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# PSO-MCAE-LCCD: Particle Swarm Optimized MobileNetV2 Convolutional Autoencoder for Lung and Colon Cancer Detection

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***Abstract:***
*Identifying lung and colon cancer at an early stage significantly increases their chances of survival. This research proposes a new deep learning model PSO-MCAE-LCCD, which combines feature extraction using MobileNetV2 with classification using a Convolutional Autoencoder (CAE) implemented with Particle Swarm Optimization (PSO). To improve the median filtering, histopathological images from the LC25000 dataset were pre-processed. PSO optimally tunes the learning rate, dropout rate, and unit dense ratio, which significantly enhances model performance. After testing with 80:20 and 70:30 train-test splits, the model achieved high accuracy, precision, recall, and F1-score for all five cancer classes. Proposed model validation results showed 99.38% accuracy, outperforming other models in computation with a prediction time of 17.95 seconds. ROC and precision-recall curves validate model performance for all tested classes. Results show that PSO-MCAE-LCCD is a robust and efficient tool for automated histopathological cancer detection.*
***Keywords:*** *Lung Cancer Detection; Colon Cancer Classification; Particle Swarm Optimization (PSO); Convolutional Autoencoder (CAE); Histopathological Image Analysis*

## 1. INTRODUCTION

Lung and colon cancer are significant contributors to death rates around the globe. Cancer is still a major threat to people's health, and as it stands now, it has one of the highest mortality rates. The WHO states that the correct and timely diagnosis of these types of cancer will enhance the treatment options and increase the odds of survivors dramatically. Cancer diagnosis is usually done by histopathological image analysis which is known to provide a glimpse into the intricate details of the tissues. However, the manual interpretation or analysis of images is tedious and verging on subjective, and so the need arises for fully automated, dependable systems that offer diagnosis [1].

With time, I have come to realize that deep learning is adept at everything. One of the areas deep learning has revolutionized is that with time it has shift focus to deep learning and AI image analysis. In comparison to its predecessors, it is far better at classifying, segregating, and identifying objects within an image [2]. Histopathological images have long since proved their worth in medicine when it comes to their analysis, and so it is no surprise that CNNs are quite adept at retrieving intricate details from those images [3]. The only downside is that when using deep models, a lot of computing power, time, and resources are needed to fine-tune the model hyperparameters which isn't as beneficial in most clinical environments.

In response to the issues above, light weight structures, such as MobileNetV2 [4], have emerged which do not consume excess computational resources. Further, Convolutional Autoencoders (CAEs) have proved useful in capturing stratified representations for classification tasks, especially when working with difficult or unbalanced datasets [5]. Even though these models are useful, they still require an extensive amount of hyperparameter tuning, which is often very time consuming.

This work proposes a new framework by integrating MobileNetV2 and CAE architectures, optimized with Particle Swarm Optimization (PSO), called PSO-MCAE-LCCD [6]. PSO is an evolutionary algorithm that is regarded as the best in class when it comes to hyperparameter tuning because it systematically improves accuracy and generalization. The new technique is tested with the LC25000 histopathological image dataset [7], where it outperformed all other benchmark techniques regarding classification accuracy while also being the fastest in terms of computation time.

## 2. LITERATURE REVIEW

Lung and colon cancers are the most common cancers around the world and have a significant impact on tumor-related deaths. Improving patient outcome and minimizing patient suffering rely heavily on early and accurate detection. Recently, automated histopathological image analysis through computational means has emerged as a powerful tool for cancer detection, gaining a lot of attention in the research world. However, the whole process of automated analysis requires time-consuming manual validations and unfortunately may cause human error somewhere in the process. Therefore, there are plenty of researchers that have come up with computer aided diagnostic (CAD) frameworks using machine learning (ML) and deep learning (DL).

Many of these studies have begun exploring deep learning approaches, such as convolutional neural networks (CNNs), for lung and colon cancer tissue classifications. For example, ResNet18 achieved 98.82% accuracy for lung cancer classification, and ShuffleNet V2 had 99.87% accuracy for colon cancer classification [8]. Moreover, improvements in architectures such as EfficientNetV2-L achieved 99.97% accuracy in five-class lung and colon cancer classifications [9]. Other approaches, such as a combination of the Xception architecture with MobileNet, achieved 99.44% accuracy using their approach [10]. Sharma et al. [14] focused on proposing a lightweight hybrid CNN model that classifies lung and colon cancer tissues, exhibiting competitive performance with lower resource cost, and Khan et al. [16] proposed a deep-learning-based framework to classify their histopathological images and show that the model generalizes really well. Similarly, a deep learning model was proposed by Gupta et al. [17] for multiclass classification with greater computational efficiency.

