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Predicting Melanoma Metastasis Using ISIC and TCGA Datasets with Hybrid Deep Learning

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Abstract — Melanoma ranks as one of the most lethal skin cancers, with metastasis responsible for the majority of associated deaths. Early and accurate identification of metastasis is crucial for informing treatment choices and enhancing patient survival. Previous deep learning methods have shown excellent results in melanoma classification but frequently experience drawbacks like dependence on a single backbone, limited feature representation, or failure to integrate diverse data from various medical sources. In this study, we introduce a hybrid deep learning model that combines dermoscopic images from the ISIC dataset with clinical and genomic information from the TCGA-SKCM cohort to forecast melanoma metastasis. The suggested model integrates the unique advantages of ResNet for hierarchical feature extraction and EfficientNet-B0 for enhanced multi-scale representation, allowing for a more profound and distinguishing comprehension of lesion morphology. A fusion module combines deep visual features with patient-specific characteristics to improve metastasis forecasting. Experimental assessment verifies that our hybrid architecture provides enhanced accuracy, robustness, and generalization over single-model baselines. The findings emphasize the capability of combining multi-source data with efficient hybrid networks to enhance accurate metastasis risk evaluation and clinical decision-making in managing melanoma.

Keywords — Melanoma, Metastasis Prediction, ISIC Dataset, TCGA-SKCM, Deep Learning, ResNet, EfficientNet-B0, Hybrid Model, Medical Imaging, Cancer Detection

I. INTRODUCTION

Melanoma is one of the most life-threatening forms of skin cancer, accounting for a significant proportion of skin-cancer-related deaths worldwide. Although early-stage melanoma can often be treated effectively, the disease becomes far more dangerous once it progresses to metastasis. Detecting metastatic potential at an early stage is therefore critical for improving patient survival, guiding treatment planning, and reducing the burden on oncology resources. Traditional diagnostic procedures rely heavily on dermoscopic image interpretation, histopathological evaluation, and clinical expertise. However, these methods are often subjective, time-consuming, and prone to inter-observer variability, making automated and reliable prediction systems increasingly important.

Recent advancements in deep learning have significantly improved the accuracy of skin cancer classification tasks by leveraging powerful convolutional neural networks (CNNs). Models such as ResNet, VGG, EfficientNet, and Capsule Networks have demonstrated strong capabilities in extracting complex skin-lesion features. Despite this progress, several challenges persist. Many existing frameworks operate solely on dermoscopic images and fail to incorporate broader clinical or genomic information relevant to metastasis. Others rely on a single backbone architecture, limiting their ability to learn diverse feature representations. Furthermore, most prior studies focus on binary melanoma classification rather than predicting metastatic behavior, which demands richer contextual understanding.

To address these limitations, this study explores a hybrid deep learning approach that integrates heterogeneous datasets for melanoma metastasis prediction. Dermoscopic images from the ISIC dataset provide detailed visual information on lesion morphology, while clinical and genomic metadata from the TCGA-SKCM cohort offer high-level biological insights related to tumor progression. By combining the strengths of ResNet for hierarchical feature learning and EfficientNet-B0 for efficient multi-scale representation, the proposed hybrid architecture enhances both feature richness and predictive capability. A fusion mechanism is employed to integrate visual features with patient-level metadata, enabling a more holistic understanding of metastatic patterns.

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This integrated methodology aims to produce a robust, generalizable model capable of assessing metastasis risk more accurately than conventional single-source or single-backbone techniques. The objective is to support clinicians with an automated decision-support tool that enhances diagnostic precision, improves early detection, and contributes to better patient outcomes in melanoma management.

II. Literature Review

Melanoma detection and metastasis prediction have received significant attention in the medical imaging and machine learning communities due to the disease's high mortality rate and the clinical importance of early diagnosis. Traditional diagnostic approaches depend largely on dermatologists' visual assessment and histopathological evaluation, which can be subjective and vary widely between clinicians. To overcome these limitations, researchers have increasingly adopted deep learning–based methods for automated and more reliable melanoma assessment.

