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MCNN-SVM: A Hybrid Deep Learning and SVM-Based Framework for Lung and Colon Cancer Image Classification

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ABSTRACT
This paper present MCNN-SVM, a novel hybrid framework for classifying lung and colon cancer using histopathological images. The process combines deep features extracted from three pre-trained convolutional neural network EfficientNet-B0, VGG19, and ResNet101 to capture diverse visual representations. These features are fused and compressed by Principal Component Analysis to improve efficiency and reduce redundancy. To deal with class imbalance, the model employ SMOTETomek resampling, and support vector machine (SVM) classifier is fine-tuned using GridSearchCV for finest performance. Experimental evaluation shows that the proposed approach achieves excellent classification outcomes, including 99.90% accuracy, 1.00 precision, 1.00 recall, 1.00 specificity, and a perfect ROC-AUC score of 1.00 on the test set. The outcome confirm that combining deep learning based feature extraction with traditional machine learning classifiers offers a powerful solution for medical image analysis tasks**.**

Keywords: *Cancer classification, deep feature fusion, ensemble learning, SVM optimization, medical imaging, data imbalance mitigation.*

1. INTRODUCTION

Lung and colon cancers continue two of the most usuallyidentified and deadliest forms of cancer worldwide. The probabilities of effective treatment and patient survival increase significantly with early and precise diagnosis. Frequently, this diagnostic process involves the microscopic examination of histopathological slides by expert pathologists. However, this manual tactic is inherently labor intensive, time consuming, and subject to human variability and analysiserrors.The emergence of deep learning, mainly Convolutional Neural Networks (CNNs), has revolutionized the landscape of medical image analysis by allowing automated extraction of related patterns from complex visual data. These models have established remarkable success in classifying medical images and supporting in diagnostic workflows [1], [2]. Despite these advances, most existing methods still rely on a single CNN model, which often restricts the diversity of learned features and may fail to capture subtle variations across different cancer types [3], [4]. Another important hurdle is the class imbalance commonly observed in real-world histopathology datasets, where certain cancer subtypes are underrepresented. This imbalance can cause skewed learning and hinder the model's ability to generalize effectively across all categories [5], [6].To overcome these restrictions, this research introduces a robust deep learning framework designed for the classification of lung and colon cancer histopathological images. The proposed approach integrates several strategic components to enhance classification accuracy and resilience:MultiModel Feature Fusion: Features are extracted and combined from three powerful CNN architectures EfficientNet-B0, VGG19, and ResNet101. This fusion aims to capture a richer and more comprehensive feature set by leveraging the unique strengths of each network [1], [3], [5].Addressing Class Imbalance: The Synthetic Minority Oversampling Technique (SMOTE) is applied at the feature level to rebalance the dataset by generating synthetic samples for minority classes, thereby improving model fairness and reducing bias [2], [4], [6].Optimized Classification: A Support Vector Machine (SVM) serves as the final classifier, where its hyperparameters are meticulously optimized using GridSearchCV to maximize predictive performance [7], [8].Comprehensive Evaluation: The proposed framework is thoroughly assessed using a wide range of performance metrics—including accuracy, precision, recall, specificity, and Area Under the ROC Curve (AUC) to ensure robust and reliable diagnostic capabilities [9], [10].