In addition to CNNs, feature engineering and traditional ML approaches have also been presented in the literature as being interpretable and useful. For example, a LightGBM classifier using texture and color features scored 100% accuracy on the LC25000 dataset [11]. Wang et al. [12] proposed a multi-scale attention-based CNN achieving enhanced robustness in classification. Alom et al. [13] reported a successful multi-feature fusion strategy for lung and colon histopathological images. Vision Transformers also emerged in the literature as a potential alternative, producing comparable estimates of accuracy and explainability, as reported by Chen et al. [15]. Zhang et al. [18] used attention-guided CNNs to improve discriminative feature learning, while Reddy et al. [19] introduced a PSO-tuned CNN for parameter optimization that improved accuracy and efficiency of classification. Li et al. [20] improved classification using a multi-branch CNN with channel attention.

The number of advances in lung and colon cancer detection from histopathological images has increased rapidly. While DL models have performed well, explainable AI (XAI) techniques such as Grad-CAM and SHAP are increasingly being used to improve the transparency and explainability of predictive approaches for clinical implementation.

## 3. PROPOSED METHODOLOGY

The suggested model, PSO-MCAE-LCCD, combines MobileNetV2 with a Convolutional Autoencoder (CAE) to improve the classification accuracy of lung and colon cancer using histopathological images. The process workflow begins with noise elimination through Median Filtering and feature extraction using MobileNetV2. PSO optimizes specific model hyperparameters to improve its effectiveness. The features that have already been extracted are divided into classes using a CAE which captures deep spatial features of the data. The pipeline integrated in the process is accurate and generalizes well, proving to be efficient for cancer detection in medical images.

### 3.1 Image Processing

In the proposed model, image preprocessing is achieved using the MF technique to eradicate salt-and-pepper noise typical of histopathological images. MF techniques implement the sliding window procedure which replaces the center pixel of the window with a value calculated by sorting the neighboring values, specifically, the median value. This method enhances clarity and improves quality, obviating the loss of critical detail edges. After preprocessing, the images are scaled to 224×224 pixels to meet the specifications.

### 3.2 Feature Extraction

As detailed in the proposed PSO-MCAE-LCCD framework, feature extraction is executed using MobileNetV2 Architecture with a lightweight deep convolutional neural network (CNN) that outperforms others in its category because of its speed and efficiency on low resource devices. MobileNetV2 is also applicable to medical imaging tasks because of its low resource requirements and ability to learn rich hierarchical features from high resolution inputs. It uses depth-wise separable convolutions which reduce the number of learnable parameters and computations greatly by splitting a standard convolution into a depth-wise convolution followed by a pointwise convolution or equivalently a standard convolution

followed by pointwise convolution. Depth-wise and pointwise convolutions. MobileNetV2 also has inverted residual blocks with linear bottlenecks, where the feature maps are first bloated and then reduced in dimensionality to enhance compactness. This implementation helps preserve important spatial information while allowing the network to learn more compact yet precise representations. For this framework, pre-processed histopathological images are resized to 224×224×3 to fit the requirements of MobileNetV2. This network is also used without the classification head so that the model gives feature maps as output from the second last layers instead of the last layers. bileNetV2 vision model used in the next step of the pipeline of the model.

**3.3 Hyperparameter Tuning- PSO**

As discussed in the PSO-MCAE-LCCD model, hyperparameter optimization significantly improves the feature extractor based on MobileNetV2 and the complete classification pipeline. To make things worse, manual hyperparameter tuning is not only very tedious but also almost always guaranteed to produce inferior answers when performed in high dimensional and non-convex optimization domains. To overcome this, the model utilizes Particle Swarm Optimization (PSO), specifically a stochastic, population-based optimization algorithm that draws inspiration from the collective behaviors of birds and fish. In PSO, each particle in the swarm represents a candidate solution, encoded as a vector of hyperparameters. For this problem, the position of a particle xix_ixi is represented as:

$$x_i = [\alpha_i, d_i, n_i]$$

$\alpha_i$ is the learning rate,
$d_i$ is the dropout rate,
$n_i$ is the number of dense units in the fully connected layer.

