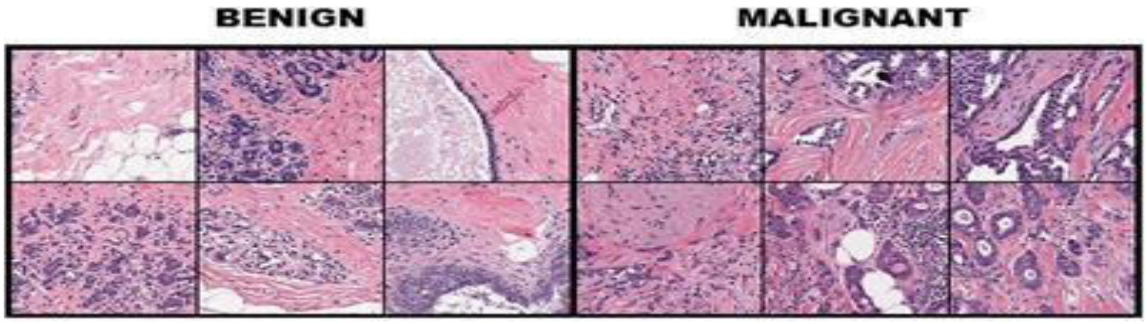

Figure-3: BreakHis Dataset

In this section we demonstrate the efficiency and accuracy of the proposed approach, compared to the standalone model. The metrics are loss, and accuracy as depicted in Table 1.

Algorithm	Loss	Accuracy
Standalone CNN model	28%	93%
Optimized CNN model	27%	97%

Table-1: Performance Analysis

The values for the hyperparameters of the convolutional neural network found by the genetic algorithm are demonstrated in Table 2.

Hyperparameters	Values
Learning rate	0.004086
Dropout rate	0.467756
Epochs	12
Batch size	116
Optimizer	adam

Table-2: potential values of hyperparameters

The proposed approach of using a Genetic Algorithm for hyperparameter tuning significantly improved the performance of a CNN. In the case of breast cancer classification using the BreakHis dataset, the optimized CNN model achieved an accuracy of 97%, compared to 93% for a standalone model with manually chosen hyperparameters. This demonstrates the effectiveness of GAs in finding superior hyperparameter combinations, leading to more accurate CNN models. Figure 4 and Figure 5 displays the accuracy and loss of the CNN models comprising both optimized and standalone models.

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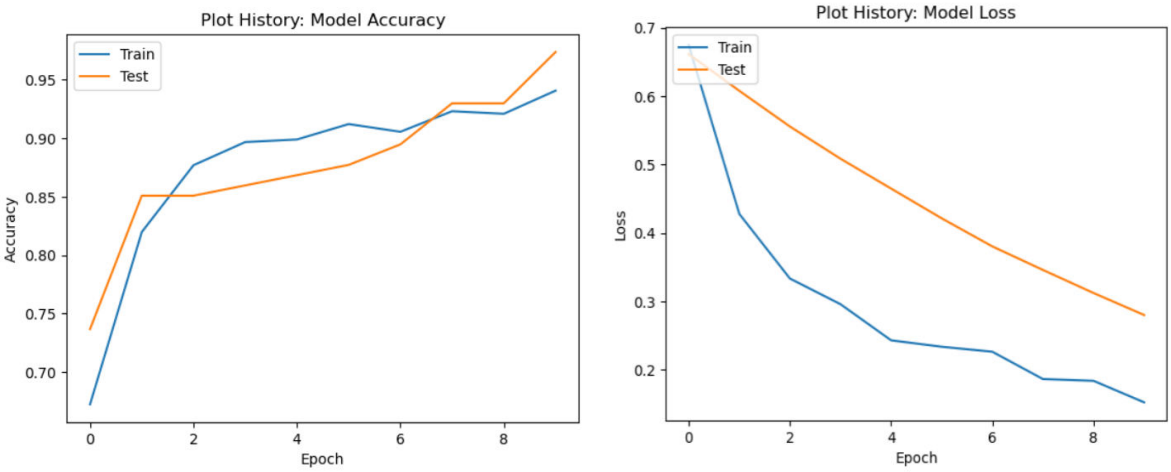

