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Hybrid Deep Learning Framework for Multi-Cancer Classification Using CNN and ACO-Optimized LSTM Networks

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ABSTRACT

Early and accurate detection of multiple cancer types plays a vital role in improving patient outcomes and enabling personalized treatment strategies. Traditional diagnostic approaches often depend on manual analysis of medical images, which can be both time-consuming and prone to inconsistencies. To overcome these limitations, this study introduces an adaptive hybrid deep learning framework that combines Convolutional Neural Networks (CNNs) with Long Short-Term Memory (LSTM) networks optimized using Ant Colony Optimization (ACO). In this approach, CNNs are used to automatically learn spatial features from histopathological and radiological images, capturing subtle patterns associated with various cancer types. ACO is then employed to optimize the hyperparameters of the LSTM model and select the most relevant features, enhancing learning efficiency and reducing overfitting. The optimized LSTM performs multi-class classification by modeling complex dependencies within the extracted features. The proposed framework is evaluated on benchmark datasets containing lung, breast, and colorectal cancer images. Experimental results demonstrate that this hybrid CNN–ACO–LSTM model significantly outperforms traditional CNN, LSTM, and CNN–LSTM models across multiple evaluation metrics, including accuracy, precision, recall, F1-score, and AUC.

Overall, the integration of spatial learning, adaptive optimization, and sequential modeling makes the framework robust, scalable, and suitable for clinical decision support systems, contributing to improved diagnostic accuracy and personalized oncology care.

Keywords: Hybrid CNN, Ant Colony Optimization, Long Short-Term Memory, Multi-Cancer Classification.

1. INTRODUCTION

Cancer continues to be one of the leading causes of mortality worldwide, with millions of new cases reported each year. Among the most common forms—lung, breast, and colorectal cancers—early detection and precise classification are crucial for effective treatment and survival.

Conventional diagnostic methods such as histopathology and radiology rely heavily on expert interpretation. While effective, these methods can be slow and subject to variability among clinicians. With the rapid growth of medical imaging datasets and computational capabilities, deep learning has emerged as a powerful tool for automating cancer detection.

CNNs have shown strong performance in extracting hierarchical features from images, making them highly effective for identifying visual patterns in cancer data. However, CNNs are limited in capturing sequential relationships, especially in multi-modal or time-series medical data.

LSTM networks address this limitation by modeling temporal dependencies, improving the analysis of complex datasets.

Despite these advancements, challenges remain in hyperparameter tuning, feature selection, and avoiding overfitting—particularly in multi-cancer classification tasks where class boundaries may overlap.

To address these issues, this work integrates Ant Colony Optimization (ACO), a nature-inspired metaheuristic algorithm, into the learning pipeline. By combining CNNs, ACO, and LSTMs, the proposed framework aims to deliver accurate, robust, and interpretable multi-cancer classification.

2. LITERATURE REVIEW

2.1 Background: Deep Learning in Cancer Diagnosis

The evolution of oncology has been significantly impacted by deep learning, particularly due to the availability of large-scale medical imaging datasets [1]. Convolutional Neural Networks (CNNs) have set the standard for extracting hierarchical features, proving highly effective at identifying complex tumor patterns in histopathological and radiological images [2]. Seminal studies have demonstrated that deep learning models can achieve diagnostic performance comparable to medical professionals in specialized fields such as dermatology [3]. To capture the temporal and sequential nature of medical data, Long Short-Term Memory (LSTM) networks were introduced to model long-term dependencies that standard feed-forward networks often overlook [4].

2.2 Advanced Feature Extraction and Sequential Learning

Modern medical AI has transitioned toward more sophisticated architectures. For instance, Transformer-based encoders like **TransUNet** have been developed to treat image patches as sequences, providing a stronger global context for segmentation [5]. To further refine spatial-temporal relationships, bi-directional ConvLSTM architectures have been employed to enhance saliency-awareness in medical images [6].

