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Melanoma Skin Cancer Detection Using Deep Learning and the Ant Colony Optimization Algorithm

A. Aliabadian [1,*]

[1] Assistant Professor, Department of Electrical and Biomedical Engineering, Shomal University, Amol, Iran

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ABSTRACT

Skin cancer is among the most common and potentially fatal forms of cancer worldwide, making early and accurate diagnosis essential for effective treatment and improved patient outcomes. Conventional diagnostic procedures, such as histopathological examination and biopsy, are often time-consuming and require significant clinical expertise. Recent advances in artificial intelligence and deep learning have enabled the development of automated diagnostic systems that can support clinicians in the early detection of skin lesions. In this study, a deep Convolutional Neural Network (CNN) is proposed for the classification of skin cancer images. To enhance the performance of the network, the Ant Colony Optimization (ACO) algorithm is employed to optimize the model parameters and reduce classification error. The proposed hybrid CNN–ACO framework is evaluated using a benchmark skin lesion dataset and compared with conventional deep learning approaches. Experimental results demonstrate that the optimization process improves classification performance and model convergence. The proposed method achieves an overall classification accuracy of 96%, outperforming baseline architectures and highlighting the effectiveness of integrating metaheuristic optimization techniques with deep learning models for automated skin cancer diagnosis. The findings suggest that the proposed framework can serve as a reliable decision-support tool for early skin cancer detection in clinical applications.

1. INTRODUCTION

Melanoma represents one of the most aggressive and lethal variants of skin cancer, characterized by its propensity to metastasize rapidly to distant vital organs if not detected and treated during its nascent stages. Early diagnostic interception significantly enhances patient survival rates and clinical therapeutic efficacy. Consequently, engineering rapid and robust methodologies for automated melanoma identification has consistently remained a primary priority within clinical research and biomedical engineering [1-3].

Precise melanoma detection not only elevates patient quality of life but also curtails long-term healthcare expenditures. Within public health infrastructures, automated computer-aided diagnosis (CAD) frameworks can act as an auxiliary tool for general practitioners in primary care clinics, empowering them to screen suspicious lesions

* Corresponding Author: a.aliabadian@shomal.ac.ir
Assistant Professor, Department of Electrical and Biomedical Engineering, Shomal University, Amol, Iran Email:

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accurately without requiring specialized or expensive diagnostic equipment. Furthermore, these intelligent technologies find extensive utility in population-wide screening initiatives and mobile personal health monitoring applications.

The automated diagnosis of melanoma is hindered by numerous computer vision challenges. These predominantly encompass the high intra-class morphological similarity between benign and malignant lesions, severe variability in skin pigmentation and lesion textures, and heterogeneous illumination conditions across clinical images. Moreover, the scarcity of large-scale, well-annotated, and validated medical repositories for model training constitutes a major bottleneck in intelligent system development. These challenges underscore the critical imperative to exploit advanced, data-driven computational paradigms [4-6].

Deep learning, particularly deep Convolutional Neural Networks (CNNs), has revolutionized digital image processing and computerized clinical diagnostics. These deep topologies are uniquely capable of automatically learning and extracting complex, hierarchical feature abstractions directly from dermoscopic images, delivering superior classification margins compared to classical hand-crafted descriptor workflows. In recent benchmark studies, deep learning models have demonstrated diagnostic performance on par with, or even exceeding, certified dermatologists [7-12].

Driven by the rapid evolution of deep neural network architectures and enhanced access to large-scale medical big data, the future trajectory of melanoma screening is veering toward edge-deployed, portable, and intelligent diagnostic software. These technologies can be embedded within smartphone applications for preliminary consumer triage or deployed in point-of-care clinics to support clinical decision-making. Nevertheless, to achieve widespread clinical translation, critical challenges regarding patient data privacy, model interpretability (explainable AI), and extensive multi-centric clinical validation must be systematically resolved.

2. 2. EXISTING METHODS

In study [1], the primary objective is to verify that the high-level feature representations learned by deep neural networks align with established clinical criteria used in dermoscopic skin lesion diagnosis. Specifically, a deep classification architecture is initially trained to map each dermoscopic input image to a calculated predictive probability score for each diagnostic class. Subsequently, a comprehensive feature importance analysis is executed to validate the clinical relevance of the internal representations.

