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Research Article

Optimising Deep Feature Maps using Genetic Algorithm for Efficient Breast Mass Classification in Mammogram Images

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ABSTRACT

Breast cancer is the most prominent cause of death of women worldwide, highlighting the importance of precise and effective diagnostic tools. Deep convolutional neural networks have already achieved substantial success. in medical image analysis but run into redundancy and computational cost problems with high-dimensional feature flattening. This paper provides a hybrid deep learning and metaheuristic approach to optimising deep feature maps prior to flattening. From the CBIS-DDSM breast cancer dataset, feature maps are drawn from the ReLU5 layer of AlexNet, and global average pooling (GAP) compresses them into a single representative value without changing size or losing information. A Genetic Algorithm (GA) is employed for optimisation at the channel level to determine the most informative and relevant channels to classify. The subset of features optimised is then fed into a softmax classifier to classify finally. This method avoids redundant calculations, accelerates convergence, and decreases training time. Experiments show that the designed model performs better than the conventional AlexNet framework in both accuracy in classification and efficiency in computations. Notably, at 40 epochs, GA_AlexNet achieved a 72.51% accuracy, surpassing AlexNet by 8.44%.

Keywords: Mammogram Image Analysis , Deep Feature Optimisation , Genetic Algorithm, Breast Mass Classification

Introduction

Breast cancer still poses a significant issue in international public health due to its high prevalence, biological heterogeneity, and high mortality. It is the most commonly found malignancy among females as well as one of the principal causes of mortality among cancer patients globally.[1] Early diagnosis is crucial for better survival as well as minimising the cost of treatments. Medical image modalities—mammography, ultrasound, as well as magnetic resonance imaging (MRI)—play the most important role in the detection of abnormalities within the tissue of the breasts.[2] However, constraints such as overlapping anatomical features and inadequate contrast, along with different levels of density of breasts, usually complicate manual analysis, sometimes resulting in the possibility of missed lesions or diagnostic mistakes.[3]

In order to address such issues, computer-aided diagnosis (CAD) systems were introduced to assist radiologists with automatic second opinions as well as minimise the possibility of human failure.[4] Over the past decade, deep learning transformed CAD strategies. Convolutional Neural Networks (CNNs), in specific, have shown exceptional performance in automatically learning hierarchical as well as discriminative features from raw medical images. They provided spectacular success in principal tasks such as the detection and segmentation, as well as the classification the classification of tumors.[5] As opposed to traditional machine learning techniques that are based on hand-crafted features, CNNs can automatically extract complex contextual as well as spatial patterns.[6]

Despite such advantages, CNN-based systems pose some challenges. The architectures typically produce high-dimensional feature representations that might involve redundant or irrelevant details, contributing to increased computational complexity as well as increased training time.[7] Secondly, the learning of CNNs from the beginning will necessitate enormous annotated medical data that is typically limited. Transfer learning overcomes such barriers through the fine-tuning of pre-trained networks—such as AlexNet, VGG, and ResNet—on domain-relevant datasets. Such an approach reduces the need for enormous training data as well as computational power while boosting the generalisation performance.[8] Then, transfer learning proved to be immensely effective as pertains to the mammogram-informed classification of breast cancer.[9]

Nevertheless, transfer learning models still may preserve redundant features to hamper classification performance. The selection of the most discriminant and informative features becomes prominent as a consequence. The feature selection can be viewed as a multi-objective optimisation problem aiming to attain high classification accuracy with the lowest feature dimensionality.[10] Inspired by natural and biological systems, metaheuristic optimisation schemes have shown enormous potential to address such optimisation problems. The Genetic Algorithm (GA), the Particle Swarm Optimisation (PSO), and the Marine Predators Algorithm (MPA) can automatically control exploration and exploitation to achieve the optimal feature subsets.[11, 12] When incorporated with the architectures of deep learning, the aforementioned schemes can utilise the intelligent optimisation of the deep feature representations to achieve higher classification accuracy with less computational cost.[13] Inspired by such advancements, the present research proposes a hybrid metaheuristic–deep learning paradigm that optimises CNN feature maps before the flattening step. Optimising at the channel level, the new strategy efficiently reduces the redundancy at the early pipeline of the net. This implies faster convergence and reduced training time, as well as superior accuracy levels in tasks of classifying breast cancer.

