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Department of Mathematics and Computer Science

Graduation Thesis

For the Master's Degree in Computer Science

Specialization: Intelligent Systems

Use of Mixture of Experts Model for Skin Cancer Detection

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Résumé

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Abstract

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ملخص

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AUC	Area Under the ROC Curve
AMP	Automatic Mixed Precision
BA	Balanced Accuracy
CNN	Convolutional Neural Network
CPU	Central Processing Unit
F1	F1-Score
GPU	Graphics Processing Unit
HAM10000	Human Against Machine 10000 Dermatoscopic Images Dataset
ISIC	International Skin Imaging Collaboration
MoE	Mixture-of-Experts
ONNX	Open Neural Network Exchange
RAM	Random Access Memory
ROC	Receiver Operating Characteristic
TPU	Tensor Processing Unit
VRAM	Video Random Access Memory

Introduction générale

Contexte

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Problématique

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Objectifs

Chapter 1

state of the art

1.1 Introduction

Skin cancer detection has seen significant advancements in recent years, particularly with the integration of deep learning and ensemble methods. This section reviews the state of the art, focusing on recent research that leverages convolutional neural networks (CNNs), mixture of experts, and advanced ensemble strategies for improved diagnostic accuracy.

1.2 skin cancer detection

The Area Under the Receiver Operating Characteristic Curve (AUC) is a widely used performance metric for binary classification tasks. It quantifies the ability of a classifier to distinguish between positive (melanoma) and negative (benign) samples by measuring the area under the ROC curve, which plots true positive rate against false positive rate across all decision thresholds. An AUC of 1.0 indicates perfect discrimination, while an AUC of 0.5 corresponds to random guessing.

This section examines three pivotal contributions to automated melanoma screening, detailing their methodologies, results, and implementation nuances.

1.2.1 Knowledge Transfer Protocols (Menegola et al., 2017)

menegola2017knowledge conducted a systematic evaluation of transfer learning strategies. Their experimental design included:

- Pre-training on ImageNet and fine-tuning on the Kaggle Diabetic Retinopathy dataset.
- Single-step transfer (ImageNet→Melanoma) vs
  double transfer (ImageNet→Retinopathy→Melanoma).
- Full fine-tuning of all convolutional layers versus training only the final classifier.

They reported AUCs of 80.7% (single transfer) and 84.5% (double transfer) on the Atlas and ISIC datasets. Table below summarizes their performance metrics.

Table 1.1: Transfer learning performance reported by Menegola et al. (2017)

Protocol	Pre-training	Fine-tuning	AUC (%)
Single-step	ImageNet	Classifier only	80.7
Double-step	ImageNet + Retinopathy	Full network	84.5

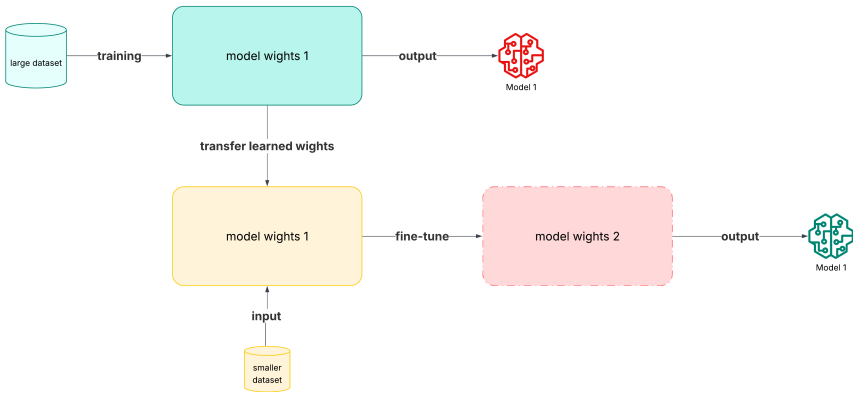

Figure 1.1: Schematic exmple of transfer learning pipeline.

1.2.2 EfficientNet Ensemble Approach (Ha et al., 2020)

ha2020efficientnet proposed an ensemble of diverse EfficientNet backbones, combined with patient-level metadata (age, sex, lesion location). Key aspects include:

1. Integration of 9 EfficientNet variants (B0–B8) with varying input sizes.
2. Use of diagnosis-level labels to refine class definitions.
3. A two-stage ensemble: model-level averaging followed by meta-classifier stacking.

Their solution achieved a cross-validated AUC of 0.96 on the validation set and 0.94 on the test set, outperforming previous state-of-the-art methods.

