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# Medical Image Classification by Genetic Algorithm and Ensemble Tree Learning Model

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**Abstract- Skin cancer represents a major global health concern, impacting millions of people across the world. This makes timely detection and precise diagnosis extremely important, with dermoscopic imaging serving as an effective tool for identifying abnormalities at an early stage. In this study, a novel classification model is presented to distinguish skin medical images as either normal or abnormal. The proposed framework is divided into two main modules. The first module focuses on enhancing image quality through noise elimination and identifying the most affected regions that contribute significantly to diagnosis. The second module is responsible for extracting histogram-based and CCM features from the processed images, which are then utilized to train the Ensemble Tree classifier. The experimental evaluation was carried out using a real-world skin cancer image dataset. The obtained results demonstrate that the MICAIML improves detection accuracy with existing approaches.**

**Keywords- Genetic algorithm, Image Processing, Feature Embedding, Extraction, Ensemble Learning.**

## I. INTRODUCTION

There have been dramatic increase in the number of medical images which are taken for treatment planning, diagnosis, and other clinical purposes [1]. In the current clinical standards, these measurements (annotations) from medical scans are done by expert physicians. These procedures are tedious, and prone to intra- and inter-observer errors, which can readily affect the diagnosis and treatment procedure [2]. The need for using expert-level automated methods (i.e. segmentation) and software with high efficacy, which can help and ease these tasks and resolve above mentioned problems, is essential.

Ever since the first images from inside the human body were taken using X-Rays in 1895, the field of medical imaging has progressed at a considerable rate. While traditional X-Ray imaging has stood the test of time and is still used today, it has been joined by ultrasound, Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), and Single Photon Emission Computed Tomography (SPECT), among others. Each of these imaging modalities fills an important and often complementary niche in clinical practice providing greater insight into the human body in both health and disease than would have ever been possible without them. The desire for detailed images of the brain has driven much of this progress, leading to the development of the field of neuro-imaging. The modern-day clinician now has an large amount of techniques at their disposal allowing for highly detailed images of individual brain structures, as well as precise measures of brain activity and processes such as metabolism and the accumulation of proteins. As per the medical image reports of a patient experts diagnose disease. As high quality image developing devices by various techniques like X-Ray, CT-Scan, MRI, etc. [3] increases the dependency of radiologist, pathologist. As most of image interpretation done by medical experts, so to reduce their load and increase the accuracy of work by automation of image diagnosis algorithms. Most of computer vision algorithms were develop to identify the image content and classify images as per visual information reflect by X-Ray, Light, Margnet, etc. [4]. Still classification of medical images into correct class for different disease is a major issue to solve.

## II. RELATED WORK

Fernando K. Malerbi et. al. in [5], Participants underwent fundus photographs using a portable retinal camera (Phelcom Eyer). The captured images were automatically analysed by deep learning algorithms RAS (retinal alteration score) and DRAS (diabetic retinopathy alteration score), consisting of convolutional neural networks trained on EyePACS datasets and fine-tuned using datasets of portable device fundus images. The ground truth was the classification of DR corresponding to adjudicated expert reading, performed by three certified ophthalmologists.

Zeru Hai et. al. [6], proposed the DRGCNN (DR Grading CNN) model. To solve the problem caused by imbalanced data distribution, our model adopts a more balanced strategy by allocating an equal number of channels to feature maps representing various DR categories. Furthermore, this paper introduce a CAM-EfficientNetV2-M encoder dedicated to encoding input retinal fundus images for feature vector generation.

D. R. Manjunath et. al. in [7], done feature engineering, by various sampling methods, and hyperparameter tuning, the models demonstrated strong performance across all dataset variations. Notably, the models also yielded robust results on the original imbalanced dataset, highlighting the strength of the algorithms and the impact of careful parameter optimization. Among the tested approaches, ensemble methods, particularly Voting and Stacking Classifiers, delivered superior outcomes, achieving nearly perfect evaluation metrics on oversampled data. Hyperparameter tuning further enhanced results by lowering RMSE and log loss, while improving accuracy and recall across different settings. These findings underscore the critical role of optimization in handling real-world clinical datasets, which are often imbalanced and noisy.