Related Work

In recent years, hybrid frameworks that integrate deep learning with feature selection and metaheuristic optimisation techniques have attracted growing research interest for breast cancer detection and classification. The research in[14] introduces a framework integrating the use of attention mechanisms, radiomic features, and bilateral asymmetry analysis to improve the classification of the mammograms, taking advantage of both the temporal as well as the spatial information to achieve higher predictive value. The research in[15] presents an adversarial robust feature learning framework to attenuate spurious correlations in mammogram data, making the deeper models more reliable. The research in[16] offers an uncertainty-aware Bayesian framework of deep learning to predict molecular subtypes from mammograms with direct predictions, allowing the classification to be done in a robust manner with the estimation of the model's predictive uncertainty.

The researchers in[17] put forward a self-adaptive quantum metaheuristic algorithm that combines teaching-learning as well as genetic algorithm techniques for feature selection. This combination strengthens classification accuracy while abating the computational complexity to some extent. Similarly, the research in[18] creates a deep learning–based hybrid framework with feature selection to detect the significant biomarkers in the case of breast lesions, achieving enhanced interpretability as well as diagnostic effectiveness. The paper in[19] presents a stacking ensemble framework combined with feature selection to improve the stability as well as the robustness of the outcome of the classification of breasts as cancerous. The research in[20] uses metaheuristic-optimised XGBoost with feature selection to maintain predictive accuracy with a reduction in redundant features.

Other developments involve the research in,[21] where the integration of SHAP-based recursive feature elimination with metaheuristic hyperparameter tuning leads to efficient dimension reduction as well as trustworthy classification during early-stage detection of breast cancer. Likewise,[22] uses binary particle swarm optimisation (BPSO) to select the best feature subset optimally, showing that classification can be maintained or even enhanced with a smaller feature set. A quantum-inspired SVM model in[23] uses genetic-algorithm-based feature selection to reach the best possible tradeoff between accuracy, sparsity, and minimisation of covariance in the case of the datasets with breast cancer.

Together, these studies highlight the increased significance of hybrid deep learning–optimisation methods in the field of medical image analysis. The vast majority of current research, nevertheless, conducts feature selection after flattening the feature maps or on the end-extracted feature vectors. Channel-level optimisation at levels pre-dating the flattening step has hardly ever been investigated with a view to eliminating redundant channels prior to the flattening step to reduce computational complexity and enhance classification accuracy. To remedy this research gap, the current research presents a genetic algorithm–driven channel selection method exploited right on the deep CNN feature maps to secure better classification performance in the case of the classification of breast cancer.

Proposed Methodology

The suggested hybrid model combines AlexNet, a Global Average Pooling (GAP), a Genetic Algorithm (GA), and a Softmax classifier. The novelty of the method is the use of GA-based optimisation on the feature maps of the CNN prior to flattening that facilitates channel-level refinement selectively. This facilitates enhanced classification accuracy as well as lowers computational complexity by minimising the number of channels that are most informative.

Feature Extraction

AlexNet is employed as a pre-trained model for deep feature extraction. Input images are resized to before being passed through the convolutional layers, which extract hierarchical spatial representations. Activations from the relu5 layer are represented as:

$$\text{act} \in \mathbb{R}^{H \times W \times C} \tag{1}$$

where and denote the spatial dimensions (height and width), and is the number of channels (feature maps). To summarize each channel while preserving spatial information, **Global Average Pooling (GAP)** is applied

$$\text{gap}_c = \frac{1}{H \times W} \sum_{i=1}^{H} \sum_{j=1}^{W} \text{act}_{i,j,c} \tag{2}$$

This reduces each 2D feature map into a single scalar, producing a compact 1×C vector per image:

$$X(i,:) = [\text{gap}_1, \text{gap}_2, \ldots, \text{gap}_C] \tag{3}$$

Thus, each image is represented by a channel descriptor vector summarizing the salient information from all convolutional feature maps.