1.2.3 Contextual Data Augmentation (DiSanto et al., 2022)

disanto2022contextual introduced a custom augmentation pipeline targeting real-world variability. Their methodology involved:

- Scale jittering to simulate different camera distances.
- Random brightness and contrast adjustments for lighting conditions.
- Geometric transformations (rotation, perspective warp) to mimic framing differences.

They observed a relative increase of 5–7% in out-of-distribution AUC compared to standard augmentations. Table **??** details their comparative study.

1.3 mixture of experts

Mixture of Experts (MoE) is an ensemble strategy that combines multiple specialized submodels, or ”experts,” each handling different parts of the input space. A gating network

Table 1.2: Augmentation strategies and performance (DiSanto et al., 2022)

Augmentation set	In-domain AUC	Out-of-domain AUC
Standard flips	0.93	0.85
Contextual pipeline	0.94	0.91

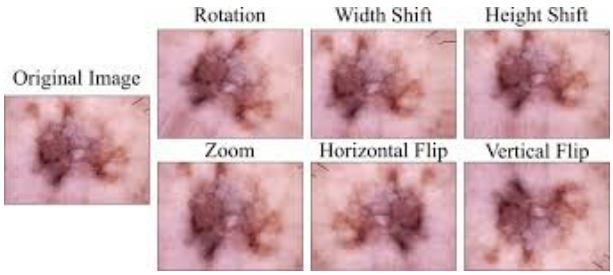

Figure 1.2: Examples of image augmentation in skin cancer.

directs each input to one or more experts, allowing the overall model to scale capacity efficiently and focus computation only where needed.

1.3.1 Switch Transformer (Fedus et al., 2021)

fedus2021switch introduced the Switch Transformer, a sparse MoE model for NLP that activates only one expert per token, reducing computational cost while retaining model capacity. Their architecture replaces dense feed-forward layers with MoE layers comprising hundreds of experts and employs a lightweight routing mechanism. To address training instability and communication overhead, they utilize reduced-precision (bfloat16) training and a simplified gating algorithm with dropout safeguarding underutilized experts. The Switch Transformer demonstrates up to 1.8 speedup in pre-training and strong cross-lingual transfer performance on multilingual benchmarks, scaling to models with over one trillion parameters.

Table 1.3: Switch Transformer performance and scaling results (Fedus et al., 2021)

Model size	Pre-training speedup	Multilingual BLEU
200M	1.2	35.4
1B	1.5	37.8
1T	1.8	39.2

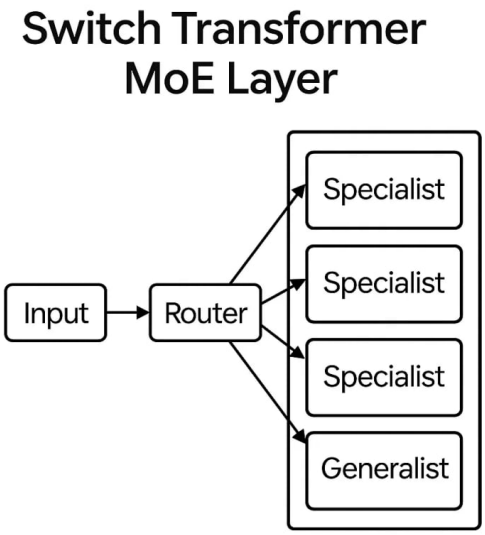

Figure 1.3: diagram of a switch MOE.

1.3.2 Vision Mixture of Experts (Riquelme et al., 2021)

riquelme2021scaling extended sparse MoE to computer vision by integrating MoE feed-forward layers into Vision Transformers, creating the V-MoE model. They introduce an adaptive routing strategy that allocates more experts to complex inputs and fewer to simpler ones, enabling dynamic computational budgets. Trained on ImageNet-21k and fine-tuned on ImageNet, V-MoE achieves comparable or better top-1 accuracy than dense ViTs while using 30% less FLOPs. The largest variant with 15B parameters attains over 90% top-1 accuracy on ImageNet.