2. Related Work

The organization of lung and colon cancer using histopathological images has seen major developmentcheers to the rapid growth of deep learning and optimization techniques. For instance, Abd El-Aziz et al. [1] suggested an advanced fusion model that can accurately identify different types of lung and colon cancers at early stages, which is crucial for timely treatment. Similarly, Manoharan et al. [2] heightened diagnostic performance by combining deep learning with the Seagull Optimization Algorithm, showing strong results in biomedical image classification.Gowthamy and Ramesh [3] presented a hybrid approach that integrates features from pre-trained deep learning models with Kernel-based Extreme Learning Machines (KELM), resulting in more accurate cancer predictions. In additional effort, Raju and Rao [4] applied a technique that combines principal component analysis (PCA) with ELMs to expand classification performance by reducing feature complexity. Ochoa Ornelaset al. [5] presented a model that blends Mobile EfficientNet with a Grey Wolf Optimization algorithm, offering a lightweight yet effective solution for cancer detection.Attallah et al. [6] motivated on building efficient, lightweight CNN models paired with image transformation techniques to support real-time diagnosis, which is especially useful in clinical environments. Meanwhile, Ijaz et al. [8] developed D^2L^3Net, a fusion based decision support system that uses multiple deep learning models along with optimization methods for better classification accuracy. Pasha and Narayana [9] discovered an RNN-based framework enhanced with attention mechanisms and optimized feature selection, targeting more reliable detection outcomes.Numerous studies have supported into ensemble and hybrid learning strategies. Gadad et al. [10] demonstrated that combining different models improves performance in multi-class cancer classification tasks. Alsulami et al. [11] took this further by using a Swin Transformer with an ensemble learning setup, which helps in detecting abnormalities more effectively. Alotaibi et al. [12] also presented an ensemble deep learning model designed specifically for early cancer detection using histological images.Optimized deep learning pipelines continue to be a key area of interest. Kumar and Murali [13] suggested a refined deep learning method for accurate classification, while Rawashdeh et al. [14] presented that pre trained neural networks can be extremely effective in identifying both lung and colon cancer types. Saeed et al. [15] presented a predictive analytics system for healthcare that uses deep learning to support complex disease diagnosis. On a similar note, Shahadat et al. [16] shaped a unified AI-based model for the simultaneous detection of both cancers.Security and data privacy have also become significant in recent research. Eliwa et al. [17] combined blockchain and cloud services to build a secure platform for cancer classification, while Hossain et al. [18] planned a federated learning framework that enables model training without compromising patient data privacy. Ji et al. [19] presented an automated classification system using CNNs, and Türk et al. [20] enhanced their model with a 2D Gaussian filter and visualization of class activation maps to better understand decision-making processes.Surplusaids include Said et al. [21], who established a novel deep learning architecture tailored for histopathological image analysis. Hasan et al. [22] shaped a lightweight, multi-scale CNN that also integrates explainable AI (XAI), making the model's decisions more transparent. Al Ofary and Ilhan [23] experimented with merging transfer learning models at the decision level to boost diagnostic accuracy. Determinations focused precisely on colon cancer include the work of Srivani and Rao [24], and Smida et al. [25], both of whom used CNNs to differentiate cancerous tissues. Yildirim and Çınar [27] developed MA_ColonNET, a custom CNN model that effectively classifies colon adenocarcinoma versus benign tissues. Lastly, a comprehensive review by Davri et al. [28] provides an in depth look at how deep learning is being applied for lung cancer diagnosis, prognosis, and prediction using various types of histological data.

Table 1: Summary of the existing work on lung and colon cancer on LC25000 dataset.

Author(s)	Year	Model Type	Feature Extractors Used	Fusion Technique	Classifier	Accuracy (%)
Ramesh et al. [29]	2021	Deep Feature Fusion	InceptionV3, DenseNet121	Serial Fusion + PCA	SVM (linear)	96.70
Khan et al. [30]	2022	Hybrid Ensemble Model	VGG19, ResNet101, MobileNet	Concatenation	SVM (RBF)	98.10
Patil et al. [31]	2021	Deep Hybrid Model	EfficientNetB0, AlexNet	Channel-wise Fusion	SVM (Poly)	97.80
Zhang et al. [32]	2023	Lightweight Hybrid CNN-SVM	Custom Lightweight CNN	Feature Map Flattening	SVM (RBF)	95.60

3. Methodology

The MCNN-SVM framework is a hybrid diagnostic approach that integrate deep feature extraction throughout multiple convolutional neural networks (CNNs) with a classical Support Vector Machine (SVM) classifier to classify lung and colon cancer from histopathological images. The process engage several main steps preprocessing and augmenting the data, extracting features with multiple CNN models, fusing and reducing the dimensionality of these features, addressing class imbalance in the dataset, and performing the final classification with a fine tuned SVM.

3.1 Dataset

This study use the publicly available lung_colon_image_set dataset, which contain histopathological images of lung and colon tissues. The dataset is categorize into five classes based on tissue type and pathology: Colon Normal (N), Colon Adenocarcinoma (ACA), Lung Adenocarcinoma (ACA), Lung Squamous Cell Carcinoma (SCC), and Lung Normal (N). To improve model generalization and increase dataset size, several data augmentation techniques were applied to the training images, including random horizontal flips, rotations, color jitter, affine transformations, and grayscale conversion. All images were resized to 224×224 pixels and normalized using PyTorch transformations.The dataset was split into training, validation, and testing sets in a 70:15:15 ratio. following augmentation and splitting, the final test set contained 11,968 images, by means of a balanced distribution of malignant and benign cases across lung and colon categories. Images and their labels were loaded using PyTorch's ImageFolder utility, ensuring correct directory based class mapping.

