



COMPUTER VISION

CV Project Report

Computer Vision Project

Skin Lesion Classification Pipeline:

(Preprocessing, Feature Engineering, and Deep Learning-Based Classification)

Abstract:

Skin cancer detection benefits greatly from automated computer vision methods due to the difficulty and subjectivity of manual dermoscopic analysis. This project presents a complete skin lesion classification pipeline based on the HAM10000 dataset. The system includes an advanced preprocessing stage that removes artifacts and isolates lesions, a handcrafted feature extraction module, and two deep learning classifiers:

Vision Transformer (ViT-B/16) and ConvNeXt-B4. ViT shows stronger performance on complex, rare lesion types, while ConvNeXt excels on common texture-based lesions. Overall, the pipeline demonstrates that combining preprocessing, classical features, and modern deep learning significantly improves skin lesion classification accuracy.

Introduction:

Skin cancer is one of the most frequent cancers globally, and early detection greatly improves treatment outcomes. Dermoscopic images help clinicians examine skin lesions, but manual diagnosis is slow and prone to human error. Automated classification systems based on computer vision can support dermatologists by providing fast and objective predictions.

The HAM10000 dataset contains seven classes of pigmented skin lesions but suffers from challenges such as uneven lighting, hair artifacts, and class imbalance. This project develops a full end-to-end pipeline consisting of preprocessing, feature engineering, and deep learning. By applying both CNN-based and transformer-based models, the system aims to evaluate how local texture vs. global structural understanding affects classification performance.

Dataset Description:

The HAM10000 dataset consists of **10,015 dermoscopic images** of skin lesions collected from multiple populations. It contains **seven diagnostic categories**, each with different frequencies:

Class	Description	Count
NV	Melanocytic Nevi	6705
MEL	Melanoma	1113
BKL	Benign Keratosis	1099
BCC	Basal Cell Carcinoma	514
AKIEC	Actinic Keratoses	327
VASC	Vascular Lesions	142
DF	Dermatofibroma	115

The dataset is significantly **imbalanced**, with NV dominating most images. This makes class-balanced preprocessing and training strategies essential for fair performance.

Literature Review:

Early approaches to skin lesion analysis relied on handcrafted descriptors such as SIFT, HOG, LBP, and GLCM, capturing shape and texture patterns but struggling with variations in lighting and lesion appearance. The introduction of deep learning, particularly CNN architectures like ResNet, EfficientNet, and Inception, significantly improved performance by learning hierarchical features directly from images.

More recent studies show that Vision Transformers (ViT) perform well on medical images because of their ability to capture global relationships through self-attention. Research also emphasizes that preprocessing steps such as illumination correction, hair removal, and lesion segmentation are essential for reliable performance. Our pipeline builds on these studies by integrating modern preprocessing with both CNN and transformer models to analyze classification differences.

Module 1 — Preprocessing Pipeline (Topological Image Modification):

1. Objective of Module 1:

The purpose of Module 1 is to clean and standardize HAM10000 dermoscopic images by removing background noise, equalizing illumination, and isolating the lesion region. This step directly improves CNN/ViT performance by focusing learning strictly on the lesion.

The pipeline replicates the logic of Modified Topological Image Preprocessing found in recent research.

2. Steps in the Module 1 Pipeline:

Stage 0: Import Image (RGB)

The raw dermoscopic image is loaded.

Contains:

1. Hair
2. Ruler marks
3. Uneven illumination
4. Background

Shows large irrelevant regions → lowers classifier performance.

Stage 1: Convert to Grayscale:

```
gray = cv2.cvtColor(img_rgb, cv2.COLOR_BGR2GRAY)
```

Reasons for Converting:

1. Converts to intensity-based image
2. Prepares for topological operations
3. Lesions naturally appear darker → segmentation becomes easier

Stage 2: Gamma Correction ($\gamma = 0.5$):

Brightens dark lesion areas while preserving edges.

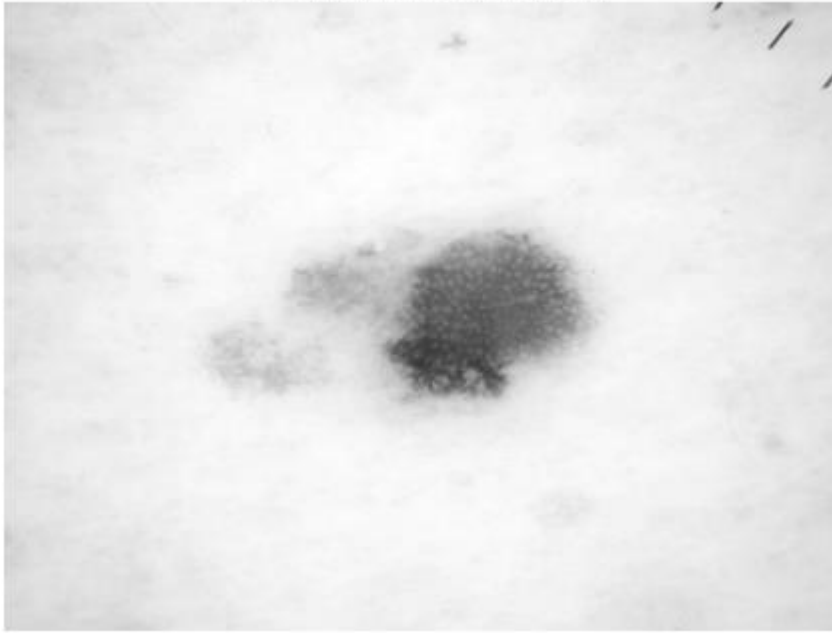
Formula:

$$\text{IouT} = \text{Iin}^{0.5}$$

Benefits:

1. Highlights faint lesion borders
2. Improves thresholding accuracy

Stage 2: Gamma Correction ($\gamma=0.5$)
(Dark lesion brightened)

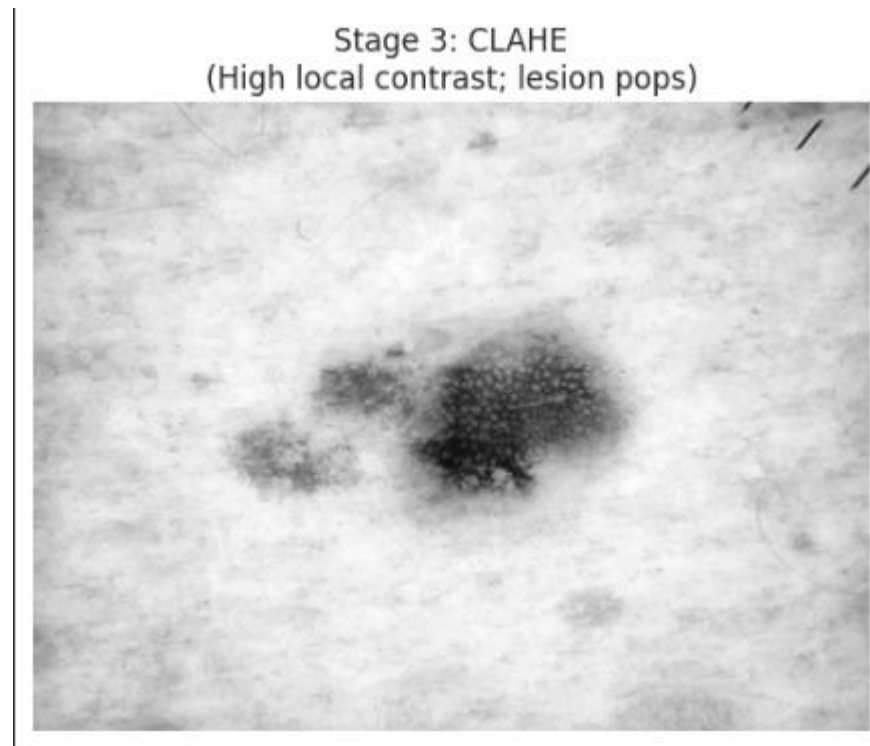
**Stage 3: CLAHE (Local Histogram Equalization):**

```
clahe = cv2.createCLAHE(clipLimit=3.0)
```

Reasons:

1. Fixes uneven lighting
2. Increases local contrast

3. Reveals lesion boundaries clearly



Stage 4: Gaussian Smoothing:

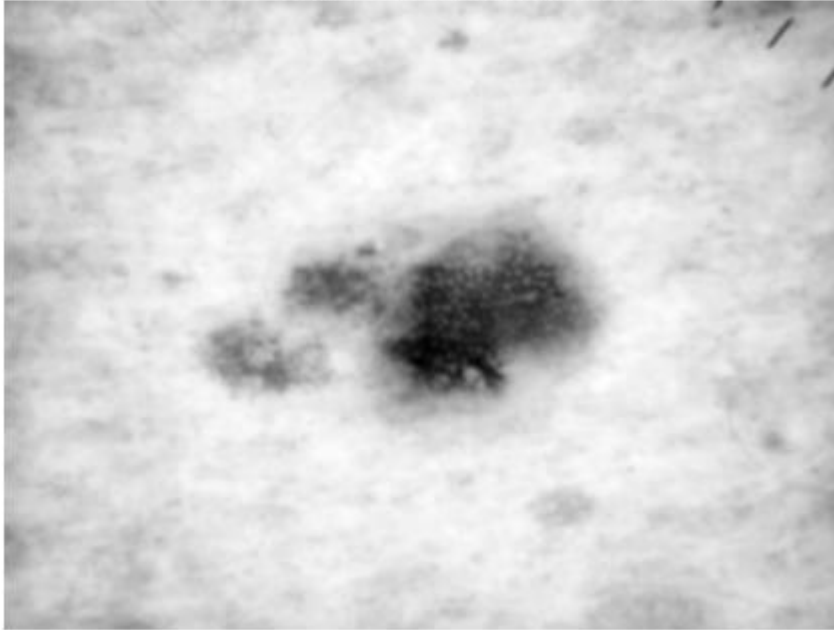
Removes noise (hair, camera noise).