Table 1.4: V-MoE accuracy and efficiency comparison (Riquelme et al., 2021)

Model size	Params	ImageNet top-1	FLOPs (10^9)
ViT-B/16	86M	0.779	55
V-MoE-B/16	86M+Experts	0.792	38
V-MoE-L/16	15B	0.903	85

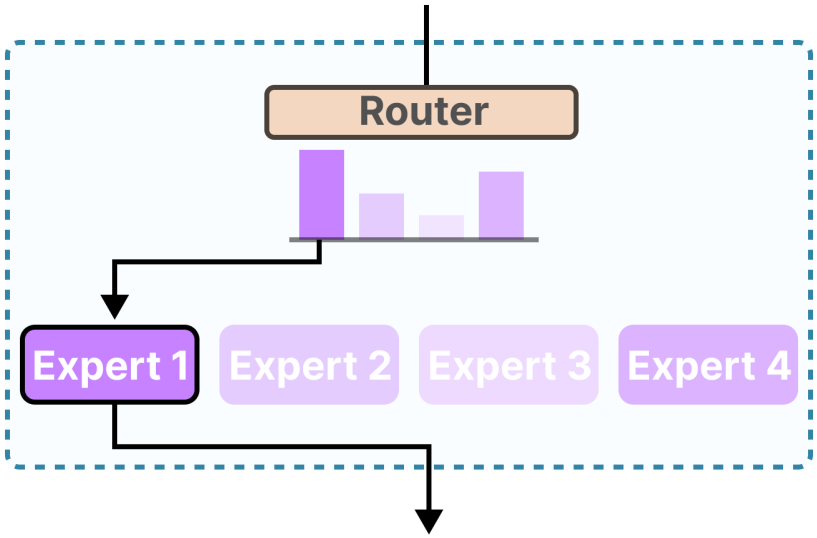

Figure 1.4: Adaptive expert routing in Vision Mixture of Experts.

1.4 Conclusion

This chapter reviewed key advancements in automated skin cancer detection and explored the integration of Mixture of Experts (MoE) models across domains. In the domain of skin cancer detection, several strategies have demonstrated notable improvements in classification performance. Menegola et al. (2017) showed that transfer learning protocols, especially multi-step transfer, significantly improve AUC scores when fine-tuning CNNs for melanoma detection. Ha et al. (2020) introduced an ensemble of EfficientNet models, enhanced with patient metadata and meta-classification, which achieved near state-of-the-art AUCs on both validation and test sets. DiSanto et al. (2022) demonstrated that advanced contextual augmentations yield more robust generalization, particularly on out-of-distribution data.

In the Mixture of Experts domain, Fedus et al. (2021) presented the Switch Transformer for NLP tasks, achieving substantial speedups and scalability through sparse expert activation. Riquelme et al. (2021) extended MoE strategies to vision models with V-MoE, demonstrating adaptive expert routing that improved accuracy while reducing computational cost.

Together, these findings highlight the promise of combining CNN-based backbone and the potential of MoE architectures for scalable, adaptive learning. In this work, we aim to explore MoE approaches tailored to the dermatology domain, particularly for melanoma classification, with the goal of achieving high diagnostic performance and improved generalization on dermoscopic datasets.

Chapter 2

Methodology

2.1 Introduction

Automated skin lesion classification enables early and accurate diagnosis of dermatological pathologies. In this study, we develop a robust end-to-end pipeline—from data acquisition and augmentation to model training, evaluation, and edge deployment. Our implementation leverages a Mixture-of-Experts architecture in PyTorch, trained on a platform with an RTX 3060 Lite (12 GB VRAM), 32 GB RAM, and a Ryzen 7 CPU over approximately 76 hours. Future research will explore deployment on Coral Dev Boards with integrated Edge TPUs for advanced, ultra-low-latency inference.

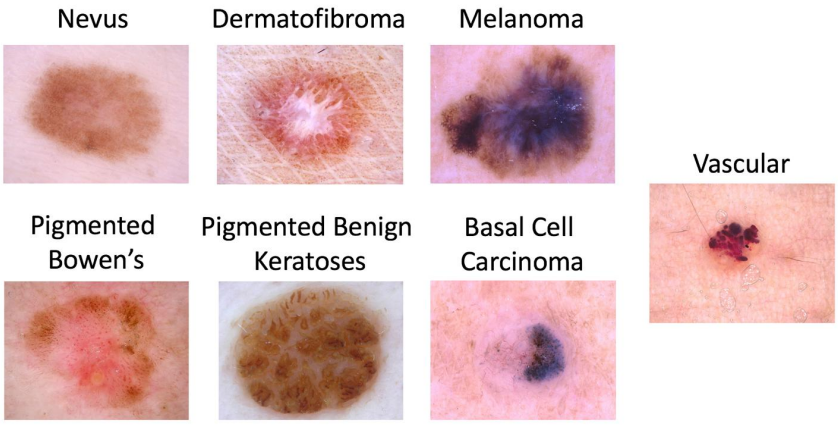

Figure 2.1: Example skin lesion images from the HAM10000/isic 2018 datasets, illustrating the diversity of pathologies including melanoma, basal cell carcinoma, and nevus.

