A project report on

Skin Cancer Detection using Deep Learning

Submitted in partial fulfillment for the award of the degree of

Bachelor of Technology in Computer Science and Engineering with Specialization in AI and Robotics

by

VEDANT KISHORE ADKA (21BRS1394)
CHAVALI SAI SREE RAM YADAV (21BRS1359)

VIT®
Vellore Institute of Technology
(Deemed to be University under section 3 of UGC Act, 1956)
CHENNAI

SCHOOL OF COMPUTER SCIENCE AND ENGINEERING

November,2024

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I hereby declare that the thesis entitled “SKIN CANCER DETECTION USING DEEP LEARNING” submitted by VEDANT KISHORE ADKA (21BRS1394), for the award of the degree of Bachelor of Technology in Computer Science and Engineering with specialization in AI and Robotics, Vellore Institute of Technology, Chennai is a record of bonafide work carried out by me under the supervision of Dr. Balasundaram A.

I further declare that the work reported in this thesis has not been submitted and will not be submitted, either in part or in full, for the award of any other degree or diploma in this institute or any other institute or university.

Place: Chennai

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This is to certify that the report entitled “Skin Cancer Detection using Deep Learning” is prepared and submitted by Vedant Kishore Adka (21BRS1394) to Vellore Institute of Technology, Chennai, in partial fulfillment of the requirement for the award of the degree of **Bachelor of Technology in Computer Science and Engineering with specialization in AI and Robotics** is a bonafide record carried out under my guidance. The project fulfills the requirements as per the regulations of this University and in my opinion meets the necessary standards for submission. The contents of this report have not been submitted and will not be submitted either in part or in full, for the award of any other degree or diploma and the same is certified.

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ABSTRACT

The rising incidence of skin cancer worldwide necessitates the development of advanced diagnostic tools to aid in early detection and improve patient outcomes. This project aims to design and implement an automated deep learning-based system for the classification of skin lesions as benign or malignant. Leveraging the Vision Transformer (ViT) model, which is known for its capability to capture complex image features through self-attention mechanisms, this research explores a novel approach to skin cancer diagnosis.

The system utilizes the HAM10000 dataset, a diverse and comprehensive collection of dermatoscopic images representing a variety of skin disorders. Initial data preprocessing includes image normalization and resizing, ensuring consistency for model input. To enhance model generalization and robustness, data augmentation techniques such as rotation, flipping, zooming, and rescaling are applied using TensorFlow's ImageDataGenerator. These steps create a more diverse training set, mitigating the risk of overfitting and improving the model's ability to perform on unseen data.

The ViT architecture is employed due to its effectiveness in capturing both local and global patterns by dividing images into patches and applying a self-attention mechanism. This approach enables the model to analyze image sections contextually, thereby enhancing its classification accuracy. Model training is performed with cross-entropy loss and the Adam optimizer, incorporating early stopping and learning rate scheduling to optimize learning and prevent overfitting. Evaluation of the model's performance involves key metrics such as accuracy, precision, recall, F1-score, and a confusion matrix for detailed insight into classification strengths and potential biases.

This project holds significant promise for real-world applications, especially in telemedicine. Deploying the system on telemedicine platforms can provide rapid, automated diagnostic support to healthcare providers and patients, facilitating timely decision-making and treatment. By addressing challenges in early skin cancer detection, this project aims to reduce diagnostic delays, enhance healthcare accessibility, and contribute to better patient outcomes. The research further highlights the potential of advanced deep learning models like Vision Transformers in revolutionizing medical diagnostics and shaping the future of AI-driven healthcare solutions.

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Place: Chennai

Date: 13 November 2024 **Vedant Kishore Adka**

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List of Abbreviations

Abbreviation	**Full Form**
AI	Artificial Intelligence
BCC	Basal Cell Carcinoma
BKL	Benign Keratosis-like Lesions
CNN	Convolutional Neural Network
CT	Computed Tomography
DF	Dermatofibroma
EDA	Exploratory Data Analysis
FN	False Negatives
FP	False Positives
GAN	Generative Adversarial Network
HAM10000	Human Against Machine with 10,000 training images dataset
LIME	Local Interpretable Model-agnostic Explanations
ML	Machine Learning
MRI	Magnetic Resonance Imaging
MSE	Mean Sensitivity Index
NLP	Natural Language Processing
NV	Melanocytic Nevi
ResNet	Residual Network
SCC	Squamous Cell Carcinoma

SHAP	SHapley Additive exPlanations
TP	True Positives
UV	Ultraviolet
ViT	Vision Transformer

Chapter 1

INTRODUCTION

Skin cancer is one of the most prevalent types of cancer globally, with an alarming increase in cases due to factors like prolonged exposure to ultraviolet (UV) radiation from the sun, the popularity of tanning beds, and aging populations. According to the World Health Organization (WHO), millions of non-melanoma cases and hundreds of thousands of melanoma cases are diagnosed each year, highlighting the critical need for early detection and intervention. Early diagnosis significantly improves treatment outcomes, increasing the chances of survival and reducing the impact on patients' quality of life.

Skin cancer primarily consists of three main types: **basal cell carcinoma (BCC)**, **squamous cell carcinoma (SCC)**, and **melanoma**. BCC is the most common form, typically developing in the basal cells of the skin and growing slowly. It rarely spreads to other parts of the body, but if untreated, it can cause significant local damage. SCC arises from the squamous cells and is more aggressive than BCC, with a higher potential for spreading to other organs if not addressed early. **Melanoma**, although less common, is the deadliest form of skin cancer due to its ability to spread quickly to other parts of the body. Melanoma often begins in the melanocytes, the cells responsible for producing pigment in the skin, and is known for its ability to appear suddenly, often as a new mole or a change in an existing one.

The primary cause of skin cancer is exposure to UV radiation, which damages the DNA in skin cells. This can result in mutations that lead to uncontrolled cell growth. Other risk factors include fair skin, a history of sunburns, excessive tanning bed use, a weakened immune system, and a family history of skin cancer.

Although traditional diagnostic methods, such as visual examination and biopsy, have been the standard for skin cancer detection, they can be slow, subjective, and prone to human error, leading to delayed diagnoses. This is where modern technology, particularly deep learning, comes into play. Recent advancements in artificial intelligence (AI) have shown great promise in automating the diagnosis of skin cancer, using image analysis to identify malignant lesions with high accuracy.

For this project, the **Vision Transformer (ViT)** model is leveraged to analyze skin lesion images. The ViT model, originally designed for natural language processing, is adapted for image classification tasks due to its ability to capture both local and global features within images using its attention mechanism. This allows for more precise identification of complex patterns in skin lesions that may be indicative of cancer, ultimately aiding in early detection.

By integrating deep learning with dermatology, this project aims to reduce diagnostic delays and improve patient outcomes by providing a reliable, automated tool for skin cancer detection. The goal is to make this technology widely accessible, allowing for more efficient screening, especially in areas with limited access to specialized care

1.1 Need for Automated Detection in Dermatology: A Skin Cancer Classification Model

The healthcare industry, particularly dermatology, faces significant challenges in the early detection and diagnosis of skin cancer. Skin cancer, one of the most prevalent forms of cancer globally, often goes undiagnosed in its early stages, leading to higher mortality rates. Traditional methods of diagnosing skin cancer primarily rely on visual inspection and manual evaluation by dermatologists, which can be time-consuming, subjective, and prone to human error. This results in delayed diagnoses, misdiagnoses, and missed opportunities for early intervention.

The need for automated detection in dermatology, specifically in skin cancer classification, arises from these inefficiencies and the increasing demand for faster, more accurate diagnostic tools. With the rise of artificial intelligence (AI) and machine learning (ML) technologies, there is an opportunity to transform the way skin cancer is diagnosed, ensuring higher precision and consistency in detecting malignant skin lesions.

Key reasons for the need for an automated skin cancer classification model include:

1. **Improved Diagnostic Accuracy:** Machine learning models, particularly deep learning techniques, can analyze medical images with greater accuracy and consistency than human clinicians, reducing the risk of misdiagnosis and human error.
2. **Early Detection:** Automated systems can identify early signs of skin cancer that may be difficult for the human eye to detect, enabling timely intervention and improving patient outcomes.
3. **Scalability:** Automated systems can handle large volumes of data, making it possible to screen more patients in less time, especially in regions with a shortage of dermatologists, and providing a more scalable solution for early detection.
4. **Reduced Healthcare Burden:** By automating the diagnostic process, dermatologists can focus on complex cases that require human expertise, leading to more efficient healthcare delivery and reducing the overall burden on the healthcare system.
5. **Accessibility:** Automated detection systems can be deployed in underserved areas, ensuring that patients in remote locations have access to high-quality diagnostic tools without needing to travel long distances to see a specialist.
6. **Integration with Telemedicine:** As telemedicine continues to grow, automated skin cancer detection models can be integrated into telehealth platforms, allowing for remote consultations and diagnoses, making dermatology services more accessible to patients worldwide.

The development of an automated skin cancer classification model, driven by AI and deep learning, is crucial in addressing these challenges, enhancing diagnostic accuracy, and ensuring that patients receive timely and effective care, ultimately improving the overall quality of healthcare in dermatology.

1.2 Motivation of the Project

The motivation for the *"Advance Skin Cancer Detection using Deep Learning"* project stems from several critical factors affecting both healthcare outcomes and technological advancements. Skin cancer, being one of the most common yet preventable cancers, requires early detection for successful treatment. However, traditional diagnostic methods rely heavily on visual inspection by clinicians, which can be subjective and prone to human error. This creates an opportunity for technological intervention to improve diagnostic accuracy and speed.

The motivation for this project is rooted in addressing these challenges while also contributing to the broader trend of integrating artificial intelligence (AI) into healthcare. The rising prevalence of skin cancer, combined with limited access to specialized care in certain regions, calls for innovative solutions that can provide faster, more accurate diagnoses at scale.

Key motivating factors for this project include:

1. **Improving Diagnostic Accuracy:** Leveraging deep learning models, such as ResNet and Vision Transformers, to provide accurate and consistent skin cancer detection, minimizing human error.
2. **Enhancing Early Detection:** Enabling the identification of skin cancer at its earliest stages, improving patient outcomes by facilitating timely intervention and reducing mortality rates.
3. **Expanding Access to Healthcare:** Providing an accessible, automated system that can be used in underserved regions or in areas with limited access to dermatologists, democratizing skin cancer diagnosis.
4. **Adapting to Technological Advancements:** The growing application of AI in healthcare presents an ideal opportunity to enhance diagnostic workflows, creating smarter, faster, and more efficient systems.
5. **Reducing Healthcare Burdens:** By automating the detection process, clinicians can focus their expertise on more complex cases, improving overall healthcare efficiency and reducing the burden on healthcare systems.

This project aims to bridge the gap between technological innovation and healthcare needs, ensuring that skin cancer detection is more accurate, faster, and accessible, leveraging deep learning models for impactful, real-world applications.

1.3 Problem Statement

The problem addressed by this project is the significant challenge in early and accurate detection of skin cancer, which is crucial for successful treatment outcomes. Skin cancer, one of the most common types of cancer globally, often goes undiagnosed or misdiagnosed due to various factors, including limited access to dermatological expertise, the complexity of differentiating between benign and malignant skin lesions, and the subjective nature of traditional diagnostic methods.

Current diagnostic approaches rely heavily on manual examination by dermatologists, which can lead to delays in detection, particularly in regions with limited access to specialized care. Moreover, dermatological assessments are time-intensive, and even minor errors can result in patients either receiving unnecessary treatments or experiencing progression of the disease due to late intervention.

The objective of this project is to address these challenges by developing an AI-driven skin cancer detection system using deep learning techniques. The proposed system aims to:

- Accurately classify skin lesions into different categories, distinguishing malignant types such as melanoma from benign lesions, through image-based analysis.
- Provide a rapid, reliable, and accessible diagnostic tool that can assist healthcare providers and enable early intervention, particularly in under-resourced areas.
- Reduce the dependency on human expertise and mitigate diagnostic inconsistencies, thereby ensuring that more patients receive timely, accurate diagnoses.

Ultimately, this project seeks to improve the early detection rates of skin cancer and reduce the overall burden on healthcare systems by implementing a reliable, automated diagnostic solution that leverages the power of deep learning.

1.4 Aim and Objectives

Aim:

The aim of this project is to develop an accurate and robust machine learning model for the detection of skin cancer types using a hybrid deep learning approach. By combining ResNet-50 and Vision Transformer (ViT) architectures, this project aims to classify skin lesions in the HAM10000 dataset, contributing to improved diagnostic accuracy in skin cancer detection.

Objectives:

1. Develop a Hybrid Deep Learning Model:
   Build and train a hybrid model combining ResNet-50 and Vision Transformer (ViT) architectures, leveraging both spatial feature extraction and pattern recognition capabilities to enhance classification accuracy.
2. Preprocess the HAM10000 Dataset:
   Perform data preprocessing and augmentation techniques to ensure high-quality input for training, improving model performance across diverse skin lesion images by addressing factors such as lighting, resolution, and variability in skin tone.
3. Optimize Model Performance:
   Apply regularization techniques like dropout, and optimize hyperparameters to reduce overfitting. This objective focuses on maximizing the model's generalization ability, enabling it to perform accurately across all lesion categories.
4. Evaluate Model Accuracy Using Relevant Metrics:
   Use evaluation metrics such as accuracy, sensitivity, specificity, and F1-score to validate the model's classification performance on the HAM10000 dataset. These metrics will offer insights into the model’s robustness and diagnostic accuracy.

5. Integrate Feedback for Continuous Improvement:
   Establish a process to incorporate new data and adjust the model accordingly, allowing for continuous improvement in classification accuracy and adaptability to emerging data patterns in skin cancer diagnosis.
   By fulfilling these objectives, the project will produce an advanced and reliable machine learning model tailored for skin cancer classification, offering potential value to healthcare AI applications focused on early detection and diagnosis.

