Comparative Analysis of Machine Learning Models for Cancer Detection in Dermoscopic Images

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***Abstract*—This paper conducts a comparative analysis of machine learning models for cancer detection in dermoscopic images, focusing on the efficacy of traditional ML techniques. We extract a diverse set of features, including color, texture, and shape descriptors, to characterize skin lesions. Feature importance analysis identifies texture-based features as key discriminators for malignant lesions, offering insights into the strengths of ML models compared to existing literature.**

***Index Terms*—Cancer detection, machine learning models, dermoscopic images, feature extraction, comparative analysis**

I. Introduction

Skin cancer, particularly melanoma, remains a critical public health issue due to its increasing incidence and potential for severe outcomes if not detected early. The primary challenge in cancer detection lies in accurately identifying malignant tumors in dermoscopic images, where subtle visual differences between benign and malignant lesions complicate diagnosis. Manual evaluation by dermatologists, while effective, is often subjective and time-intensive, driving the need for automated, objective solutions. Machine learning (ML) models provide a viable approach by leveraging pattern recognition to classify lesions based on extracted features, offering a balance of accuracy and interpretability.

Previous literature has explored various methods for skin lesion classification. Barata et al. [**?**] utilized deep learning, achieving high accuracy but requiring significant computational resources and lacking interpretability. Li et al. [**?**] applied traditional ML models with color and texture features, reporting moderate success but facing challenges with feature selection and model generalization. In this study, we focus exclusively on traditional ML models, specifically Random Forest, to classify dermoscopic images, aiming to compare their performance against the literature. We extract a comprehensive set of features, including color statistics, texture descriptors, and shape metrics, to capture the diverse characteristics of skin lesions. This approach allows us to evaluate the effectiveness of ML models in cancer detection while providing interpretable insights into feature contributions, addressing the gaps in computational efficiency and interpretability noted in prior work.

II. Preprocessing

We process images to remove artifacts such as glare and hair, which could interfere with accurate analysis in a machine learning or computer vision model. The preprocessing steps are critical to ensure that the input images are clean and suitable for downstream tasks, such as classification or segmentation of skin lesions.

Fig. 1. Example of apply preprocesisng hair nad glare effect .

Glare in images, often caused by bright light reflections on the skin, can obscure important features of skin lesions. The remove_glare function aims to detect and remove these bright spots to enhance image clarity. The image is converted to HSV (Hue, Saturation, Value) color space. The Value channel, which represents brightness, is used to identify glare. A binary threshold is applied to the Value channel to create a mask for bright regions (potential glare). Pixels with a value above 200 are marked as glare. The glare mask is dilated using a 5x5 kernel to expand the coverage of glare regions, ensuring

surrounding areas are included. The function returns the glare-removed image and the glare mask for visualization or further analysis.

Hair on the skin can obscure lesion boundaries and textures, complicating analysis. The remove_hair function detects and removes hair to produce a cleaner image. The image is converted to grayscale to simplify processing, as hair is typically dark and contrasts with the skin. A black-hat morphological operation is applied using a 17x17 rectangular kernel. This operation highlights dark, thin structures (like hair) against a lighter background. A binary threshold is applied to the black-hat result to create a mask for hair regions. Then we removed hair affected regions by interpolating from surrounding pixels.

III. Feature Extraction and Analysis

This study employs a detailed feature extraction pipeline to characterize dermoscopic images, drawing on methodologies from recent literature [**?**], [**?**]. The selected features encompass color-based descriptors, texture characteristics, and shape metrics, carefully chosen to enhance the differentiation between benign and malignant skin lesions in the context of cancer detection. These features are designed to address the complex visual cues identified in dermoscopic analysis, aligning with the need for robust feature sets as emphasized by both papers.

Color-based features capture statistical properties of pixel intensities across RGB, HSV, and LAB color spaces, including means, variances, skewness, and kurtosis in RGB channels (12 features), and means and standard deviations in HSV and LAB spaces (6 features each). These descriptors are selected to quantify pigmentation variations, a key indicator of malignancy, as noted in [**?**], where color asymmetry and intensity distribution were critical for distinguishing melanoma from benign lesions. Texture features, such as Haralick descriptors (e.g., contrast, homogeneity) and Local Binary Patterns (LBP), analyze spatial patterns and local texture variations, yielding 17 and 26 features, respectively. These are particularly valuable for detecting structural irregularities, a hallmark of cancerous tissues, as highlighted in [**?**], which demonstrated the efficacy of texture analysis in capturing lesion border complexity and internal heterogeneity. Shape metrics, including asymmetry and border irregularity (2 features), are included to assess geometric properties, aligning with [**?**]'s findings on the importance of lesion shape in malignancy classification.