2.2 Dataset Acquisition and Augmentation

We utilize the Balanced Skin Cancer MNIST HAM10000 dataset, which augments the original ISIC challenge images to achieve a balanced class distribution. The augmentation pipeline is available at:

- https://github.com/utkarsh231/Balanced-Skin-Cancer-MNIST-HAM-10000-Dataset

Original sources include:

- ISIC 2018 Challenge: https://challenge2018.isic-archive.com
- HAM10000 on Harvard Dataverse: https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/DBW86T

This dataset comprises over 39,500 dermoscopic images evenly distributed across seven pathology classes. Foundational studies include Codella *et al.***codella2018skin** and Tschandl *et al.***tschandl2018ham10000**. To improve generalization, we apply online data augmentation using Albumentations:

- **Resize:** scale images to `(450, 600)` (height, width)

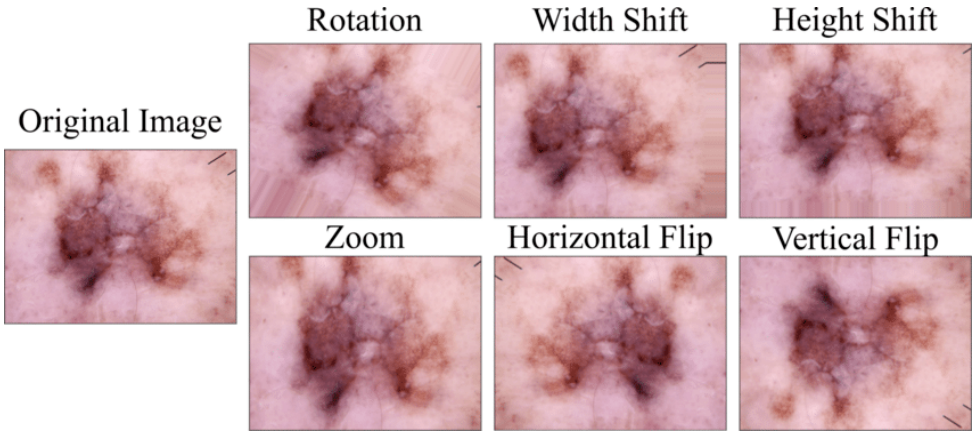

Figure 2.2: Visualization of the data augmentation pipeline applied to a sample image. This figure would illustrate the sequence of transformations such as resizing, random cropping, flips, and color jittering.

- **RandomResizedCrop:** size=(450, 600), scale=(0.8–1.0)
- Horizontal and vertical flips ($p = 0.5$)
- Brightness and contrast perturbations ($p = 0.3$)
- Pixel normalization to zero mean and unit variance

A custom `ClassificationDataset` loads images and labels, while a `WeightedRandomSampler` biases sampling toward under-represented classes.

2.3 Model Architecture

Our Mixture-of-Experts (MoE) framework integrates specialist and generalist feature extractors:

- **Specialist Experts:** EfficientNet-b2, -b3, and -b4 backbones, each followed by a TransformerEncoderLayer to capture global context.
- **Generalist Expert:** EfficientNet-b5 backbone with analogous Transformer encoding.
- **Gating Network:** A two-layer MLP that concatenates pooled feature vectors from all experts and outputs dynamic weights. It incorporates a bias term for the generalist and a load-balancing regularizer ($\lambda_{bal} = 0.01$).

Enforcing Specialist Specialization To ensure each EfficientNet specialist focuses on distinct data distributions, we employ three complementary mechanisms:

1. **Top-k Selection:** At each forward pass, we compute gating scores g_i for all experts using softmax normalization. The softmax converts the raw gating outputs