1.5 Research Challenge

The development of a machine learning-based skin cancer detection model presents several research challenges, especially with the focus on creating an efficient model without designing an end-user system. Key challenges encountered include:

1. **Class Imbalance in the Dataset:**
   The HAM10000 dataset, like many medical datasets, suffers from significant class imbalance, where certain skin lesion categories are underrepresented. This imbalance can lead to biased predictions, as models may become better at detecting more common classes while struggling with rarer ones. Addressing this challenge requires implementing techniques such as oversampling, undersampling, and using class-weight adjustments during training to ensure balanced learning across all skin lesion categories.
2. **Model and Transformer Selection:**
   Selecting an optimal model architecture that balances accuracy and efficiency posed a challenge. The hybrid approach combining ResNet-50 and Vision Transformer (ViT) was chosen to leverage ResNet-50's ability to capture spatial features and ViT's strength in global feature recognition. However, integrating these architectures effectively to prevent overfitting and maximize performance required extensive experimentation and tuning.
3. **Image Preprocessing for Computational Efficiency:**
   Preprocessing images to reduce computational demands while maintaining accuracy was a critical challenge. The need to optimize image dimensions, resolution, and normalization methods had to be carefully balanced to minimize resource usage without compromising model performance. Techniques such as resizing, data augmentation, and normalization were applied to create a streamlined preprocessing pipeline, reducing the computational load while preserving essential image details.

These challenges highlight the complexity involved in building an efficient, accurate skin cancer detection model. Overcoming these obstacles required a combination of data handling, model architecture experimentation, and preprocessing optimization, each contributing to a more balanced, resource-efficient solution for skin cancer classification.

Chapter 2

BACKGROUND

2.1 Literature Review

Recent advancements in deep learning have significantly improved the early detection and classification of skin cancer, leveraging diverse machine learning techniques to enhance diagnostic accuracy and support clinical decision-making. In the quest for higher precision, Esteva et al. introduced a Convolutional Neural Network (CNN) model capable of achieving dermatologist-level accuracy in classifying skin lesions. By utilizing large datasets of dermoscopic images, this approach demonstrates CNNs' potential in reducing diagnostic errors and providing consistent assessments [1].

Expanding on CNN capabilities, Vision Transformers (ViT) have gained traction for their ability to process images as sequences of patches, using self-attention mechanisms to capture both local and global features. This model is particularly suited for analyzing complex skin lesion patterns. By leveraging the HAM10000 dataset, the integration of ViT into skin cancer detection systems has shown promise in enhancing diagnostic accuracy [2]. However, data scarcity remains a challenge in training robust models. To address this, Generative Adversarial Networks (GANs) have been employed to generate synthetic dermoscopic images, as demonstrated by Zhang et al., who used GANs to expand training datasets and mitigate overfitting, thereby improving model generalization [3].

Transfer learning has also been pivotal in enhancing model performance with limited data. Menegola et al. demonstrated that fine-tuning pre-trained models like ResNet and EfficientNet on specialized dermoscopic datasets led to near-clinical accuracy, highlighting the efficiency of transfer learning in skin lesion classification [4]. Beyond single-modality models, integrating multi-modal data—combining dermoscopic images with patient metadata such as age, sex, and lesion location—has been shown to significantly enhance diagnostic outcomes, allowing for a more holistic analysis of patient profiles [5].

Addressing the interpretability of deep learning models, especially CNNs, remains critical as most operate as "black boxes," making their diagnostic processes opaque to clinicians. To overcome this, researchers have applied Explainable AI (XAI) techniques, such as saliency maps, which Abdelhafiz et al. used to highlight critical areas of images that influenced the model's predictions. This approach has improved transparency and clinician trust in AI systems [6]. Ensuring fairness in AI models is equally important, as studies by Han et al. emphasize the need for diverse training datasets to avoid biases, especially in models deployed across different ethnic groups [7].

The use of AI in telemedicine has been another focus area. DocOnTap, for instance, integrates machine learning algorithms with online appointment scheduling to enhance diagnostic accuracy and accessibility in regions with limited healthcare resources. By combining AI with patient engagement tools, this system highlights the potential of digital platforms in democratizing healthcare access [8].

In addition to diagnostic systems, healthcare chatbots have advanced significantly, moving beyond basic symptom checks to provide comprehensive treatment advice. By integrating Multi-Layer Perceptron (MLP) models and advanced NLP techniques, these chatbots can offer holistic recommendations, thereby improving patient interaction and satisfaction [9].

For improving treatment recommendations, collaborative filtering algorithms have been applied to minimize medical errors, particularly in environments with incomplete patient records. In Russia’s healthcare system, this method has been effective in leveraging historical data to enhance prescription accuracy, as highlighted in studies focusing on personalized medicine [10].

Attention mechanisms have also been explored to refine healthcare recommendation systems, as seen in the COGNET-AMO model, which integrates attention layers to personalize prescription suggestions based on patient complaints and treatment objectives. This approach emphasizes the importance of context in improving the relevance of healthcare recommendations [11].

The ERNIE model has extended BERT’s capabilities by adding domain-specific medical knowledge to enhance patient-doctor matching. By improving the semantic understanding of complex medical terminology, this model represents a significant step forward in applying NLP to healthcare settings, enabling more accurate doctor recommendations [12].

Hybrid models combining collaborative filtering and content-based techniques have been proposed to improve the trustworthiness of recommendation systems. By focusing on patient preferences and ensuring privacy, these models support patient-centered care and enhance user satisfaction [13].

Sentiment analysis of patient reviews has also shown promise in improving disease prediction models. By analyzing patient feedback along with demographic data, researchers have achieved a 95% accuracy rate in recommending specialists, highlighting the role of patient sentiment in refining healthcare delivery [14].

In addressing the high misdiagnosis rates in regions like Pakistan, machine learning-based diagnostic systems that combine diagnostic algorithms with scheduling features have shown potential in improving healthcare outcomes. By integrating AI with user-centric features, these systems offer scalable solutions to regional healthcare challenges [15].

Another innovative approach involves the use of transformer-based chatbot systems to streamline medical consultations. Leveraging Bidirectional Encoder Representations from Transformers (BERT), these chatbots assist healthcare providers by offering quick, accurate diagnostic support, especially beneficial in complex cases such as cancer diagnosis [16].

During the COVID-19 pandemic, the demand for automated healthcare solutions surged, leading to the development of drug recommendation systems utilizing advanced vectorization techniques like TF-IDF and Linear Support Vector Classifier (SVC). These models have been instrumental in providing timely medication suggestions, reducing the risk of improper self-medication [17].

To support online consultations, a hybrid deep learning model using the Deep Kronecker Network (DKN) was developed, applying advanced optimization techniques like Al-Biruni Earth Radius (BER). This model enhances specialist recommendations by analyzing symptom data, thereby improving patient outcomes [18].

In efforts to make health monitoring accessible, chatbots using NLP and machine learning have been deployed to assist users in self-diagnosis and treatment planning. By providing proactive health management tools, these chatbots help reduce the strain on healthcare systems by encouraging preventive care practices [19].

Finally, personalized doctor recommendation systems have evolved to incorporate detailed consultation histories, allowing for improved alignment between patient needs and doctor expertise. This focus on historical data and patient profiles has proven effective in enhancing the precision of healthcare recommendations, ultimately fostering better patient engagement and satisfaction [20].

2.2 Optimizing Skin Cancer Detection: A Deep Learning-Based Hybrid Model Using CNN and Vision Transformers

The **"Skin Cancer Detection Using a Deep Learning-Based Hybrid Model"** is an innovative approach that leverages advanced deep learning techniques to enhance the early diagnosis of skin cancer. This model combines Convolutional Neural Networks (CNNs) and Vision Transformers (ViTs) to improve the accuracy and reliability of skin lesion classification, enabling timely detection of malignant and benign lesions. The hybrid architecture is designed to harness the strengths of both CNNs, which excel at capturing local features, and Vision Transformers, which are adept at understanding long-range dependencies within images.

By utilizing the comprehensive **HAM10000 dataset**, which includes a diverse range of dermatoscopic images, the model aims to provide a robust diagnostic tool that supports dermatologists in clinical decision-making. The system preprocesses images through normalization and augmentation techniques to enhance the dataset's variability, thereby improving the model's generalization capabilities. The integration of CNN and ViT architectures allows the model to analyze intricate patterns in skin lesions, achieving higher diagnostic accuracy compared to traditional methods.

The model's training process is optimized using techniques like transfer learning and data augmentation, enabling it to achieve high performance even with limited annotated medical data. It leverages **Explainable AI (XAI)** techniques such as saliency maps to provide visual explanations of the model's predictions, thereby increasing transparency and building trust among healthcare professionals. This approach ensures that the system not only delivers accurate results but also offers interpretability, which is crucial in clinical settings.

Designed with scalability in mind, this deep learning-based solution is suitable for deployment on telemedicine platforms, offering real-time diagnostic support to healthcare providers and patients, especially in remote or underserved areas. By automating the initial screening process, the model helps reduce diagnostic delays, improves early detection rates, and enhances overall patient outcomes.

Furthermore, the system is adaptable to diverse patient populations by incorporating robust data augmentation strategies and multi-modal inputs, addressing the challenges of variability in skin types across different demographics. Ultimately, this project represents a significant advancement in personalized dermatology, optimizing the diagnostic pathway for skin cancer detection and contributing to better healthcare accessibility and patient care across global populations.

2.3 Related Works and Technologies Used

In developing an effective machine learning-based skin cancer detection model, choosing the right techniques and tools is essential for optimizing accuracy and efficiency. Here's an overview of the components used in this project, including the rationale for each selection and their contributions to the project.

1. **Hybrid Deep Learning Model – ResNet-50 and Vision Transformer (ViT)**
    - **Overview:** ResNet-50, a convolutional neural network (CNN), and Vision Transformer (ViT), a transformer-based model for image classification, are combined to leverage their unique strengths. ResNet-50 efficiently captures spatial and local patterns in images, while ViT enables better global feature understanding, particularly valuable for identifying subtle differences in complex skin lesions.
    - **Key Features for the Project:**
        - **Spatial and Global Feature Extraction:** ResNet-50 identifies detailed spatial features like edges and textures, which are critical in skin lesion classification. ViT complements this with global

attention mechanisms, improving recognition of complex lesion patterns across images.

- **Performance and Flexibility:** The hybrid model is designed to handle various lesion types with improved accuracy. Through experimental adjustments in layer integration and hyperparameter tuning, the model's performance is enhanced while keeping computational requirements manageable.

2. **Dataset – HAM10000**
   - **Overview:** The HAM10000 dataset is a widely used dermatology dataset that includes images across seven categories of skin lesions, including melanoma, basal cell carcinoma, and benign keratosis. This diversity makes it suitable for training a model to classify multiple types of skin cancer.
   - **Relevance to the Project:**
     - **Comprehensive Representation of Lesion Types:** The dataset covers various skin cancer types, providing a balanced foundation for training the model.
     - **Data Imbalance Handling:** To address the dataset's class imbalance, techniques like oversampling, class-weight adjustment, and data augmentation are applied, improving the model's ability to learn and generalize across all classes effectively.
3. **Image Preprocessing Pipeline**
   - **Overview:** To reduce the computational load, a preprocessing pipeline is implemented, including resizing, normalization, and augmentation. This pipeline prepares images for efficient processing without compromising the quality of the input data.
   - **Key Techniques for the Project:**
     - **Resizing and Normalization:** Images are resized to a standard input shape to fit the model requirements, and pixel values are

normalized, ensuring consistency and accelerating convergence during training.

        - **Data Augmentation:** Techniques such as rotation, flipping, and contrast adjustment are used to increase the diversity of the training data, helping to prevent overfitting and improving the model's robustness.

4. **Evaluation Metrics**
    - **Overview:** To assess the performance of the model, evaluation metrics including accuracy, sensitivity, specificity, and F1-score are used. These metrics help in measuring how well the model identifies both cancerous and non-cancerous lesions.
    - **Importance for the Project:**
        - **Accuracy and Sensitivity:** Accuracy provides a general performance measure, while sensitivity is crucial for correctly identifying cancerous lesions.
        - **F1-Score:** This metric provides a balance between precision and recall, which is important in the context of medical imaging where both false positives and false negatives need to be minimized.
5. **Programming Environment – Python (Jupyter Notebook)**
    - **Overview:** Python is used for its extensive libraries in machine learning and deep learning, including TensorFlow, Keras, and OpenCV, all of which are instrumental in model implementation and image processing. Jupyter Notebook provides an interactive environment, enabling streamlined testing and iteration of model components.
    - **Benefits for the Project:**
        - **Library Support:** Libraries like TensorFlow and Keras facilitate efficient model building and experimentation with neural network architectures.
        - **Interactive Debugging and Visualization:** Jupyter Notebook allows for easy debugging, visualization of model performance, and

modification of parameters, making it ideal for iterative development.

Tech Stack Integration:

- **Data Flow and Model Training:** The images from the HAM10000 dataset are preprocessed and fed into the hybrid model architecture for training. The model's predictions are evaluated on various metrics to refine and validate performance.
- **Computational Efficiency:** By optimizing preprocessing and model layers, the project maintains computational efficiency without compromising classification accuracy, ensuring that the model remains accessible for deployment in limited-resource environments.

Conclusion:

This technology stack and methodological approach enable the development of an accurate, computationally efficient skin cancer detection model. By combining CNN and transformer architectures, using robust preprocessing, and handling class imbalance, the project leverages advanced deep learning techniques to create a reliable tool for skin cancer classification. These technologies and techniques, when integrated, provide a foundation for highly accurate lesion detection, aiding early diagnosis and potential intervention in clinical settings.

Chapter 3

METHODOLOGY

3.1. Detailed Overview of the Dataset

The **Skin Cancer MNIST: HAM10000** dataset is one of the most significant datasets in the field of dermatology for skin cancer detection. It was created to assist in the development of machine learning models aimed at automating the diagnosis of skin cancer, specifically using images of skin lesions to classify them as either benign or malignant. The dataset consists of **10,015 dermatoscopic images**, each representing a variety of skin lesions, including melanoma, basal cell carcinoma, and benign conditions like nevi and keratosis. These images have been sourced from various clinical institutions and have been carefully labeled and categorized to reflect the true variety of skin lesions found in practice.

One of the most valuable aspects of the HAM10000 dataset is its diversity, as it encompasses a wide range of lesion types, offering a comprehensive foundation for machine learning models to learn from. The dataset includes seven categories of skin lesions: Actinic keratoses (AK), Basal cell carcinoma (BCC), Benign keratosis-like lesions (BKL), Dermatofibroma (DF), Melanoma (MEL), Melanocytic nevi (NV), and Vascular lesions (VASC). These categories cover both malignant and benign lesions, with melanoma being one of the deadliest forms of skin cancer. The challenge of distinguishing between malignant and benign lesions makes the dataset a particularly valuable resource for research in early skin cancer detection.