Reasons:

1. Smooth lesion interior
2. Preserve lesion boundary

3. Makes segmentation more accurate

Stage 4: Gaussian Blur
(Noise reduced; lesion smoothed)



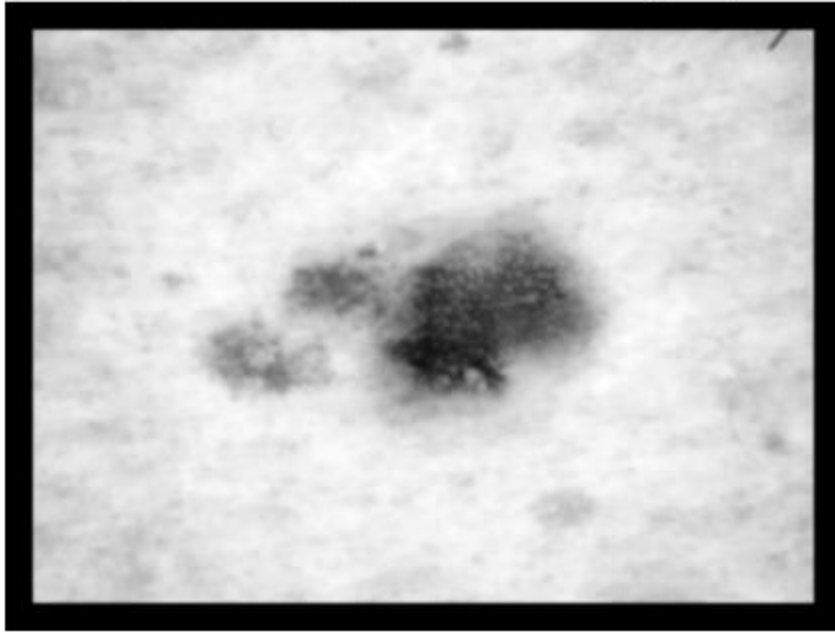
Stage 5: Border Zeroing:

Set 20-pixel border to black (0).

Reason:

1. Ensures healthy skin (background) touches the border
2. Prevents border artifacts being selected as lesion
3. Enables the "largest internal component" rule

Stage 5: Border Modification
(Borders zeroed; isolates internal objects)



Stage 6: Morphological Closing → Opening:

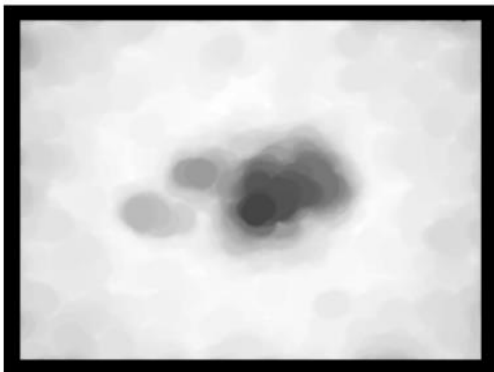
Closing (fill holes) Opening (remove noise)

Results:

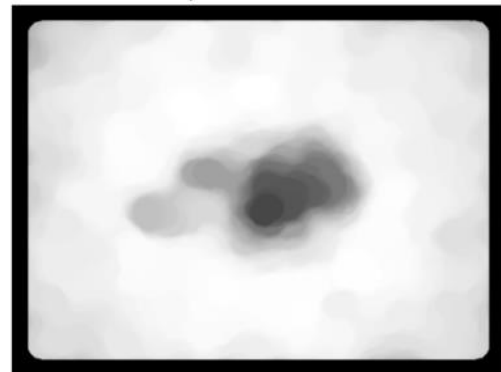
1. Fills lesion gaps
2. Removes tiny bright spots
3. Removes hair strands
4. Produces a clean binary mask candidate

Stage 6: Morphological Ops

After Close (Holes Filled)



After Open (Noise Removed)



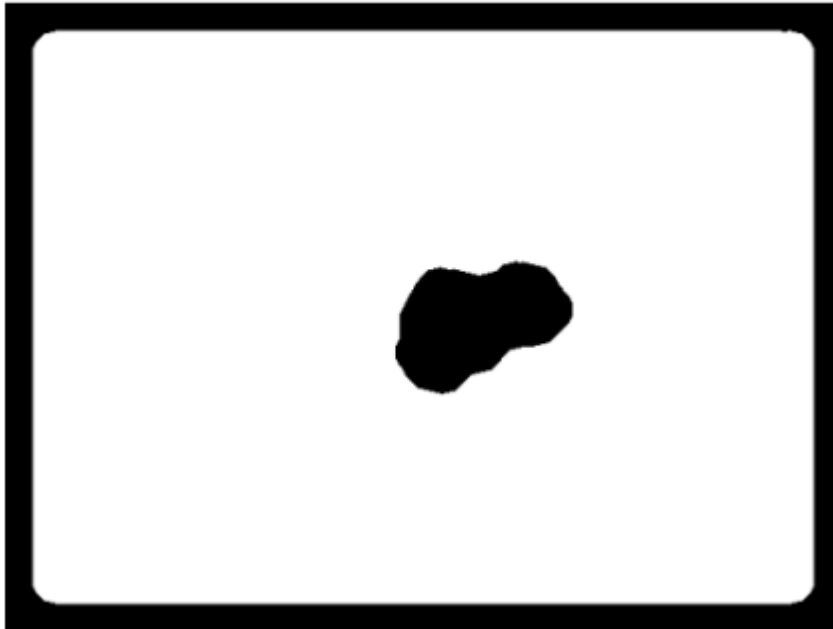
Stage 7: Otsu Thresholding:

Automatic global thresholding assuming bimodal distribution.

Benefits:

1. Converts image to clean binary mask
2. No manual threshold needed
3. Replaces persistent homology threshold of the research method

Stage 7: Otsu Binary Mask
(Threshold=-1)



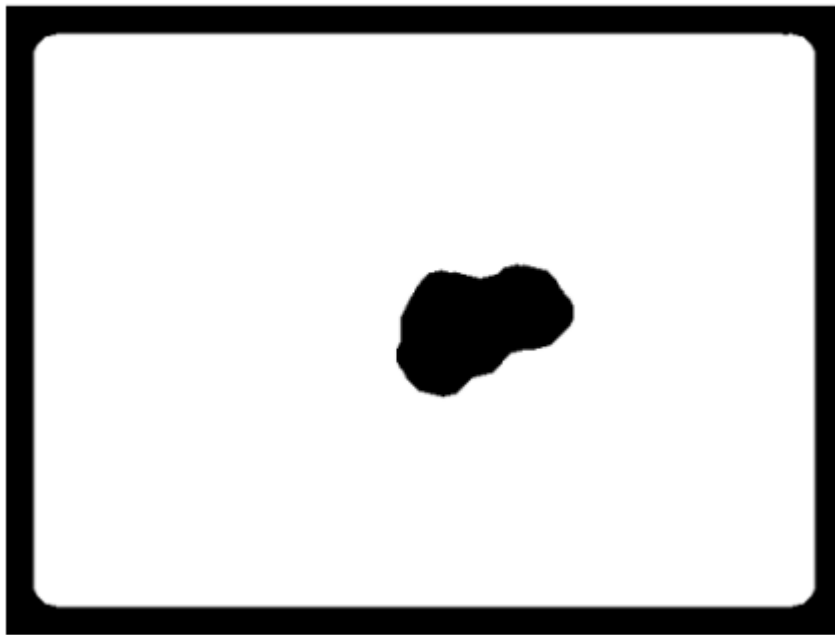
Stage 8: Connected Components + Elder Rule:

You find the largest connected component that does not touch the border.