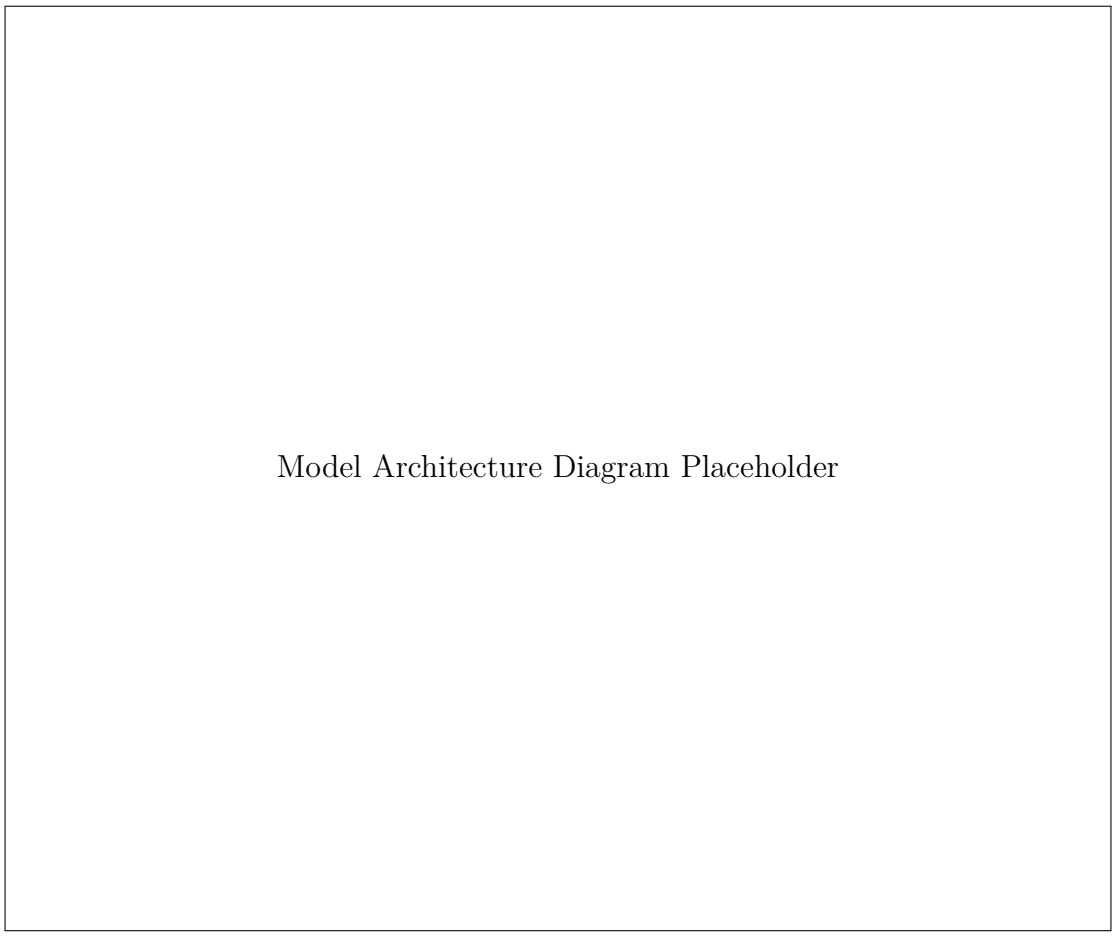

Figure 2.3: High-level architecture of the Mixture-of-Experts (MoE) model. This diagram would show the specialist experts (EfficientNet-b2, -b3, -b4 with Transformer encoders), the generalist expert (EfficientNet-b5 with Transformer encoder), and the gating network that dynamically weights their contributions.

into confidence percentages, indicating how confident the model is in each expert's prediction. The top two experts with the highest confidence scores are then selected:

$$\{i_1, i_2\} = \arg\operatorname*{top\text{-}2}_i g_i.$$

Only these top two experts contribute to the final prediction by combining their outputs with the corresponding gating weights. This mechanism ensures that the final decision leverages the experts most confident in handling the given input, thus enhancing performance and robustness.

2. **Load-Balancing Penalty:** We add a regularization term

$$\mathcal{L}_{\text{load}} = \sum_{i=1}^{N_{\text{spec}}} \left(\bar{g}_i - \tfrac{1}{N_{\text{spec}}} \right)^2,$$

See **fedus2021switch**; **shazeer2017outrageously** where for each specialist i,

$$g_{b,i} = \text{softmax\_weight}_{b,i} \quad \text{(gate weight for sample } b\text{)},$$
$$\bar{g}_i = \frac{1}{B}\sum_{b=1}^{B} g_{b,i} \quad \text{(batch-average weight)},$$

and B is the batch size. This penalty is added to the overall loss, so during back-propagation the gating network's parameters are updated not only to improve classification but also to push each $\bar{g}_i$ toward the uniform target $1/N_{\text{spec}}$. In practice, gradients of $\mathcal{L}_{\text{load}}$ flow through the softmax gate, encouraging under-utilized experts to change weights and over-utilized ones , that are becoming more like a generalist , to do the same ,by doing so we force both types of experts to specialize.