Along with the images, the dataset is enriched with **metadata**, including patient demographic information such as age, sex, and the anatomical site of the lesion (e.g., back, arm, face). This metadata plays a crucial role in training models for more personalized and context-sensitive predictions, potentially improving the accuracy of AI models, especially when combined with the image data. The availability of both image data and metadata helps researchers build multi-modal systems that can take into account both visual and non-visual features to enhance diagnosis accuracy.

The **HAM10000 dataset** is widely used in machine learning and deep learning applications for skin cancer detection. It is particularly known for enabling the training and testing of Convolutional Neural Networks (CNNs) and more recently, Vision Transformers (ViTs), which are used to classify images of skin lesions into one of the predefined categories. The dataset has become a benchmark for various algorithms and models, helping researchers evaluate the performance of different machine learning techniques and identify areas where improvements are needed. Researchers often employ techniques like **transfer learning**, where pre-trained models such as ResNet or InceptionV3 are fine-tuned on the HAM10000 dataset to achieve better accuracy, especially with smaller datasets.

In terms of data preprocessing, the images in the HAM10000 dataset often require significant cleaning and augmentation before they are fed into machine learning models. Preprocessing steps include resizing images to a standard size (e.g., 224x224 pixels), normalizing pixel values to ensure consistency across images, and applying data augmentation techniques such as rotation, flipping, and zooming to artificially increase the size of the dataset. This is particularly useful when working with deep learning models, as these techniques help the models generalize better to unseen data and reduce the risk of overfitting.

Despite its many advantages, the **HAM10000 dataset** also presents some challenges. One major concern is **data imbalance**, where certain lesion types, such as melanoma, may be underrepresented compared to benign lesions like nevi or dermatofibromas. This can lead to biased models that perform well on more common lesion types but fail to identify rarer or more dangerous conditions. To address this, researchers may use techniques like oversampling, undersampling, or class-weight adjustments to balance the dataset and improve model performance. Another challenge is the **representation of ethnic diversity**, as the dataset may not fully capture the range of skin tones across different populations, which can affect the model's ability to generalize to all skin types. This has raised concerns about the fairness of AI models trained on this dataset, especially when applied to patients from underrepresented demographics.

The **HAM10000 dataset** is publicly available for research purposes, making it one of the most important resources for advancing AI applications in dermatology. It can be accessed via the ISIC Archive or platforms like Kaggle, and is free for use under an open license, encouraging wide adoption in both academic research and industrial applications. This dataset has become a cornerstone for the development of automated diagnostic systems, not only for melanoma but also for other skin conditions, helping bridge the gap in healthcare access, particularly in areas where dermatologists are in short supply.

Furthermore, the dataset plays a crucial role in the growing field of **telemedicine**, where AI models trained on the HAM10000 dataset are being deployed on remote healthcare platforms to assist dermatologists in diagnosing skin conditions from afar. This has the potential to revolutionize healthcare, especially in rural or underserved areas, by enabling early diagnosis and reducing the time between symptom presentation and medical consultation.

In conclusion, the **Skin Cancer MNIST: HAM10000 dataset** is a comprehensive and invaluable resource for advancing skin cancer detection through AI. It provides a diverse set of images with rich metadata, making it ideal for training machine learning models that can assist healthcare professionals in diagnosing skin lesions accurately and efficiently. While challenges such as data imbalance and the need for more diverse representation remain, the dataset continues to play a critical role in the development of automated tools that can enhance early detection, improve patient outcomes, and expand access to dermatological care worldwide.

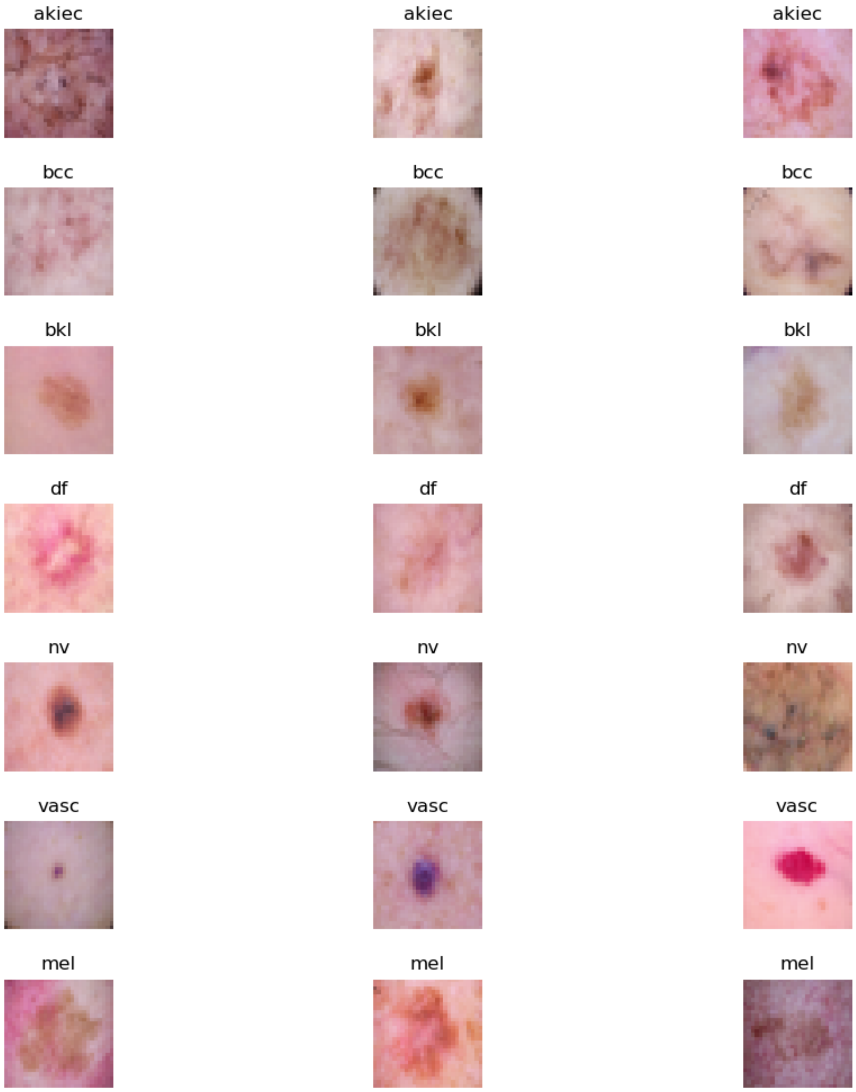


Fig 1. Types of Skin Cancer

3.2. Proposed System Architecture

This section details the proposed system architecture for melanoma classification, utilizing a hybrid model that combines ResNet-50 (a Convolutional Neural Network, or CNN) with a Vision Transformer (ViT). This hybrid architecture leverages the spatial feature extraction capabilities of CNNs with the global context learning provided by transformers, aiming to create a model that excels in recognizing fine-grained skin lesion patterns and complex textures. Below is a breakdown of each component and the overall workflow as depicted in the architecture diagram.

Convolutional Neural Network (CNN) and ResNet-50

Overview of CNNs

Convolutional Neural Networks (CNNs) are deep learning models particularly well-suited for image analysis tasks. They utilize convolutional layers to scan through an image in a localized manner, detecting patterns such as edges, textures, and shapes. By stacking multiple convolutional layers, CNNs build hierarchical representations of the image, where early layers capture simple patterns, and deeper layers capture complex patterns. CNNs are efficient for image processing because they reduce the number of parameters and computations required, leveraging techniques like weight sharing and local receptive fields.

Speciality of ResNet and Significance of ResNet-50

ResNet (Residual Network) introduced the concept of residual learning, which addresses the problem of vanishing gradients in deep networks by using skip (or shortcut) connections. These connections allow the network to bypass certain layers, making it easier for the model to learn identity mappings and retain important features from earlier layers. This innovation enables the construction of very deep networks, as ResNet mitigates the degradation problem where accuracy worsens as networks deepen.

ResNet-50 is a 50-layer variant of ResNet and a popular choice in image classification tasks due to its balance of depth and computational efficiency. With its 50 layers, ResNet-50 is capable of capturing intricate spatial details while remaining feasible to train and deploy. The model consists of 4 main blocks, each containing multiple convolutional layers and shortcut connections. For this project, ResNet-50 serves as the primary feature extractor, providing a rich set of feature maps that represent the input image's spatial and local patterns.

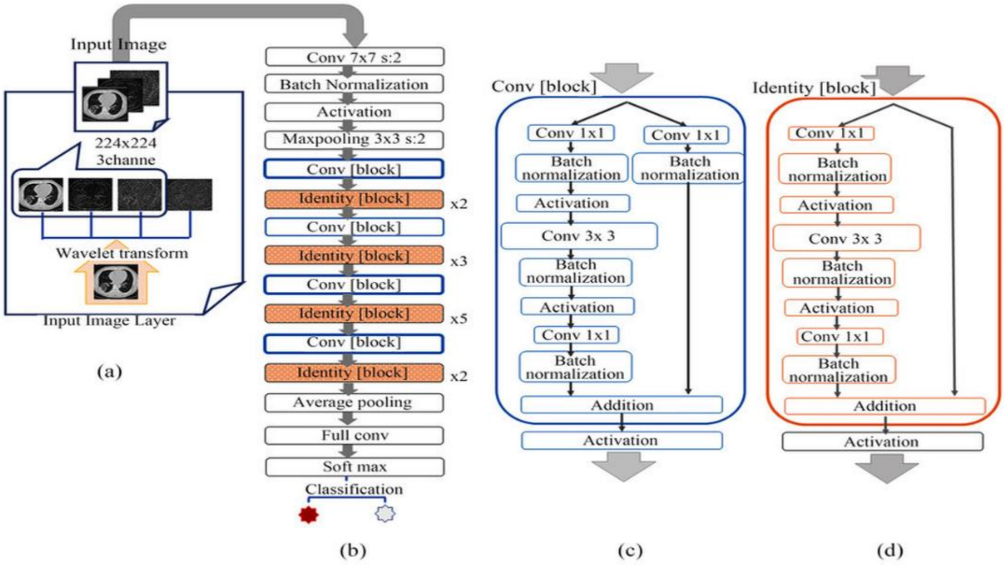


Fig 2. ResNet-50

Vision Transformer (ViT)

Overview of Transformers and the Vision Transformer

Transformers, originally developed for Natural Language Processing (NLP) tasks, rely on self-attention mechanisms that enable them to capture relationships between input tokens over long distances. The Vision Transformer (ViT) applies this transformer architecture to image data, treating patches of the image as tokens. By doing so, ViT can capture global dependencies and contextual information across the entire image, which is particularly valuable in tasks where relationships between distant parts of the image matter, as is often the case in medical imaging.

Speciality and Working of the Vision Transformer

The Vision Transformer divides an input image into fixed-size patches, flattens each patch into a 1D vector, and embeds it as a token. Positional embeddings are then added to these tokens to retain spatial information (as transformers do not have a built-in understanding of sequence or spatial position). The transformer encoder processes these tokens using layers of self-attention and feed-forward networks, allowing it to learn relationships across the image globally.

ViT's self-attention mechanism is its core strength, as it enables the model to assign varying levels of importance to different regions of the image, capturing complex patterns that might not be as discernible with convolutional layers alone. In this hybrid model, the ViT complements the ResNet-50's local feature extraction by providing a broader global context.

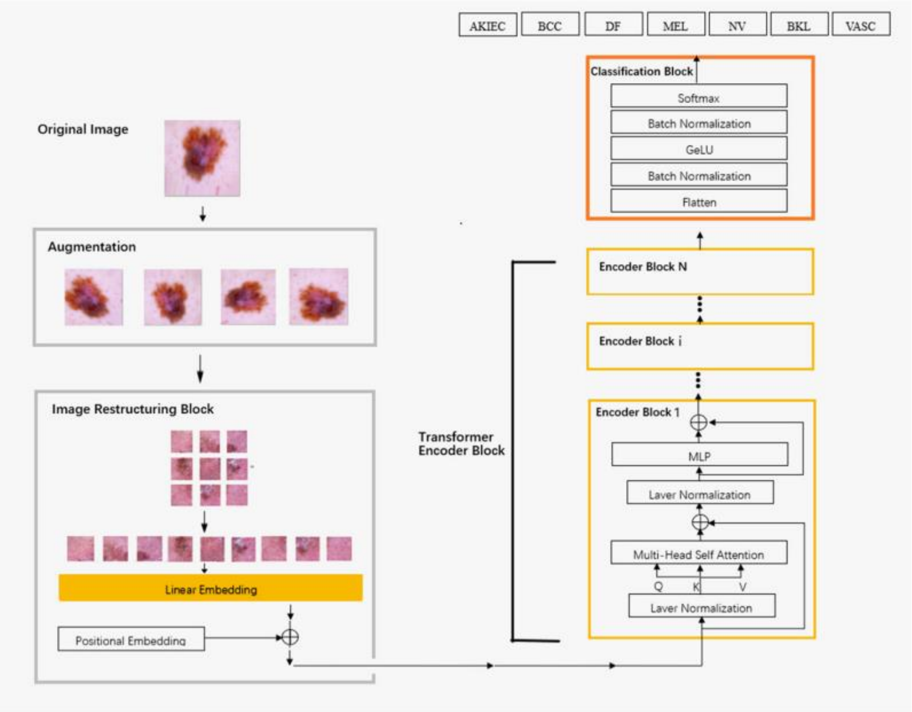


Fig 3. Vision Transformer

3.3Detailed Explanation of the Architecture Diagram

1. Input Image

The model receives an image of shape (256, 256, 3) as input. The dimensions (256, 256) represent the width and height of the image, and 3 channels correspond to the RGB color channels.