Al-Waisy et. al. in [8], This study introduces Skin-DeepNet, a novel deep learning-based framework designed for the automated early diagnosis and classification of skin cancer lesions from dermoscopy images. Skin-DeepNet incorporates a two-step pre-processing stage to enhance image contrast, followed by robust skin lesion segmentation using Mask R-CNN and GrabCut algorithm.

Ashfaq et al. [9] introduced a hierarchical framework for automated skin cancer detection that employs a multi-level classification process. This layered strategy allows the system to first separate benign lesions from malignant ones and then further classify cancer subtypes, leading to more accurate and interpretable diagnostic outcomes. By progressively analyzing lesion characteristics across multiple abstraction levels, the model captures subtle visual patterns that are often overlooked, thereby supporting clinicians with more informed and reliable decision-making.

Lin TL et al. [10] proposed an advanced hyperspectral imaging-based method known as the Spectrum-Aided Vision Enhancer (SAVE) to improve the visual distinction of skin lesions. The technique transforms standard RGB images into narrow-band images by integrating hyperspectral data, significantly enhancing lesion-to-tissue contrast. The study evaluates the effectiveness of this enhanced imaging approach using ten machine learning and deep learning models—including CNNs, Random Forest, YOLOv8, ResNet50, MobileNetV2, Logistic Regression, and multiple SVM variants—to accurately classify actinic keratosis (AK), basal cell carcinoma (BCC), and seborrheic keratosis (SK).

## III. PROPOSED METHODOLOGY

The study introduces a framework named MICAIML for the classification of medical images. As illustrated in Fig. 1, the proposed framework consists of two major modules. The first module is dedicated to image feature optimization, while the second module focuses on training the mathematical classification model. The input image is initially processed through the first module to enhance data quality using artificial immune-inspired genetic operations. After optimization, relevant image features are extracted and utilized for training the Ensemble Tree classifier.

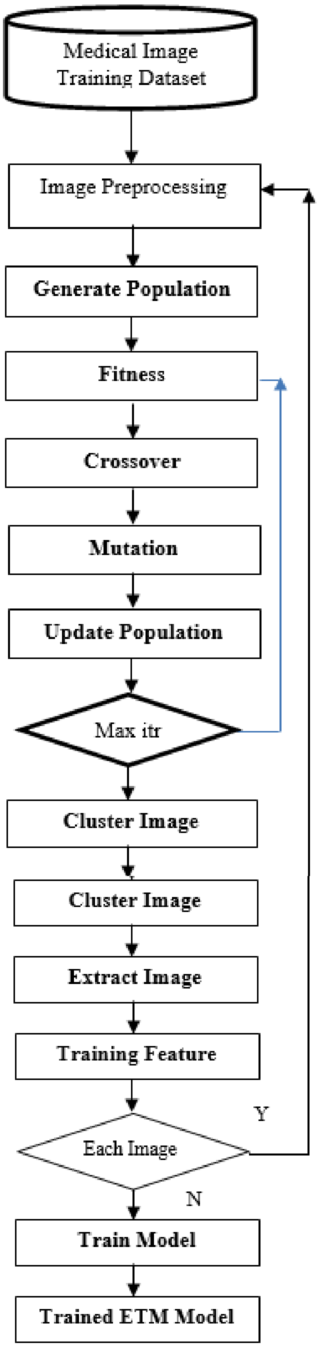

Fig. 1 Block diagram of proposed MICAIML model.

**Input Raw Dataset**

Input raw data comprises a collection of medical images used for experimentation. The complete dataset is divided into two subsets: the training set and the testing set. In both subsets, the class labels of each image are predefined and known, enabling supervised learning and evaluation.

**First Module**

This module performs the preprocessing and optimization of input images. Each input image i obtained from the input data undergoes several processing steps to improve its quality and prepare it for feature extraction.

**Pre-processing**

Initially, the training images from the MRD are converted into the required matrix dimensions for further processing. To improve image clarity, filtering is applied to minimize unwanted noise. In this work, a median filtering technique is employed for effective noise reduction. The preprocessed image is then transformed into grayscale format, which helps in identifying the most significant affected feature regions for further analysis.