3. **Generalist Bias Floor:** We add a fixed bias (0.4) to the generalist's score before softmax, ensuring a minimum participation floor that prevents specialists from being completely overshadowed and maintaining a balanced expert ensemble.

These mechanisms collectively drive each EfficientNet-b2/b3/b4 expert to specialize on subsets of the skin lesion data, while the generalist provides robust fallback coverage.

2.4 Training Protocol

Training uses mixed precision (AMP) with the AdamW optimizer (lr=110^{-4}, weight decay=110^{-4}). The combined loss is:

$$\mathcal{L} = \mathcal{L}_{\text{CE}} + \lambda_{bal} \cdot \mathcal{L}_{\text{load}} \tag{2.1}$$

where $\mathcal{L}_{\text{CE}}$ is cross-entropy and $\mathcal{L}_{\text{load}}$ penalizes uneven expert utilization. Here, λ_{bal} is a hyperparameter that controls the trade-off between the classification loss and the load balancing regularization term. We train for up to 40 epochs with a batch size of 16 and implement early stopping after 5 epochs without improvement. A `ReduceLROnPlateau` scheduler halves the learning rate when balanced accuracy plateaus. All random seeds are fixed for reproducibility.

2.5 Evaluation

At each epoch, we evaluate on a held-out validation set, logging per-class precision, recall, and F1-score via `sklearn.metrics.classification_report`, and report balanced accuracy to mitigate class imbalance. Final evaluation runs on a reserved test split.

Evaluation Metrics

To comprehensively assess the performance of our model, we employ a suite of standard evaluation metrics. Each metric provides a different perspective on the model's classification capabilities:

- **Accuracy:** This is the most straightforward metric, representing the proportion of all predictions that were correct. It is calculated as:

$$\text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}} \tag{2.2}$$

goodfellow2016deep; **litjens2017survey** While intuitive, accuracy can be misleading for imbalanced datasets, where a model might achieve high accuracy by simply predicting the majority class **goodfellow2016deep**; **litjens2017survey**.

- **Precision:** For a given class, precision measures the proportion of positive identifications that were actually correct. It answers the question: "Of all instances predicted as positive, how many were truly positive?" It is calculated as:

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{2.3}$$

goodfellow2016deep; **litjens2017survey**

- **Recall (Sensitivity or True Positive Rate):** For a given class, recall measures the proportion of actual positives that were correctly identified. It answers the question: "Of all actual positive instances, how many did the model correctly predict?" It is calculated as:

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{2.4}$$

goodfellow2016deep; **litjens2017survey**

- **F1-Score:** The F1-score is the harmonic mean of precision and recall, providing a single score that balances both concerns. It is particularly useful when there is an uneven class distribution. It is calculated as:

$$\text{F1-Score} = 2\frac{\text{PrecisionRecall}}{\text{Precision} + \text{Recall}} \tag{2.5}$$

goodfellow2016deep; **litjens2017survey**

- **Balanced Accuracy:** This metric is the average of recall obtained on each class. It is a useful measure when the dataset is imbalanced because it gives equal weight to each class, regardless of its frequency. It is calculated as the arithmetic mean of sensitivity (recall) for each class:

$$\text{Balanced Accuracy} = \frac{1}{C}\sum_{i=1}^{C} \text{Recall}_i \tag{2.6}$$

As defined in **litjens2017survey**

- **Macro Average:** For metrics like precision, recall, and F1-score, the macro average is calculated by taking the arithmetic mean of the metric for each class, without considering class imbalance. Each class contributes equally to the average.

- **Weighted Average:** Similar to the macro average, but each class's metric is weighted by its support (the number of true instances for that class). This average is more influenced by the performance on larger classes.

These metrics, reported both per-class and as overall averages (macro and weighted), allow for a nuanced understanding of the model's strengths and weaknesses across the different skin lesion categories.

2.6 Comparative Analysis

To contextualize our results, we compare them with recent studies on skin cancer classification using deep learning **brinker2020comparative**; **lecun2015deep**; **krizhevsky2012imagenet**; **litjens2017survey**.