Channel Optimization via Genetic Algorithm

The Genetic Algorithm (GA) is used to optimize the subset of GAP channels that contribute most to classification performance. Each GA chromosome is a binary vector representing channel selection, where 1 indicates inclusion and 0 exclusion.

The fitness function is defined as:

$$\text{Fitness} = \text{Accuracy}(\text{Softmax}(X_{\text{selected}})) - \lambda \cdot \frac{|\text{Selected Channels}|}{C} \tag{4}$$

where is a penalty factor discouraging selection of excessive channels.

GA operations—including selection, crossover, and mutation—iteratively improve the channel subsets by evaluating classification accuracy on the selected channels. This ensures that only the most informative and non-redundant channels are retained for final classification.

Classification using Softmax

The optimized channel subset obtained from GA is fed into a Softmax classifier for final prediction. Given the optimized feature matrix , where is the number of selected channels, the class probabilities are computed as:

$$P(y = j \mid x_i) = \frac{\exp(W_j^{\top} x_i)}{\sum_{k=1}^{K} \cdot \ \exp(W_k^{\top} x_i)} \tag{5}$$

where represents the learned weights for class . The class with the highest probability is assigned as the predicted label. This probabilistic mapping ensures interpretable and confidence-based outputs, distinguishing between benign and malignant breast lesions.

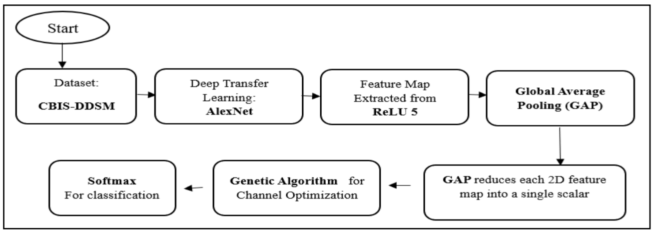


Figure 1.Proposed Methodology Workflow

Materials and Methods

Alex

AlexNet is a convolutional neural network that was introduced in 2012 by Krizhevsky, Sutskever, and Hinton. The net consists of five convolutional layers with three fully connected layers, including ReLU activation functions and max pooling layers. Extensive data augmentation and dropout regularisations were introduced by the model to avoid overfitting as well as to enhance generalisation. AlexNet made history in the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) 2012 with spectacular performance, birthing the field of computer vision as a prominent field of deep learning.[24]

Genetic Algorithm

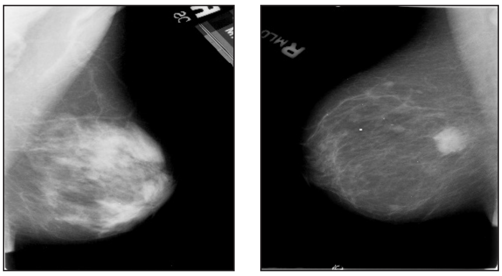
The Genetic Algorithm (GA) is a metaheuristic that is based on populations and is inspired by the natural evolution of Charles Darwin. The procedure starts with an initial set of candidate solutions from which the best one evolves over several generations based on processes similar to biological reproduction—i.e., selection, crossover, and mutation. Those operators push the fitter folks to lead the group toward better fixes. GA fits best for those tough optimisation puzzles. It digs through huge search areas pretty fast. Plus,, it skips getting trapped in local highs too soon. The thinghing is, GA really shines with how flexible it gets. And it'ss solid too. too. That is why this metaheuristic works well in things like feature selection. It helps with scheduling too. And machine learning optimisation has seen it in action.[25]

Global Average Pooling

Global Average Pooling, or GAP, shows up a lot as a way to cut down dimensions in convolutional neural networks. Instead of flattening feature maps to long vectors, GAP takes the mean value along each feature map to produce one representative number per channel. The strategy retains global spatial information yet dramatically reduces the number of parameters. As such, overfitting is prevented, computational complexity is decreased, as well as generalization power enhanced. GAP is one of the de facto components within state-of-the-art deep architectures, particularly image classification and object recognition tasks, wherein compact yet informative feature representations are favoured.[26]