**Generate Antibody:** At the beginning of the genetic algorithm, an initial population of candidate solutions is generated randomly. Each candidate solution, referred to as a chromosome, represents a possible segmentation pattern for the input image. The population consists of multiple chromosomes, each encoding a set of pixel segment values that will be optimized during subsequent iterations.

**Fitness Evaluation:** Each chromosome is evaluated using a fitness function to measure its suitability for image segmentation. The fitness value is determined by calculating the difference between pixel values and their corresponding segment center values. Chromosomes with lower difference values indicate better segmentation quality and are therefore considered more optimal. The fitness evaluation helps in identifying promising solutions within the population.

**Crossover:** Crossover is performed to combine the characteristics of two selected parent chromosomes and generate new offspring solutions. In this process, portions of genetic information are exchanged between parents, allowing the offspring to inherit useful features from both. This operation enhances the exploration of the search space and increases the likelihood of obtaining improved segmentation solutions.

**Mutation:** In this step mutation has further modify the population matrix. Each chromosome modify its set and generate new chromosome.

**Population Update:** After crossover and mutation, the newly generated offspring are evaluated and compared with the existing population. Chromosomes with better fitness values are retained, while weaker solutions are discarded. This replacement strategy ensures that the overall quality of the population improves over successive generations.

**Termination and Final Solution**: The above steps are repeated for a predefined number of iterations or until the algorithm reaches convergence. At the end of the optimization process, the chromosome with the best fitness value is selected as the final optimal segmentation solution. The segmented image is then divided into significant and non-significant regions, where the important segmented region is utilized for feature extraction and further classification in the next module.

**Second Module**

Feature Extraction and Ensemble Training: This study extracts histogram and co-occurrence matrix (CCM) features from the affected image segment. Sixteen grayscale histogram bins are used to generate 16 feature values from each image. Additionally, the image is transformed into RGB and HSV color spaces to compute CCM-based texture features, including contrast, energy, inverse difference, and entropy. Features are extracted from the Red, Green, Hue, and Saturation matrices, producing another 16 values, which are then normalized for consistency. These combined features are used to train an Ensemble Tree classifier. The training process involves preprocessing, feature selection, and bootstrap-based learning, where multiple decision trees are generated using different subsets of training data. The final classification is obtained through majority voting, improving accuracy, stability, and robustness for reliable skin cancer image classification.

## IV. EXPERIMENT AND RESULTS

The model was implemented using MATLAB 2016a. All experiments were carried out on a system equipped with a 12th generation Intel i3 processor and 8 GB of RAM. Comparison of proposed MICAIML (Medical Image Classification using Artificial Immune Machine Learning) with MICWSN and model proposed in [15]. Experiment was done real medical images taken from [19].

### Results

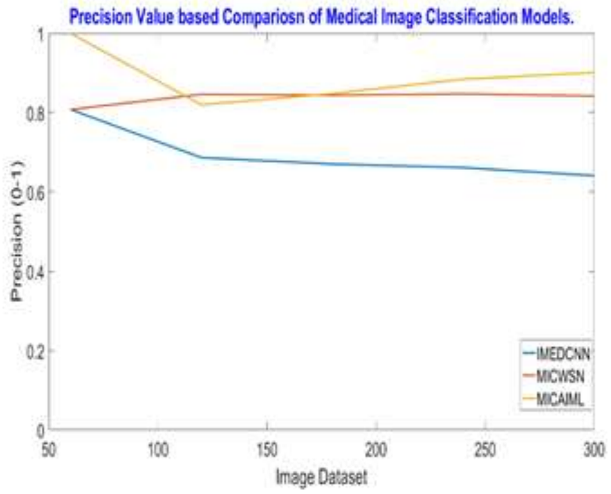

Fig. 2 Precision value based comparison of image classification models.

Fig. 2 shows the precision value of medical image classification models where MICAIML MICWSN has high values. It was shown that with increase in dataset size values of precision value of MICAIML increases while previous decreases.