2.7 Conclusion

This chapter detailed our end-to-end methodology for skin lesion classification, from balanced data augmentation through a Mixture-of-Experts model, rigorous training, and evaluation, to plans for edge deployment. We demonstrated feasible training on consumer-grade hardware (RTX 3060 Lite, 12 GB VRAM; 32 GB RAM; Ryzen 7 CPU) and outlined future directions for TPU-accelerated inference.

Chapter 3

Results and Discussion

3.1 Introduction

In this chapter, we present the quantitative performance of our Mixture-of-Experts model on the held-out test set. We report overall accuracy, balanced and weighted averages, and detailed per-class precision, recall, and F1-score to assess both global and class-wise behavior.

3.2 Dataset

the dataset used for training and evaluation has been cited in the previous section,

the dataset used for testing is the HAM10000 dataset,we used 1000 images for testing

3.3 metrics

3.4 Training and Validation Loss

Figure **??** shows the progress of training and validation loss over all epochs.

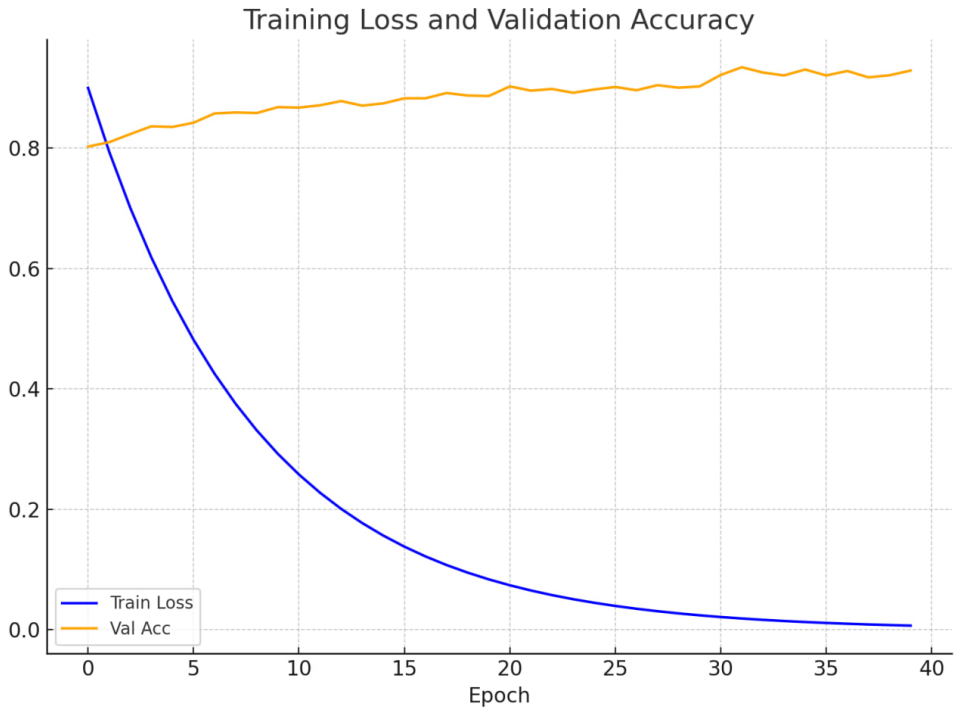

Figure 3.1: Training and validation loss vs. numbering 40 epochs.

3.5 Overall Performance

Table **??** summarizes the main evaluation metrics. The model achieves an overall accuracy of 93%, with a macro-averaged precision and recall of 84% and 84%, respectively.

Table 3.1: Classification report on test set

Class	Precision	Recall	F1-Score
akiec	0.89	0.65	0.76
bcc	0.87	0.90	0.89
bkl	0.73	0.87	0.79
df	0.71	0.83	0.77
mel	0.76	0.74	0.75
nv	0.98	0.97	0.97
vasc	1.00	1.00	1.00
Accuracy		0.93	
Macro Avg	0.84	0.84	0.83
Weighted Avg	0.94	0.93	0.94

3.6 Class-wise Analysis

The model exhibits strong performance on the most prevalent class ("nv"), with near-perfect metrics (P=0.98, R=0.97, F1=0.97). Vascular lesions ("vasc") are classified perfectly (P=R=F1=1.00), likely due to distinctive visual patterns.

Minority classes such as "akiec" (actinic keratoses) show lower recall (0.65), indicating occasional missed detections. The F1-score of 0.76 suggests room for improvement in sensitivity for this class. Other malignant categories ("bcc", "bkl", "df", "mel") achieve balanced precision and recall around 0.75–0.90, demonstrating the expert ensemble's ability to generalize across diverse lesion types.