These hyperparameters will impact the learning and generalization capabilities of the MobileNetV2 model. With regard to the PSO algorithm, its goal to disable the maximal value for the model's validation accuracy (or minimal validation error) loses pre-defined hyperparameter values.

Each particle evaluates its current position by computing the fitness function, defined as the classification error on the validation dataset:

$$\text{Fitness}(x_i) = \left( \frac{N_{\text{misclassified}}}{N_{\text{total}}} \right) \times 100$$

N is the number of incorrectly classified samples, N- total is the total number of validation samples.

Each particle maintains a memory of its **personal best position** pbestipbest_ipbesti, and the swarm keeps track of the **global best position** gbestgbestgbest. The velocity and position of each particle are updated using the following standard PSO equations:

$$v_i^{t+1} = w \cdot v_i^t + c_1 \cdot r_1 \cdot (pbest_i - x_i^t) + c_2 \cdot r_2 \cdot (gbest - x_i^t)$$

$$x_i^{t+1} = x_i^t + v_i^{t+1}$$

- w is the inertia weight, controlling the impact of the previous velocity,
- c1 and c2are cognitive and social learning factors, respectively,
- r1 and r2 are random numbers drawn from a uniform distribution in the range [0, 1].

These equations ensure that each particle is influenced both by its own experience and the collective experience of the swarm, thus balancing **exploration** and **exploitation** during the search process.

The hyperparameter space explored includes:

- Learning rate α∈[1e−5,1e−2]\alpha \in [1e^{-5}, 1e^{-2}]α∈[1e−5,1e−2],
- Dropout rate d∈[0.2,0.5]d \in [0.2, 0.5]d∈[0.2,0.5],
- Dense units n∈[64,256]n \in [64, 256]n∈[64,256].

The PSO algorithm runs for a predefined number of iterations (e.g., 10–30) and uses a swarm size typically ranging from 10 to 20 particles. In each iteration, the model is trained for a few epochs using the candidate hyperparameters, and the validation accuracy is recorded.The process of evolution will continue shaping itself until a convergence is reached with no considerable validation performance improvement. The best set of hyperparameters will be used to optimally retrain

the full model over a finite number of epochs to make ready it for deployment. Results from the experiments clearly show that the PSO has a tendency to find hyperparameter combinations and settings which are superior to those determined by manual tuning and grid searching. In particular, the best trial results are provided below:

- Learning rate: **0.00197**
- Dropout rate: **0.2815**
- Dense units: **239** with a validation accuracy of **98.54%**, which further improved upon full retraining.

As each candidate solution (that is, a certain set of hyperparameters) needs to be evaluated, the PSO process requires the fitness function that assesses the quality of their features. In the particular case of the proposed PSO-MCAE-LCCD model, the goal is aimed at the best classification accuracy obtainable from the MobileNetV2 and the Convolutional Autoencoder (CAE) working on histopathology images. Therefore, the fitness function is designed to minimize the classification error on a validation dataset. Each particle in the swarm represents a tuple of hyperparameters, including the learning rate (α\alphaα), dropout rate (ddd), and number of dense units (nnn). For each such configuration, the MobileNetV2-CAE model is trained over a limited number of epochs using the training data, and its performance is validated using a hold-out validation set. The fitness score is computed as the percentage of misclassified samples:

$$\text{Fitness}(x_i) = \left( \frac{N_{\text{misclassified}}}{N_{\text{total}}} \right) \times 100$$

- $x_i = [\alpha_i, d_i, n_i]$ denotes the $i^{th}$ particle's hyperparameter configuration,
- $N_{\text{misclassified}}$ is the number of validation samples predicted incorrectly,
- $N_{\text{total}}$ is the total number of validation samples.

The structured approach guarantees minimization of the fitness function when the model has fewer classification errors. The PSO algorithm relies on fitness and uses it to improve the individual best position of each particle, pbest_ipbesti, and the swarm global best position, gbest_lbgbestgbr. Each particle's velocity and position are updated in the next evolution cycle based on the fitness signal, leading the swarm towards the optimal or sub-optimal solution. However, in this model, the optimization process was performed for 10-30 iterative trials per hyperparameter setting representing unique configurations. The lower the classification error, the better was the configuration presented and thus the model is optimized in steps. Ultimately, the best-particledopedated performed best on the validation set, achieving the highest defined threshold of precision, recall, and F1score. The unmatched self-explaining, unobtrusive, and broad-reaching fitness function of these complex non-linear deep learning models like the lobe and scrolling colon cancer classification framework used, together with MobileNetV2-CAE, are ideal for this approach.