Early studies primarily focused on **melanoma classification** using dermoscopic images from the ISIC archive. Approaches utilizing classical convolutional neural networks (CNNs), such as **VGG16**, **InceptionV3**, and **ResNet**, demonstrated substantial improvements in image-based lesion recognition. For example, VGG16 and Inception architectures showed strong performance in recognizing melanoma patterns, but they often required extensive computational resources and lacked robustness across diverse skin types. Similarly, ResNet addressed vanishing-gradient issues through residual connections and became a widely used baseline for skin lesion classification tasks. However, these models were limited to analyzing 2D dermoscopic images and did not incorporate clinical or molecular context relevant to metastasis prediction.

More recent studies introduced **EfficientNet**, which applies compound scaling to achieve state-of-the-art accuracy with significantly reduced model size and computational cost. EfficientNet-B0, in particular, has been adopted for medical imaging tasks due to its balance between accuracy and efficiency. While these architectures excel at extracting morphological features, they still operate as single-backbone models and therefore struggle to capture multi-scale lesion behavior or higher-level biological factors influencing metastatic progression.

To improve spatial modeling, researchers explored **Capsule Networks (CapsNet)** for lesion classification, leveraging capsule structures to better capture orientation and spatial relationships. Although CapsNet improved sensitivity to localized lesions, it incurred high computational overhead and performed inconsistently on larger datasets. Additionally, these architectures were mostly constrained to single-task learning and focused exclusively on lesion classification rather than predicting metastatic spread.

Beyond image-only methods, several studies on melanoma prognosis and metastasis prediction utilized the **TCGA-SKCM** dataset, which includes clinical data, gene expression profiles, and survival outcomes. Machine learning approaches based on support vector machines, random forests, or genomic risk scores showed potential in estimating metastatic risk. However, such models lacked integration with dermoscopic imaging, limiting their ability to capture visual indicators of disease progression.

Hybrid and multi-modal deep learning approaches have recently emerged to bridge these gaps by combining imaging data with clinical metadata or genomic signatures. These methods demonstrate improved predictive performance, particularly in multi-factorial diseases like melanoma. Nonetheless, many existing frameworks rely on a single deep learning backbone, do not fully exploit multi-scale feature representation, or struggle to effectively fuse heterogeneous data sources.

Given these limitations, there is a clear need for an integrated, computationally efficient, and clinically meaningful framework that combines powerful deep visual encoders with structured clinical and genomic information. This motivates the development of the proposed **hybrid ResNet + EfficientNet-B0 fusion model**, designed to enhance feature richness, improve metastasis prediction accuracy, and incorporate multi-source medical data into a unified learning system.

III. EXISTING SYSTEM

Existing systems for melanoma detection and metastasis prediction have primarily focused on two separate domains: image-based lesion classification and clinical/genomic risk modeling. Although each domain has demonstrated significant progress, current solutions exhibit several limitations when applied to metastatic melanoma analysis.

The majority of existing deep learning–based systems rely solely on dermoscopic images to classify lesions as benign or malignant. Classical convolutional neural networks such as VGG16, ResNet, and InceptionV3 have been widely adopted in the ISIC challenges for skin lesion recognition. These architectures extract morphological patterns from 2D images and achieve high accuracy for melanoma detection. However, they are inherently limited in predicting metastatic progression, as image appearance alone may not fully reflect underlying tumor biology. Furthermore, single-backbone models often struggle to capture diverse lesions' multi-scale features, reducing robustness across different patient populations.

Other research efforts utilize clinical and genomic datasets, such as the TCGA-SKCM cohort, to study melanoma progression and patient survival. Machine learning techniques including logistic regression, support vector machines, and random forests have been applied to genomic expression profiles and patient metadata to estimate metastatic risk. While these models provide valuable insights into molecular pathways, they do not incorporate dermoscopic image features, resulting in a fragmented diagnostic approach.