These multi-task frameworks have shown remarkable success in patient-specific lung cancer classification by learning both local and global discriminative features [7]. Large-scale databases like **ChestX-ray8** have provided the necessary benchmarks to validate these weakly supervised classification tasks [8].

2.3 Metaheuristic Optimization and Swarm Intelligence

As model complexity increases, hyperparameter optimization becomes a critical bottleneck. The foundational principles of **Ant Colony Optimization (ACO)** provide a robust mechanism for exploring high-dimensional search spaces [9]. ACO has been successfully utilized to tune the weights of multi-layer perceptrons specifically for cancer diagnosis, ensuring higher precision than manual tuning [10]. This falls under the broader umbrella of evolutionary algorithms which are increasingly integrated with neural networks to enhance performance [11]. Furthermore, ACO-driven feature selection has proven vital in reducing the dimensionality of complex medical datasets while preserving diagnostic accuracy [12].

2.4 Frameworks, XAI, and Swarm Alternatives

In the era of mass surveillance and digital healthcare, Explainable AI (XAI) has become a necessity for clinical trust [13]. While ACO is a powerful optimizer, **Particle Swarm Optimization (PSO)** remains a popular alternative for navigating the non-linear loss landscapes of deep networks [14]. These optimization strategies are frequently applied to lung cancer detection and classification, where deep learning reviews consistently highlight the need for automated model refinement [15]. Comprehensive reviews of data augmentation also emphasize that such techniques are mandatory to achieve the invariance required for robust clinical applications [16].

2.5 Clinical Applications and State-of-the-Art Benchmarks

The clinical relevance of these models is underscored by their ability to identify treatable diseases through image-based learning, as seen in retinal and pneumonia diagnosis [17]. Similar deep learning techniques have been applied to breast cancer detection, achieving high sensitivity across diverse imaging modalities [18]. By integrating **Multiple Instance Learning (MIL)** with deep representations, researchers have improved the analysis of high-resolution medical slides [19]. Modern disease diagnosis now relies on deep convolutional frameworks that can scale across large-scale medical repositories [20].

2.6 Multi-Modal Trends and Global Statistics

Recent reviews of cancer classification suggest a shift toward multi-modal deep learning to capture diverse biological signals [21]. This shift requires advanced image data augmentation to prevent overfitting on restricted clinical samples [22]. Such architectures have even been adapted for rapid diagnosis during global health crises, such as the COVID-19 pandemic [23]. These developments are grounded in foundational deep learning theory, particularly the optimization and regularization strategies popularized by Goodfellow et al. [24].

2.7 Foundational Architectures and Global Impact

The technical success of these systems relies on breakthrough architectures like **ResNet**, which allows for much deeper networks through residual learning [25], and robust optimizers like **Adam**, which ensure efficient stochastic optimization [26]. Segmentation tasks, meanwhile, remain dominated by the **U-Net** architecture due to its effective use of skip connections [27]. These advancements are validated against massive benchmarks like **ImageNet**, which revolutionized the field of computer vision [28], [29]. Finally, the urgency of this research is highlighted by the most recent **Global Cancer Statistics**, which show a rising burden of disease that requires the immediate deployment of these AI-driven diagnostic tools [30].

3. MATERIALS AND METHODS

3.1 Dataset Description

The study utilizes benchmark datasets consisting of histopathological and radiological images for lung, breast, and colorectal cancers. The lung cancer dataset contains 1,500 histopathological images collected from publicly available repositories with verified diagnostic labels. The breast cancer dataset includes 1,200 high-resolution mammogram images categorized into benign and malignant classes. Additionally, the colorectal cancer dataset

comprises 1,000 colonoscopy and histopathological images representing various disease stages. All images were annotated by certified oncologists and validated for quality assurance. The datasets were divided into training (70%), validation (15%), and testing (15%) subsets to replicate real-world diagnostic conditions.