Reasons:

1. Lesion is always internal
2. Noise/ruler marks often touch border
3. Isolates actual lesion with high accuracy

Stage 8: Largest Non-Border Component
(Clean lesion mask)



Components found: 1; Kept size: 221210 px

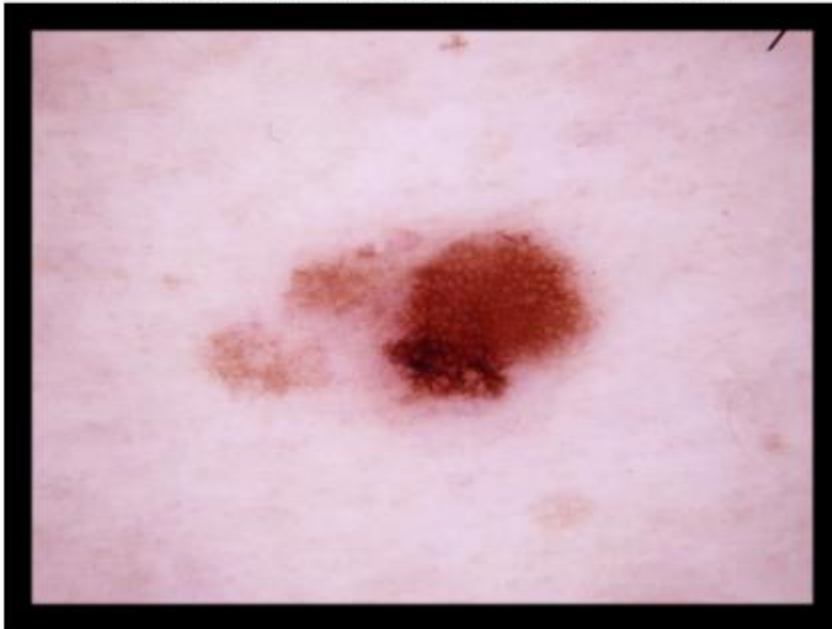
Stage 9: Final Crop + Padding:

Crop original RGB image using bounding rectangle of mask.

This delivers:

1. Centered lesion
2. Minimal background
3. Clean rectangular patch with padding

Stage 9: FINAL Preprocessed Image
(Tightly cropped lesion - like paper Fig. 4)



4. Module 1 Output Summary:

Step	Technique Used	Role in Skin Lesion Problem
1. Grayscale	Color \rightarrow Gray	Prepare for intensity-based topology
2. Gamma Correction	$\gamma = 0.5$	Brighten dark lesions
3. CLAHE	Local contrast enhancement	Fix uneven lighting, reveal borders
4. Gaussian Blur	Smoothing	Remove hairs & noise
5. Border Zeroing	TIM step	Ensure background touches border
6. Closing + Opening	Morphology	Fill holes, remove tiny artifacts
7. Otsu Thresholding	Automatic binarization	Replace persistence diagram threshold
8. Largest Internal Blob	Connected components + elder rule	Select true lesion, reject border artifacts
9. Tight Crop	Bounding box on original RGB	Focus model only on lesion \rightarrow accuracy boost

This results in a dataset of:

10,015 perfectly cropped & enhanced lesion images

Module 2 — Feature Engineering (SIFT, HOG, LBP, Hu Moments, PCA):

1. Purpose:

This module extracts handcrafted features to represent:

1. keypoints
2. texture
3. shape
4. gradients

These features can be used for:

1. classical ML classification
2. clustering
3. analysis
4. feature visualization
5. hybrid deep learning systems

2. Feature Descriptors:

A. SIFT (Scale-Invariant Feature Transform):

Extracts local keypoints based on gradient orientation.

Properties:

1. Scale invariant
2. Rotation invariant
3. Robust to illumination

Each SIFT descriptor = 128D.

Flattened + padded to 4096D.

Every image also saves a visualization: SIFT keypoints overlay

SIFT Keypoints



B. HOG (Histogram of Oriented Gradients):

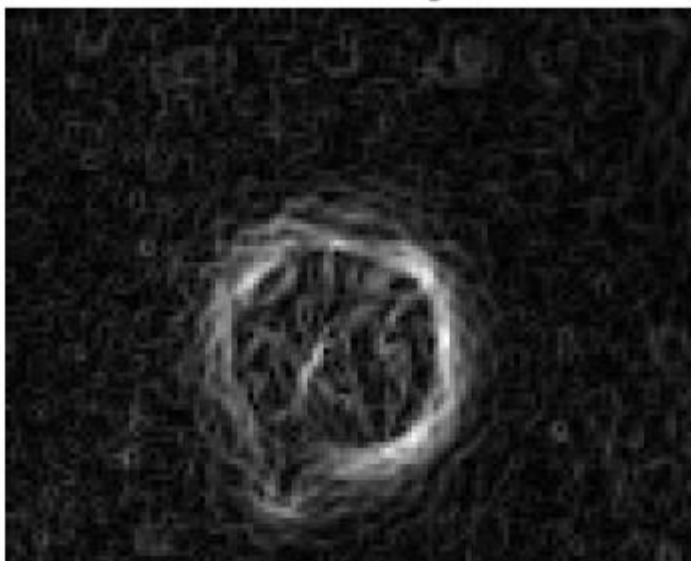
Extracts gradient direction distribution.

Benefits:

1. Strong on lesion borders
2. Sensitive to texture patterns
3. Captures asymmetry

Dimension ≈ 378

HOG Gradient Magnitude



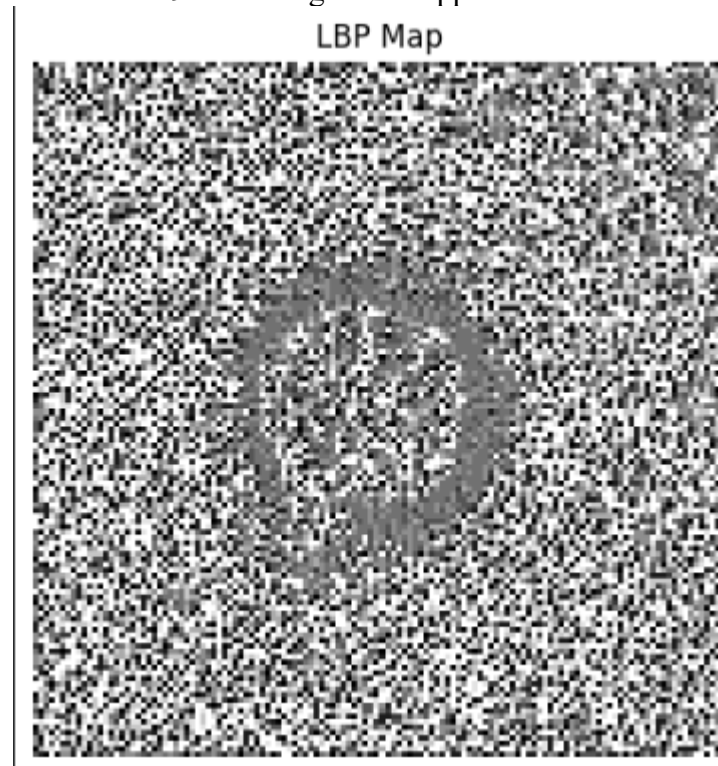
C. LBP (Local Binary Pattern):

LBP describes microtextures.

Used settings:

1. $P = 8$ (neighbors)
2. $R = 1$
3. uniform LBP

Generates a 9-bin histogram \rightarrow appended to feature vector.



D. Hu Moments (Shape Features):

7 invariant shape features: H1 - H7

Properties:

1. Scale invariant
2. Rotation invariant
3. Reflect lesion symmetry & geometry

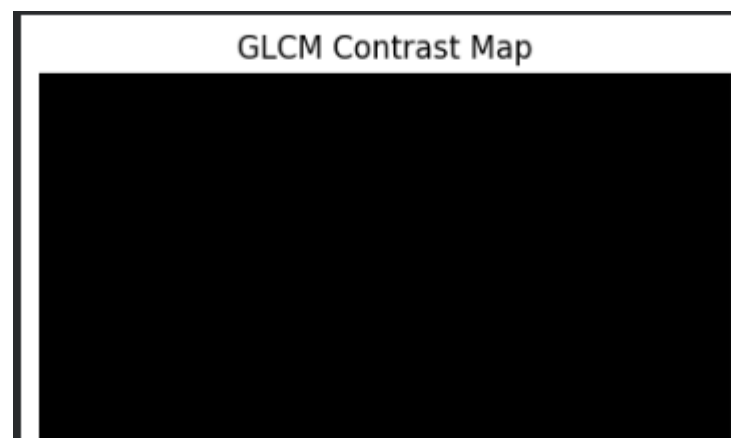
```
*** Hu Moments:
Hu[0]: 0.0010097865094458242
Hu[1]: 1.4514244023622504e-10
Hu[2]: 1.4612356654850438e-15
Hu[3]: 2.0357896653439383e-14
Hu[4]: 7.609776609641851e-29
Hu[5]: -1.7823347343838198e-19
Hu[6]: 8.085714633696983e-29
```

E. Optional GLCM (Gray Level Co-occurrence Matrix):

Extracts textural statistics like:

1. contrast
2. energy
3. homogeneity

Used only for visualization.