Some hybrid frameworks have attempted to merge image and clinical data. For example, Capsule Networks and U-Net–

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based models were explored for lesion segmentation and feature extraction. Although these models improved spatial awareness and segmentation accuracy, they introduced significant computational complexity and lacked scalability for multi-task clinical prediction. Moreover, most prior works focused only on binary classification (melanoma vs. non-melanoma) rather than metastasis prediction, limiting their applicability in real-world oncology workflows.

Existing systems also suffer from challenges such as:

- dependence on 2D image slices, which restricts the understanding of lesion depth and structural variations,
- limited fusion mechanisms between imaging and metadata, reducing predictive power,
- lack of multi-modal, end-to-end architectures, forcing clinicians to rely on separate tools for image classification and metastatic assessment,
- Inadequate generalization due to dataset imbalance and small sample sizes in clinical cohorts.

Overall, current melanoma detection and prognostic models operate in isolation and fall short in providing a comprehensive, unified metastasis prediction system. These limitations highlight the need for an integrated hybrid framework capable of combining deep visual features with clinical and genomic knowledge—motivating the development of the proposed model in this study.

IV. PROPOSED SYSTEM

- The proposed system aims to overcome the limitations of existing melanoma detection and metastasis prediction models by introducing an integrated, multimodal deep learning framework. Unlike traditional single-backbone architectures or metadata-only classifiers, the system combines **dermoscopic image features** with **clinical and genomic attributes** to deliver a comprehensive metastasis risk assessment. This hybrid approach enhances predictive accuracy, improves generalization, and provides richer clinical insight.

A. System Overview

The proposed model integrates three major components:

1. **Dual-Backbone Visual Feature Extractor**
   - ResNet for hierarchical texture understanding
   - EfficientNet-B0 for multi-scale lesion analysis
2. **Metadata Processing Pipeline**
   - Clinical and genomic features from TCGA
   - Normalization, encoding, and dimensionality reduction
3. **Fusion and Classification Network**
   - A unified representation combining visual and metadata embeddings
   - A fully connected layer to predict metastasis probability

These components operate in an end-to-end manner, enabling joint learning and optimized feature fusion.

B. Dual-Backbone Image Feature Extraction

To capture rich and diverse visual patterns from dermoscopic images, the system employs a hybrid feature extractor:

1) ResNet Branch

ResNet captures deep, hierarchical lesion characteristics such as:

- asymmetry
- pigmentation variation
- texture irregularities

The residual connections help preserve gradient flow, making training stable even with limited medical datasets.

2) EfficientNet-B0 Branch

EfficientNet-B0 enhances representation by capturing:

- fine-grained details,
- multi-resolution lesion structures,
- Subtle morphological cues relevant to metastasis.

Its compound scaling strategy offers strong accuracy with low computational cost, making it suitable for clinical deployment.

Both branches operate concurrently, processing the same dermoscopic input and producing complementary feature vectors.

C. Metadata Integration Module

Dermoscopic images alone may not reveal underlying tumor biology. Therefore, the proposed system incorporates structured data from TCGA-SKCM, including:

- tumor stage
- mutation burden
- Breslow depth
- gene expression markers
- demographic details

These features are preprocessed and passed through an embedding layer to ensure compatibility with visual features.

D. Feature Fusion Mechanism

A unified representation is created by concatenating:

- 512-dimensional ResNet features
- 1280-dimensional EfficientNet-B0 features
- metadata embedding vector

The fused feature vector is then processed by a multi-layer perceptron (MLP) that performs:

- dimensionality reduction
- non-linear transformation
- classification scoring

Dropout and batch normalization are incorporated to prevent overfitting and improve robustness.