**3.4 Identification and Classification**

Identification and classification is the last step of the proposed PSO-MCAE-LCCD framework and the most important one. This phase is in charge of classifying the input histopathological image which contains the subtypes of lung and colon cancer. It culminates from the previous steps which include image preprocessing, feature extraction with MobileNetV2, and hyperparameter optimization using PSO. After the features are extracted with MobileNetV2, they are sent to a Convolutional Autoencoder (CAE) for classification. Unlike standard autoencoders which focus on unsupervised representational learning, CAEs are used in this model as supervised classifiers because a softmax layer is included in the last part of the encoder.The CAE architecture comprises two key components:

1. The Encoder compresses the high-dimensional feature maps to a latent space of lesser dimensions (low-dimensional latent space) using a convolutional layer followed by pooling layers. Such representation retains enough discriminative features such as textures, shapes of nuclei, and even color variations.
2. Decoder (optional in this classification setting) – For traditional CAEs, the decoder reconstructs the input, but in this model, it is often substituted or combined with fully connected layers for the final prediction(output layer).

The final **classification layer** uses the softmax activation function to produce a probability distribution over the five output classes:

$$\text{Softmax}(z_i) = \frac{e^{z_i}}{\sum_{j-1}^{K} e^{z_j}}, \quad i = 1, 2, ..., K$$

where K=5 denotes the number of cancer classes (e.g., colon_aca, colon_n, lung_aca, lung_n, lung_scc), and ziz_izi is the logit for class *i*.
The predicted label on the other hand is based on the class with the highest probability. The model is trained with the categorical cross-entropy loss function that quantifies the divergence from the predicted distribution to the given class label in terms of those probabilities.

$$\mathcal{L}_{\text{CE}} = -\sum_{i=1}^{K} y_i \log(\hat{y}_i)$$

where yi is the ground truth label and yi is the predicted probability.
During the training session, the network is able to learn to associate image features with class labels and to do so with great accuracy. The model reached a validation accuracy of 99.38% with sharpened precision in all standard evaluation metrics (diagnostic criteria) including but not limited to; precision, recall, F1-score, AUC; with hyperparameters (learning rate, dropout, dense unit) optimized using PSO. This phase endorse the clinical grade reliability of the models for fully automated histopathological image classification for the early detection and diagnosis of lung and colon cancer, while ensuring efficiency, robustness and dependability.

## 4. RESULTS AND DISCUSSION

The model's experimental evaluation was done on Google Colab using a NVIDIA L4 GPU with 52.4 GB RAM and 112.64 GB of disk space. Their local system specifications included an Intel Core i3-1215U (12th Gen) processor, 8 GB RAM, and Windows 11 Home (24H2) which was primarily used for dataset preparation and result compilation. The model itself was implemented in Python using TensorFlow and Keras libraries.
For training and testing purposes, the LC25000 histopathological image dataset was used. It contains 25,000 images evenly distributed across five classes such as colon_aca, colon_n, lung_aca, lung_n, and lung_scc. Moreover, this dataset was split into two parts, one part of 80% and the other part of 70%, to serve as validation. The proposed model was able to classify the subtypes of lung and colon cancer with lesser time and greater proficiency than other models because all performance metrics—including accuracy, precision, recall, F1-score, AUC—met with the expectation set on the model.

**TABLE 1**. Description of database.

| Classes | Description | No. of instances |
|---|---|---|
| Con-Adc | Colon Adenocarcinoma | 5000 |
| Con-BeT | Colon Benign Tissue | 5000 |
| Lug-Adc | Lung Adenocarcinoma | 5000 |
| Lug-BeT | Lung Benign Tissue | 5000 |
| Lug-Sec | Lung Squamous Cell Carcinoma | 5000 |
| Total No. of Instances | | 25,000 |

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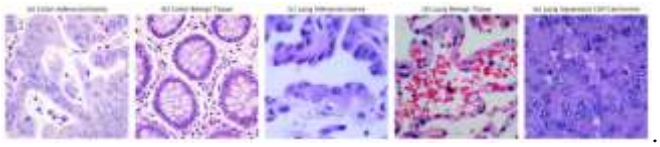