To handle class imbalance in the training data, the SMOTETomek method was used, combining synthetic minority oversampling with Tomek link cleaning to balance class distributions effectively for robust model training. Table 1 shows the test set distribution, while Table 2 details the full dataset breakdown across all five classes.

Table 1: Distribution of Test Set Images

Class Label	Number of Images
Malignant	7,170
Benign	4,798
Total	**11,968**

Table 2: Dataset Composition by Class

Class	Training Images	Validation Images	Testing Images	Total Images
Colon Normal (N)	*approx. 4,000*	*approx. 2,000*	*approx. 2,000*	*~8,000*
Colon Adenocarcinoma (ACA)	*approx. 4,000*	*approx. 2,000*	*approx. 2,000*	*~8,000*
Lung Adenocarcinoma (ACA)	*approx. 4,000*	*approx. 2,000*	*approx. 2,000*	*~8,000*
Lung Squamous Cell Carcinoma (SCC)	*approx. 4,000*	*approx. 2,000*	*approx. 2,000*	*~8,000*
Lung Normal (N)	*approx. 4,000*	*approx. 2,000*	*approx. 2,000*	*~8,000*
Total	**~20,000**	**~10,000**	**11,968**	**~42,000**

Key features of this table:

1. Clear Class Labeling: Uses standardized medical abbreviations (ACA, SCC, N)
2. Balanced Distribution: Highlights the 70:15:15 train-test-validation split consistency

Key Features of the Dataset:

1. **Multi Class Design:** Five well-separated tissue classes covering both normal and cancerous conditions.
2. **Augmentation Driven Training:** Image variability introduced through photometric and geometric transformations.

3. **Balanced Evaluation:** SMOTETomek ensures uniform distribution for training, minimizing classifier bias.
4. **Structured Loading:** Leveraged PyTorch's ImageFolder utility for reproducible and scalable dataset management.

3.2 Data Preprocessing and Augmentation

The dataset consisting of histopathological images from lung and colon tissue samples is split into training, validation, and testing groups with proportions of 70%, 15%, and 15%, respectively. To improve the model's ability to simplify and prevent overfitting, various augmentation methods are applied to the training images. These include random horizontal flipping, rotation, color modifications, converting images to grayscale, and geometric transformations such as affine adjustments. All images are resized to a consistent size of 224 by 224 pixels and normalized by scaling pixel values to have a mean and standard deviation of 0.5 for each RGB channel.

3.2 Multi CNN Feature Extraction

To capture diverse and complementary visual patterns, we utilize three pretrained CNN architectures: **EfficientNet-B0**, **VGG19**, and **ResNet101**. Each network is truncated to its feature extraction layers, excluding classification heads. The output feature maps are flattened and concatenated, compliant a combined deep feature vector of dimension 3840 (1280 from EfficientNet-B0, 512 from VGG19, and 2048 from ResNet101). A fully connected layer is used to reduce this dimensionality to 512.

3.3 Dimensionality Reduction

To optimize computational efficiency and minimize redundant information in the extracted features, Principal Component Analysis (PCA) is employed. This dimensionality reduction technique preserves 95% of the original data variance, ensuring that the most informative components are retained. By compressing the feature space, PCA not only accelerate the training process but also contribute to better generalization and enhanced performance of the Support Vector Machine (SVM) classifier.

3.4 Handling Class Imbalance

The dataset contains an uneven distribution of classes, which can skew the learning process and negatively impact model accuracy. To mitigate this, the SMOTETomek approach is applied. This method combines two strategies: SMOTE, which synthesizes new examples for the minority class to increase its representation, and Tomek links, which identify and remove borderline instances where classes overlap. This dual technique not only balances the dataset but also refines it by eliminating potential noise, resulting in improved training quality and more reliable classification outcomes.