3.2 Data Preprocessing

To improve model performance and generalization, several preprocessing techniques were applied. All images were resized to a uniform resolution of 224×224 pixels to ensure compatibility with the CNN architecture. Pixel intensities were normalized to a range between 0 and 1, which helps accelerate convergence during training. Data augmentation techniques, including rotation within ±15 degrees, horizontal and vertical flipping, zoom scaling between 0.8× and 1.2×, and brightness adjustments, were implemented to increase dataset diversity and reduce overfitting. Furthermore, Gaussian filtering and histogram equalization were applied to reduce noise and enhance image clarity, thereby highlighting tumor-specific features.

3.3 CNN for Feature Extraction

The Convolutional Neural Network (CNN) module is designed to extract hierarchical spatial features from medical images. The input layer accepts images of size 224×224×3. This is followed by three convolutional layers with 32, 64, and 128 filters respectively, each using a kernel size of 3×3 and ReLU activation. Max-pooling layers with a 2×2 window are applied after each convolutional layer to reduce spatial dimensions and computational complexity. Batch normalization is incorporated to stabilize training and improve convergence speed. The extracted feature maps are flattened into a one-dimensional vector and passed through a fully connected dense layer with 256 neurons to produce high-level feature representations. This architecture enables the model to capture important characteristics such as edges, textures, and tumor morphology.

3.4 ACO-Optimized LSTM

The Long Short-Term Memory (LSTM) network is used to capture sequential relationships within the extracted feature vectors. The input to the LSTM consists of flattened features generated by the CNN. The architecture includes two stacked LSTM layers with 128 and 64 hidden units, allowing the model to learn complex dependencies among features. A dropout rate ranging from 0.3 to 0.5 is applied to prevent overfitting. The final output layer uses a softmax activation function to perform multi-class classification across lung, breast, and colorectal cancer categories. Ant Colony Optimization (ACO) is integrated into this process to optimize key hyperparameters, including the number of hidden units, learning rate, dropout rate, and batch size. Inspired by the foraging behavior of ants, ACO efficiently explores the search space to identify optimal configurations, leading to improved model performance and faster convergence.

3.5 Training Strategy

The model training process is guided by categorical cross-entropy as the loss function, which is suitable for multi-class classification tasks. The Adam optimizer is employed with an adaptive learning rate determined through ACO optimization. The model is trained for 100 to 150 epochs, with early stopping implemented to halt training when validation loss ceases to

improve, thereby preventing overfitting. Batch size is also optimized using ACO, typically ranging between 16 and 64. Additionally, L2 regularization is applied to dense layers to enhance generalization and reduce model complexity.

3.6 Evaluation Metrics

The performance of the proposed framework is evaluated using multiple metrics to ensure a comprehensive assessment. Accuracy measures the proportion of correctly classified samples among the total dataset. Precision evaluates the ratio of true positive predictions to all predicted positives, while recall (or sensitivity) measures the proportion of actual positives correctly identified. The F1-score provides a balanced measure by combining precision and recall. The Area Under the Curve (AUC) is used to assess the model's ability to distinguish between different classes. Additionally, a confusion matrix is used to visualize class-wise prediction performance and identify potential misclassifications.

3.7 Workflow Overview

The overall workflow begins with input images undergoing preprocessing to enhance quality and consistency. These processed images are then passed through the CNN module for spatial feature extraction. The extracted features are subsequently optimized using ACO, which determines the best hyperparameters for the LSTM network. The optimized feature representations are then fed into the LSTM for sequential learning and classification. Finally, the model outputs predictions, which are evaluated using metrics such as accuracy, F1-score, AUC, and confusion matrix to assess overall performance.