In paper [2], the multi-class classification of diverse skin lesions including basal cell carcinoma, benign keratosis, dermatofibroma, vascular lesions, melanoma, and melanocytic nevi is reported using a pre-trained VGG-16 network, yielding an overall accuracy exceeding 80%. Implementing a sparse coding algorithm mitigated the structural demand for massive manually annotated datasets to extract robust features. Furthermore, data redundancy schemes coupled with a convolutional topology improved the global classification accuracy. This research utilized the validated PH2 database, comprising 1,600 melanoma and 1,600 non-melanoma labeled dermoscopic samples.

In reference [3], a convolutional neural network paradigm is proposed to enhance the boundary segmentation of skin lesions. The methodology leverages hybrid deep learning architectures specifically VGG19-UNet and DeepLabV3 frameworks to maximize the precision of lesion margin extraction. Computational evaluations were executed on the benchmark ISIC 2018 dataset containing 2,594 dermoscopic images. The dataset was randomly partitioned into a 80% split for model training and a 20% hold-out cohort for validation. The empirical findings demonstrated that the proposed hybrid model achieved a global segmentation accuracy of 93.6%, consistently outperforming conventional baseline methods.

Early diagnostic stratification of skin malignancies dramatically improves clinical therapeutic success. In recent years, CNNs have emerged as a powerful instrument for this objective. In paper [4], the HAM database was utilized to benchmark different classification strategies. Three specific models comprising standard VGG16, VGG19, and a custom-designed deep CNN topology were architected, trained, and evaluated. During the experimental validation, an 80/20 train/test split was enforced, with a subset of the training pool reserved for in-loop validation. The results delineated a performance comparison of the respective models based on mean classification accuracy and net objective loss.

In paper [5], an automated framework for the diagnosis of malignant skin lesions is introduced. The methodology mathematically replicates the two-stage clinical diagnostic workflow practiced by dermatologists. In the initial stage, a deep learning model categorizes the skin lesions into two macro-classes: melanocytic and non-melanocytic. In the second stage, specialized separate deep architectures are leveraged to identify the specific malignant sub-types. The evaluation profiles verified that isolating melanocytic from non-melanocytic lesions is achievable with exceptionally high precision. Furthermore, the findings indicated that malignant melanocytic lesions are classified with higher relative accuracy than their malignant non-melanocytic counterparts.

In research [6], a deep convolutional neural network architecture is introduced to classify melanoma images into binary benign and malignant cohorts. The network topology comprises sequential blocks of alternating convolutional and max-pooling layers, followed by a regularization Dropout layer and a terminal fully connected (dense) layer. Model evaluation conducted on 352 test frames demonstrated an overall accuracy, sensitivity, and specificity of 84.76%, 91.97%, and 78.71%, respectively. This operational profile indicates that the proposed architecture possesses strong translation potential for practical clinical deployment, assisting medical professionals in executing more effective therapeutic strategies.

The medical sector has undergone a profound paradigm shift through the integration of automated diagnostic decision-support systems that assist clinicians in disease identification. In paper [7], a hybrid ensemble methodology for melanoma skin cancer detection is presented, suitable for screening any anomalous lesion. The predictive pipeline relies on an ensemble of three models: a deep convolutional neural network and two classical machine learning classifiers trained on extracted lesion attributes including border irregularity, texture descriptors, and color variance. These three distinct predictive streams are subsequently aggregated using a majority voting ensemble mechanism. Experimental results verified that this combined ensemble configuration yielded the highest classification accuracy compared to any of the constituent models evaluated in isolation.

One of the most widely adopted clinical frameworks for melanoma screening is the ABCDE criteria, which serves as an effective diagnostic heuristic. This clinical guideline differentiates malignant melanoma from benign cutaneous lesions based on five distinct morphological properties: Asymmetry (A), Border irregularity (B), Color variation (C), Diameter exceeding 6 mm (D), and Evolving structural changes over time (E). The standard computerized melanoma diagnostic pipeline generally encompasses several sequential phases: image acquisition and pre-processing, lesion segmentation, feature extraction, and terminal lesion classification. While the sequence and technical execution of these phases vary across methodologies, state-of-the-art frameworks often hybridize these distinct stages to optimize global classification precision.