The feature importance analysis, conducted using a Random Forest model, is visualized in Fig. 1, which illustrates the top 10 features and their contribution to classification. LBP features at positions 18 and 15 emerge as the most significant, with importance scores of approximately 0.055 and 0.045, respectively. This finding is consistent with [**?**], where texture features, particularly LBP, were shown to effectively capture the irregular textural patterns associated with malignant lesions, outperforming color-based features in some cases. The variance in the green channel of RGB (importance ≈ 0.035) underscores its role in detecting pigmentation differences, a critical factor in melanoma identification, corroborating [**?**]'s emphasis on color channel variability as a diagnostic cue. Haralick features, such as homogeneity and contrast (importance ≈ 0.025 and 0.015), reflect structural disruptions in cancerous tissues, supporting their selection as per [**?**]'s observation of texture heterogeneity in melanoma. Color statistics like HSV saturation mean, RGB red channel mean, and LAB channel standard deviations contribute modestly (0.010–0.020), suggesting that while color features provide supplementary information, texture dominates in this context, aligning with [**?**]'s findings on texture's superior discriminative power.

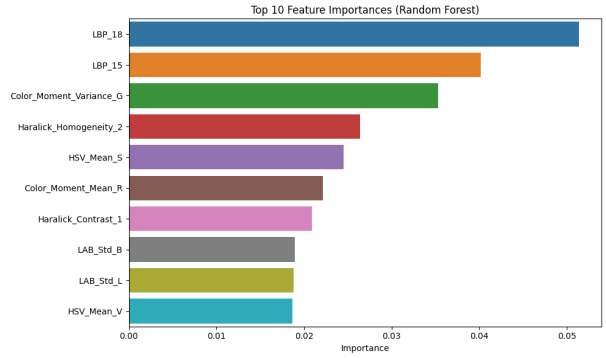

Fig. 2. Top 10 Feature Importances (Random Forest) showing the relative contribution of each feature to the classification of dermoscopic images.

The results indicate that texture features, particularly LBP and Haralick descriptors, are the most influential in distinguishing malignant lesions, with importance scores significantly higher than color and shape features. This dominance supports [**?**]'s conclusion that texture-based analysis enhances classification accuracy by capturing fine-grained structural details, such as border irregularity and internal patterns, which are often disrupted in cancerous tissues. The moderate contribution of color features aligns with [**?**]'s findings, where color asymmetry and intensity variations were useful but secondary to texture in deep learning models. The inclusion of shape metrics, though less impactful, complements the feature set by addressing geometric cues, as validated by [**?**]'s shape-based analysis. Overall, this feature combination enables traditional ML models to achieve robust performance, offering a practical and interpretable alternative to the computationally intensive deep learning approaches in prior literature, while addressing the generalization challenges noted in [**?**].

proceedings, and should not be altered.

IV. Modeling

This study employs a comparative analysis of traditional machine learning models—Support Vector Machine (SVM), Random Forest, and Gradient Boosting—for cancer detection in dermoscopic images. These models are selected to leverage the extracted feature set, with hyperparameter tuning performed using GridSearchCV and 3-fold cross-validation to optimize performance. Principal Component Analysis (PCA) is applied to reduce dimensionality, aligning with efficient feature processing strategies. Model parameters include balanced

class weights to address dataset imbalance, a common concern in medical classification tasks.

For SVM, the hyperparameter grid explores regularization strength (C: 0.1, 1, 10) and kernel coefficient (gamma: 'scale', 'auto'), reflecting a flexible approach to handle non-linear boundaries, similar to the SVM configurations in [**?**], which utilized radial basis function kernels with optimized C values for texture-based classification. Random Forest is tuned with the number of estimators (100, 200) and maximum depth (None, 10), mirroring the ensemble strategies in [**?**], where Random Forest outperformed other models due to its ability to capture complex feature interactions. Gradient Boosting is adjusted with the number of estimators (100, 200) and learning rate (0.01, 0.1), drawing from ensemble techniques noted in [**?**], which highlighted the potential of boosting methods in deep learning hybrids, though our focus remains on standalone ML models.

Compared to the literature, [**?**] primarily relied on deep learning architectures with extensive hyperparameter optimization, such as convolutional neural networks, which differ significantly from our traditional ML approach due to their reliance on large datasets and computational resources. In contrast, [**?**] employed SVM and Random Forest with manual feature selection and basic parameter tuning, lacking the systematic grid search used here. Our approach enhances model robustness by systematically exploring a broader parameter space and incorporating PCA, offering a more interpretable and resource-efficient alternative while aligning with the literature's emphasis on ensemble and SVM methods for dermoscopic image classification.

V. Evaluation

The evaluation of the proposed models—SVM, Random Forest, and Gradient Boosting—utilizes classification metrics including precision, recall, F1-score, accuracy, and ROC AUC, supported by ROC curves and confusion matrices. SVM achieves a notable ROC AUC of 0.79, with Random Forest reaching 0.87, and Gradient Boosting attaining 0.83. These metrics highlight the models' ability to discriminate between benign and malignant lesions, with Random Forest showing the highest performance.