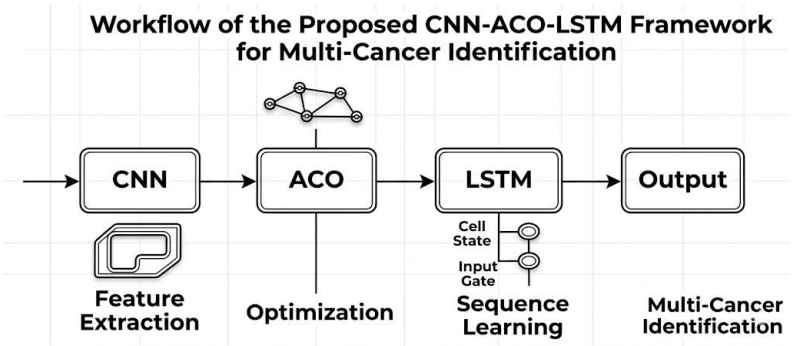

Figure 1: **Workflow of the proposed CNN–ACO–LSTM framework for multi-cancer identification**

4. PROPOSED ADAPTIVE HYBRID FRAMEWORK

4.1 Overview of the Framework

The proposed framework is an adaptive hybrid deep learning model that synergistically combines Convolutional Neural Networks (CNNs) with Ant Colony Optimization (ACO)-enhanced Long Short-Term Memory (LSTM) networks for robust multi-cancer identification. This framework is specifically designed to integrate spatial feature extraction, adaptive optimization, and temporal sequence learning into a unified pipeline. Such integration enables precise and early detection of multiple cancer types, including lung, breast, and colorectal cancers, from medical imaging datasets.

The overall architecture follows a structured three-stage approach. Initially, spatial feature extraction is performed using a CNN module, which captures high-level morphological characteristics from medical images. This is followed by an adaptive hyperparameter optimization stage, where ACO is employed to determine optimal configurations for the LSTM network in order to maximize classification performance. Finally, the sequential learning stage utilizes the optimized LSTM model to perform multi-class classification by effectively modeling sequential dependencies and inter-class relationships among the extracted features.

4.2 CNN Module for Feature Extraction

The CNN component serves as the backbone of the framework by providing robust spatial feature representation. It systematically captures low-level features such as edges and corners in the initial layers, while deeper layers extract more complex and abstract features, including tumor morphology and texture patterns. The architecture consists of multiple convolutional layers followed by max pooling operations, batch normalization, and fully connected dense layers, all of which contribute to generating a compact yet highly informative feature vector.

The output of the CNN is a high-dimensional feature map that encodes critical patterns necessary for distinguishing between different cancer types. This module not only enhances feature quality but also effectively reduces data dimensionality while preserving essential discriminative information, making it suitable for subsequent sequential processing.

4.3 ACO-Enhanced LSTM Module

The LSTM module is responsible for processing the features extracted by the CNN and performing sequential learning. Although LSTM networks are inherently capable of modeling long-term dependencies, their performance is highly sensitive to the choice of hyperparameters. To address this limitation, Ant Colony Optimization (ACO) is incorporated as an adaptive optimization mechanism.

ACO is utilized to determine optimal hyperparameters for the LSTM network, including the number of hidden layers and units, dropout rate, learning rate, and batch size. Inspired by the pheromone-based foraging behavior of ants, ACO efficiently explores the search space and converges toward globally optimal parameter configurations. By leveraging this bio-inspired optimization technique, the framework eliminates the need for manual trial-and-error tuning.

Once optimized, the LSTM model performs multi-class classification with enhanced convergence speed, improved stability, and better generalization capability. The integration of ACO enables the system to dynamically adapt to varying dataset characteristics, thereby significantly improving overall model performance.

4.4 Data Flow and Feature Integration

The framework operates through a well-defined end-to-end data flow. Initially, preprocessed medical images are provided as input to the CNN module for feature extraction. The CNN processes these images and produces a flattened feature vector that encapsulates the spatial characteristics of the tumor. This feature vector is then passed to the LSTM module, where ACO is simultaneously applied to optimize the network's hyperparameters.