In paper [9], a hybrid diagnostic framework for melanoma detection is presented to evaluate suspicious skin lesions. The predictive architecture incorporates three concurrent streams: a convolutional neural network alongside two classical machine learning classifiers trained on an ensemble of hand-crafted structural, textural, and color features. These three independent classifiers are subsequently consolidated using a majority voting fusion mechanism to boost the global system throughput and enhance classification precision.

3. PROPOSED METHODOLOGY

The comprehensive execution of the proposed data clustering framework is delineated sequentially below:

Step 1: Data Preparation The initial input dataset is compiled and subjected to standardized pre-processing pipelines. Concurrently, the target number of clusters (k) is mathematically initialized, which can be dynamically computed leveraging partition-evaluation heuristics such as the Elbow method or Silhouette analysis. This phase establishes the critical foundation for successful down-stream global optimization and stable data partitioning.

Step 2: Formulating Clustering as an Optimization Problem The spatial clustering task is mathematically transformed into a metaheuristic global optimization problem. Each discrete agent (ant) within the Ant Colony Optimization (ACO) algorithm represents a candidate solution vector for the k cluster centroids. Consequently, the spatial coordinates of each ant encode a prospective configuration of cluster centers within the high-dimensional feature space. The objective function is formulated as the Sum of Squared Errors (SSE), representing the total

squared Euclidean distances of data points to their respective assigned cluster centroids, which the optimization loop aims to globally minimize.

Step 3: Initial Centroid Selection via ACO The pheromone matrix is initialized, dictating the probabilistic likelihood of selecting any given data vector as a cluster centroid. Each ant dynamically selects a subset of k points to serve as cluster centers, driven by a probabilistic transition rule governed by the pheromone intensity and heuristic visibility (attractiveness) information. The heuristic visibility metric can be formulated based on spatial isolation, rendering data vectors that exhibit maximum distance from alternative points more attractive. Following cluster-center assignment, the fitness quality of each individual ant's solution is quantitatively measured by evaluating the net SSE metric.

Step 4: Pheromone Update Mechanism Pheromone intensities are dynamically updated across the search space based on the optimization performance of individual ants. Consequently, agents that converge upon superior topological solutions with lower SSE metrics deposit a higher density of pheromone. Concurrently, a mathematical pheromone evaporation factor is applied to decay existing trails over time. This decay limits premature convergence and prevents the swarm from stagnating in sub-optimal local minima, guaranteeing that the swarm explores the hyper-dimensional search landscape effectively.

Step 5: ACO Iterative Loop The sequential execution of cluster center selection and pheromone tracking is repeated iteratively for a predefined number of generations or until the swarm satisfies an explicit convergence threshold. The optimal configuration of centroids yielding the global minimum objective function value is extracted to serve as the highly optimized initial seed coordinates for the subsequent K-means clustering routine. This critical phase guarantees that the local fine-tuning phase initiates from the most mathematically sound topological coordinates.

Step 6: Execution of the K-means Algorithm Initialized with the optimized initial centroids derived from the ACO stage, the remaining data points are systematically mapped to their nearest spatial cluster head based on Euclidean proximity. The cluster centroids are subsequently recomputed and updated by calculating the mathematical mean of all data vectors assigned to each respective partition. This execution loops recursively until the displacement of cluster centers falls below a designated convergence tolerance threshold, yielding the terminal optimized cluster partitions.

Step 7: Evaluation and Performance Analysis Following the termination of the hybrid optimization-clustering routine, the global quality of the resulting partitions is quantitatively validated using robust unsupervised metrics, such as the Silhouette Score, the Davies–Bouldin Index, or the ratio of intra-cluster to inter-cluster spatial distances.

To execute the classification of the images generated by the preceding clustering phase, the deep neural network architecture must be explicitly defined. Within this structural framework, an imageInputLayer serves as the network gateway, receiving normalized input images constrained to a fixed spatial dimension.