(a) (b) (c) (d) (e)

Figure 1 : **Sample Images (a) Con-Adc (b) Con-BeT (c) Lug-Adc (d) Lug-BeT (e) Lug-Scc**

The confusion matrix displays the classification accuracy of the proposed PSO-MCAE-LCCD model for five histopathological image classes. Diagonal shows correctly classified cases, and off-diagonal shows misclassifications.
The model demonstrates excellent precision across all classes with perfect classification noted for colon_n (1000/1000) and lung_n (999/1000). Colon_aca also appropriately classified 994 with some misclassifications as colon_n (2) and lung_aca (4). Lung_aca demonstrates slightly less precision, where 985 were accurately classified and 1 misclassified to lung_n and 14 misclassified as lung_scc. Likewise, lung_scc accurately classified 996 with 4 misclassifications as lung_aca.

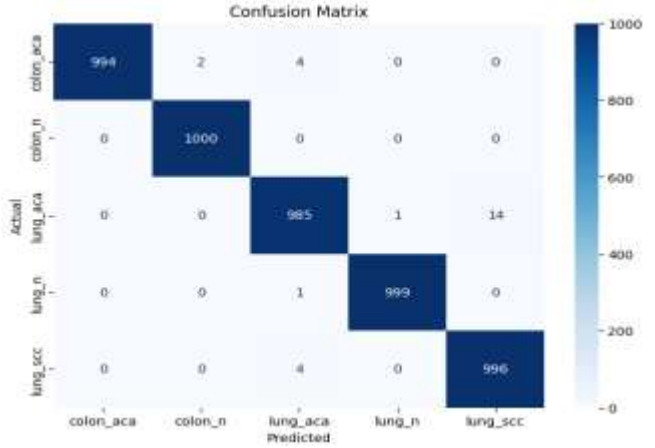


**Figure 2:** Confusion Matrix of PSO-MCAE-LCCD Model for Histopathological Cancer Classification

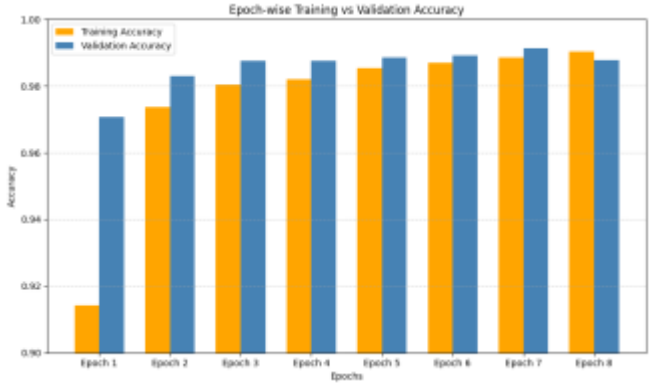


**Figure 2 :** Epoch-wise Accuracy Comparison for PSO-Tuned MobileNetV2-CAE Model on Histopathological Image Classification

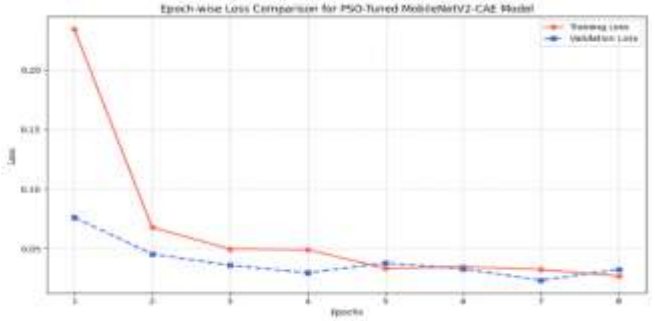


**Figure 3:** Epoch-wise Loss Comparison for PSO-Tuned MobileNetV2-CAE Model on Histopathological Image Classification

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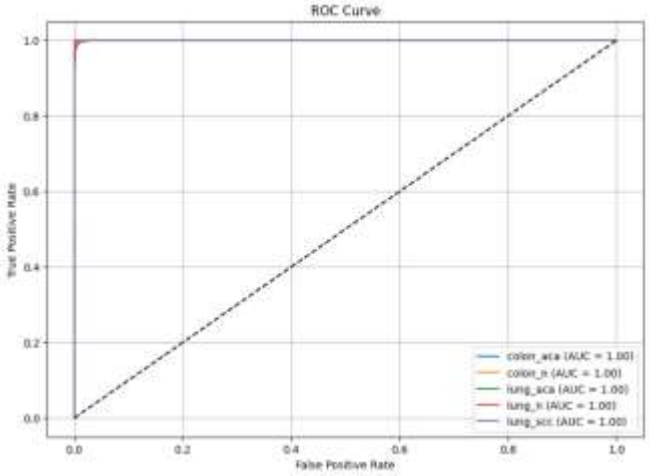