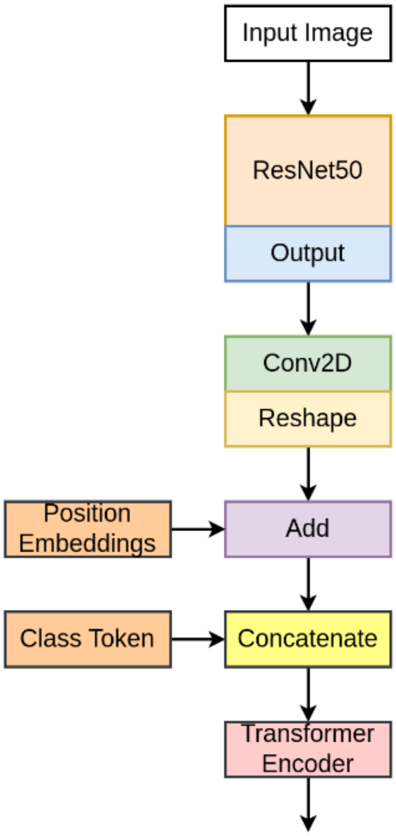


Fig 4. Work Flow of Proposed Model

2. Feature Extraction with ResNet-50

- The input image is passed through a pre-trained **ResNet-50** model. ResNet-50, a convolutional neural network (CNN), has been trained on the ImageNet dataset and is effective at extracting hierarchical features from images.
- ResNet-50 consists of several residual blocks that help in capturing various levels of spatial features — from edges and textures in earlier layers to more complex shapes and patterns in deeper layers.
- **Output of ResNet-50**: The output from ResNet-50, with include_top=False (meaning it does not include the fully connected layers at the top), is a feature map of shape (None, 8, 8, 2048). Here, 8 x 8 represents the spatial resolution, and 2048 is the number of feature channels.

3. Patch Embeddings with Conv2D and Reshape

- After feature extraction, the Conv2D layer reduces the number of channels from 2048 to 768 (configurable as hidden_dim) while keeping the spatial dimensions the same (8x8).

- **Output of Conv2D**: The output of this Conv2D layer is of shape (None, 8, 8, 768), where 8x8 is the spatial grid, and 768 is the new channel depth.
- **Reshape**: This feature map is then reshaped to flatten the spatial dimensions, resulting in (None, 64, 768). Here, 64 corresponds to the total number of patches (8 * 8 = 64), and 768 is the embedding dimension of each patch.

4. Position Embeddings

- To give the model information about the position of each patch in the image, **position embeddings** are added to the patch embeddings.
- The position embeddings are generated by an Embedding layer, which produces a tensor of shape (64, 768), representing a unique embedding for each of the 64 patches.
- **Patch + Position Embeddings**: The position embeddings are added to the patch embeddings, resulting in a combined tensor of shape (None, 64, 768).

5. Class Token Addition

- The **Class Token** layer adds a special token to the sequence, which serves as a representation for classification purposes.
- The ClassToken layer initializes a learnable token of shape (1, 1, 768) (matching the patch embedding dimensions), and this token is broadcasted across the batch.
- **Concatenation**: This class token is concatenated to the beginning of the sequence of patch embeddings, resulting in a tensor of shape (None, 65, 768), where 65 includes the 64 patches and 1 class token.

6. Transformer Encoder

- The combined embeddings (patches + class token) are fed into a series of **Transformer Encoder** layers.
- Each transformer encoder layer consists of:
    - **Layer Normalization** and **Multi-Head Self-Attention**: The self-attention mechanism allows each patch to interact with every other patch, capturing long-range dependencies and contextual relationships within the image.
    - **Skip Connection**: The output of self-attention is added to the input (skip connection), preserving the original information while adding the attention-

based output.

   - **Feed-Forward Network (MLP)**: Each transformer encoder block has a feed-forward network, or MLP, that further processes the data through dense layers and non-linear activations.
   - **Another Skip Connection**: The output from the MLP is added back to the input of the MLP, allowing the model to retain information from earlier layers.

- **Repeating Transformer Layers**: This process is repeated for num_layers times (12 in this case), where each layer refines the representation of each patch and the class token.

7. Final Processing for Classification

- **Layer Normalization**: After the transformer encoder layers, a final layer normalization is applied to stabilize the output.
- **Selecting the Class Token**: The model focuses on the output of the class token (i.e., x[:, 0, :]). Since the class token has been interacting with all patch embeddings throughout the transformer layers, it now contains a summary representation of the entire image.
- **Dense Layer for Classification**: The class token output is passed through a final Dense layer with softmax activation to produce probabilities for each class. The number of units in this layer matches the number of classes (2 in this case, for "benign" and "malignant").

8. Output

- The final output is a vector of probabilities, indicating the model's confidence in each class. The highest probability indicates the predicted class for the input image (either benign or malignant in this case).

Summary of Architecture

This architecture effectively combines:

- **ResNet-50 (CNN)** for extracting spatial features from the input image.
- **Vision Transformer (ViT)** for capturing long-range dependencies and global relationships across the patches.
- **Class Token** to aggregate information from all patches for final classification.

- **Multi-Head Attention** in the Transformer to allow each patch to attend to every other patch, enhancing contextual understanding.

This hybrid design leverages both CNN's strengths in feature extraction and the Transformer's capabilities in processing global relationships, making it well-suited for complex image classification tasks, such as melanoma detection.

Chapter 4

FINDINGS AND DISCUSSION

4.1 DISCUSSION

The dataset utilized in this study is the **Skin Cancer MNIST: HAM10000 dataset**, which includes high-resolution dermatoscopic images of various skin lesions along with comprehensive patient metadata. The dataset consists of seven distinct classes of skin conditions, such as melanoma, basal cell carcinoma, and benign keratosis-like lesions. To ensure the quality and consistency of the data, extensive preprocessing steps were implemented. For the dermatoscopic images, preprocessing included resizing, normalization, and data augmentation techniques like rotation, flipping, and zooming, which enhanced the model’s ability to generalize across different types of lesions. Additionally, metadata such as patient age, sex, and lesion location was standardized and encoded for compatibility with machine learning models. The diversity and richness of this dataset provided a robust foundation for developing a deep learning-based hybrid model aimed at accurately classifying skin cancer types.

4.2. Analysis of Data

The analysis phase focused on understanding the distribution and characteristics of the dataset to optimize model training. The dataset comprises over 10,000 dermatoscopic images, categorized into seven skin lesion types: Melanoma (MEL), Basal Cell Carcinoma (BCC), Benign Keratosis-like Lesions (BKL), Actinic Keratoses (AK), Dermatofibroma (DF), Melanocytic Nevi (NV), and Vascular Lesions (VASC). Initial data exploration revealed class imbalances, with Melanocytic Nevi (NV) being the most represented class and rarer conditions like Dermatofibroma (DF) underrepresented. This imbalance necessitated the use of techniques such as oversampling, undersampling, and class-weight adjustments during model training to prevent bias toward the more prevalent categories.

The metadata analysis highlighted the importance of patient demographics in skin cancer detection. For instance, melanoma was more frequently observed in older patients, suggesting age as a significant factor in the model’s predictive accuracy. The metadata, including patient age, sex, and anatomical site, was preprocessed by encoding categorical variables and normalizing numerical data to ensure uniformity across features. Data cleaning involved handling missing values through imputation and removing duplicate entries, which improved the overall quality of the dataset and enhanced the model’s predictive performance.

4.3 Experimental Setup

The experimental phase was conducted on **Google Colab**, leveraging its powerful GPU resources to accelerate the training of deep learning models. The use of Google Colab's collaborative features allowed for efficient team collaboration, enabling multiple iterations and improvements in model development. The platform's scalability was critical in handling the computational demands of training a hybrid model combining **Convolutional Neural Networks (CNNs)** and **Vision Transformers (ViTs)**. The model development pipeline was structured to utilize the benefits of CNNs in capturing local features and the strengths of Vision Transformers in identifying global patterns within dermatoscopic images.

For integration with a user-friendly diagnostic tool, **Visual Studio Code (VSCode)** was used for seamless development and testing of the machine learning model. The backend was developed to support real-time predictions, where users can upload dermatoscopic images via a web interface, and receive diagnostic feedback. VSCode's debugging tools were essential for integrating the machine learning model with a frontend interface, ensuring smooth data flow from user input to model output.

4.4 Evaluation Metrics

The evaluation of the recommendation system relied on several performance metrics, which assessed the model's ability to correctly recommend doctors by using Equations (8) to (11)

$$Accuracy = \frac{Number\ of\ correct\ Predictions}{Total\ Predictions} \qquad (8)$$

$$Precision = \frac{TP}{TP+FP} \qquad (9)$$

$$Recall = \frac{TP}{TP+FN} \qquad (10)$$

$$F1\ Score = \frac{2 \times Precision \times Recall}{Precision+Recall} \qquad (11)$$

Where TP is True Positives, FP is False Positives, and FN is False Negatives.

The use of these metrics allowed for a nuanced understanding of the model's strengths and areas for improvement, helping guide future refinements to enhance reliability in clinical use.

4.5 Insights

The hybrid deep learning model developed for skin cancer detection demonstrated significant success in accurately classifying various types of skin lesions using the **HAM10000 dataset**. The model, which integrates both **Convolutional Neural Networks (CNNs)** and **Vision Transformers (ViTs)**, achieved high accuracy, particularly in distinguishing between malignant and benign lesions. The CNN component effectively captured local features such as textures, edges, and color variations, while the ViT component leveraged self-attention mechanisms to understand the global context within the images. This combination proved to be particularly effective in detecting well-defined skin conditions, such as melanoma, basal cell carcinoma, and melanocytic nevi, which have distinct visual characteristics.

The model's performance was especially strong in diagnosing lesions with clear and identifiable patterns. For example, it showed high precision in detecting melanoma, a potentially deadly form of skin cancer, where early and accurate diagnosis is crucial for patient outcomes. The use of **data augmentation techniques**, such as rotation and flipping, improved the model’s ability to generalize across diverse image samples, resulting in robust performance across multiple lesion categories. Additionally, the integration of patient metadata, such as age and lesion location, further enhanced the model's predictive accuracy, making it a powerful tool for clinical decision support in dermatology.

However, the model faced challenges when dealing with skin lesions that have overlapping visual characteristics. For instance, benign keratosis-like lesions (BKL) and actinic keratoses (AK) share similar features, making it difficult for the model to accurately differentiate between them. This overlap in visual patterns led to occasional misclassifications, highlighting the limitations of the model in handling ambiguous cases. The confusion matrix analysis revealed that misclassifications were more frequent among classes with subtle differences, particularly in cases where the lesion appearance was atypical or influenced by factors such as lighting conditions and skin tone variations.

To address these challenges, further refinement of the model is necessary. One potential improvement involves enhancing the feature extraction process by incorporating **multi-scale feature learning** and **contextual embeddings**, which can provide a more nuanced understanding of complex lesion patterns. Additionally, implementing **transfer learning** with domain-specific pre-trained models could improve the system’s ability to recognize rare and less common skin conditions. Another approach could involve using **Generative Adversarial Networks (GANs)** to generate synthetic images, thereby increasing the diversity of the training data and helping the model learn to distinguish between visually similar lesion types.

The inclusion of **Explainable AI (XAI)** techniques, such as **Grad-CAM (Gradient-weighted Class Activation Mapping)**, was instrumental in interpreting the model’s predictions. By generating heatmaps that highlight the areas of the image most influential in the decision-making process, the system provided dermatologists with greater transparency and confidence in the AI-driven diagnosis. This interpretability is essential in clinical settings, where trust in automated systems is critical for adoption.

Despite the model’s overall success, there are opportunities for enhancement in handling cases with high intra-class variability and inter-class similarity. Future work may include incorporating additional data sources, such as patient medical history and genetic factors, to improve the model’s diagnostic precision. Exploring advanced architectures like **Hybrid Transformers with Dynamic Convolutional Layers** could also enhance feature representation, leading to better differentiation between complex and overlapping lesion types.

Overall, the hybrid deep learning model presents a promising approach to improving skin cancer detection. Its ability to accurately classify common and well-defined lesions underscores its potential for integration into telemedicine platforms, where quick and reliable diagnosis can significantly improve patient outcomes. By addressing the current limitations and expanding the system’s capabilities, this AI-driven solution can provide a more comprehensive tool for early skin cancer detection, ultimately supporting dermatologists in delivering better patient care.