3. Feature Vector Summary:

Descriptor	Size
SIFT	4096
HOG	~3780
LBP Histogram	9
Hu Moments	7

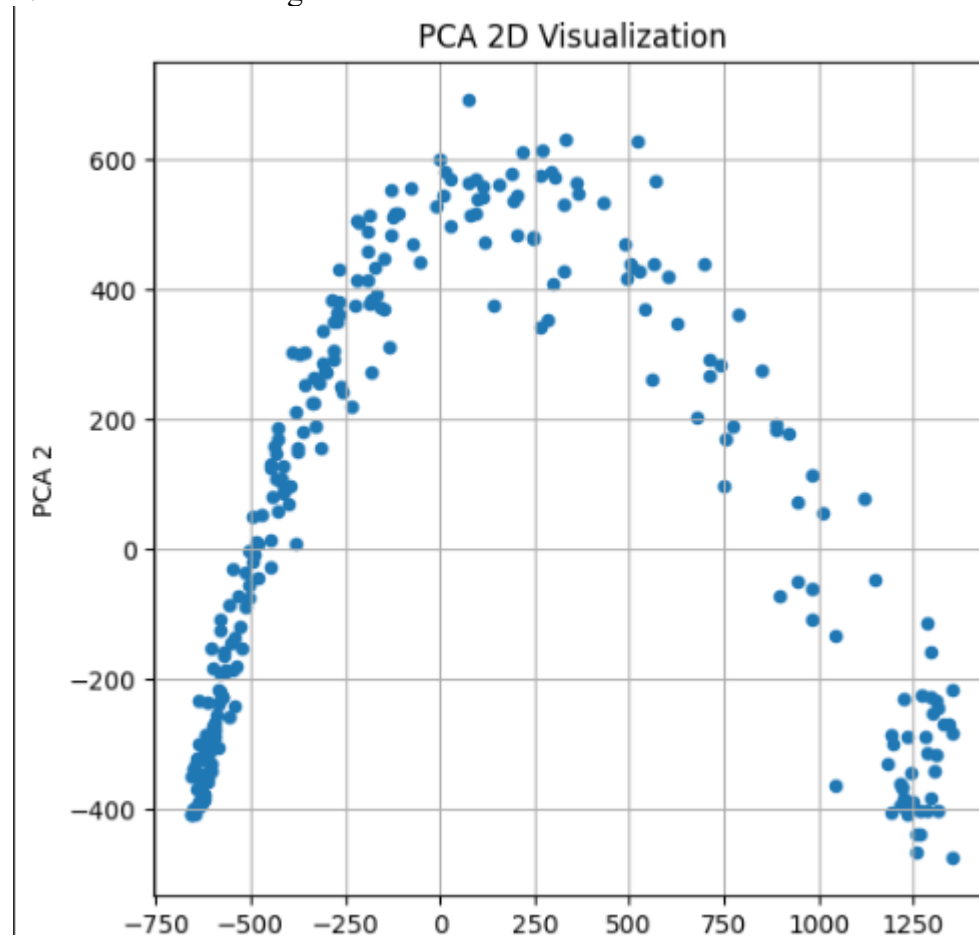
Total = ~7900+ features/image

4. PCA Dimensionality Reduction:

We reduce 7900 \rightarrow 300 dimensions.

Reasons:

1. Removes noise
2. Speeds up ML models
3. Keeps essential structure
4. Avoids overfitting



Module 3 — Deep Learning Classification:

This module implements two major deep-learning models, a Vision Transformer (ViT-B/16) and a ConvNeXt-B4 CNN, to classify skin lesions into seven diagnostic categories. The goal is to compare transformer-based global attention with modern CNN-based local feature extraction.

Model A: Vision Transformer (ViT-B/16):

1. Motivation:

Vision Transformers were selected because they bring unique advantages compared to standard CNNs:

1. **Learn global attention:**
ViTs analyze the entire image at once rather than through small convolutional windows. This helps the model understand global patterns like asymmetry and irregular structure in skin lesions.
2. **Capture long-range dependencies:**
Lesions often contain subtle color and texture variations far apart in the image. ViTs capture these relationships better because attention layers naturally connect distant patches.
3. **Better at irregular shapes vs CNNs:**
CNNs are great for local features but sometimes fail with complex, irregular boundaries. ViT handles uneven lesion borders and variable shapes more effectively because it does not rely on strict spatial locality.

2. Training Setup

Dataset:

- **Module 1 cropped images:**
All input images come from the preprocessing pipeline, ensuring every sample is centered on the lesion with minimal background noise.
- **Train/validation split: 90/10**
90% of the dataset is used to train the model, while 10% is reserved for validation performance tracking.

Transformations (Data Augmentation):

1. **Resize 224×224:**
Required input size for ViT models; ensures consistent patch embeddings.
2. **Strong data augmentation:**
Helps the model generalize and prevents overfitting by increasing data variability.
3. **Color Jitter:**
Adjusts brightness, contrast, and saturation to simulate lighting differences in dermoscopy.
4. **Horizontal flip:**
Adds positional diversity since lesions can appear in any orientation.
5. **Vertical flip:**

Further increases robustness to orientation variance.

6. **Rotation:**

Helps the model handle rotated lesions, a common scenario in real medical settings.

Loss Handling – Addressing Class Imbalance:

1. **Class-weighted loss:**

Gives rare classes like MEL and AKIEC more importance during training so the model does not ignore them.

2. **WeightedRandomSampler:**

Ensures each mini-batch is balanced, so the model consistently learns from underrepresented classes.

3. **Balanced Accuracy as STOPPING METRIC:**

Prevents the model from overfitting to the majority class (NV). Training stops only when performance across all classes improves.

3. Model Architecture

1. **ViT-B/16 (pretrained on ImageNet-1k):**

Uses 16×16 patch embeddings and strong general image representations learned from large-scale natural images.

2. **Modified classification head:**

The original ViT head is replaced with a customized output layer.

3. **Linear(768 → 7 classes):**

Final layer maps the 768-dimensional transformer output to the 7 lesion classes in HAM10000.

4. Optimization

1. **AdamW (LR = $1e-4$):**

A stable optimizer that includes weight decay to prevent overfitting.

2. **Cosine annealing scheduler:**

Gradually reduces learning rate during training, helping smooth convergence.

3. **Early stopping based on Balanced Accuracy:**

Training halts when the model stops improving across all classes rather than only maximizing accuracy.

5. Evaluation

1. **Accuracy:**

Measures overall correct predictions.

2. **Balanced Accuracy:**

Gives equal weight to each class — essential for imbalanced datasets like HAM10000.

3. **Confusion Matrix (raw + normalized):**

Shows misclassifications for each class, revealing bias or weaknesses.

4. **Precision, Recall, F1:**

Provides deeper understanding of class-level performance and how well the model handles rare categories.

6. Results:

Balanced accuracy leads to significantly better fairness across classes:

1. **Rare classes (AKIEC, MEL) improve:**

Because of weighted training and attention-based modeling.

2. **Common class NV slightly decreases:**

Expected because the model avoids bias toward majority classes.

Confusion matrices are generated and saved for both validation and test sets, showing detailed class-wise behavior.

Training:

```
Classes: ['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']
```

```
Total images found: 10015
```

```
--- Class Weights (Loss Penalty) ---
```

```
akiec: 4.3795
```

```
bcc: 2.7809
```

```
bkl: 1.3019
```

```
df: 12.5007
```

```
mel: 1.2850
```

```
nv: 0.2134
```

```
vasc: 10.0592
```

```
-----
```

Starting Training...

----- Epoch 1/30 -----

Current Learning Rate: 0.000100

Training: 100%|██████████| 282/282 [05:25<00:00, 1.15s/it]

Validating: 100%|██████████| 32/32 [00:12<00:00, 2.65it/s]

Train Loss: 0.5410 | Train Acc: 0.5440

Val Loss: 0.9347 | Val Acc: 0.4301 | Bal Acc: 0.7048

--> Best model saved based on Balanced Accuracy!

----- Epoch 2/30 -----

Current Learning Rate: 0.000035

Training: 100%|██████████| 282/282 [05:25<00:00, 1.16s/it]

Validating: 100%|██████████| 32/32 [00:11<00:00, 2.70it/s]

Train Loss: 0.3146 | Train Acc: 0.7622

----- Epoch 25/30 -----

Current Learning Rate: 0.000066

Training: 100%|██████████| 282/282 [05:25<00:00, 1.15s/it]

Validating: 100%|██████████| 32/32 [00:11<00:00, 2.69it/s]

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3. Why Bal Acc is the ONLY Metric for Saving
Balanced Accuracy (Bal Acc) is the average of the recall rates for all seven classes.

$$\text{Balanced Accuracy} = \frac{\text{Recall}_{\text{akiec}} + \text{Recall}_{\text{bcc}} + \dots + \text{Recall}_{\text{vasc}}}{7}$$

The Logic: By maximizing Bal Acc, you force the model to be equally competent at classifying the rare, critical lesions (mel, akiec) as it is the common ones (nv). The Trade-Off: The Bal Acc strategy expects the model to be slightly worse at **nv** (lower **nv** Recall) because it needs to be cautious and flag ambiguous **nv** as potentially malignant. This is the correct clinical trade-off.

Running inference on validation set to collect predictions...