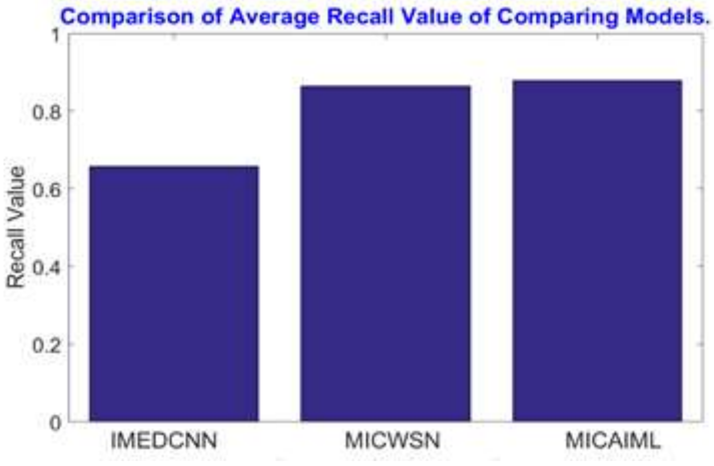

Fig. 3 Average recall value of comparing models on different testing datasets.

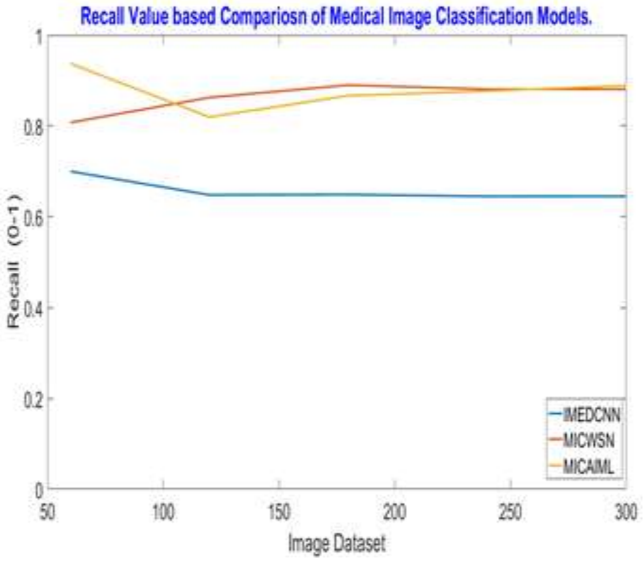

Fig. 4 Recall value based comparison of image classification models.

Fig. 3 and fig. 4 shows the recall comparison between the models. The MICAIML approach significantly enhances classification recall, achieving up to 25.11% for smaller datasets and consistently higher performance for larger datasets as well.

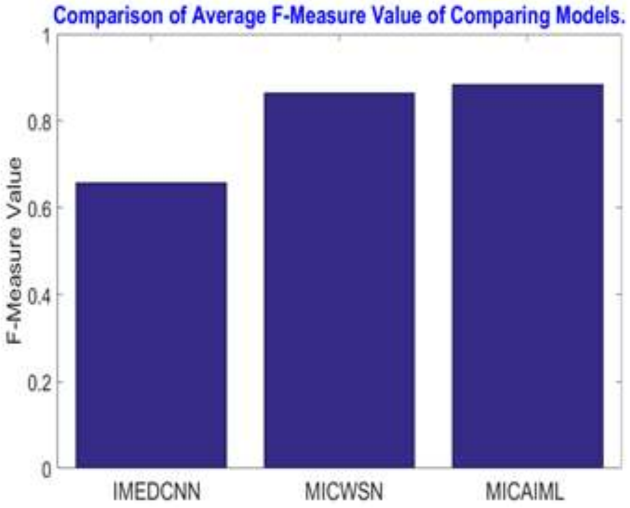

Fig. 5 Average F-measure value based comparison of image classification models.

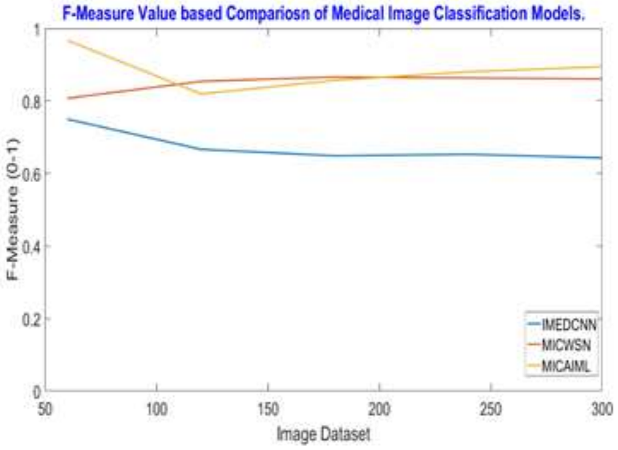

Fig. 6. F-Measure value based comparison of models of medical image diagnosis.