Chapter 5

RESULTS

5.1 Results from ResNet-50

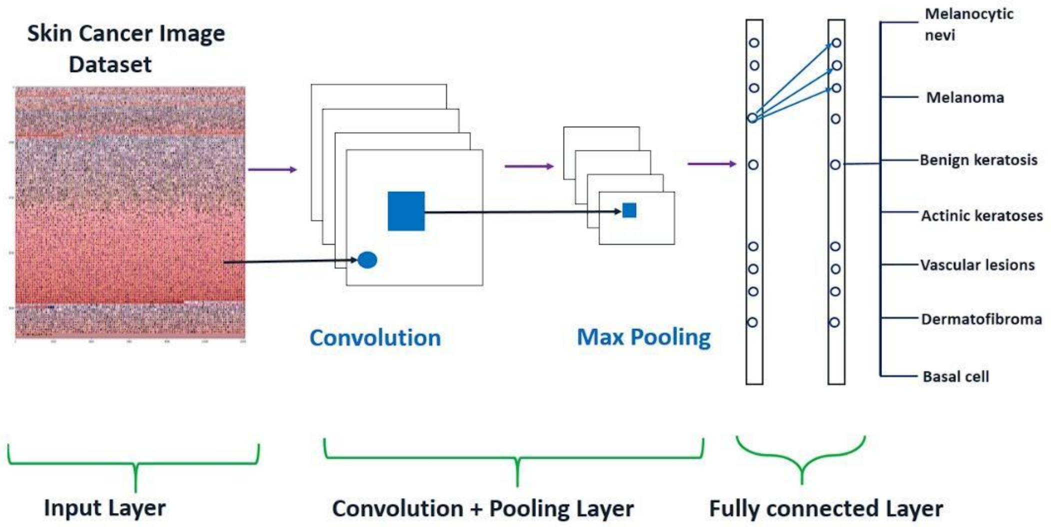


Fig 5. Pretrained ResNet-50

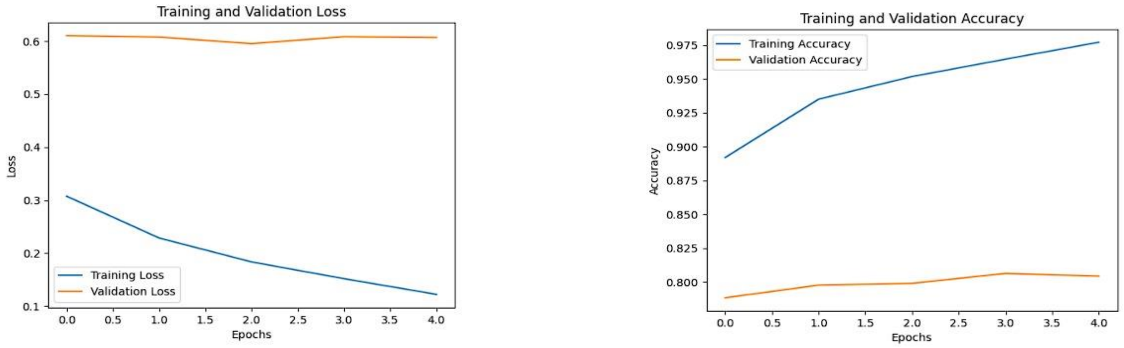


Fig 6. Training and Validation Results

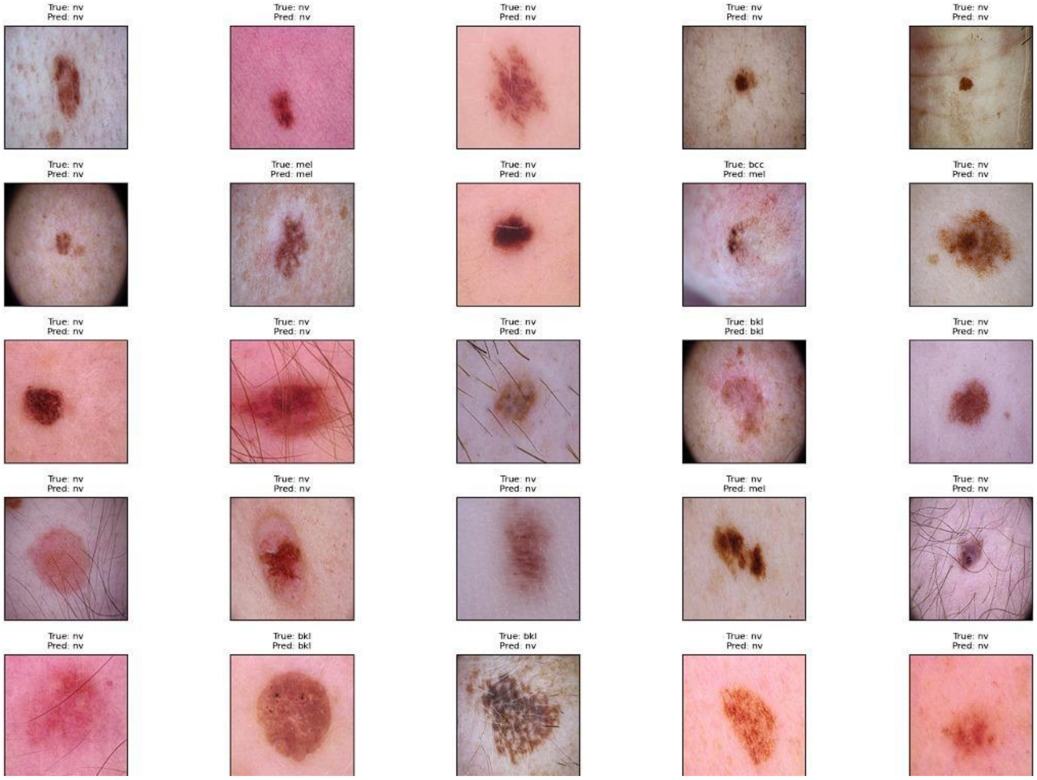
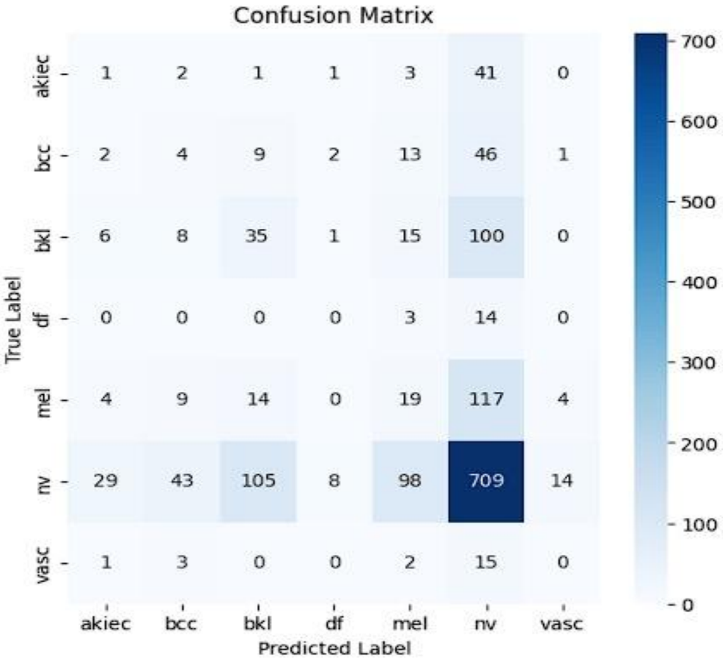
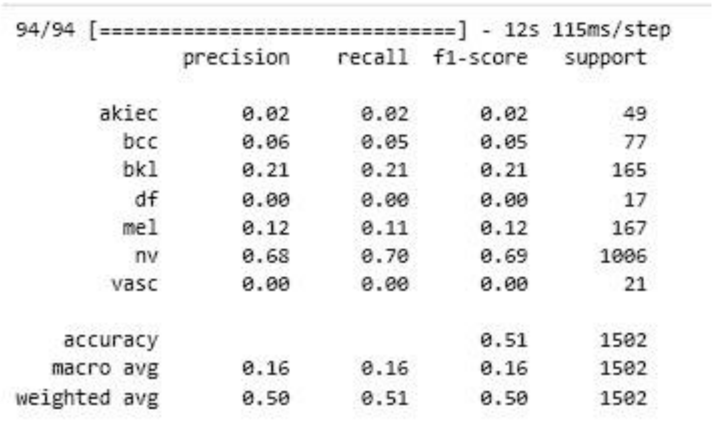


Fig 7. Results of pretrained ResNet-50



	akiec	bcc	bkl	df	mel	nv	vasc
akiec	1	2	1	1	3	41	0
bcc	2	4	9	2	13	46	1
bkl	6	8	35	1	15	100	0
df	0	0	0	0	3	14	0
mel	4	9	14	0	19	117	4
nv	29	43	105	8	98	709	14
vasc	1	3	0	0	2	15	0

Fig 8. Confusion matrix of pretrained ResNet-50



```
94/94 [==============================] - 12s 115ms/step
              precision    recall  f1-score   support

       akiec       0.02      0.02      0.02        49
         bcc       0.06      0.05      0.05        77
         bkl       0.21      0.21      0.21       165
          df       0.00      0.00      0.00        17
         mel       0.12      0.11      0.12       167
          nv       0.68      0.70      0.69      1006
        vasc       0.00      0.00      0.00        21

    accuracy                           0.51      1502
   macro avg       0.16      0.16      0.16      1502
weighted avg       0.50      0.51      0.50      1502
```

Fig 9. Classification Report of pretrained ResNet-50

5.2 Results from ViT(Vision Transformer)

i) ViT B – 32

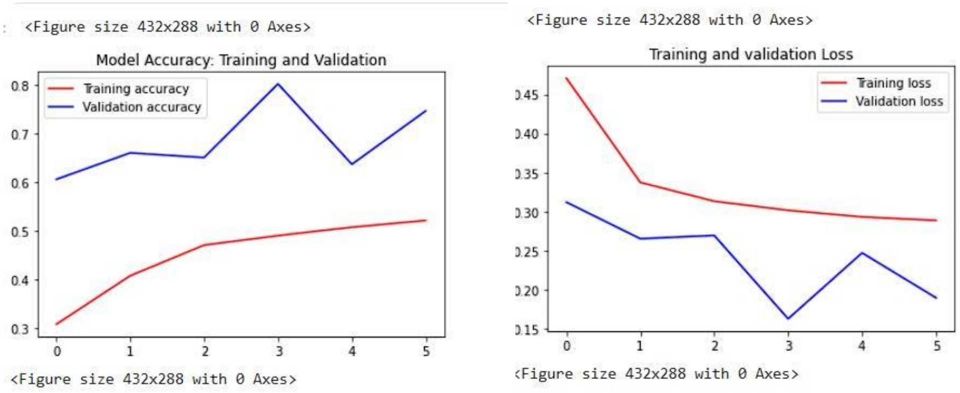


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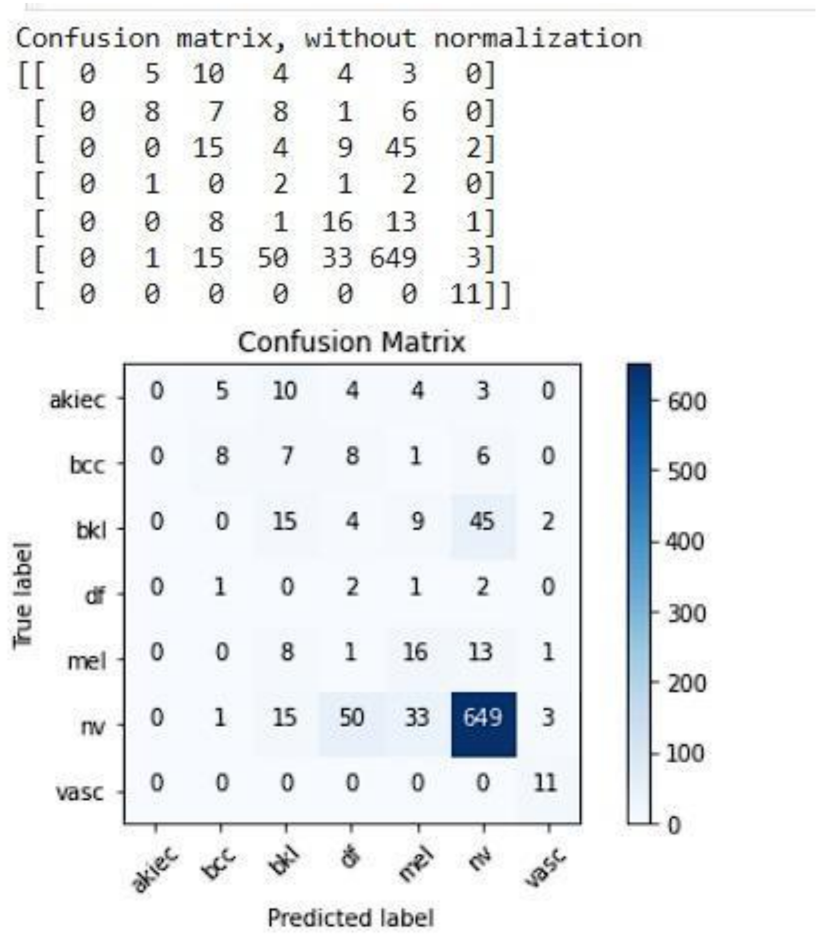
Fig 10. Training and Validation results of ViT B -32



```
Confusion matrix, without normalization
[[  0   5  10   4   4   3   0]
 [  0   8   7   8   1   6   0]
 [  0   0  15   4   9  45   2]
 [  0   1   0   2   1   2   0]
 [  0   0   8   1  16  13   1]
 [  0   1  15  50  33 649   3]
 [  0   0   0   0   0   0  11]]
```

Fig 11. Confusion matrix of ViT B -32

ii) ViT B – 16

```
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```

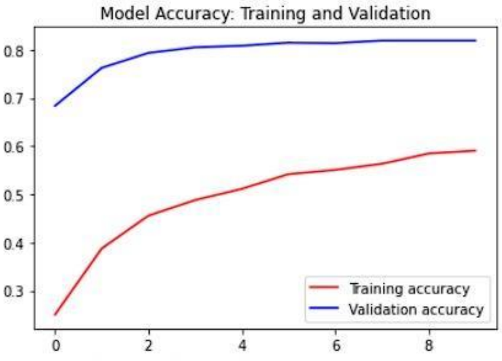

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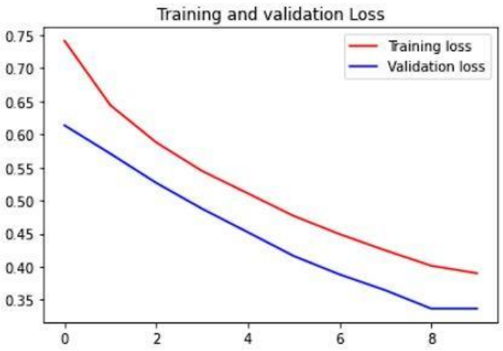

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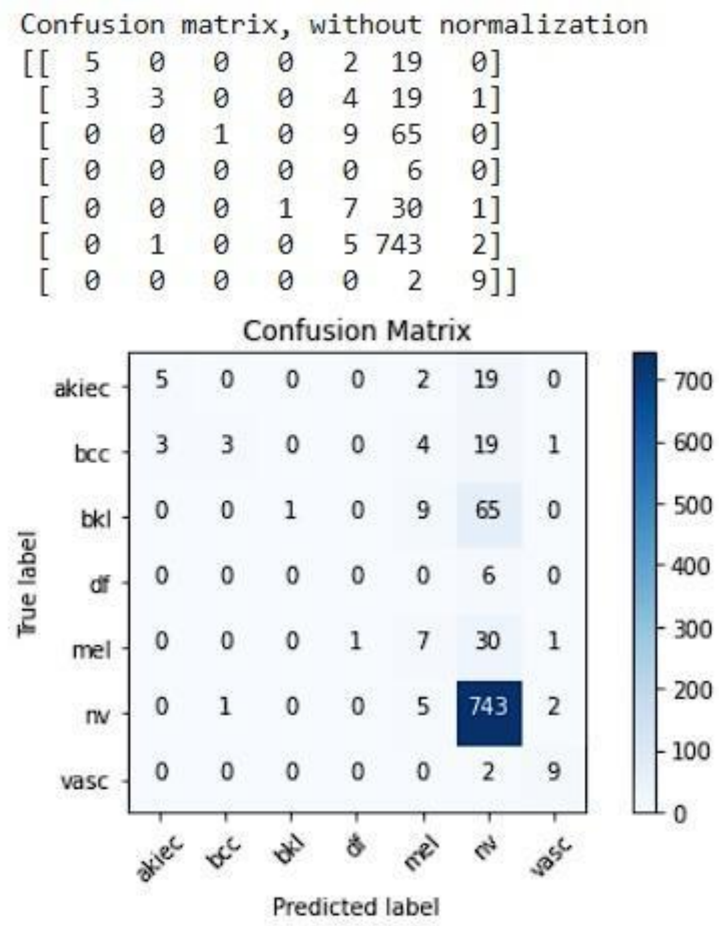
Fig 12. Training and Validation results of ViT B -16