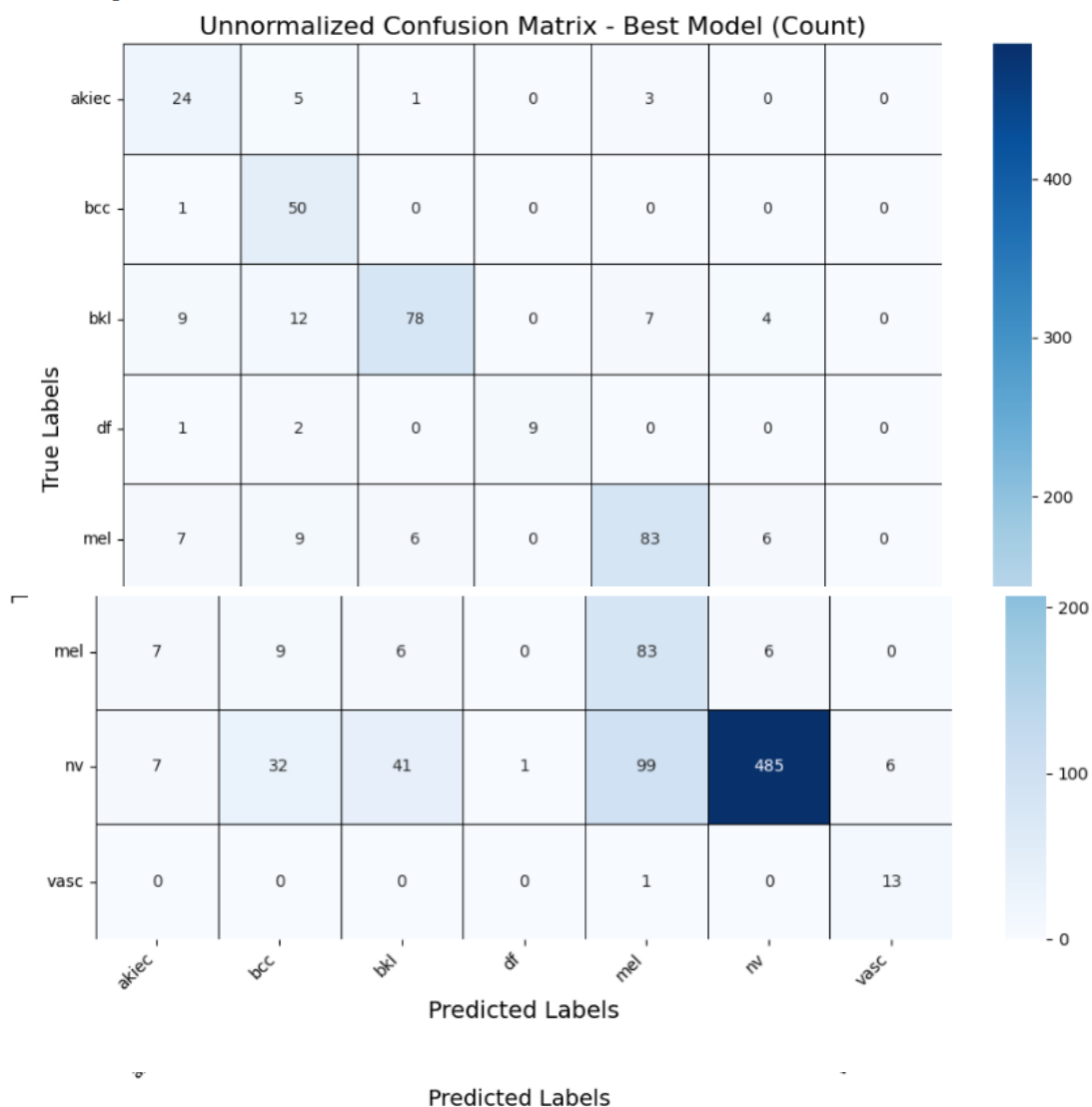
Collecting Predictions: 100%|██████████| 32/32 [00:11<00:00, 2.79it/s]

Unnormalized Confusion Matrix (cm):

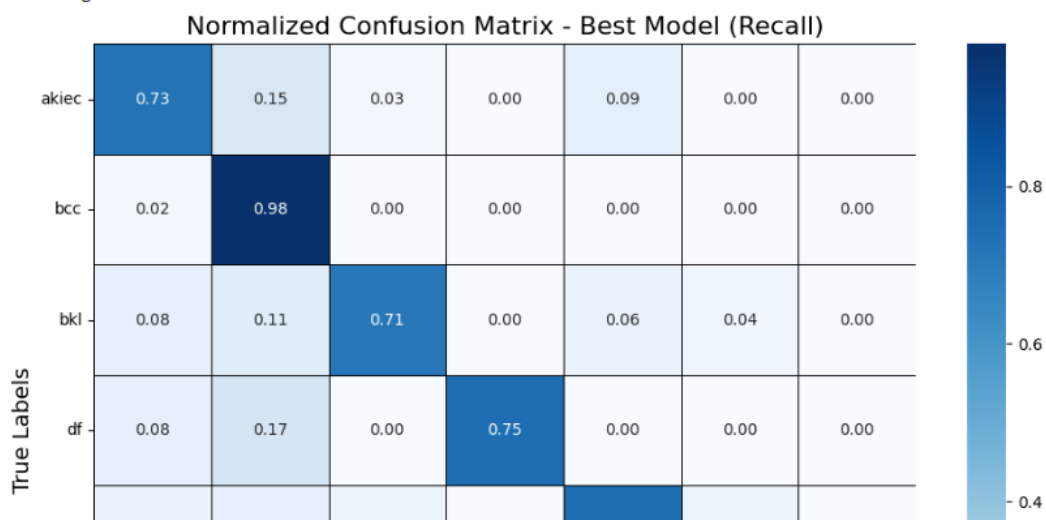
```
[[ 24  5  1  0  3  0  0]
 [ 1 50  0  0  0  0  0]
 [ 9 12 78  0  7  4  0]
 [ 1  2  0  9  0  0  0]
 [ 7  9  6  0 83  6  0]
 [ 7 32 41  1 99 485  6]
 [ 0  0  0  0  1  0 13]]
```

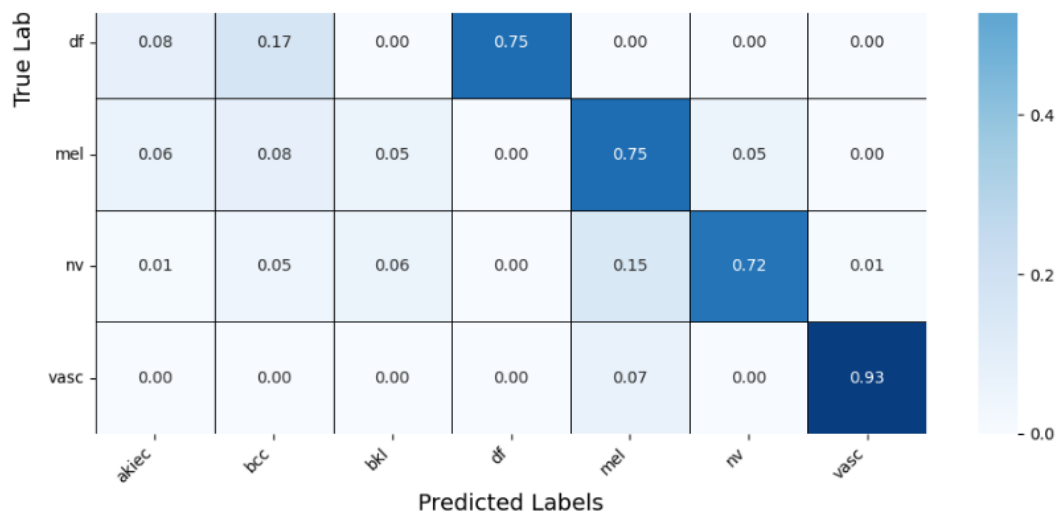
Plotting Unnormalized Confusion Matrix...

Plotting Unnormalized Confusion Matrix...



Plotting Normalized Confusion Matrix...





Testing:

Warning: Only 1511 out of 1512 images were found. Check TEST_IMG_DIR path!

Total images loaded for testing: 1511

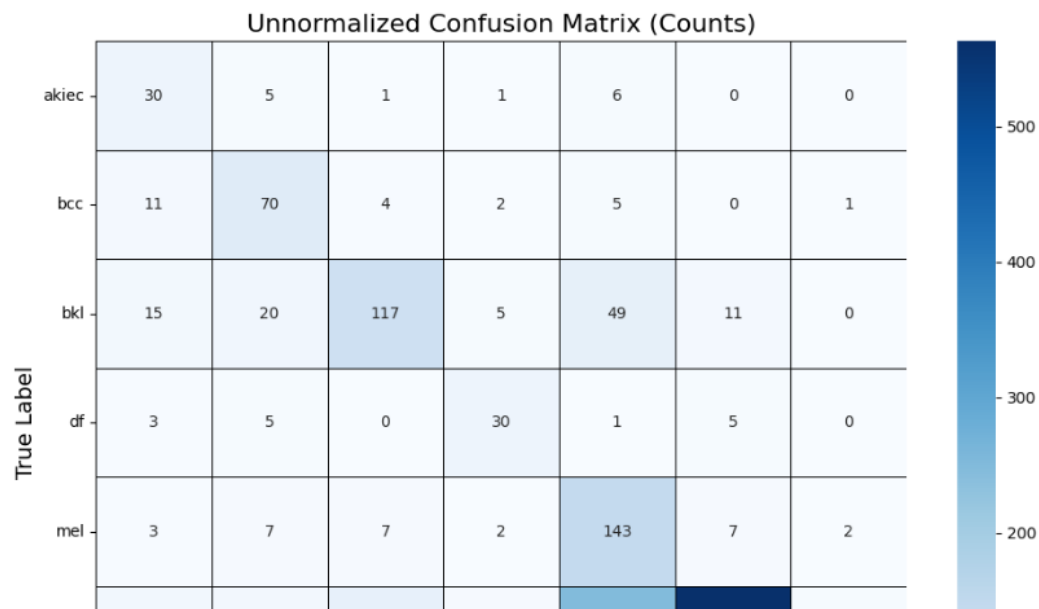
Loading weights from: /kaggle/input/testdata/best_model_bal_acc.pth...