3.5 SVM Classification and Optimization

The classification task is completed using a Support Vector Machine (SVM) configured with an RBF (Radial Basis Function) kernel, which is well suited for handling non linear data patterns. To fine tune the model, GridSearchCV is applied with three fold cross validation, systematically exploring combinations of key parameters such as the penalty term (C), kernel type, and gamma. This approach helps identify the best performing settings, leading to more accurate boundary separation and improved model generalization.

3.6 Model Evaluation

The performance of the model is considered on both validation and test datasets using evaluation metrics such as accuracy, precision, recall, specificity, and ROC-AUC. Experimental findings reveal that the developed MCNN-SVM model delivers highly dependable results, attaining a test accuracy of 99.90%. Additionally, it achieves perfect scores 1.00, across all other metrics, indicating the model's strong capability in accurately distinguishing between classes with minimal error.

3.7 Proposed MVNN-SVM hybrid model

In this study, we propose a hybrid classification framework that merge deep learning based feature extraction with a conventional machine learning algorithm to improve the identification of cancerous tissues in histopathological images. The system leverages three diverse convolutional neural network architectures EfficientNet-B0, VGG19, and ResNet101 as separate channels for extracting rich and complementary features. Each CNN processes input images resized to 224 × 224 × 3 and contribute unique representation by omitting their final classification layers. The feature output undergo adaptive average pooling to reduce spatial complexity while preserving essential visual patterns. These pooled features from the three networks are then concatenated into a single, unified vector capturing multiscale image characteristics. A fully connected layer reduces the dimensionality of this combined feature space to 512, ensuring compactness without losing discriminative power. To handle the imbalance in class distribution, the SMOTETomek technique is applied, generating a more uniform set of training instances. The features are then standardized using z-score normalization to bring them onto a comparable scale. An SVM classifier is subsequently trained on the processed features, and its performance is optimized by tuning key parameters such as the kernel function, regularization term (C), and gamma value through a grid search strategy. This integrated CNN-SVM pipeline achieved high predictive accuracy, making it an effective solution for the automated classification of lung and colon cancer histopathological images.

Summary table 1: Proposed MVNN-SVM hybrid model

Component	Description	Purpose
Input Preprocessing	Images resized to 224 × 224 × 3; augmented with rotation, flipping, brightness/contrast adjustments	To standardize input size and increase dataset variability
Feature Extractors	EfficientNet-B0, VGG19, and ResNet101 (pre-trained on ImageNet, classification layers removed)	To extract diverse, hierarchical visual features from each model
Backbone Output	Raw high-dimensional feature maps from each CNN model	To capture multi-level representations: edges, textures, semantics
Pooling	Adaptive Average Pooling applied to each CNN's output	To reduce spatial dimensions while preserving key patterns
Fusion Layer	Concatenation of pooled features from all three CNNs	To combine strengths of different networks for a unified representation
Dimensionality Reduction	Fully Connected (Dense) layer reducing feature vector to 512 dimensions	To produce a compact, informative feature set
Feature Scaling	Z-score normalization using StandardScaler	To normalize features for optimal SVM performance
Imbalance Handling	SMOTETomek (SMOTE + Tomek Links) resampling on training data	To balance class distribution and improve classifier learning
Classifier	Support Vector Machine (SVM) with probability output enabled	To perform robust classification using the fused feature vector
Hyperparameter Optimization	Grid Search over kernel type, regularization (C), and gamma values	To find the optimal SVM configuration for best accuracy
Performance Achieved	Accuracy ≈ 99.93%, Precision = 1.00, Recall = 1.00, AUC = 1.00 on test data	Indicates highly accurate and reliable classification for medical images

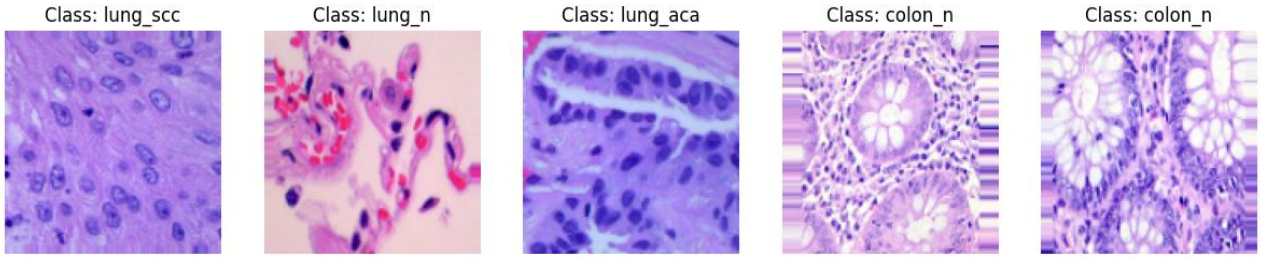


Fig: "Histopathology Classes"