Fig. 5 shows the f-measure values of comparing models where MICWSN model perform better as compared to IMEDCNN model by 0.1782. This enhancement was clearly seen in fig. 6, achieved by the combination of wolf algorithm that reduces the unwanted data of image and spiking neural network that gain from the optimized feature set.

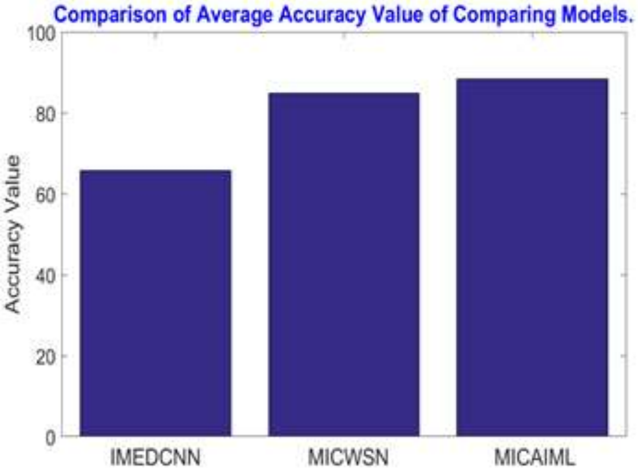

Fig. 7 Average accuracy value of comparing models on different testing datasets.

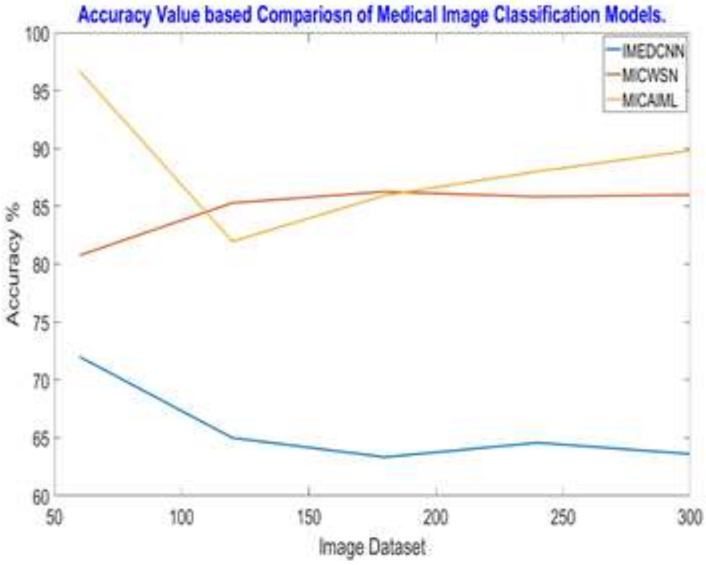

Fig. 8 Accuracy value based comparison of models of medical image diagnosis.

Fig. 7 shows the correct class detection accuracy of the models against various testing dataset. Fig. 4.7 shows that that use of histogram feature with DWT frequency has increases the learning capacity of spiking neural network in MICWSN. Fig. 4.8 shows the detection accuracy was improved by 19.125% as compared to IMEDCNN model.

## V. CONCLUSION

This study proposed the model effective skin cancer image classification through a two-module approach. In the first module, raw medical images are preprocessed using median filtering to remove noise and improve image quality, followed by genetic algorithm. This optimized segmentation ensures that only relevant image portions are selected for further analysis. Further histogram and co-occurrence matrix (CCM) features are extracted from the segmented regions to capture important statistical and texture information. Experimental analysis on skin cancer medical image datasets demonstrates that the proposed model achieves improved detection accuracy from existing models. In furture scholars can develop similar models for other diseases.

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