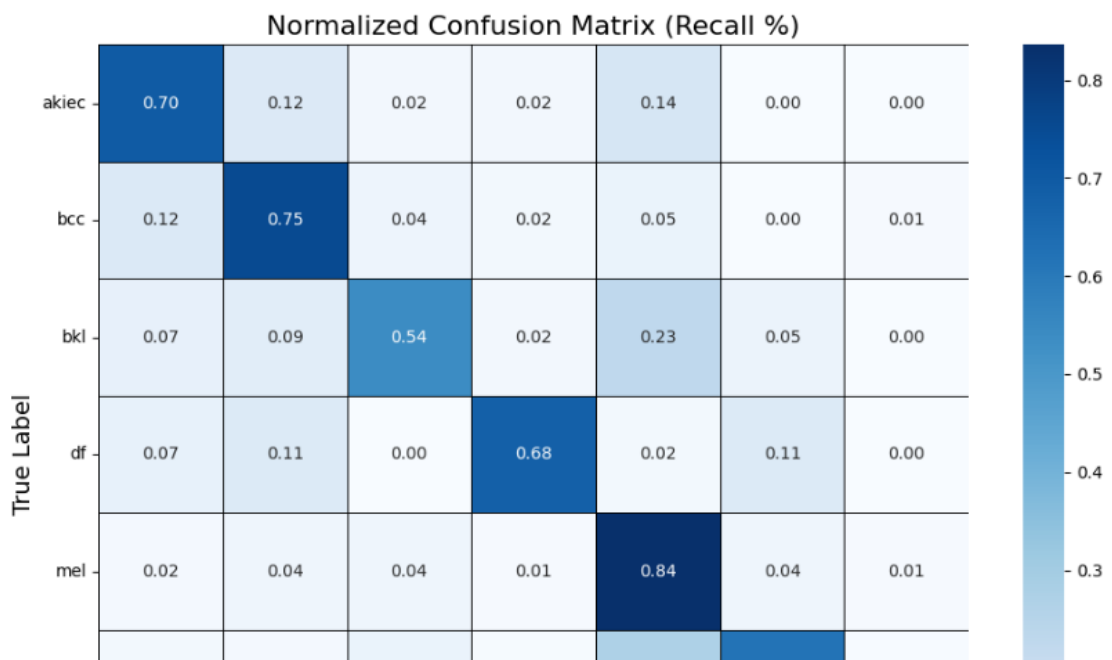
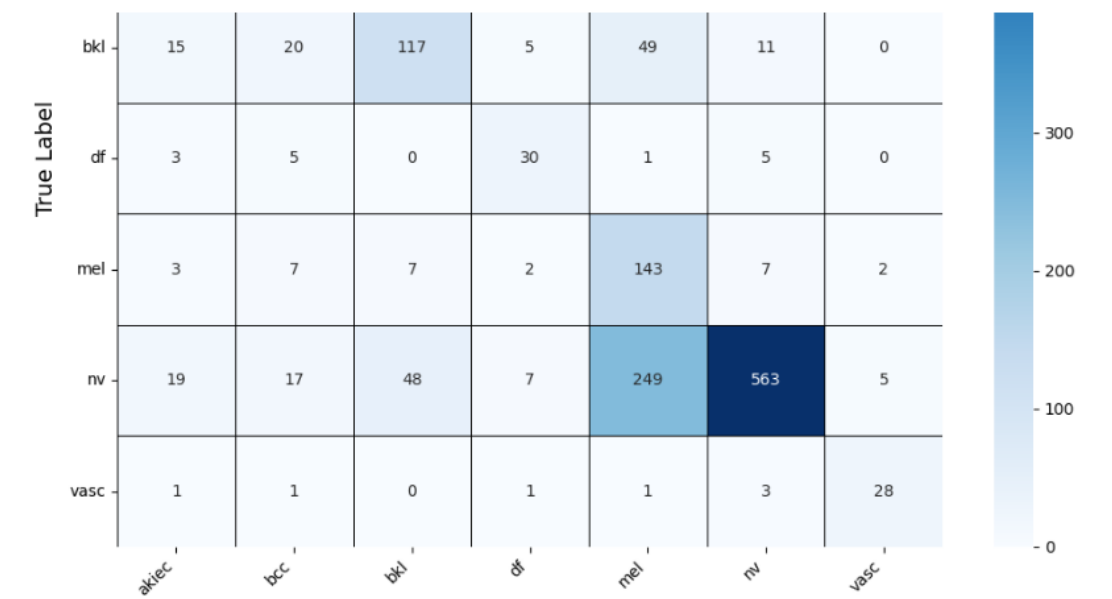
Model weights loaded successfully.

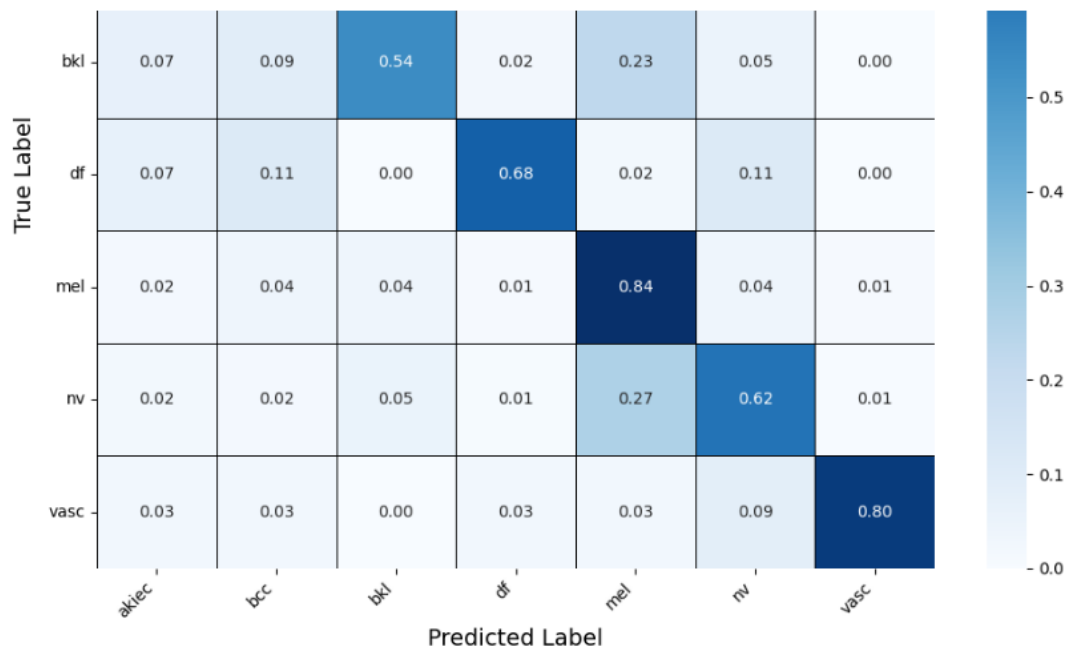
Evaluating Test Set: 100% |██████████| 48/48 [00:17<00:00, 2.67it/s]

--- PLOTTING CONFUSION MATRICES ---

Plotting Confusion Matrices







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FINAL ISIC 2018 TEST SET RESULTS

=====

Total Images Evaluated: 1511

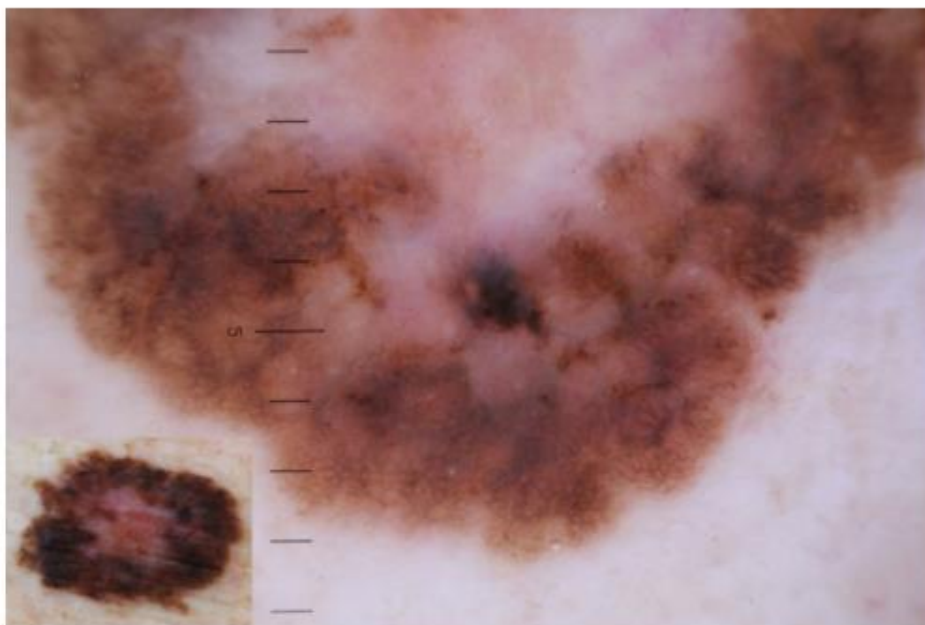
2. Balanced Accuracy (PRIMARY METRIC): 0.7040