Subsequently, a convolution2dLayer slides a bank of 2D convolutional kernels across the input tensor to automatically extract high-level feature maps and spatial abstractions. This is directly followed by a batchNormalizationLayer, which normalizes the activations across mini-batches to accelerate the optimization process and stabilize gradient propagation.

Next, a non-linear activation function is introduced via a reluLayer (Rectified Linear Unit), embedding crucial non-linear function approximation capabilities so the network can decode complex relations among visual descriptors. A maxPooling2dLayer is then implemented to perform spatial downsampling, which condenses the dimensionality of the feature maps to enforce spatial translation invariance while strictly preserving dominant feature descriptors.

Down-stream in the pipeline, a fullyConnectedLayer flattens and maps all preceding local activations to a global dense network layer, consolidating the extracted structural information for terminal classification. Finally, a softmaxLayer applies a normalized exponential function to compute the output class probability distributions, and a terminal classificationLayer computes the cross-entropy loss to yield the definitive classification results.

This deep diagnostic architecture is illustrated schematically in Figure 1.

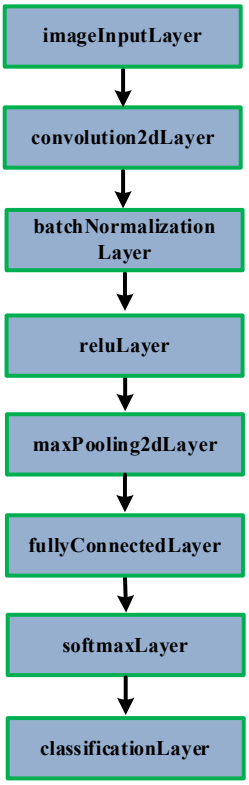

Fig. 1. Schematic architecture of the Convolutional Neural Network (CNN).

4. SIMULATION RESULTS

The proposed methodology and the existing comparative techniques were implemented within the MATLAB software environment developed by MathWorks. The hardware configuration utilized for the simulations consisted of an Intel(R) Core™ i5-4460 CPU @ 3.2 GHz processor equipped with 16 GB of RAM.

The hybrid K-means and ACO clustering algorithm was applied to a representative sample image, illustrated in Figure 2, to execute the optimal partitioning of lesions or Regions of Interest (ROIs). In this instance, the segmentation outputs corresponding to two distinct clusters are visualized to clearly demonstrate the data separation efficiency (Figure 3). Furthermore, the optimization convergence profile derived from the ACO algorithm is plotted to illustrate the tracking trajectory and global convergence toward the optimal cluster centroids (Figure 4).

In this study, classification accuracy was adopted as the primary performance metric to evaluate the proposed framework and benchmark it against existing methods. The PH2 database contains 200 dermoscopic images stratified into three clinical categories: 80 benign tumors, 80 atypical nevi, and 40 malignant melanomas. The classification accuracy of the proposed hybrid algorithm on this dataset reached 96%, demonstrating the high efficiency of the approach. The accuracy comparison chart of the evaluated algorithms is provided in Figure 5. A paramount architectural advantage of the proposed method over baseline techniques is the deployment of ACO for the optimal selection of initial cluster centers. Under this approach, the operational parameters of the clustering model are dynamically tuned via ACO, significantly boosting the final classification precision.

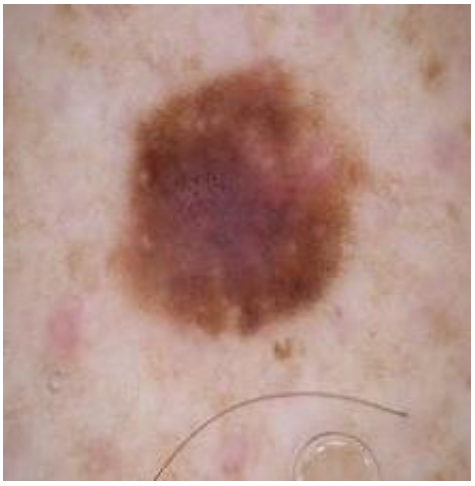

Fig. 2. Original sample dermoscopic image.