Figure-4: Accuracy and loss of optimized model

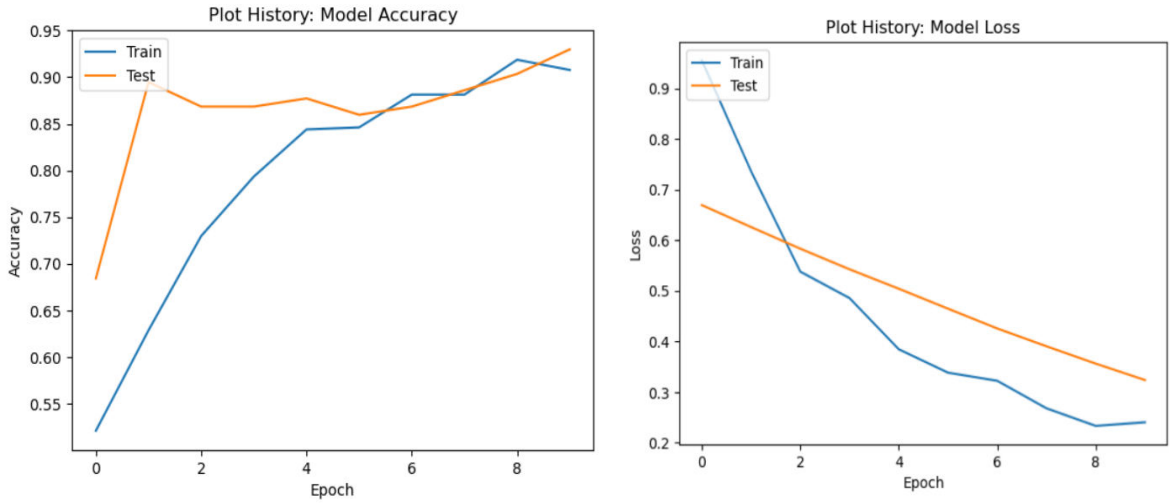

Figure-5: Accuracy and loss of standalone model

The accuracy and loss plots depict the training process for both the optimized and standalone CNN models. The standalone model's accuracy plot exhibits a slower rise and plateaus at a lower accuracy level (around 93%) compared to the optimized model's plot, which has a steeper rise and reaches a higher final accuracy (around 97%). Conversely, the loss plot for the standalone model shows a slower decrease and stabilizes at a higher loss value, while the optimized model's loss plots a more rapid decrease and reaches a lower final loss value. This visual comparison suggests that the optimized hyperparameters from the genetic algorithm enabled the CNN to learn more effectively, achieving both higher accuracy and lower loss compared to the manually configured standalone model.

V. CONCLUSION AND FUTURE SCOPE

The application of convolutional neural network (CNN) for breast cancer detection emphasizes the potential of progressed deep learning methods in moving forward the precision and effectiveness of breast cancer diagnosis. By leveraging the control of convolutional neural networks (CNNs), the study exhibits the potential for deep learning algorithms to upgrade the accuracy, effectiveness, and reliability of breast cancer detection from histopathological images, subsequently offering an important tool for early discovery and treatment. Through the investigation of different datasets and the development of strong convolutional neural network (CNN) models, researchers have illustrated the capacity to identify unobtrusive patterns and anomalies in breast imaging and by employing a Genetic Algorithm (GA), we have achieved substantially remarkable outcomes by competently searching for optimal configuration of the model. This approach allows for precise tuning beyond the specified parameters used in this

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instance as in the system offers fine-grained control for a wide range of other parameters which can be adjusted with similar precision.

The approach described offers extensive flexibility for fine-tuning multiple parameters beyond those initially selected. While Genetic Algorithms were employed in this instance, comparable outcomes can be achieved through alternative optimization techniques. These include methods such as Particle Swarm Optimization and Ant Colony Optimization, demonstrating the versatility of this framework. This adaptability suggests significant potential for future applications and refinements across various optimization scenarios.