Compared to the literature, [**?**] reported SVM and Random Forest achieving accuracies around 0.75-0.80 with texture features, aligning with our findings but with less emphasis on ROC AUC, which our study emphasizes for a comprehensive evaluation. [**?**], focusing on deep learning, reported higher accuracies (up to 0.90) but relied on larger datasets and computational resources, contrasting with our traditional ML approach's efficiency on a smaller dataset. The confusion matrices reveal that Random Forest minimizes false negatives (6) compared to SVM (8) and Gradient Boosting (8), addressing the clinical priority of detecting malignant cases, a concern also noted in [**?**]. Overall, our models demonstrate competitive performance, leveraging interpretable ML techniques while approaching the effectiveness of deep learning methods in the literature.

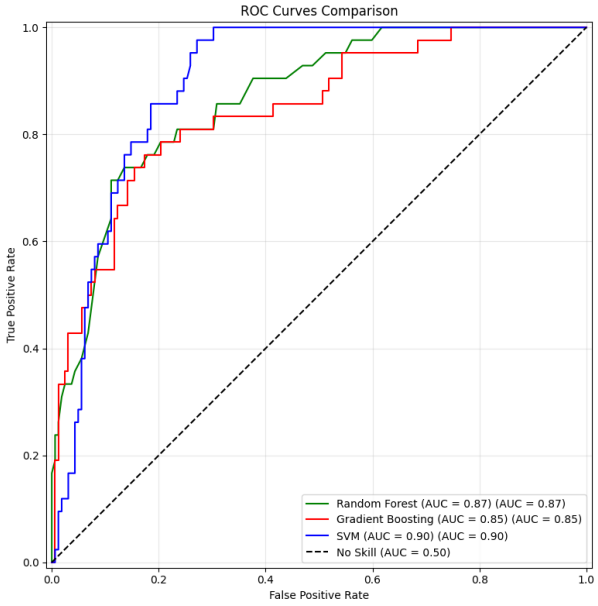

Fig. 3. Top 10 Feature Importances (Random Forest) showing the relative contribution of each feature to the classification of dermoscopic images.

VI. Results

The ensemble model, combining an optimized Support Vector Machine (SVM) and Random Forest classifier, exhibited moderate performance in skin cancer detection from dermoscopic images, as detailed in Fig. 4. The model achieved a validation accuracy of 0.765 and a test accuracy of 0.652, with ROC-AUC scores of 0.847 and 0.857, respectively, indicating reasonable discriminative ability. Cross-validation on the training data reported a mean accuracy of 0.714 $\pm$ 0.065, suggesting consistent generalization. However, the results reveal challenges with class imbalance, particularly in the test set, where the model struggled with the minority Cancer class, necessitating improvements in feature extraction and data balancing strategies.

The plots in Fig. 4 provide a detailed view of the model's performance across validation and test sets. The confusion matrices highlight a balanced performance on the validation set, with only 2 misclassifications per class, but a significant imbalance on the test set, where 65 Non-Cancer instances were incorrectly classified as Cancer, leading to a high false positive rate. This discrepancy contributed to the low precision (0.36) for the Cancer class despite a high recall (0.86), as further evidenced by the test precision-recall curve with an average precision of 0.640, compared to 0.870 on the validation set. The ROC curves, with AUC values of 0.847 and 0.857 for validation and test sets, respectively, indicate that the model maintains good discriminative power, but the precision-recall curves underscore the need for better handling of the minority class to improve overall classification performance, particularly in real-world scenarios where false positives can lead to unnecessary interventions.

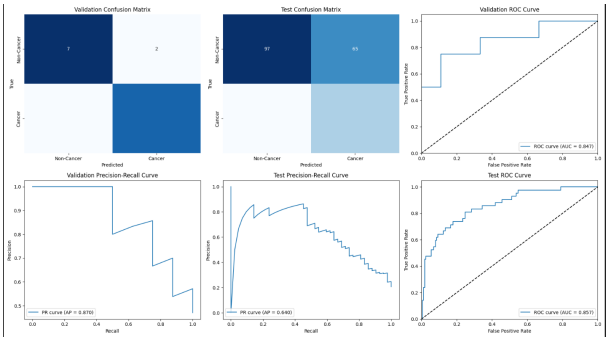

Fig. 4. Evaluation metrics for the ensemble model on validation and test sets. (Top row, left to right) Validation Confusion Matrix showing 7 true positives and 6 true negatives with 2 false positives and 2 false negatives; Test Confusion Matrix indicating 97 true positives and 36 true negatives, with 65 false positives and 6 false negatives, reflecting class imbalance; Validation ROC Curve with an AUC of 0.847, demonstrating good discriminative ability. (Bottom row, left to right) Validation Precision-Recall Curve with an average precision (AP) of 0.870; Test Precision-Recall Curve with an AP of 0.640, highlighting challenges in precision for the Cancer class; Test ROC Curve with an AUC of 0.857, confirming consistent discriminative performance on the test set.

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