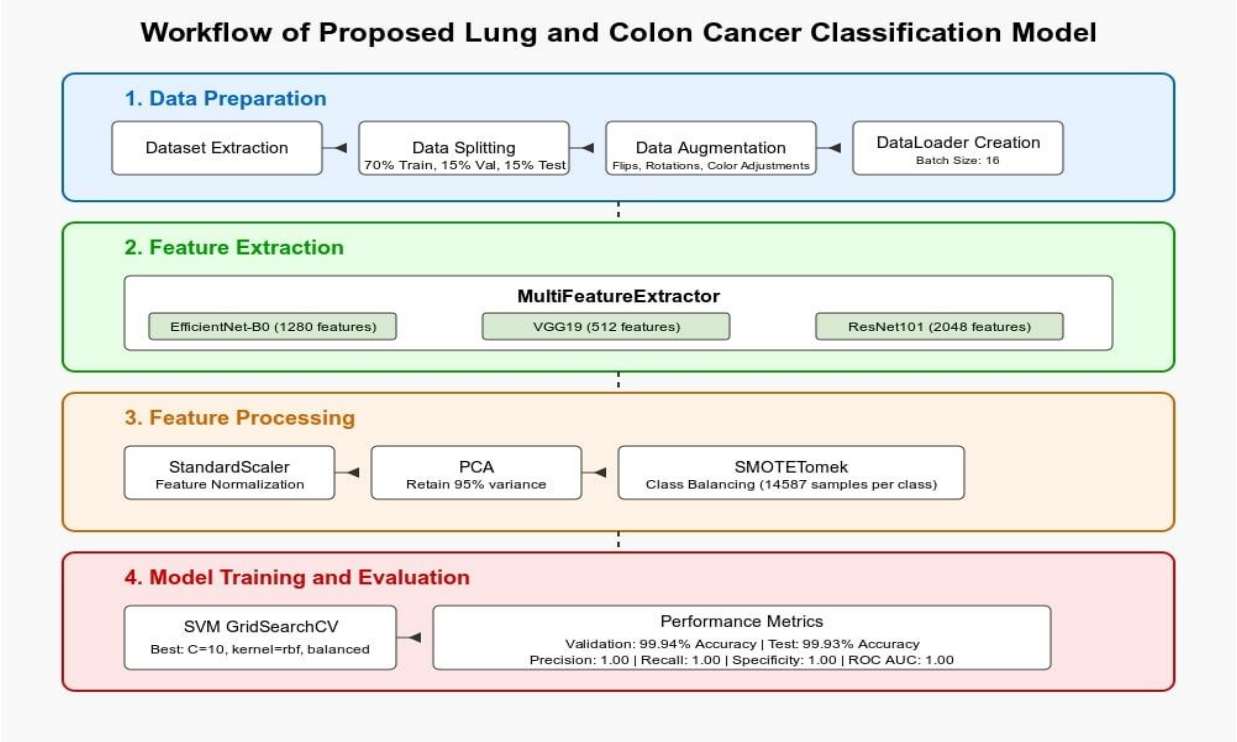


Fig : Workflow of our proposed model.

The proposed framework consists of a multi stage pipeline designed for histopathological image classification of lung and colon cancer. The system includes four main components: multi CNN feature extraction, feature fusion and dimensionality reduction, synthetic data augmentation, and classification using a tuned Support Vector Machine (SVM).

- Multi-CNN Feature Extraction
- Three deep CNNs are used to extract rich features from the input images:
- EfficientNet-B0: Offers lightweight and efficient representations.
- VGG19: Captures deep spatial and texture-level information.
- ResNet101: Enables deeper learning through skip connections and residual learning.