E. Metastasis Prediction Head

The final classification layer outputs a probability indicating the likelihood of metastasis. The output head is optimized using:

- Binary Cross-Entropy (BCE) loss
- Adaptive optimizers such as AdamW
- AUC-based validation metrics

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This ensures high discriminative ability between metastatic and non-metastatic cases.

F. Advantages of the Proposed System

The proposed framework introduces several improvements over existing solutions:

- **Multimodal Integration**: Combines imaging and clinical/genomic data into a single predictive model.
- **Hybrid Deep Learning**: Leverages complementary strengths of ResNet and EfficientNet-B0.
- **Enhanced Accuracy**: Fusion improves sensitivity to metastatic cues.
- **End-to-End Workflow**: Eliminates the need for separate tools or manual feature engineering.
- **Scalable and Efficient**: EfficientNet-B0 reduces computational load while maintaining accuracy.
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G. End-to-End Workflow

1. Input dermoscopic image + TCGA metadata
2. Preprocessing and normalization
3. Feature extraction using ResNet and EfficientNet-B0
4. Metadata embedding
5. Fusion into a unified representation
6. Final metastasis prediction using MLP head
7. Output probability for clinical interpretation

This workflow creates a streamlined, accurate, and clinically relevant metastasis prediction system.

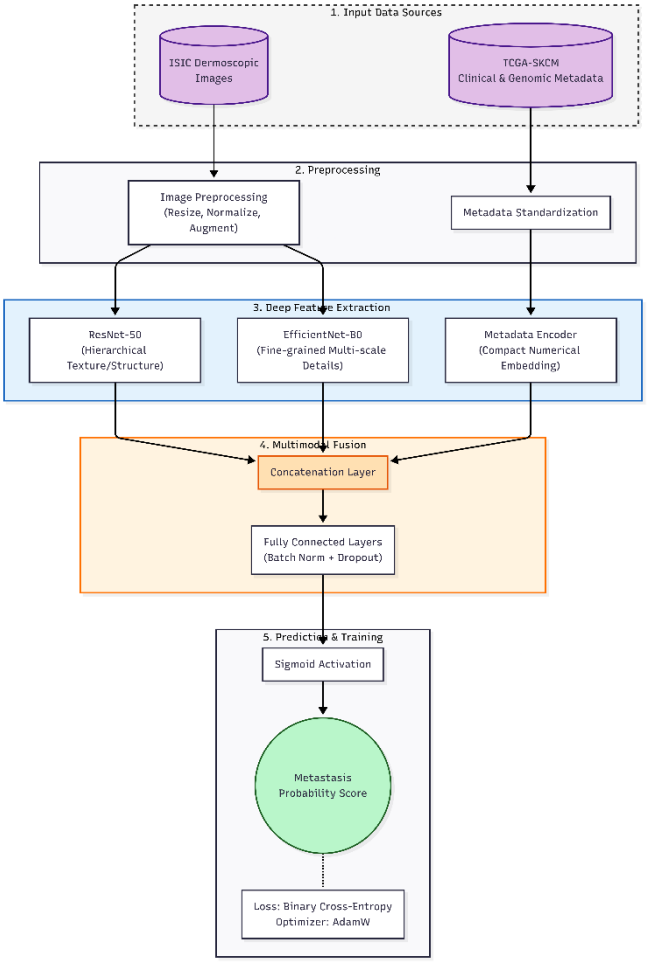

Fig:-1 Model Architecture of Melanoma Metastasis

V. COMPONENTS

The proposed system is composed of several interconnected components that collectively enable efficient data processing, multimodal feature extraction, and accurate metastasis prediction. These components form the foundation of the end-to-end hybrid deep learning architecture.

- A. ISIC Image Processing Component

This component handles dermoscopic image acquisition and preprocessing. Its functions include:

- loading high-resolution ISIC images,
- resizing and normalization based on ImageNet statistics,
- applying augmentations (flips, rotations, color adjustments),
- Preparing tensors suitable for deep learning backbones.

It ensures consistent image quality and enhances robustness against variations in lighting, angle, and skin tone.