```
Confusion matrix, without normalization
[[  5   0   0   0   2  19   0]
 [  3   3   0   0   4  19   1]
 [  0   0   1   0   9  65   0]
 [  0   0   0   0   0   6   0]
 [  0   0   0   1   7  30   1]
 [  0   1   0   0   5 743   2]
 [  0   0   0   0   0   2   9]]
```

Fig 13. Confusion Matrix of ViT B -16

Chapter 6

CONCLUSION

6.1 CONCLUSION

This project focused on developing a robust deep learning-based solution for early skin cancer detection, leveraging advanced neural network architectures to enhance diagnostic accuracy. The study demonstrated the effectiveness of **Vision Transformers (ViTs)** over traditional **Convolutional Neural Networks (CNNs)** in the domain of medical image processing. Unlike CNNs, which primarily excel at capturing local patterns, Vision Transformers leverage self-attention mechanisms to capture both local and global features, making them particularly suitable for complex medical images like dermatoscopic scans. This ability to understand long-range dependencies within images allowed the ViT models to achieve superior classification performance, particularly in distinguishing between benign and malignant skin lesions.

Among the Vision Transformer variants tested, **ViT-B/16** outperformed **ViT-B/32**, highlighting the impact of patch size on model accuracy. The smaller patch size in ViT-B/16 enabled the model to capture finer details in dermatoscopic images, leading to more precise feature extraction and improved diagnostic accuracy. This was especially important in detecting subtle differences between visually similar lesions, such as benign keratosis and melanoma, which are critical for early and accurate diagnosis. The results confirm that Vision Transformers, particularly ViT-B/16, offer a significant advantage in skin cancer detection tasks by providing higher sensitivity and specificity compared to traditional CNN models.

The importance of early and accurate skin cancer detection cannot be overstated. Skin cancer, particularly melanoma, is one of the most aggressive and potentially fatal forms of cancer if not diagnosed and treated early. This project aimed to address this challenge by leveraging state-of-the-art AI models to assist dermatologists in making timely and accurate diagnoses, thereby improving patient outcomes. The superior performance of Vision Transformers in this study not only demonstrates their potential in the medical imaging field but also paves the way for their integration into clinical decision support systems. By enhancing the accuracy of automated skin cancer screening, this technology can play a crucial role in reducing the mortality rates associated with skin cancer and expanding access to high-quality dermatological care, especially in regions with limited medical resources.

In conclusion, the combination of Vision Transformers, particularly ViT-B/16, with deep learning techniques offers a promising solution for improving the accuracy and reliability of skin cancer detection. This advancement underscores the transformative potential of AI in healthcare, enabling faster, more accurate diagnoses that can lead to better patient care and outcomes. Future work may explore further optimization of ViT models and the incorporation of multi-modal data to enhance the system's diagnostic capabilities even further.

6.2 SCOPE FOR IMPROVEMENT

Scope for Improvement

While the current hybrid deep learning model for skin cancer detection has shown promising results in accurately classifying skin lesions, there are several areas where the system can be further enhanced to improve its performance, efficiency, and scalability. These enhancements can significantly increase the model's utility in real-world clinical settings and telemedicine platforms. Below are some key areas identified for potential improvements:

1. **Custom Evaluation Metrics**:

   The current model evaluation primarily relies on standard metrics such as accuracy, precision, recall, and F1-score. However, skin cancer detection in clinical settings demands a deeper understanding of the model's performance, especially in terms of sensitivity to malignant lesions like melanoma. Introducing **custom evaluation metrics** such as the **Mean Sensitivity Index (MSI)**, **Specificity for High-Risk Categories**, and **False Negative Rate (FNR)** for critical conditions can provide a more nuanced assessment of the model’s diagnostic capabilities. These tailored metrics would ensure that the model prioritizes minimizing false negatives in high-risk cases, thereby enhancing patient safety.

2. **Reduced Computational Resource Requirements**:
   The current hybrid architecture, which combines Convolutional Neural Networks (CNNs) and Vision Transformers (ViTs), is computationally intensive, requiring high-end GPU resources for efficient training and inference. To make the model more accessible and deployable in resource-constrained environments, such as rural healthcare facilities or mobile devices, optimizations can be implemented. **Model pruning**, **quantization**, and the use of **lightweight architectures** like **MobileNet** or **EfficientNet-Lite** can significantly reduce the computational overhead without compromising accuracy. These adjustments will make the model more adaptable for real-time applications in telemedicine.
3. **Advanced Data Augmentation Techniques**:
   Although basic data augmentation techniques like rotation, flipping, and zooming are currently employed, there is scope to incorporate more sophisticated augmentation strategies to improve the model's robustness. **CutMix**, **MixUp**, and **Random Erasing** are advanced techniques that can generate more diverse training samples, helping the model to generalize better to unseen data. Additionally, **style transfer augmentation** can simulate variations in skin tones, lighting conditions, and imaging devices, thus addressing biases and improving the model's performance across different demographic groups
4. **Enhanced Interpretability with Explainable AI**:
   While the use of **Grad-CAM** and **Saliency Maps** has added a layer of interpretability, further improvements can be made to increase clinician trust. Integrating **Local Interpretable Model-agnostic Explanations (LIME)**, **SHAP (SHapley Additive exPlanations)**, or **Counterfactual Explanations** can provide deeper insights into the model's decision-making process. This would not only improve transparency but also assist dermatologists in validating the AI-generated diagnoses, ultimately leading to better adoption in clinical practice.

5. **Continuous Learning and Model Adaptation**:
   Skin cancer detection is an evolving field, with new types of lesions and variations being discovered. Implementing a **continuous learning framework** where the model can be periodically updated with new data can ensure that it remains accurate over time. Techniques like **Incremental Learning** and **Online Learning** can be employed to adapt the model to new lesion types without requiring a complete retraining, thereby saving computational resources.

Chapter 7

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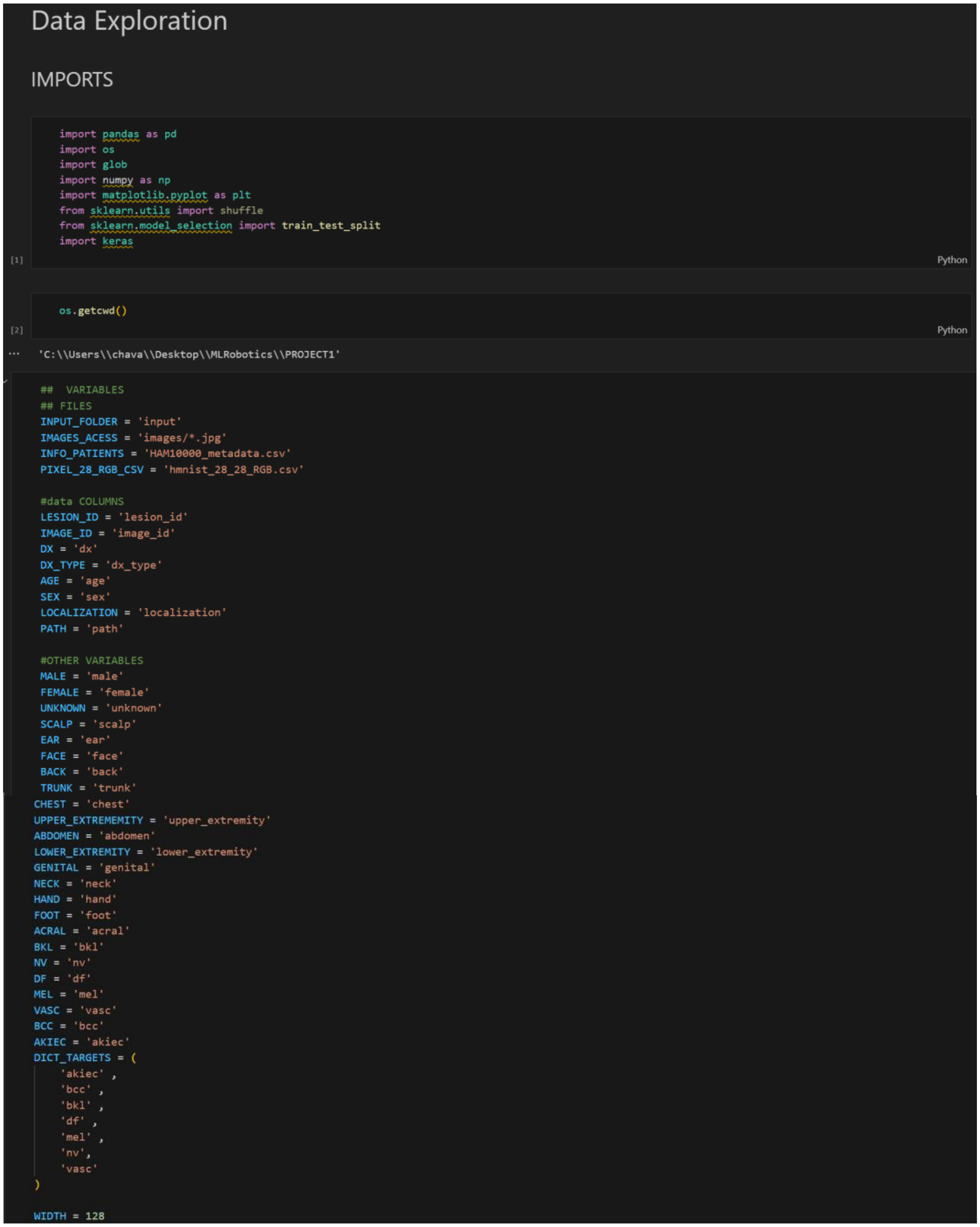
APPENDIX A – Sample Code



Data Exploration

IMPORTS

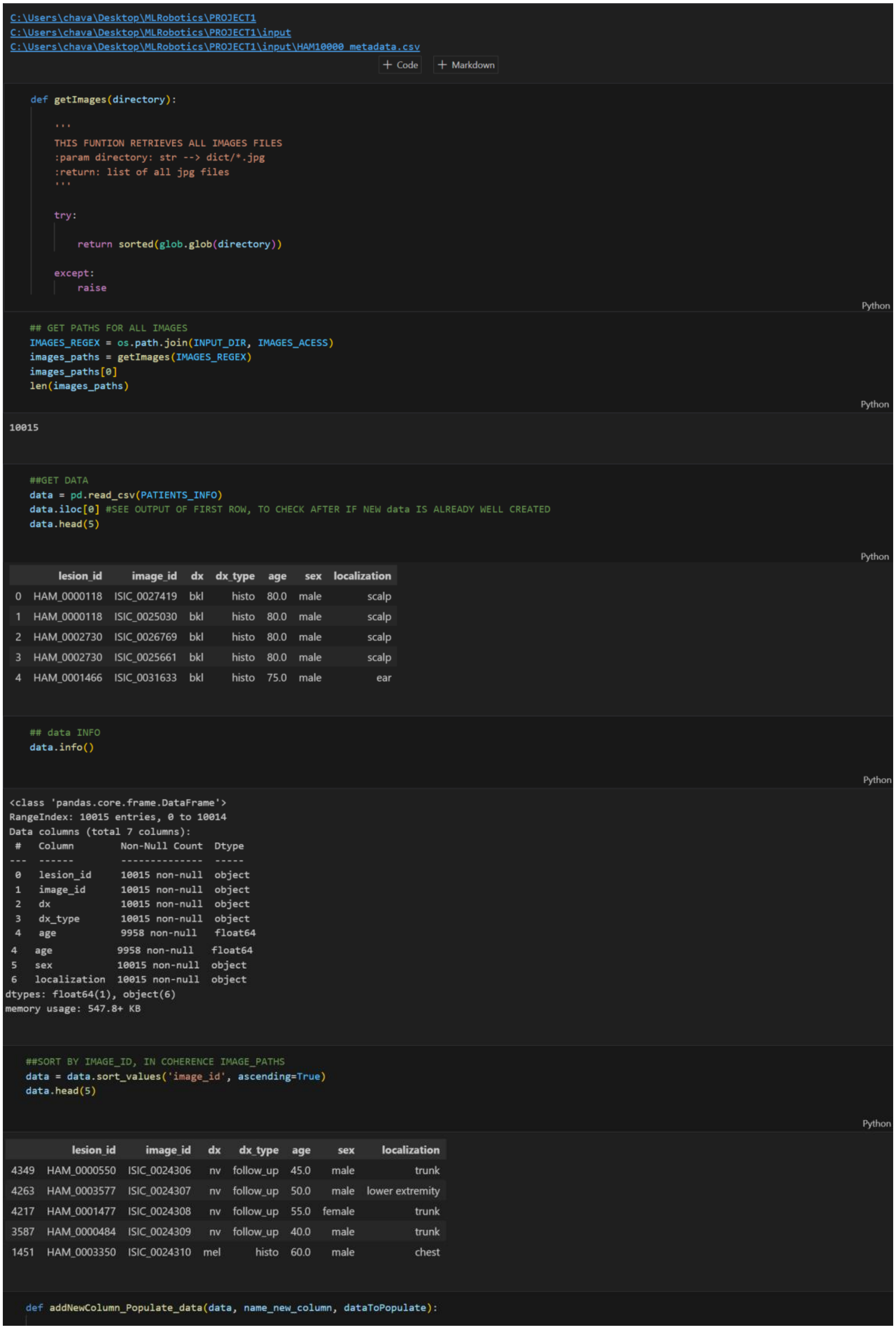
```python
import pandas as pd
import os
import glob
import numpy as np
import matplotlib.pyplot as plt
from sklearn.utils import shuffle
from sklearn.model_selection import train_test_split
import keras
```