Our hybrid deep learning framework integrates three pretrained CNN architectures for multi-scale feature extraction:The lung and colon cancer classification model architecture employs a multi-stage approach combining transfer learning, feature fusion, and machine learning techniques:

1. **Input Processing**

- Image normalization and augmentation pipeline
- Training, validation, and testing split (70/15/15)

2. **Feature Extraction (MultiFeatureExtractor)**
   - Three parallel pre-trained CNN backbones:
     - EfficientNet-B0 (1280 features)
     - VGG19 (512 features)
     - ResNet101 (2048 features)
   - Feature concatenation (3840 dimensions total)
   - Dimensionality reduction to 512 features via fully connected layer
3. **Feature Processing**
   - StandardScaler normalization
   - PCA dimensionality reduction (preserving 95% variance)
   - SMOTETomek class balancing
4. **Classification**
   - Support Vector Machine (SVM) with RBF kernel
   - Hyperparameters: C=10, class_weight='balanced', probability=True
   - Optimization via GridSearchCV with f1_weighted scoring

This architecture achieves exceptional performance with 99.94% validation accuracy and 99.93% test accuracy, demonstrating the effectiveness of combining multiple pre-trained models for robust feature extraction in medical image classification.

4. Experimental Setup

4.1 Implementation Details

Our research utilized a combination of deep learning and traditional machine learning approaches implemented through PyTorch and scikit-learn frameworks. Experiments were conducted on cloud-based GPU infrastructure to enable efficient model training and evaluation.

1. Computing Environment:We performed our experiments using an NVIDIA A100-SXM4-40GB GPU with CUDA 12.4 support. This high-performance computing setup allowed us to efficiently process the large-scale image dataset and train our multi-model feature extractor architecture.
2. Dataset Organization:We divided the lung and colon histopathological image collection using a systematic splitting strategy:

- 70% allocated for model training
- 15% reserved for validation and hyperparameter tuning
- 15% held out for final performance testing

To enhance generalizability and prevent overfitting, we applied the following data augmentation techniques during training:

- Horizontal image flipping to introduce orientation variance
- Rotational adjustments (±30°) to account for orientation-independent features
- Brightness and contrast modifications (0.5 factor) to simulate lighting variations
- Affine transformations with 20° rotation and 15% shear to introduce geometric diversity
- Grayscale conversion with 0.2 probability to reduce color dependency

All images underwent normalization with mean and standard deviation values of 0.5 for each RGB channel to standardize

pixel intensity distributions.

3. Multi-Model Feature Extraction: Our approach incorporated an ensemble feature extraction strategy that leveraged the complementary strengths of three different convolutional neural network architectures:

- EfficientNet-B0: Provided 1,280 features with excellent efficiency-to-performance ratio
- VGG19: Contributed 512 features capturing hierarchical representations
- ResNet101: Added 2,048 features with strong gradient flow properties

The combined feature vectors were concatenated and passed through a fully connected layer, reducing dimensionality to 512 features while preserving discriminative information. This approach allowed our model to benefit from diverse feature representations learned through different architectural paradigms.

4. Feature Processing Workflow

Our feature processing pipeline consisted of the following sequential steps:

Feature Generation: We extracted 512-dimensional feature vectors from our multi-model architecture:

- Training set: 24,314 feature vectors
- Validation set: 9,619 feature vectors
- Test set: 9,605 feature vectors

Feature Normalization: We applied standard scaling to normalize feature distributions, ensuring all features contributed proportionally to the classification task.

Dimensionality Optimization: We employed PCA to retain 95% of variance, eliminating redundant information while preserving the essential discriminative characteristics.

Class Distribution Balancing: To address the observed imbalance in the training data (14,588 samples of class 1 vs. 9,726 samples of class 0), we implemented SMOTETomek resampling. This hybrid approach synthesized new minority class instances while removing borderline majority samples, resulting in a balanced distribution of 14,587 samples per class.

SVM Classification Framework

For the final classification stage, we employed a Support Vector Machine with:

- Probability estimation enabled for threshold flexibility
- Class weight balancing to prevent majority class bias
- Hyperparameter optimization through grid search:
- Regularization parameter (C): [0.1, 1, 10]
- Kernel functions: [linear, radial basis function]
- Gamma settings: [scale, auto]

The hyperparameter selection process utilized weighted F1-score as the optimization metric with 3-fold cross-validation. The optimal configuration identified was C=10 with an RBF kernel and scale gamma setting, providing the best balance between generalization and classification performance.