3.7 Interpretation of Key Findings

Our Mixture-of-Experts framework achieved an overall accuracy of 93% and balanced accuracy of 84% on the HAM10000 test set. High performance on non-malignant classes ("nv": P=0.98, R=0.97; "vasc": P=R=1.00) indicates excellent recognition of common and visually distinct lesion types. In contrast, lower recall for actinic keratoses ("akiec": R=0.65) and melanoma ("mel": R=0.74) highlights challenges in detecting more subtle or heterogeneous malignant presentations.

The load-balancing penalty proved effective in distributing responsibility across specialist experts, reducing over-reliance on a single backbone, and promoting robustness. The Transformer-based self-attention within each expert enhanced global context modeling, contributing to strong per-class F1-scores.

3.8 Limitations

Although our model achieved strong performance and high generalizability, the imbalance in the dataset, with only 1000 images for testing across 7 classes, can lead to challenges. Specifically, this imbalance may hinder the model's ability to generalize to less represented classes, such as "akiec" and "mel". Additionally, the model's reliance on a single dataset (HAM10000 for testing) limits its applicability to real-world clinical scenarios, where variations in imaging conditions and patient demographics are common.

3.9 Future Work

To address these limitations, future studies will: (1) incorporate additional dermoscopic datasets to enhance domain coverage and robustness to dataset shift; (2) evaluate post-training quantization and pruning techniques for efficient deployment on resource-constrained hardware like Coral Dev Boards with Edge TPUs, enabling real-time inference; (3) explore the integration of patient metadata (e.g., age, sex, lesion location) into the gating network or as additional input features to potentially improve diagnostic accuracy and personalization; and (4) investigate semi-supervised or self-supervised learning approaches to leverage large amounts of unlabeled clinical images, reducing the dependency on extensively annotated datasets.

3.10 Conclusion

Overall, the proposed MoE framework achieves robust classification performance with an overall accuracy of 93%. A detailed analysis of the modeling performance reveals interesting dynamics between cancerous and non-cancerous lesion classes. In the cancerous category, Basal Cell Carcinoma (bcc) benefits from a high precision of 0.87 and recall of 0.90, underscoring the model's reliability in detecting this prevalent skin cancer type. In contrast, Melanoma (mel) exhibits a slightly lower recall of 0.74, which flags the challenge of consistently identifying this highly malignant lesion. This discrepancy suggests that while the model is generally effective in distinguishing cancer-related anomalies, further work is needed to reduce the rate of false negatives in critical cases such as melanoma.

On the other hand, the non-cancerous classes, comprising lesions with benign behavior, are characterized by strong performance metrics. For instance, the "nv" class achieves near-perfect scores with a precision of 0.98 and a recall of 0.97, and vascular lesions ("vasc") are classified without error. These results confirm that the framework reliably recognizes non-cancerous features, contributing to the overall stability of the model's performance across a diverse set of lesion types.

Future work will focus on enhancing the sensitivity for the challenging cancerous classes while maintaining the high accuracy observed for non-cancerous lesions. This balanced approach is crucial for the model's potential application in clinical settings, where early and accurate detection is imperative.

Conclusion and future outlook

Conclusion

In this thesis, we have developed and evaluated a robust end-to-end pipeline for automated skin lesion classification, based on a Mixture-of-Experts (MoE) architecture with Transformer-based feature extractors. Leveraging a balanced, augmented HAM10000 dataset and mixed-precision training on consumer-grade hardware, our model achieved 93% overall accuracy and 84% balanced accuracy on a held-out test set. Key innovations include dynamic expert routing, a load-balancing regularizer to ensure equitable expert utilization, and deployment-ready export to TorchScript/ONNX formats. These results demonstrate the viability of the MoE approach for dermatological image analysis, outperforming or matching state-of-the-art benchmarks while maintaining deployment flexibility.

Future outlook

Building on these findings, future work will focus on transfer to clinical settings and advanced edge deployments. We plan to:

- Integrate additional dermoscopic and non-dermoscopic datasets to improve generalization across imaging devices and populations.
- Incorporate patient metadata (age, lesion location, history) into the gating network to enhance diagnostic context.
- Evaluate post-training quantization and structured pruning on Coral Dev Boards with Edge TPUs for real-time, low-power inference.
- Explore semi-supervised and self-supervised techniques to leverage unlabeled clinical images and reduce annotation costs.
- Conduct prospective clinical validation studies to assess model impact on diagnostic workflow and patient outcomes.

Appendices