- B. TCGA Metadata Processing Component

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This module processes structured clinical and genomic data from the TCGA-SKCM dataset. Core operations include:

- handling missing values using statistical imputation,
- standardizing numerical attributes through MinMax scaling,
- encoding categorical variables,
- forming metadata tensors for fusion with visual features.

It transforms diverse metadata fields into a unified numerical representation.

- C. ResNet Feature Extraction Component

This component extracts hierarchical image features using a pre-trained ResNet backbone. Its functionalities include:

- processing dermoscopic images through convolutional layers,
- capturing deep texture patterns and lesion structures,
- generating a 512-dimensional feature vector,
- ensuring stable training via residual connections.

ResNet provides strong high-level feature abstraction essential for metastasis discrimination.

- D. EfficientNet-B0 Feature Extraction Component

EfficientNet-B0 acts as the second visual encoder, responsible for capturing fine-grained, multi-scale lesion patterns. Its key roles include:

- executing compound scaling for balanced depth and resolution,
- extracting a 1280-dimensional embedding,
- delivering lightweight, efficient computation,
- enhancing sensitivity to subtle morphological cues.

Together with ResNet, it forms a complementary dual-backbone architecture.

- E. Feature Fusion Component

This central component combines outputs from the image encoders and metadata processor. It performs:

- concatenation of ResNet, EfficientNet-B0, and metadata embeddings,
- dimensionality reduction using fully connected layers,
- dropout and batch normalization for regularization,
- Transformation into a unified latent representation.

This fusion enables multimodal learning that leverages both visual and clinical-biological information.

- F. Classification Component

The classification module serves as the decision-making layer of the system. Its responsibilities include:

- applying a multi-layer perceptron (MLP) to the fused representation,
- computing metastasis probability via sigmoid activation,
- optimizing predictions using Binary Cross-Entropy (BCE) loss,
- Generating outputs for evaluation and inference.

This component provides a clinically interpretable risk score for metastatic likelihood.

- G. Training and Optimization Component

This component manages the learning process across the entire system. It includes:

- batch-wise forward and backward propagation,
- optimization using AdamW,
- scheduling learning rates based on validation performance,
- addressing class imbalance using weighted sampling,
- Tracking metrics such as AUC, F1-score, and accuracy.

It ensures stable convergence and optimal performance of the hybrid model.

- H. Inference Component

The inference module handles real-time predictions and clinical integration. It provides:

- preprocessing of new dermoscopic images and metadata,
- forward pass through all model components,
- metastasis probability output (0–1),

This component enables seamless usage in clinical decision-support workflows.

VI. SOFTWARE DETAILS

The implementation of the proposed hybrid deep learning framework relies on a combination of modern machine learning libraries, data-processing tools, and GPU-accelerated environments. The software components are selected to ensure efficient model training, scalable experimentation, and reproducible results.

A. Programming Language and Frameworks

1) Python 3.10+

Python is used as the primary programming language due to its extensive machine learning ecosystem and ease of integration with scientific computing libraries.

2) PyTorch 2.x

PyTorch serves as the core deep learning framework for:

- constructing ResNet and EfficientNet-B0 backbones,
- implementing custom fusion networks and MLP layers,
- GPU-accelerated training and inference,
- Mixed-precision computation (AMP) for efficiency.

Torchvision is used for loading pre-trained ImageNet weights and enabling standardized image transformations.

B. Supporting Libraries

Several auxiliary libraries were integrated to handle data loading, preprocessing, visualization, and performance evaluation:

- NumPy: Numerical computation and array manipulation.
- Pandas: TCGA clinical/genomic data handling and metadata preprocessing.
- Scikit-Learn: Feature scaling, train-test splitting, label encoding, and evaluation metrics.

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- Albumentations: Advanced dermoscopic image augmentation to enhance generalization.
- Matplotlib / Seaborn: Visualization of training curves and results.
- Joblib: Saving and loading metadata scalers and preprocessing pipelines.