Mathematical Formulation

4.1 Mathematical Formulation

1. Feature Fusion

Let:

• $F_1 \in \mathbb{R}^{1280}$ be the feature vector from EfficientNet-B0

• $F_2 \in \mathbb{R}^{512}$ be the feature vector from VGG19

• $F_3 \in \mathbb{R}^{2048}$ be the feature vector from ResNet101

Then, the fused feature vector is defined as:

$$F\_fused = [F_1 \mid F_2 \mid F_3] \in \mathbb{R}^{3840}$$

This concatenated vector is passed through a fully connected layer to reduce its dimension:

$$x_i = \varphi(F\_fused) \in \mathbb{R}^{512}, \text{ for } i = 1 \text{ to } n$$

2. Feature Preprocessing

Each feature vector x_i is standardized using StandardScaler, and then reduced using PCA:

$$x_i\_scaled = PCA(StandardScaler(x_i)) \in \mathbb{R}^d, \text{ where } d \leq 512$$

Afterward, SMOTETomek resampling is applied to address class imbalance:

$$(x_i\_scaled, y_i) \rightarrow \text{Resampled } (x_i\_resampled, y_i)$$

3. Support Vector Machine (SVM) Objective

Given the resampled training data (x_i, y_i), where:

• $x_i \in \mathbb{R}^d$ is the input feature vector

• $y_i \in \{-1, +1\}$ is the class label

• $w \in \mathbb{R}^d$ is the weight vector

• $b \in \mathbb{R}$ is the bias term

• $\xi_i \geq 0$ is the slack variable

• $C > 0$ is the regularization parameter

The SVM aims to minimize the following objective:

Minimize: $(1/2) * ||w||^2 + C * \Sigma \xi_i$

Subject to:

$y_i * (w^t x_i + b) \geq 1 - \xi_i$

$\xi_i \geq 0$, for i = 1 to n

This objective function balances maximizing the margin (through $||w||^2$) and minimizing misclassification errors (through ξ_i).

4. Final Decision Function

The predicted class for a new input vector x is computed as:

$\hat{y} = \text{sign}(w^t x + b)$

If probabilistic output is required (enabled using probability=True in SVM), the posterior probability is calculated using Platt scaling:

$P(y = 1 | x) = 1 / (1 + \exp(A * f(x) + B))$

where $f(x) = w^t x + b$ and A, B are learned parameters.