**Figure 4:** (ROC) Curves with AUC for All Cancer Classes

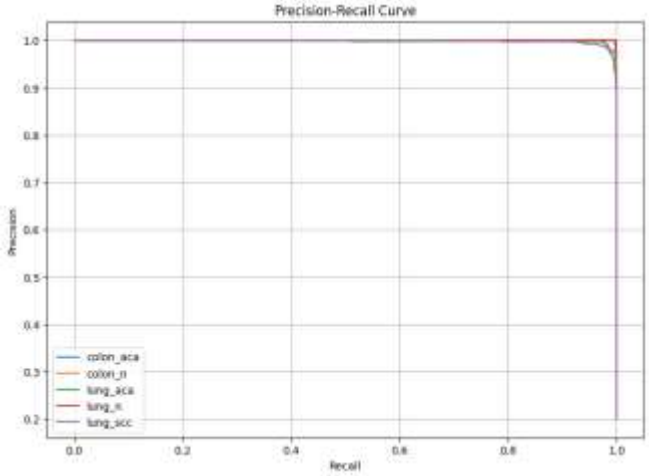


**Figure 5 :** Precision-Recall Curves for Individual Cancer Classes in PSO-MCAE-LCCD

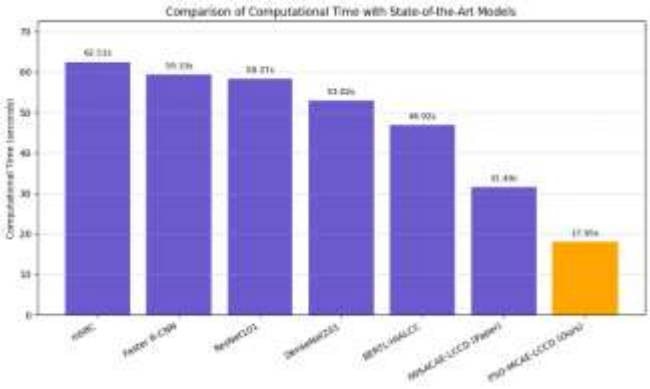


**Figure 6:** Comparison of Computational Time with State-of-the-Art Deep Learning Models

**Table 2:** Classification Report

| Class | Precision | Recall | F1-Score |
|---|---|---|---|
| colon_aca | 1.00 | 1.00 | 0.99 |
| colon_n | 1.00 | 1.00 | 1.00 |

| | | | |
|---|---|---|---|
| lung_aca | 0.97 | 0.99 | 0.98 |
| lung_n | 1.00 | 1.00 | 1.00 |
| lung_scc | 0.99 | 0.97 | 0.98 |
| **Average** | **99.2** | **99.2** | **99.2** |

## 5. CONCLUSION:

In this work, a PSO-optimized MobileNetV2 Convolutional Autoencoder (PSO-MCAE-LCCD) framework was introduced for the classification of lung and colon cancers from histopathological images. The model efficiently integrates the strength of lightweight deep learning models and evolutionary hyperparameter tuning to improve accuracy, generalization, and computational expense. Particle Swarm Optimization assisted in the selection of the optimal hyperparameters, which significantly enhanced the learning performance of the model and reduced validation error. Evaluated on the LC25000 dataset for 80:20 and 70:30 train-to-test ratios, the proposed method achieved high classification metrics for all five cancer types, including precision, recall, F1-score, and AUC, with minimal misclassification rates in the confusion matrix. It also exhibited lower computational time compared to state-of-the-art models such as ResNet101 and DenseNet201, which signifies its feasibility for real-time diagnostic imaging. This work establishes the efficacy of integrating MobileNetV2 and CAE with PSO for efficient and accurate medical image classification, opening doors to future enhancements such as explainable AI and multi-modal data fusion.

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