```python
os.getcwd()
```

```
'C:\\Users\\chava\\Desktop\\MLRobotics\\PROJECT1'
```

```python
##  VARIABLES
## FILES
INPUT_FOLDER = 'input'
IMAGES_ACESS = 'images/*.jpg'
INFO_PATIENTS = 'HAM10000_metadata.csv'
PIXEL_28_RGB_CSV = 'hmnist_28_28_RGB.csv'

#data COLUMNS
LESION_ID = 'lesion_id'
IMAGE_ID = 'image_id'
DX = 'dx'
DX_TYPE = 'dx_type'
AGE = 'age'
SEX = 'sex'
LOCALIZATION = 'localization'
PATH = 'path'

#OTHER VARIABLES
MALE = 'male'
FEMALE = 'female'
UNKNOWN = 'unknown'
SCALP = 'scalp'
EAR = 'ear'
FACE = 'face'
BACK = 'back'
TRUNK = 'trunk'
CHEST = 'chest'
UPPER_EXTREMEMITY = 'upper_extremity'
ABDOMEN = 'abdomen'
LOWER_EXTREMITY = 'lower_extremity'
GENITAL = 'genital'
NECK = 'neck'
HAND = 'hand'
FOOT = 'foot'
ACRAL = 'acral'
BKL = 'bkl'
NV = 'nv'
DF = 'df'
MEL = 'mel'
VASC = 'vasc'
BCC = 'bcc'
AKIEC = 'akiec'
DICT_TARGETS = (
    'akiec' ,
    'bcc' ,
    'bkl' ,
    'df' ,
    'mel' ,
    'nv',
    'vasc'
)

WIDTH = 128
```

Appendix 1.1 Imports and Required Variables



```
C:\Users\chava\Desktop\MLRobotics\PROJECT1
C:\Users\chava\Desktop\MLRobotics\PROJECT1\input
C:\Users\chava\Desktop\MLRobotics\PROJECT1\input\HAM10000_metadata.csv
```

```python
def getImages(directory):

    '''
    THIS FUNTION RETRIEVES ALL IMAGES FILES
    :param directory: str --> dict/*.jpg
    :return: list of all jpg files
    '''

    try:

        return sorted(glob.glob(directory))

    except:
        raise
```

```python
## GET PATHS FOR ALL IMAGES
IMAGES_REGEX = os.path.join(INPUT_DIR, IMAGES_ACESS)
images_paths = getImages(IMAGES_REGEX)
images_paths[0]
len(images_paths)
```

```
10015
```

```python
##GET DATA
data = pd.read_csv(PATIENTS_INFO)
data.iloc[0] #SEE OUTPUT OF FIRST ROW, TO CHECK AFTER IF NEW data IS ALREADY WELL CREATED
data.head(5)
```

	lesion_id	image_id	dx	dx_type	age	sex	localization
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp
2	HAM_0002730	ISIC_0026769	bkl	histo	80.0	male	scalp
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear

```python
## data INFO
data.info()
```

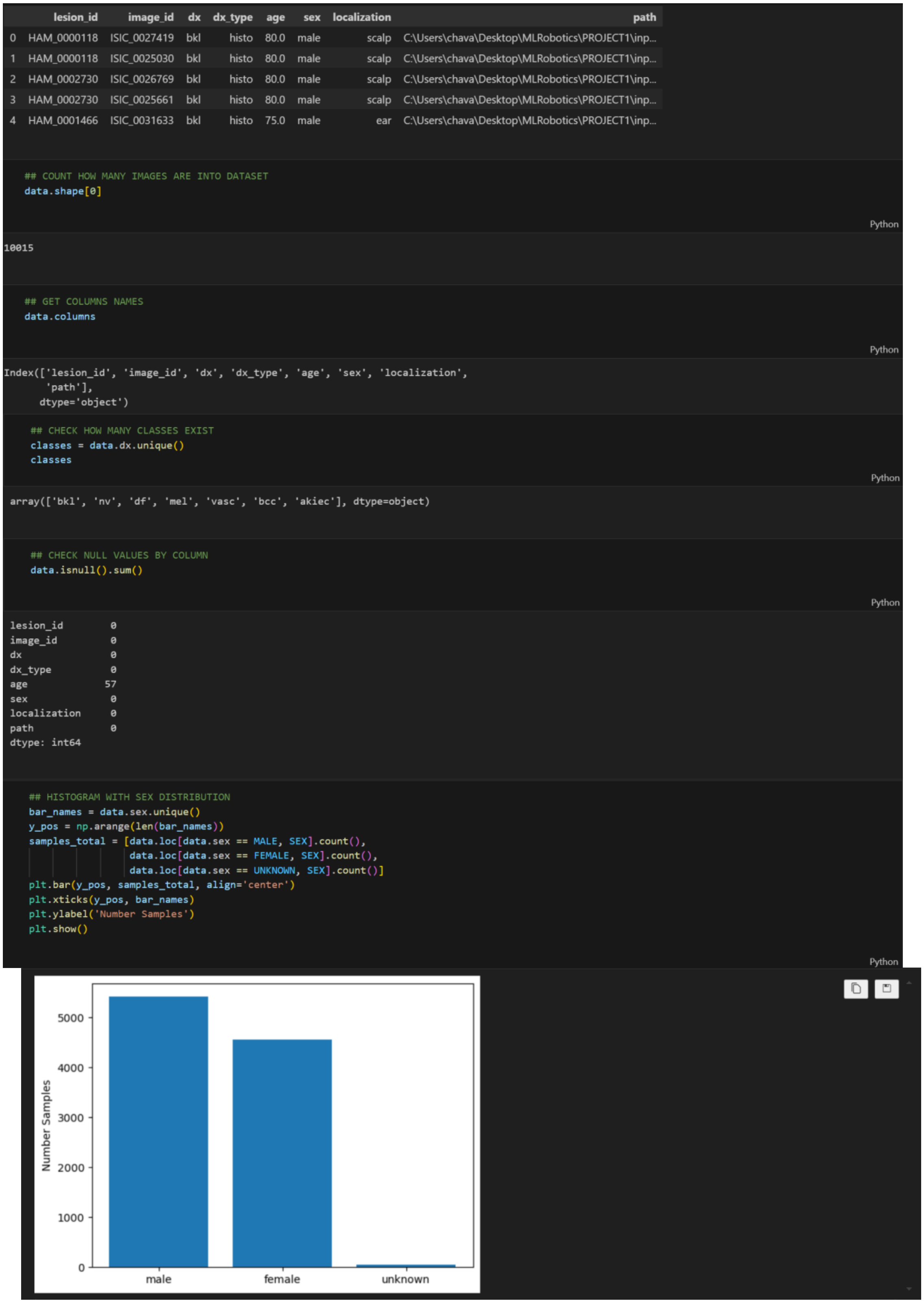
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 10015 entries, 0 to 10014
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   lesion_id     10015 non-null  object
 1   image_id      10015 non-null  object
 2   dx            10015 non-null  object
 3   dx_type       10015 non-null  object
 4   age           9958 non-null   float64
 4   age           9958 non-null   float64
 5   sex           10015 non-null  object
 6   localization  10015 non-null  object
dtypes: float64(1), object(6)
memory usage: 547.8+ KB
```

```python
##SORT BY IMAGE_ID, IN COHERENCE IMAGE_PATHS
data = data.sort_values('image_id', ascending=True)
data.head(5)
```

	lesion_id	image_id	dx	dx_type	age	sex	localization
4349	HAM_0000550	ISIC_0024306	nv	follow_up	45.0	male	trunk
4263	HAM_0003577	ISIC_0024307	nv	follow_up	50.0	male	lower extremity
4217	HAM_0001477	ISIC_0024308	nv	follow_up	55.0	female	trunk
3587	HAM_0000484	ISIC_0024309	nv	follow_up	40.0	male	trunk
1451	HAM_0003350	ISIC_0024310	mel	histo	60.0	male	chest

```python
def addNewColumn_Populate_data(data, name_new_column, dataToPopulate):
```

Appendix 1.2 Importing Dataset



	lesion_id	image_id	dx	dx_type	age	sex	localization	path
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp	C:\Users\chava\Desktop\MLRobotics\PROJECT1\inp...
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp	C:\Users\chava\Desktop\MLRobotics\PROJECT1\inp...
2	HAM_0002730	ISIC_0026769	bkl	histo	80.0	male	scalp	C:\Users\chava\Desktop\MLRobotics\PROJECT1\inp...
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp	C:\Users\chava\Desktop\MLRobotics\PROJECT1\inp...
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear	C:\Users\chava\Desktop\MLRobotics\PROJECT1\inp...

```
## COUNT HOW MANY IMAGES ARE INTO DATASET
data.shape[0]
```

```
10015
```

```
## GET COLUMNS NAMES
data.columns
```

```
Index(['lesion_id', 'image_id', 'dx', 'dx_type', 'age', 'sex', 'localization',
       'path'],
      dtype='object')
```

```
## CHECK HOW MANY CLASSES EXIST
classes = data.dx.unique()
classes
```

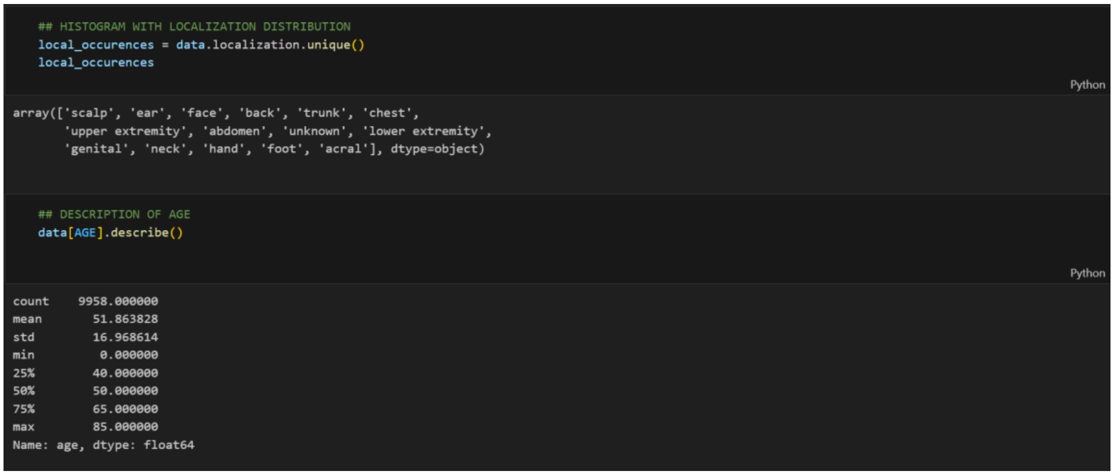
```
array(['bkl', 'nv', 'df', 'mel', 'vasc', 'bcc', 'akiec'], dtype=object)
```

```
## CHECK NULL VALUES BY COLUMN
data.isnull().sum()
```

```
lesion_id        0
image_id         0
dx               0
dx_type          0
age             57
sex              0
localization     0
path             0
dtype: int64
```

```
## HISTOGRAM WITH SEX DISTRIBUTION
bar_names = data.sex.unique()
y_pos = np.arange(len(bar_names))
samples_total = [data.loc[data.sex == MALE, SEX].count(),
                 data.loc[data.sex == FEMALE, SEX].count(),
                 data.loc[data.sex == UNKNOWN, SEX].count()]
plt.bar(y_pos, samples_total, align='center')
plt.xticks(y_pos, bar_names)
plt.ylabel('Number Samples')
plt.show()
```

Appendix 1.3 Importing Dataset

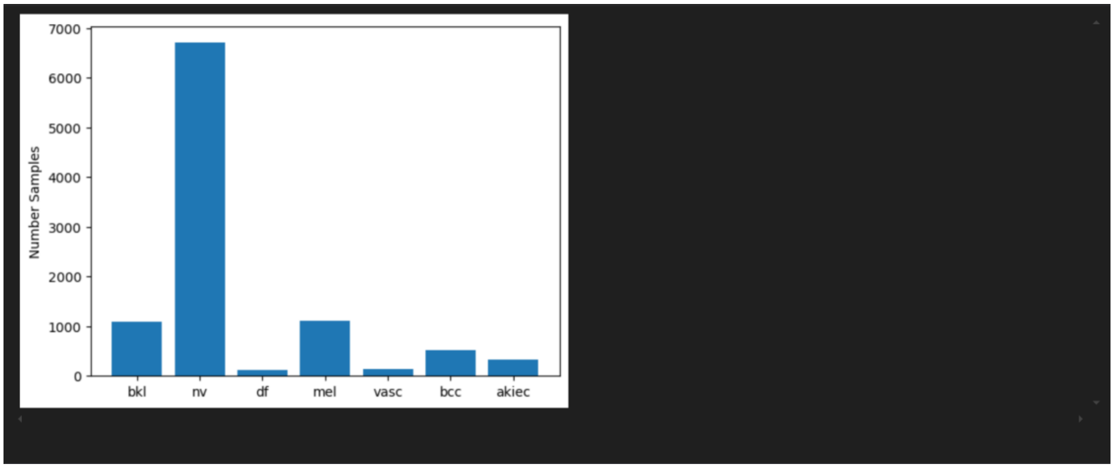


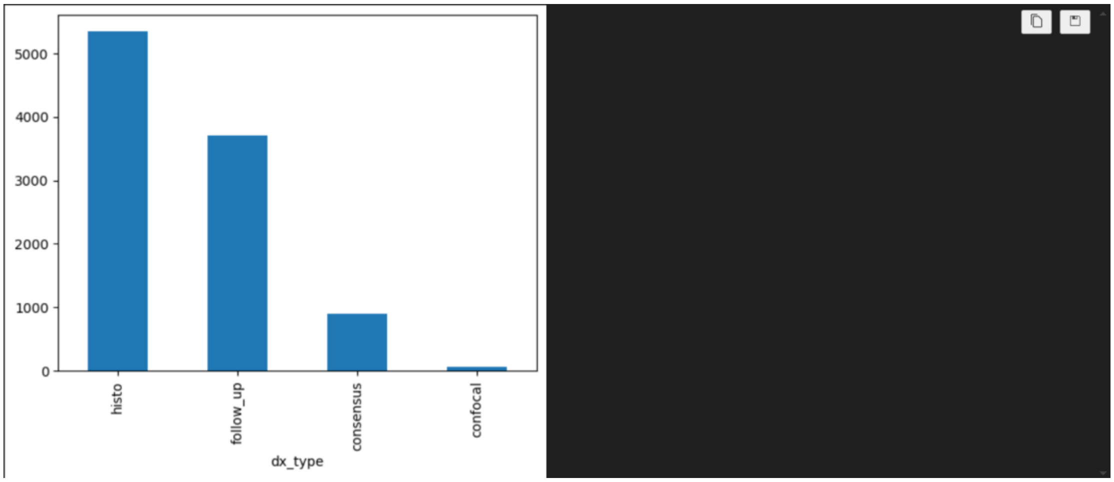
```
## HISTOGRAM WITH LOCALIZATION DISTRIBUTION
local_occurences = data.localization.unique()
local_occurences
```

```
array(['scalp', 'ear', 'face', 'back', 'trunk', 'chest',
       'upper extremity', 'abdomen', 'unknown', 'lower extremity',
       'genital', 'neck', 'hand', 'foot', 'acral'], dtype=object)
```