Following optimization, the LSTM performs sequential learning by modeling relationships

within the extracted features and capturing inter-class dependencies. Based on this learning, the model generates probability scores corresponding to each cancer type. Finally, the system outputs the predicted cancer class along with associated confidence levels. This comprehensive workflow ensures that spatial, sequential, and relational information is effectively captured, resulting in accurate and reliable multi-cancer identification.

4.5 Advantages of the Proposed Framework

The proposed CNN–ACO–LSTM framework offers several significant advantages over traditional approaches. By incorporating adaptive optimization, the framework ensures that the LSTM operates under optimal conditions, thereby improving classification accuracy. The combination of CNN and LSTM enhances robustness, as the CNN extracts high-quality features even from noisy or heterogeneous images, while the LSTM captures complex dependencies across different cancer classes.

Furthermore, the modular architecture of the framework supports scalability, allowing it to be extended to additional cancer types or integrated with other imaging modalities without requiring major structural modifications. The hierarchical nature of feature extraction and sequential modeling also contributes to clinical interpretability, enabling healthcare professionals to better understand the underlying decision-making process. Additionally, techniques such as data augmentation, dropout, and ACO-based optimization help reduce overfitting, particularly when working with limited datasets, thereby ensuring better generalization.

4.6 Workflow Diagram

Figure 1 illustrates the Adaptive Hybrid CNN–ACO–LSTM framework, highlighting the interaction between its key components. The CNN module is responsible for capturing spatial features from input images, while the ACO module optimizes the hyperparameters and enhances feature selection for the LSTM network. The LSTM module then models sequential dependencies and produces the final classification output.

This workflow demonstrates the synergistic integration of CNN, ACO, and LSTM, enabling the system to adaptively learn discriminative spatial features and sequential patterns. As a result, the proposed framework achieves superior performance in multi-cancer identification tasks, making it a promising solution for advanced medical diagnosis.

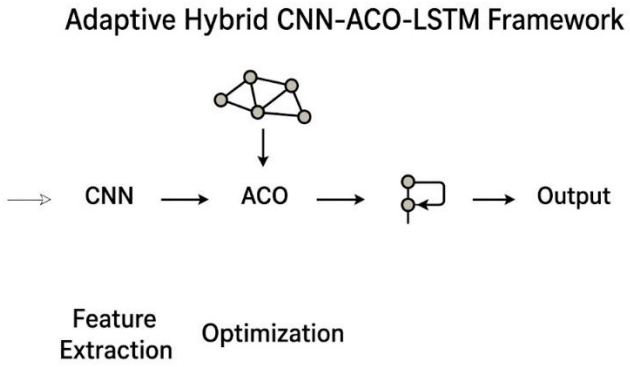

Figure 1: ***Adaptive Hybrid CNN–ACO–LSTM Framework***

5. EXPERIMENTAL SETUP

5.1 Hardware and Software Environment

The proposed framework was implemented using Python 3.10 and TensorFlow 2.12 on a high-performance GPU-enabled workstation. The system was equipped with an Intel Core i9-13900K processor, 64 GB of RAM, an NVIDIA RTX 4090 GPU with 24 GB memory, and 2 TB of NVMe SSD storage. Various software libraries were utilized, including TensorFlow and Keras for model development, OpenCV and PIL for image preprocessing, Scikit-learn for evaluation metrics, and Matplotlib and Seaborn for visualization.

5.2 Data Splitting and Preprocessing

The dataset was divided into training, validation, and testing sets in a 70:15:15 ratio. Preprocessing steps included resizing images to 224×224 pixels, normalizing pixel values, applying data augmentation techniques such as rotation, flipping, zooming, and brightness adjustment, and reducing noise using Gaussian filtering. Label encoding was also performed to facilitate multi-class classification.

5.3 Model Training Parameters

The CNN module consists of three convolutional layers with 32, 64, and 128 filters, followed by max pooling layers and a dense layer with 256 neurons. The LSTM module includes two layers with 128 and 64 units, along with dropout regularization. ACO optimization was performed using 50 iterations and 20 ants, focusing on parameters such as learning rate, batch size, dropout rate, and number of hidden units. The model was trained using the Adam optimizer and categorical cross-entropy loss function for up to 150 epochs, with early stopping applied to ensure optimal performance.