To establish, a variety of hyperparameters can be tuned by utilizing a profound Convolutional Neural Networks (CNN) model by incorporating methods like Genetic Algorithm (GA) along with exceptional accuracy, eventually contributing to improved diagnostic results and healthcare delivery within the battle against breast cancer.

REFERENCES

1. Tehnan I.A. Mohamed, Absalom E. Ezugwu, Jean Vincent Fonou-Dombeu, Abiodun M. Ikotun, Mohanad Mohammed (2023). A bio-inspired convolution neural network architecture for automatic breast cancer detection and classification using RNA-Seq gene expression data.
2. Mukesh Kumar, Saurabh Singhal, Shashi Shekhar, Bhisham Sharma, Gautam Srivastava (2022). Optimized Stacking Ensemble Learning Model for Breast Cancer Detection and Classification Using Machine Learning
3. Vijayalakshmi S, John A, Sunder R, Senthilkumar Mohan, Sweta Bhattacharya, Rajesh Kaluri, Guang Feng, Usman Tariq (2020). Multi-modal Prediction of Breast Cancer using Particle Swarm Optimization with Non-dominating Sorting
4. Sanaz Karimi Jafarbigloo, Habibollah Danyali (2021). Nuclear atypia Grading in Breast Cancer Histopathological Images Based on CNN Feature Extraction and LSTM Classification
5. Muhammet Fatih Ak (2020). A Comparative Analysis of Breast Cancer Detection and Diagnosis using Data Visualization and Machine Learning Applications
6. Meha Desai, Manan Shah (2020). An Anatomization on Breast Cancer Detection and Diagnosis Employing Multi-layer Perceptron Neural Network (MLP) and Convolutional Neural Network (CNN)
7. Reza Rabiei, Seyed Mohammad Ayyoubzadeh, Solmaz Sohrabei, Marzieh Esmaeili, Alireza Atashi (2022). Prediction of Breast Cancer using Machine Learning Approaches
8. Basem S Abunasser, Mohammed Rasheed J AL-Hiealy, Ihab S Zaqout, Samy S Abu-Naser (2023). Convolution Neural Network for Breast Cancer Detection and Classification using Deep Learning
9. Amira Mofreh Ibraheem, Kamel Hussein Rahouma, Hesham F. A. Hamed (2021). 3PCNNB-Net: Three Parallel CNN Branches for Breast Cancer Classifcation Through Histopathological Images
10. Basem S Abunasser, Mohammed Rasheed J AL-Hiealy, Ihab S Zaqout, Samy S Abu-Naser (2023). Convolution Neural Network for Breast Cancer Detection and Classification using Deep Learning
11. Khatereh Davoudi and Parimala Thulasiraman (2021). Evolving Convolutional Neural Network Parameters through the Genetic Algorithm for the Breast Cancer Classification Problem.
12. Somayeh Raiesdana (2021). Breast Cancer Detection Using Optimization-Based Feature Pruning and Classification Algorithms
13. Deva, R., & Narsimha, G. (2023). Erythemato-Squamous Disease Detection using Best Optimized Estimators of ANN. International Journal of Advanced Computer Science and Applications, 14(2).
14. Rajashekar Deva, D. G. N. (2022). Trlu: A Customized Activation Function to Detect Erythemato-Squamous Skin Cancer at Early Stage. Journal of Algebraic Statistics, 13(1), 511-516.
15. Rajashekar Deva, D. G. (2022). A Soft Hyper Tuned Voting Ensemble Classifier integrated with One Versus All Approach to Identify the Erythemato-Squamous Disease. Journal of Optoelectronics Laser, 41(5), 2022.
16. Deva, R., & Narsimha, G. (2021, December). A Tuned Stacking Algorithm to Detect Skin Cancer Using Multi-classification Algorithms. In International Virtual Conference on Industry (pp. 83-93). Singapore: Springer Nature Singapore.
17. Rajashekar Deva, D. G. N. (2021). EPFSESD: An Enhanced Pipeline Feature Selection Algorithm for Erythemato-Squamous Disease Detection. Design Engineering, 2373-2388.
18. Goldberg, David E.: Genetic Algorithms in search, optimization and Machine Learning. Addison-Wesley Longman Publishing Co., Inc

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