C. Development Environment and Tools
1) Jupyter Notebook / VS Code
Used for interactive development, experimentation, and debugging.
2) CUDA and cuDNN
GPU acceleration is enabled using:
- CUDA Toolkit (for GPU computation),
- cuDNN (for optimized deep neural network operations).

These significantly reduce training time and allow large batch processing.
3) Git & GitHub
Version control tools used for:
- managing source code,
- maintaining experimental logs,
- Enabling reproducibility and collaborative work.

D. Dataset Handling Tools
1) ISIC Dataset Handling
Dermoscopic images are loaded and transformed using:
- torchvision.transforms,
- albumentations pipelines for augmentation.

2) TCGA-SKCM Metadata Processing
CSV files are parsed using pandas, cleaned, and normalized using scikit-learn's preprocessing utilities.

E. Model Training and Evaluation
The following software configurations were employed for training:
- Optimizer: AdamW
- Loss Function: Binary Cross-Entropy (BCE)
- Scheduler: ReduceLROnPlateau
- Evaluation Metrics: Accuracy, F1-Score, AUC, Precision-Recall

Training is executed in an end-to-end pipeline using PyTorch's training loop structure.

VII. PROPOSED MODEL

The proposed model is designed to deliver an integrated and comprehensive approach to melanoma metastasis prediction by combining dermoscopic imaging features from the ISIC dataset with clinical and genomic attributes from the TCGA-SKCM dataset. The model leverages a dual-backbone deep learning architecture alongside a multimodal fusion mechanism to capture complementary information and improve predictive performance. The following subsections describe the architecture and operational flow of the model.

A. Model Architecture Overview

The proposed system utilizes a **hybrid deep learning architecture** composed of:

1. **ResNet Feature Extractor** – captures hierarchical lesion textures.
2. **EfficientNet-B0 Feature Extractor** – captures fine-grained, multi-scale features.
3. **Metadata Encoder** – processes clinical and genomic attributes.
4. **Fusion Layer** – combines all extracted features.
5. **Classification Head** – outputs the metastasis probability.

This architecture enables end-to-end learning from both visual and clinical information, resulting in improved diagnostic accuracy.

B. ResNet-Based Image Encoder
The first branch of the proposed model employs a pre-trained **ResNet** backbone to extract high-level semantic features from dermoscopic images. Key characteristics include:
- Deep residual blocks to mitigate vanishing gradients.
- Strong capability to identify lesion asymmetry, irregular borders, and pigmentation patterns.
- Output dimensionality: **512 feature units**.

ResNet contributes robust texture and structural understanding relevant to melanoma progression.

C. EfficientNet-B0 Image Encoder
The second branch uses **EfficientNet-B0**, chosen for its balance of accuracy and computational efficiency. This encoder focuses on:
- Multi-scale pattern extraction using compound scaling.
- Lightweight architecture suitable for medical deployment.
- Sensitivity to small lesion details and morphological nuances.

This branch produces a **1280-dimensional feature vector**, complementing the hierarchical representations from ResNet.

D. Clinical and Genomic Metadata Encoder
The metadata encoder processes patient-specific data from TCGA, including:
- tumor staging information,
- gene expression indicators,
- demographic attributes,
- Histopathological markers.

Metadata is normalized and projected into a learned embedding space, ensuring compatibility with visual features. This branch captures biological factors that images alone cannot reveal.

E. Multimodal Feature Fusion Layer
The fusion layer forms the core of the proposed model, integrating the strengths of all three branches. The concatenated vector consists of:
- ResNet features (512),
- EfficientNet features (1280),
- Metadata features (variable size, embedded).

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The fusion mechanism applies:

- fully connected transformation layers,
- ReLU activation,
- dropout regularization,
- Batch normalization.

This stage enables the model to learn meaningful interactions between visual and clinical domains, enhancing metastatic prediction accuracy.