Dataset

The Curated Breast Imaging Subset of the Digital Database for Screening Mammography (CBIS-DDSM) is a refined and standardised subset of the DDSM original collection. The DDSM collection includes about 2,620 digitised film mammography studies, including normal and benign as well as malignant cases. The CBIS-DDSM offers refined annotations along with standardised image formats to aid in developing as well as in benchmarking deep learning architectures to analyse breast cancers. In this research, the data is used to classify the breast mass with the help of a deep transfer learning model. For example, architectures like AlexNet—consisting of various convolutional along with residual layers—facilitate the extraction of discriminative deep features from mammograms. The extracted features act as the basis to carry out optimisation as well as classification procedures to precisely differentiate between various types of breast masses.[27]



(a) (b)

Figure 2.(a) Benign (b) Malignant

Results and Discussion

The performance of the proposed genetic algorithm-based channel selection, which is integrated with AlexNet (GA_AlexNet), was evaluated on the breast mass classification task using the CBIS-DDSM dataset. Two key metrics were considered: classification accuracy and training time across different total epochs (5, 10, 20, and 40). The baseline AlexNet model without channel selection was used for comparison.

Training Time Analysis

The results showed a real drop in training time for the GA_AlexNet setup. It happened especially with more epochs. After forty epochs, that time fell by forty-five per cent from the usual AlexNet. Mostly because the genetic algorithm picks out the right channels. It cuts away the redundant feature maps, and computation goes down.

Table 1.Total Training Time

Total Epochs	AlexNet	GA_AlexNet
5	16 min 40 sec	8 min 52 sec
10	24 min 23 sec	22 min 7 sec
20	31 min 51 sec	28 min 9 sec
40	93 min 35 sec	51 min 8 sec

Classification Accuracy Analysis

The proposed GA_AlexNet consistently outperformed baseline AlexNet in terms of accuracy, especially at higher epochs. Notably, at 40 epochs, GA_AlexNet achieved a 72.51% accuracy, surpassing AlexNet by 8.44%.

Table 2.Classification accuracy

Total Epochs	AlexNet	GA_AlexNet
5	65.58%	65.58%
10	62.34%	64.29%
20	68.61%	69.91%
40	64.07%	72.51%

The results demonstrate the effectiveness of Genetic Algorithm-based channel selection in retaining the most discriminative feature maps, which enhances the representational power of the network Interestingly, both models show fluctuating accuracy trends at different epochs. While AlexNet achieved its peak accuracy at 20 epochs (68.61%), GA_AlexNet continued to improve up to 40 epochs. It shows that GA_AlexNet is not only reducing the computational overhead but also stabilizes feature learning, particularly during longer training.

By selecting the most relevant channels before the flattening layer, the model achieves faster training times, which is

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particularly beneficial for large-scale mammogram datasets. These results support the potential of metaheuristic optimisation techniques in enhancing deep transfer learning models for medical image analysis.

Conclusion and Future Work

This paper introduces an effective hybrid framework combining deep transfer learning and metaheuristic optimisation for the task of classifying breast masses. By adding a Genetic Algorithm (GA)-based channel selection mechanism to AlexNet's Global Average Pooled (GAP) feature maps before the flattening step, the introduced model effectively eliminates redundant channels while maintaining the most discriminative channels. This selective optimisation improves the representational capability of deep features and considerably speeds up the overall classification process. Experimental assessments made on the CBIS-DDSM dataset prove that the present GA-optimised AlexNetoffers better classification accuracy with less computational time than the traditional AlexNetmodel. Channel-level optimisation reduces the dimensionality of the features, solves overfitting, and improves generalisation performance for different numbers of training epochs. These findings substantiate that the incorporation of metaheuristic optimisation in deep feature extraction flows can represent a robust and time-saving solution for computer-aided breast cancer diagnosis.

For the future, the integration of explainable AI (XAI) methods can also enhance interpretability to enable clinicians to better understand the decision-making process of the optimised deep learning model. Finally, the suggested method establishes a solid groundwork for the development of accurate, robust, and efficient diagnostic systems for medical image analysis.

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