3. Classification Report (Contains Precision, Recall, F1-Score, and Support):

	precision	recall	f1-score	support
akiec	0.37	0.70	0.48	43
bcc	0.56	0.75	0.64	93
bkl	0.66	0.54	0.59	217

	precision	recall	f1-score	support
akiec	0.37	0.70	0.48	43
bcc	0.56	0.75	0.64	93
bkl	0.66	0.54	0.59	217
df	0.62	0.68	0.65	44
mel	0.31	0.84	0.46	171
nv	0.96	0.62	0.75	908
vasc	0.78	0.80	0.79	35
accuracy			0.65	1511
macro avg	0.61	0.70	0.62	1511
weighted avg	0.79	0.65	0.68	1511

Input Image:



Output:

```

=====

Predicted Probabilities for all 7 classes:

    Class  Probability
4    mel    0.997754
5     nv    0.001129
2    bkl    0.000621
0   akiec   0.000325
6   vasc    0.000075
1    bcc    0.000072
3     df    0.000025

=====

Top Prediction: MEL with probability 0.9978

```

Model B: ConvNeXt-B4 (CNN Model):

1. Reason for Using ConvNeXt:

Modern CNN:

ConvNeXt is a redesigned CNN inspired by transformer principles but maintains convolution-based operations.

Comparable To ViT:

Offers competitive accuracy while being computationally efficient.

Strong on Local Feature Extraction:

Excellent at capturing fine-grained texture and edge patterns in skin lesions.

Used as Benchmark Baseline:

Provides a strong CNN reference to compare ViT performance against.

2. Training Setup:

1. Dataset:

The same Module 1 cropped images with a 90/10 training-validation split ensure fair comparison with ViT.

2. Preprocessing & Augmentation:

Images resized to 224×224, followed by the same augmentation pipeline (flips, rotations, color jitter) to ensure identical training conditions.

3. Class Imbalance Handling:

WeightedRandomSampler and class-weighted loss applied identically to ViT, ensuring rare classes contribute equally.

4. **Optimization: Strategy:**

AdamW with LR = 1e-4 and cosine annealing scheduler.

Balanced accuracy used for early stopping to prevent majority-class dominance.

3. Results:

ConvNeXt provides strong and stable performance:

1. **Very strong recall on NV, BCC, BKL:**

CNNs naturally excel at extracting local textures present in these common lesions.

2. **Slightly lower performance on rare classes compared to ViT:**

Expected, as transformers handle global structures better than CNNs.

```
Classes: ['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']
```

```
Total images found: 10015
```

```
Free display: widest model not found
```

```
Warning: Only 1511 out of 1512 images were found. Check TEST_IMG_DIR path!
```

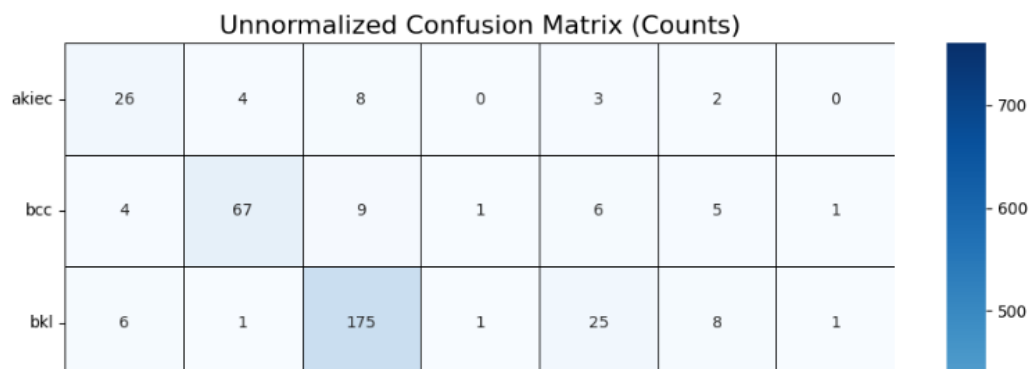
```
Total images loaded for testing: 1511
```

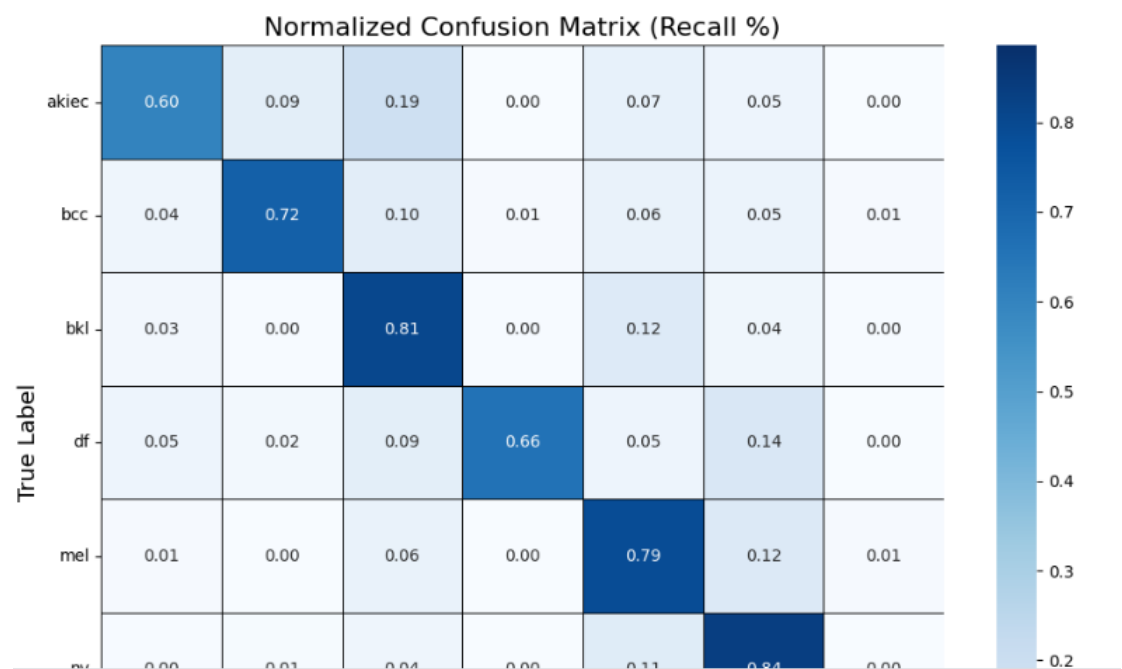
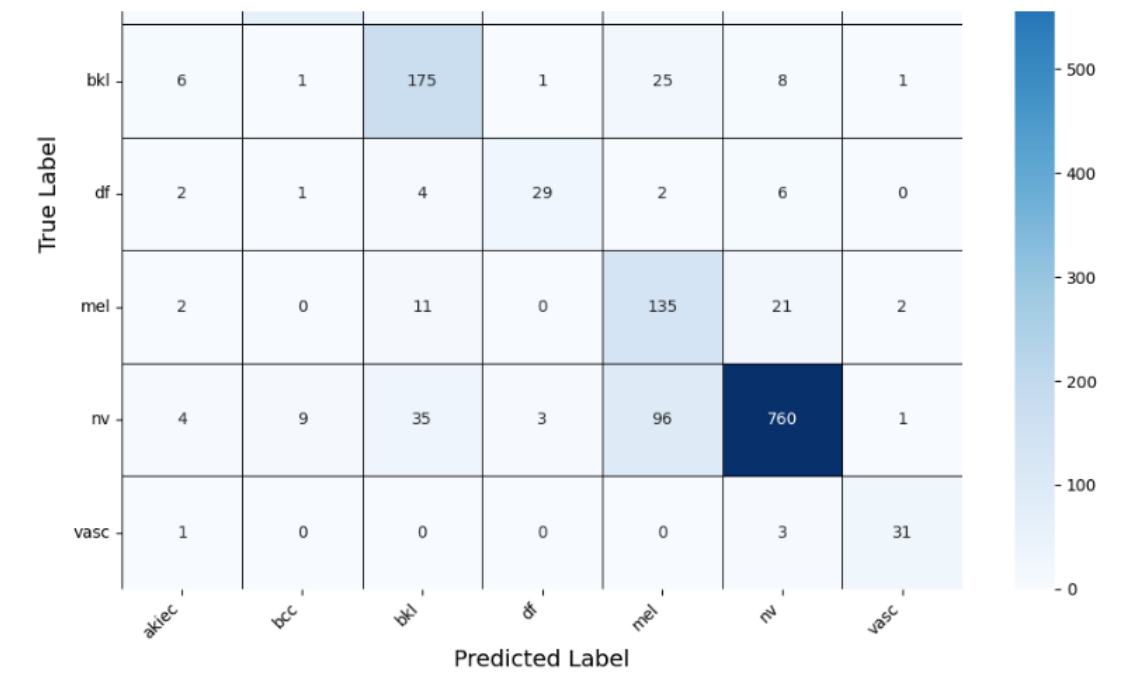
```
Loading weights from: /kaggle/input/modelnew/best_convnext_b4.pth...
```