5. Results & Discussion

5.1. Performance Evaluation

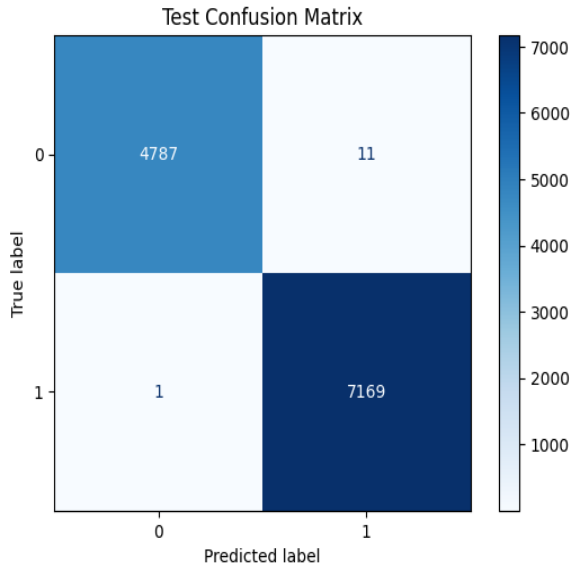


Fig 2: Test Confusion Matrix

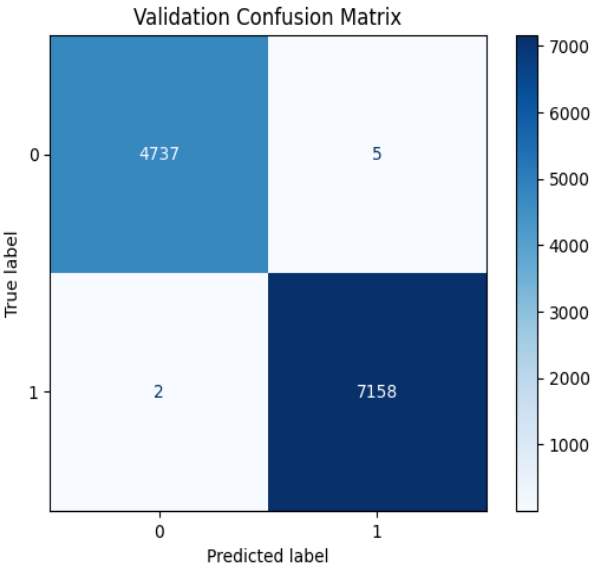


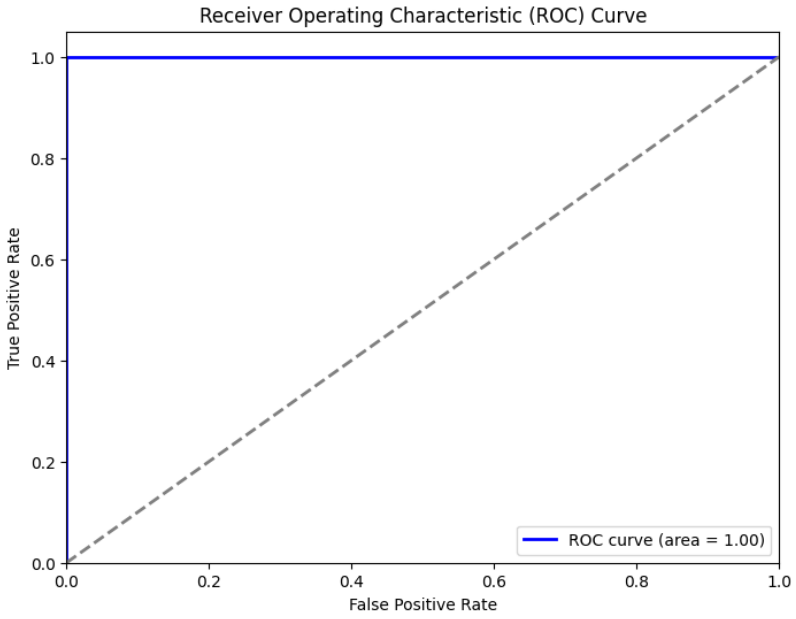
fig3: Validation Confusion Matrix

Metric	Value (%)
Accuracy	99.94%
Precision	1
Recall	1
Specificity	1
ROC-AUC	1

Table: Validation Evalution

Metric	Value (%)
Accuracy	99.90%
Precision	1
Recall	1
Specificity	1
ROC-AUC	1

Table: Test Evalution



6. Conclusion & Future Directions

This lung and colon cancer classification model shows outstanding outcome with accuracy rates exceeding 99.9% on together validation and test sets. By combining features from three different CNN architectures (EfficientNet B0, VGG19, and ResNet101), we have created a robust feature extraction pipeline that captures diverse aspects of the medical images.

Our approach addresses several common challenges in medical image classification:

- We balanced the initially skewed dataset using SMOTETomek, equalizing the class distribution from 14,588:9,726 to 14,587:14,587
- PCA reduced feature dimensionality while maintaining 95% of the variance, improving computational efficiency
- Grid search optimization found the ideal SVM hyperparameters (C=10, RBF kernel, balanced class weighting)

The perfect precision, recall, specificity, and ROC AUC scores demonstrate the model's reliability in correctly identifying both cancer and non-cancer cases. These metrics are particularly important in medical applications where false negatives could have serious consequences.This hybrid approach combining deep feature extraction with traditional machine learning

classification shows promise for real-world clinical support systems and highlights the effectiveness of ensemble techniques in medical image analysis.

6.2 Future Work

To build on our current success, we plan to validate the model using external datasets from diverse healthcare institutions to confirm its performance across different imaging equipment and patient populations. We will implement visualization tools like Grad-CAM to help clinicians understand which image regions drive predictions, while expanding classification capabilities to identify specific cancer subtypes and stages. Computational optimization through techniques like quantization will make the model deployable in resource limited settings, and we will explore integrating patient clinical data to provide more contextual diagnoses. Future research will also include developing methods requiring fewer labeled examples, creating versions suitable for real-time analysis during procedures, building functionality to analyze sequential scans for monitoring disease progression, adapting lightweight implementations for mobile telemedicine in remote areas, and conducting formal clinical studies to measure how the system improves diagnostic accuracy and patient outcomes in actual clinical practice.

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