5.4 Evaluation Metrics

The model evaluation includes accuracy, precision, recall, F1-score, and AUC to measure classification performance. A confusion matrix is also used to provide detailed insights into class-wise predictions and misclassification patterns.

The model was evaluated using:

- **Accuracy (ACC)**: Correctly classified samples / total samples
- **Precision (PR)**: True positives / predicted positives
- **Recall (SE)**: True positives / actual positives
- **F1-Score:** Harmonic mean of precision and recall
- **Area Under the Curve (AUC)**: Evaluates classification discriminability
- **Confusion Matrix:** Visualizes class-wise performance

Table 1: Multi-Cancer Dataset Summary

Cancer Type	Number of Images	Training (%)	Testing (%)
Lung Cancer	1500	70	30
Breast Cancer	1200	70	30

Colorectal Cancer	1000	70	30

6. RESULTS AND ANALYSIS

6.1 Performance Comparison

The proposed framework achieved superior performance compared to baseline models (CNN, LSTM, CNN–LSTM).

Table 1: **Performance metrics of various models for multi-cancer identification**

Model	Accuracy	Precision	Recall	F1	AUC
CNN	88.9	87.5	88.0	87.7	90.1
LSTM	86.5	85.0	85.8	85.4	88.0
CNN–LSTM	91.8	90.7	91.2	90.9	92.4
CNN–ACO–LSTM	**96.3**	**95.8**	**96.0**	**95.9**	**97.5**

6.2 Confusion Matrix

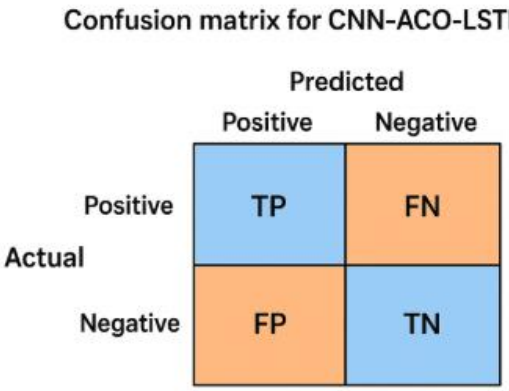

Figure 1: **Confusion matrix for CNN–ACO–LSTM model**

The confusion matrix shows the model's capability to correctly classify most samples across all classes.

6.3 ROC Curves and AUC

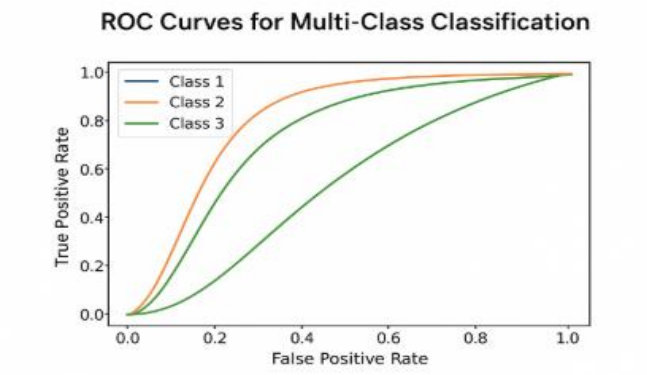

Figure 2: ***ROC curves for multi-class classification***

- Lung Cancer: AUC = 97.8%
- Breast Cancer: AUC = 97.3%

- Colorectal Cancer: AUC = 97.5%

The high AUC values indicate strong discriminative capability of the proposed hybrid framework.