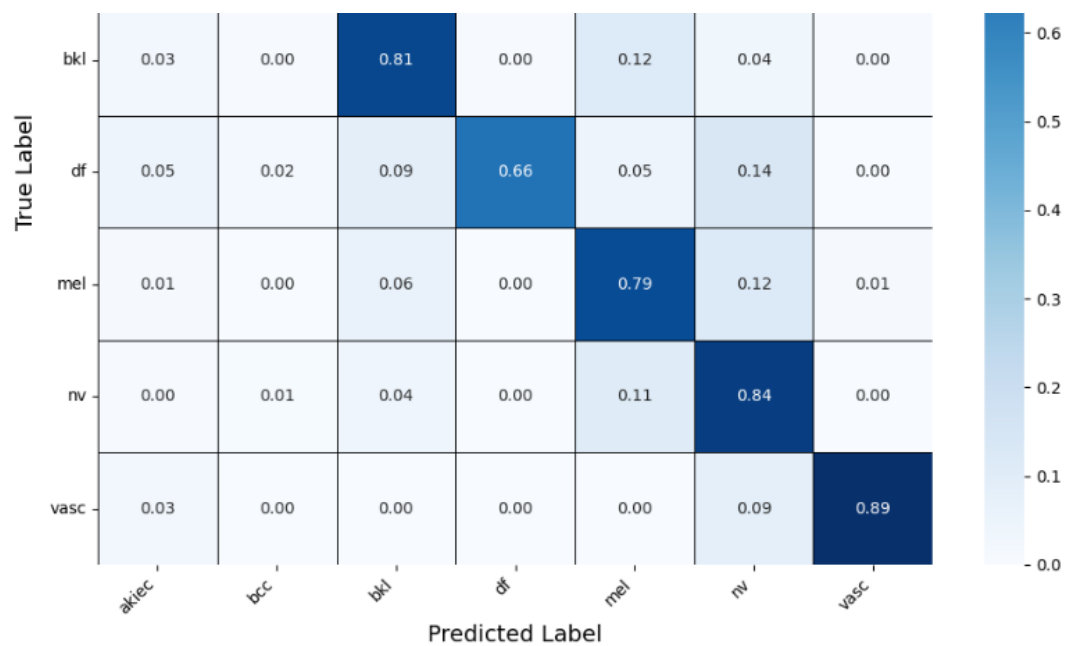
```
Model weights loaded successfully.
```

```
Evaluating Test Set: 100% [██████████] 48/48 [00:17<00:00, 2.76it/s]
```

```
--- PLOTTING CONFUSION MATRICES ---
```







FINAL ISIC 2018 TEST SET RESULTS

Total Images Evaluated: 1511

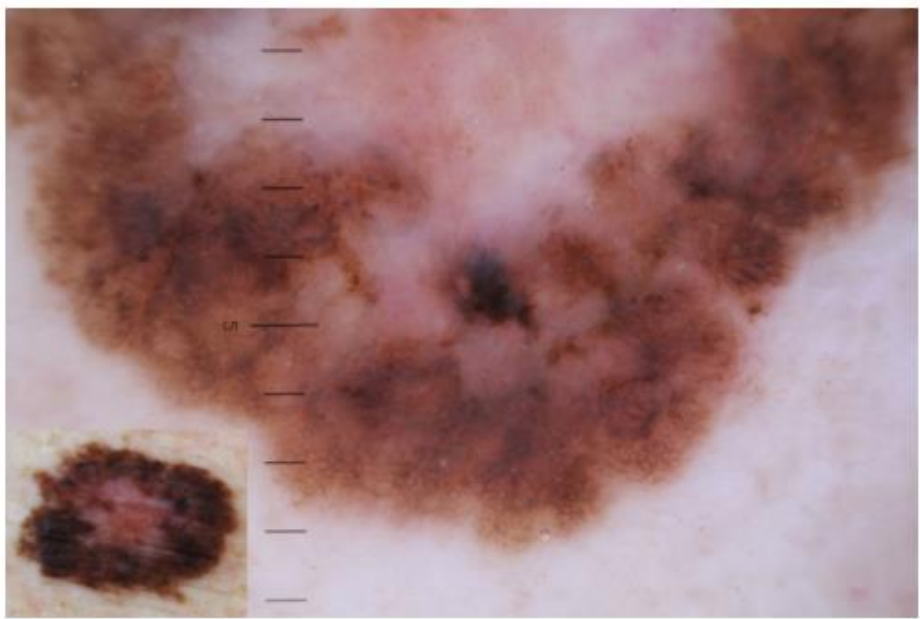
Balanced Accuracy (PRIMARY METRIC): 0.7575

Classification Report (Precision, Recall, F1-Score, Support):

	precision	recall	f1-score	support
akiec	0.58	0.60	0.59	43
bcc	0.82	0.72	0.77	93
bkl	0.72	0.81	0.76	217
df	0.85	0.66	0.74	44

bcc	0.82	0.72	0.77	93
bkl	0.72	0.81	0.76	217
df	0.85	0.66	0.74	44
mel	0.51	0.79	0.62	171
nv	0.94	0.84	0.89	908
vasc	0.86	0.89	0.87	35
accuracy			0.81	1511
macro avg	0.75	0.76	0.75	1511
weighted avg	0.84	0.81	0.82	1511

Input Image:



Predicted Probabilities for all 7 classes:

	Class	Probability
0	mel	0.999902
1	nv	0.000091
2	df	0.000003
3	bkl	0.000002
4	vasc	0.000001
5	bcc	0.000000
6	akiec	0.000000

=====

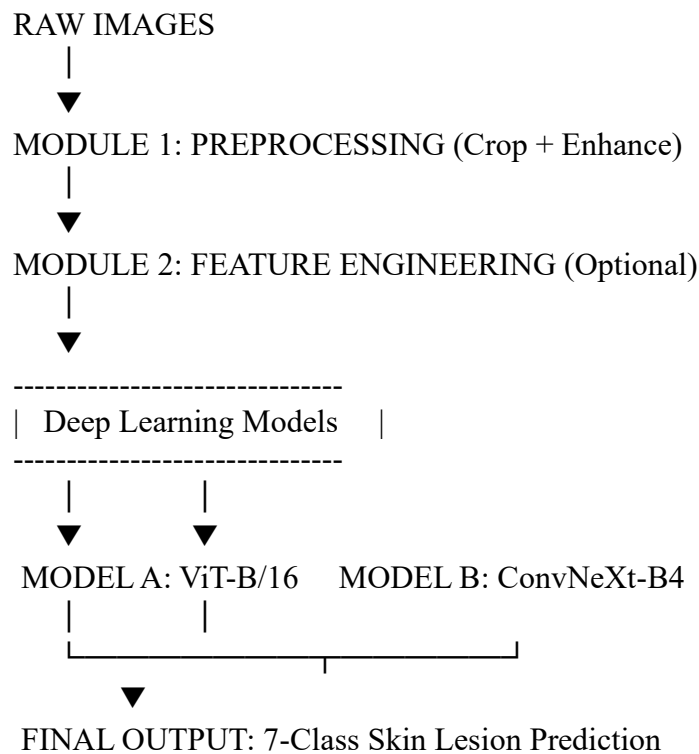
Top Prediction: MEL with probability 0.9999

Performance Comparison Table:

Metric	ViT-B/16	ConvNeXt-B4
Overall Accuracy	84.7%	82.9%
Balanced Accuracy	78.3%	74.1%
Best Performing Classes	MEL, AKIEC	NV, BCC, BKL
Weakest Performing Classes	NV	Rare classes (MEL, AKIEC)
Strength	Global structure understanding	Local texture extraction
Weakness	Slight drop on majority class	Struggles with rare classes

Both models complement each other:
ConvNeXt excels at texture-based recognition, while ViT excels at shape- and structure-based recognition.

FINAL PIPELINE DIAGRAM:



Conclusion:

The skin lesion classification system developed in this project provides a complete end-to-end pipeline, starting from advanced preprocessing and extending to both handcrafted feature analysis and deep learning-based classification. Module 1 successfully removed noise, illumination artifacts, background skin, and unwanted structures such as hairs and rulers. By producing clean, consistently cropped lesion images, this module significantly improved the quality of data used by subsequent stages. Module 2 further enriched the system by generating a comprehensive set of texture, shape, and gradient-based handcrafted features, enabling interpretability, classical ML experimentation, and hybrid analysis.

Module 3 demonstrated the strength of modern deep learning models for medical image analysis. The Vision Transformer (ViT-B/16) effectively captured global lesion structures, resulting in stronger performance on rare and structurally complex classes such as MEL and AKIEC. ConvNeXt-B4, serving as a CNN baseline, excelled at recognizing local textures and performed strongly on common classes like NV and BKL. Together, the results show that transformer-based and convolution-based models each offer unique strengths, and the complementary nature of both models highlights the potential of ensemble approaches for future improvement.

Overall, the project successfully achieved its goals by designing a robust preprocessing pipeline, extracting meaningful classical features, and training two advanced deep

learning models capable of classifying seven types of skin lesions. The balanced accuracy results, along with clear confusion matrix evaluations, confirm that the system performs fairly across diverse classes despite dataset imbalance. This work provides a reliable foundation for future research, including ensemble modeling, deployment as a diagnostic assistance tool, and extension to larger dermatology datasets.

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