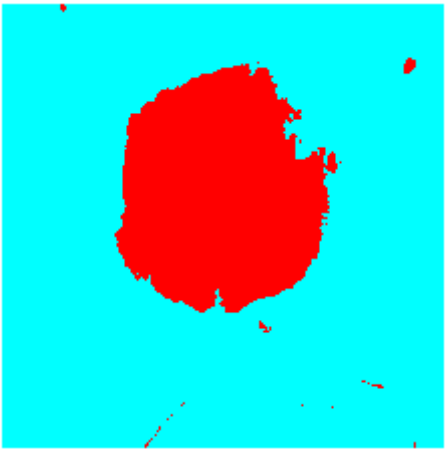

Fig. 3. Segmented and clustered output image.

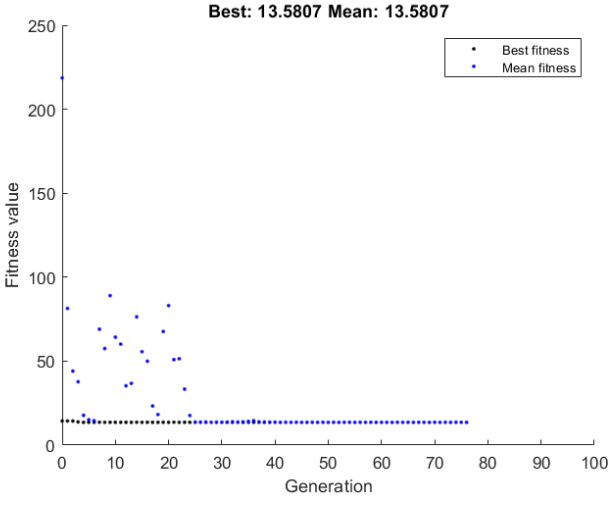

Fig. 4. Optimization convergence curve driven by the proposed ACO framework.

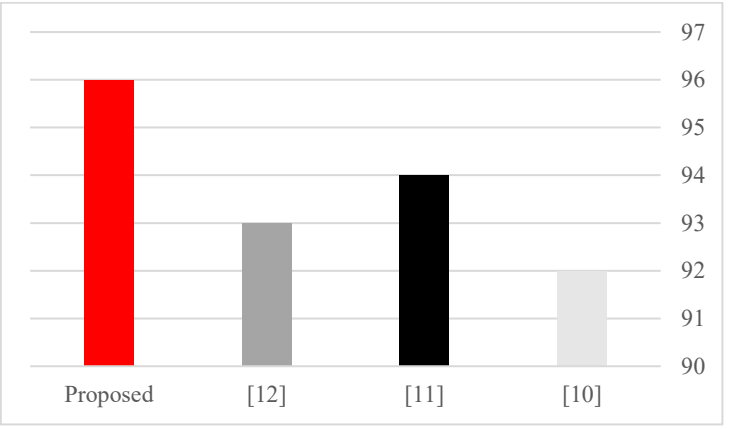

Fig. 5. Comparative accuracy analysis between the proposed method and existing state-of-the-art approaches.

5. CONCLUSION

In this paper, a hybrid diagnostic framework for skin cancer detection and classification was presented by synergizing Deep Convolutional Neural Networks and the Ant Colony Optimization (ACO) algorithm. The initial cluster centroids were globally optimized using ACO to enhance the partitioning throughput of the K-means algorithm. Empirical evaluations conducted on the benchmark PH2 database demonstrated that the proposed intelligent algorithm achieves an outstanding classification accuracy of 96%, consistently outperforming alternative state-of-the-art methods. This research verifies that coupling metaheuristic swarm intelligence with deep learning architectures can dramatically accelerate and refine melanoma screening, offering highly effective computer-aided decision support for clinical practitioners.

Declaration

We acknowledge that we used ChatGPT to enhance the academic writing of our manuscript while ensuring the originality and integrity of our work.

Transparency Statement

The data supporting this study are available upon reasonable request to the corresponding author, subject to ethical and confidentiality considerations.

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Declaration of Interest

The authors declare that they have no competing interests.

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