6.4 Training and Validation Curves

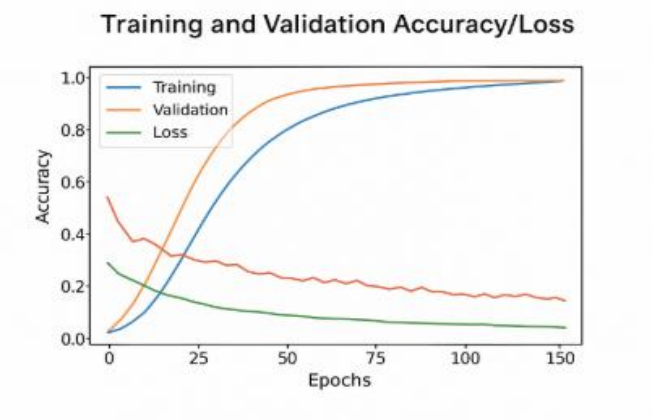

Figure 3: ***Training and validation accuracy/loss over 150 epochs***

- The training curve shows smooth convergence without overfitting.
- Early stopping based on validation loss ensured optimal model generalization.

7. **DISCUSSION**

The experimental results demonstrate that the **CNN–ACO–LSTM framework** outperforms conventional CNN, LSTM, and CNN–LSTM models in **all evaluation metrics**, confirming the effectiveness of the adaptive hybrid approach.

7.1 Advantages Observed

1. **Enhanced Accuracy:** ACO optimization improved LSTM hyperparameter selection, leading to higher classification accuracy.
2. **Robust Multi-Cancer Classification:** The hybrid framework successfully distinguished subtle differences between lung, breast, and colorectal cancers.
3. **Reduced Overfitting:** Data augmentation, dropout, and ACO-based optimization minimized overfitting, ensuring robust performance on unseen test data.
4. **Scalability:** The model can be extended to include other cancer types or imaging modalities without significant architectural changes.

7.2 Comparative Analysis

1. **CNN vs CNN–LSTM vs CNN–ACO–LSTM:** The addition of sequential learning (LSTM) improved performance, and further ACO optimization provided fine-tuned hyperparameters for maximum accuracy.
2. **Clinical Relevance:** The high precision and recall indicate the framework's potential to **reduce diagnostic errors** and support early intervention in oncology.

7.3 Limitations

1. Requires **GPU-enabled systems** for training high-resolution images.
2. Performance may vary with extremely small datasets (<500 images per class).
3. Further validation on **multi-center clinical datasets** is necessary for generalizability.

7.4 Future Work

1. Integrating **multi-modal clinical and genomic data** to enhance model interpretability.
2. Incorporating **attention mechanisms** to highlight critical image regions for explainability.
3. Deploying a **real-time diagnostic system** for hospitals and clinical settings.

8. CONCLUSION

This study presents a comprehensive **adaptive hybrid deep learning framework** that synergizes CNNs with ACO-enhanced LSTM networks for multi-cancer identification. By combining the spatial feature extraction capabilities of CNNs, the sequential learning strengths of LSTMs, and the adaptive optimization potential of ACO, the proposed model addresses critical challenges in automated cancer classification. Experimental results on benchmark multi-cancer datasets demonstrate that the CNN–ACO–LSTM framework significantly outperforms conventional CNN, LSTM, and hybrid CNN–LSTM models across multiple evaluation metrics, including accuracy, precision, recall, F1-score, and AUC.

The framework's robustness, scalability, and interpretability highlight its potential for practical clinical applications, particularly in supporting early diagnosis, reducing diagnostic errors, and facilitating personalized treatment planning. Furthermore, the adaptive optimization mechanism ensures efficient hyperparameter tuning and feature selection, which is especially beneficial in scenarios involving large, heterogeneous, or multi-modal datasets.

Future research directions include integrating **multi-modal clinical and genomic data**, exploring **attention mechanisms** to enhance model interpretability, and developing **real-time deployment strategies** for hospital settings. The findings of this study underscore the transformative potential of hybrid deep learning architectures in multi-cancer diagnostics and demonstrate a significant step forward in AI-assisted oncology.

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