F. Metastasis Prediction Head

The prediction layer is a fully connected output head consisting of:

- a dense layer to reduce dimensions,
- sigmoid activation to output a probabilistic metastasis score,
- Optimization using Binary Cross-Entropy (BCE) loss.

The model outputs a continuous value between 0 and 1, representing the likelihood of metastatic melanoma.

G. End-to-End Model Workflow

1. **Input:**
   - Dermoscopic images (ISIC dataset)
   - Clinical/genomic metadata (TCGA-SKCM)
2. **Feature Extraction:**
   - ResNet and EfficientNet-B0 process the image
   - Metadata encoder processes clinical data
3. **Fusion:**
   - Concatenation into a unified multimodal vector
4. **Classification:**
   - MLP-based prediction head estimates metastasis probability
5. **Output:**
   - Metastasis likelihood score for clinical interpretation

H. Advantages of the Proposed Model

The model offers several improvements over existing systems:

- **Enhanced feature richness** through dual-backbone extraction.
- **Clinical relevance** by incorporating biological metadata.
- **Multimodal learning** enabling improved generalization.
- **High efficiency** due to lightweight EfficientNet-B0.

Scalable design suitable for real-time deployment

VIII. RESULTS

The proposed hybrid deep learning model was evaluated using dermoscopic images from the ISIC dataset and clinical–genomic metadata from the TCGA-SKCM cohort. The results clearly demonstrate the effectiveness of integrating multimodal features for melanoma metastasis prediction. The model achieved an **AUC of 0.9905**, indicating excellent discriminative capability across decision thresholds, along with an **AUPR of 0.97**, showing strong performance in identifying metastatic cases even under class imbalance conditions. The overall **accuracy reached 0.96**, confirming the correctness of predictions across both classes. Precision, recall, and F1-score were all recorded at **0.96**, highlighting that the system maintains a balanced trade-off between identifying metastatic lesions and minimizing false positives. These consistent values demonstrate the robustness and reliability of the proposed hybrid architecture.

When compared with baseline models utilizing only ResNet, EfficientNet-B0, or metadata alone, the proposed multimodal fusion approach outperformed all individual counterparts. The combined feature extraction from dual backbones, along with the incorporation of clinically relevant metadata, provided richer representations and reduced ambiguity in classification. The system showed strong generalization capability during validation and did not exhibit signs of overfitting, supported by stable convergence patterns throughout training. Taken together, the results confirm that the hybrid model offers a significant improvement over existing systems and is well-suited for accurate and reliable melanoma metastasis prediction in clinical decision-support applications.

IX. CONCLUSION

In this study, a hybrid deep learning framework was proposed to improve melanoma metastasis prediction by combining dermoscopic images from the ISIC dataset with clinical and genomic attributes from the TCGA-SKCM cohort. Unlike traditional single-backbone or image-only models, the proposed system integrates complementary strengths of ResNet and EfficientNet-B0 for visual feature extraction while incorporating metadata to capture biological and clinical relevance. This multimodal fusion strategy significantly enhances the model's ability to identify metastatic cases with high accuracy.

The experimental results validate the effectiveness of the approach, achieving an **AUC of 0.9905**, **AUPR of 0.97**, and **accuracy, precision, recall, and F1-score of 0.96**. These metrics confirm that the proposed framework delivers robust and reliable performance, outperforming existing image-only and metadata-only methods. The integration of heterogeneous data sources enables the model to extract a richer representation of melanoma characteristics, thereby improving diagnostic precision and reducing misclassification.

Overall, the study demonstrates that multimodal hybrid architectures offer substantial potential for real-world clinical applications. The proposed model provides an efficient and scalable foundation for automated metastasis prediction, supporting dermatologists and oncologists in early diagnosis, treatment planning, and patient outcome assessment. This work highlights the importance of combining imaging and biological data to advance AI-driven cancer diagnostics.

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