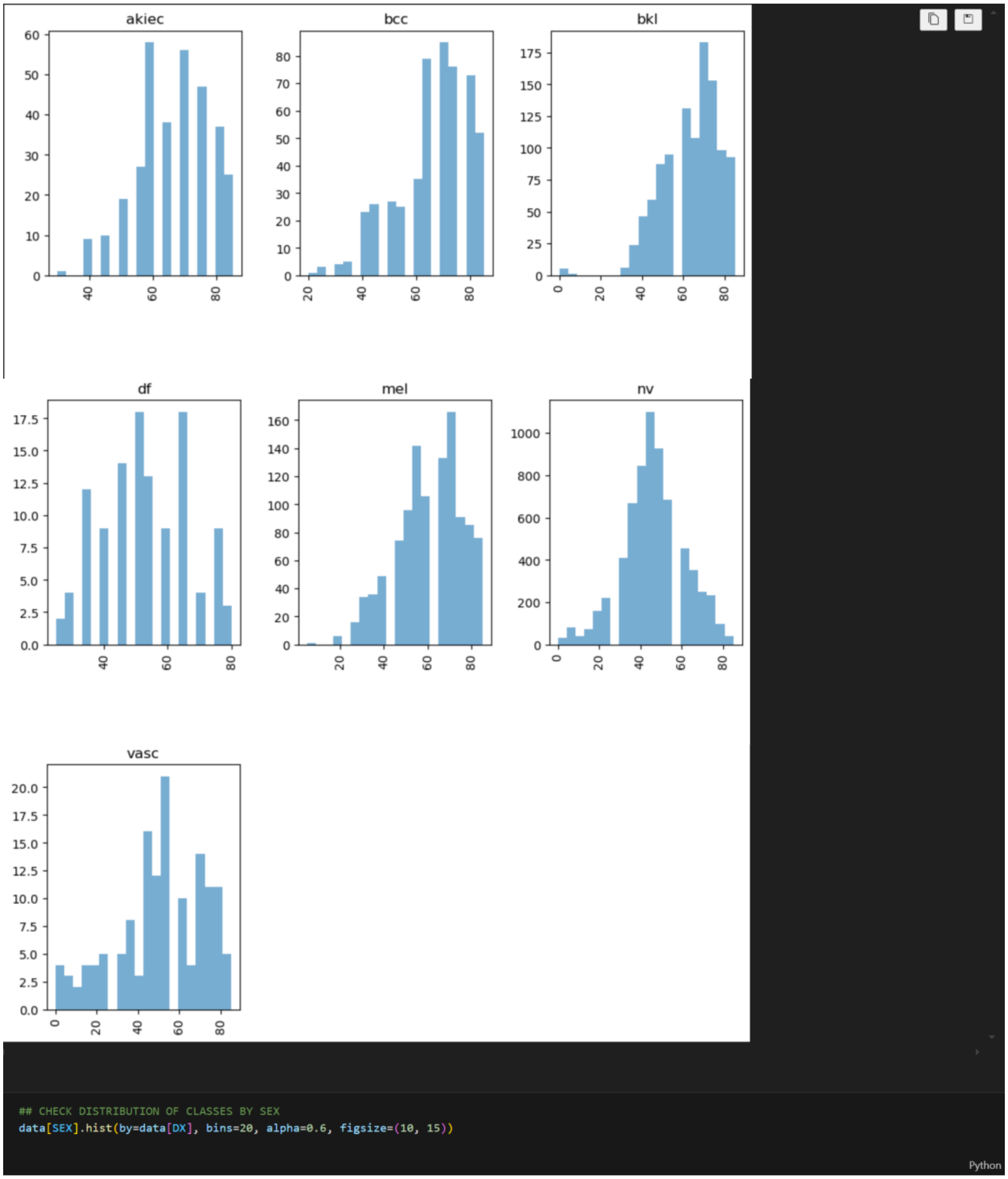
```
## DESCRIPTION OF AGE
data[AGE].describe()
```

```
count    9958.000000
mean       51.863828
std        16.968614
min         0.000000
25%        40.000000
50%        50.000000
75%        65.000000
max        85.000000
Name: age, dtype: float64
```



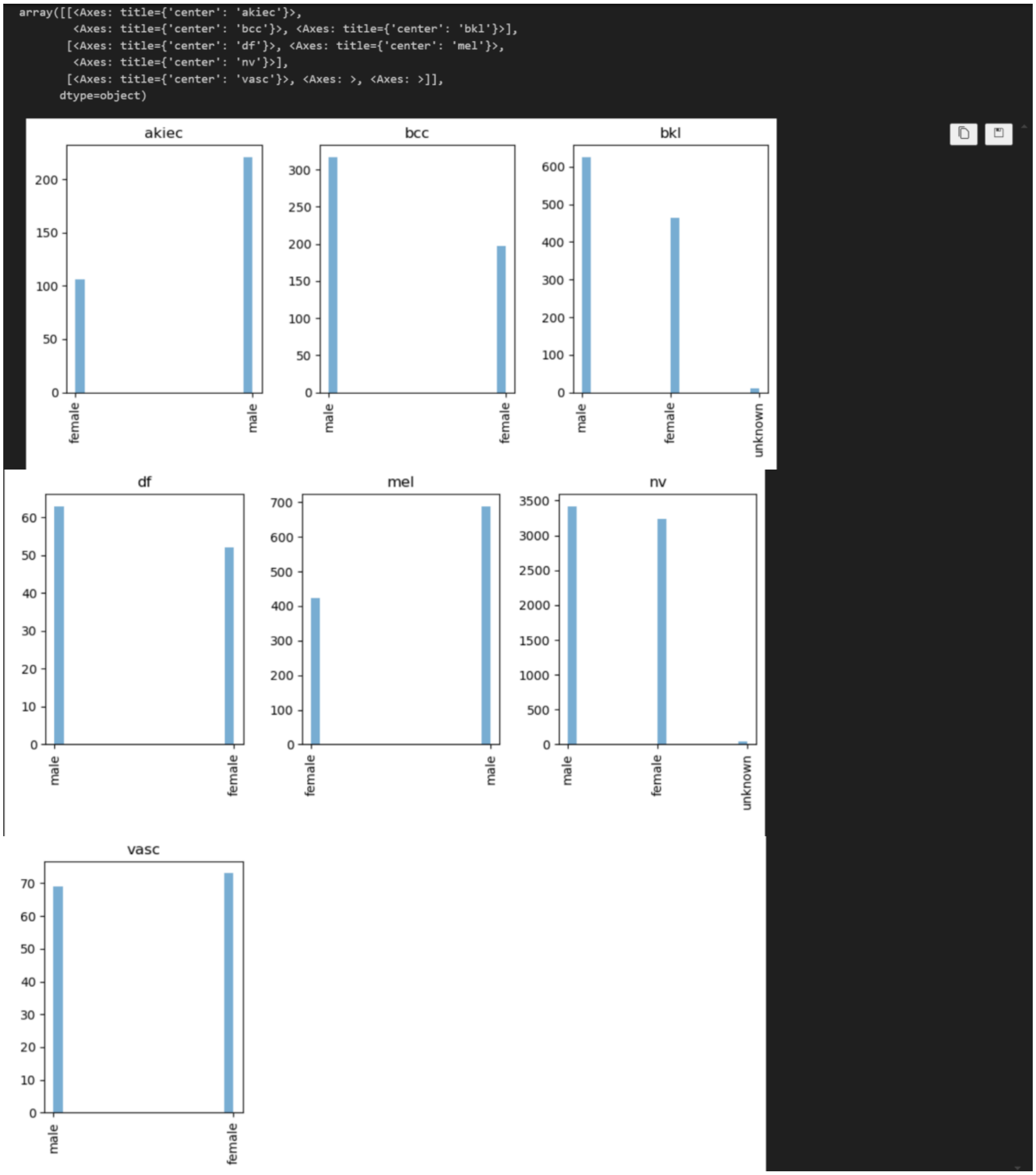


Appendix 1.4 Data Exploration



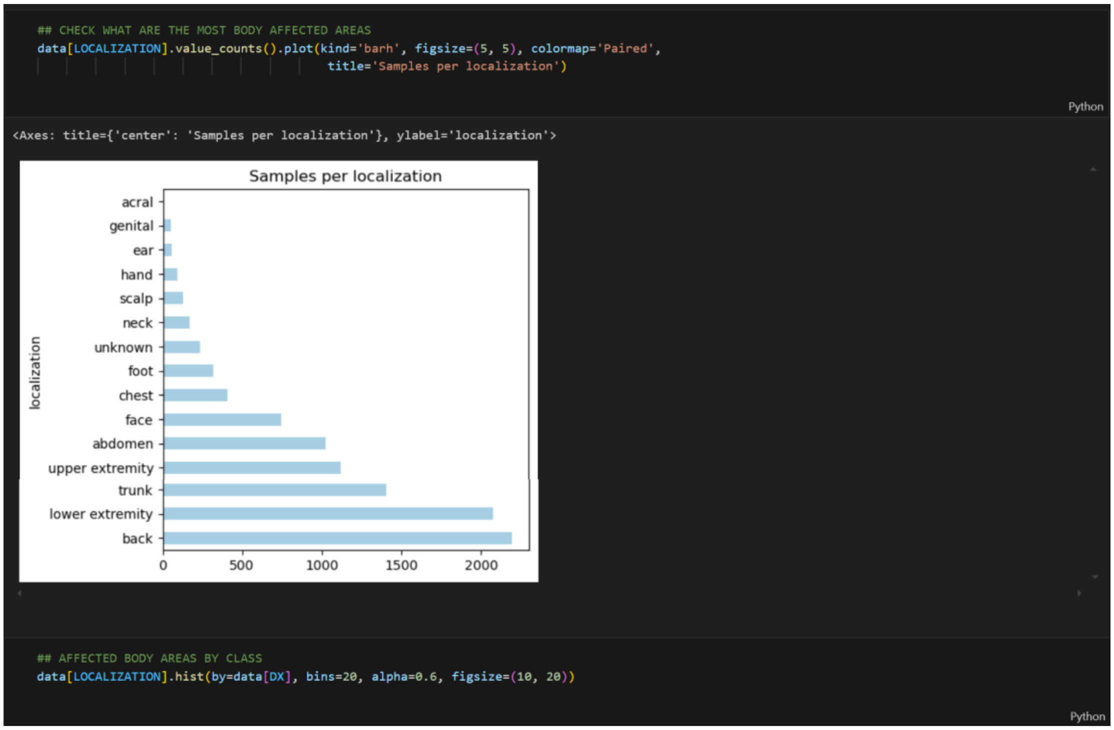
```
## CHECK DISTRIBUTION OF CLASSES BY SEX
data[SEX].hist(by=data[DX], bins=20, alpha=0.6, figsize=(10, 15))
```

Appendix 1.5 Data Exploration



```
array([[<Axes: title={'center': 'akiec'}>,
        <Axes: title={'center': 'bcc'}>, <Axes: title={'center': 'bkl'}>],
       [<Axes: title={'center': 'df'}>, <Axes: title={'center': 'mel'}>,
        <Axes: title={'center': 'nv'}>],
       [<Axes: title={'center': 'vasc'}>, <Axes: >, <Axes: >]],
      dtype=object)
```

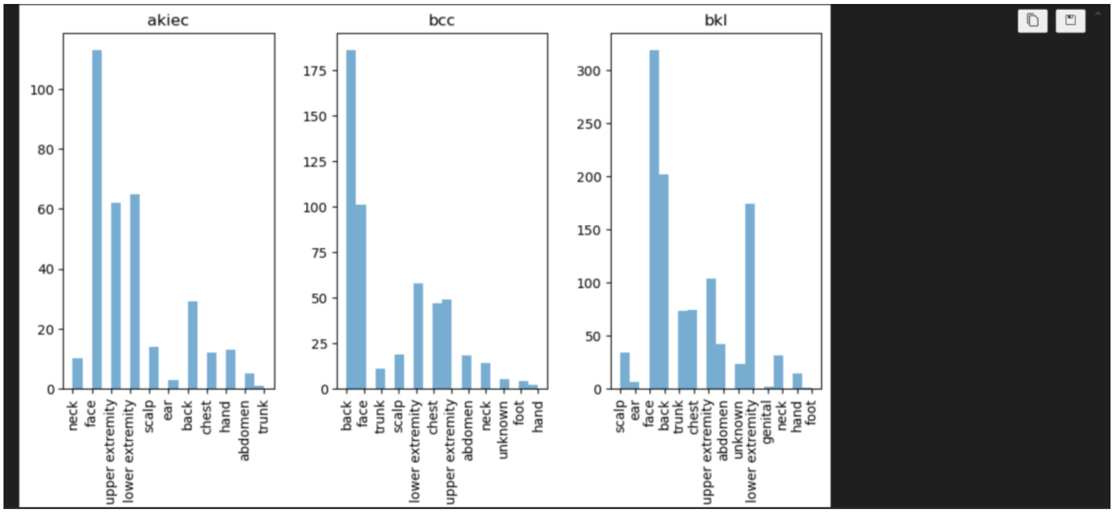
Appendix 1.6 Data Exploration



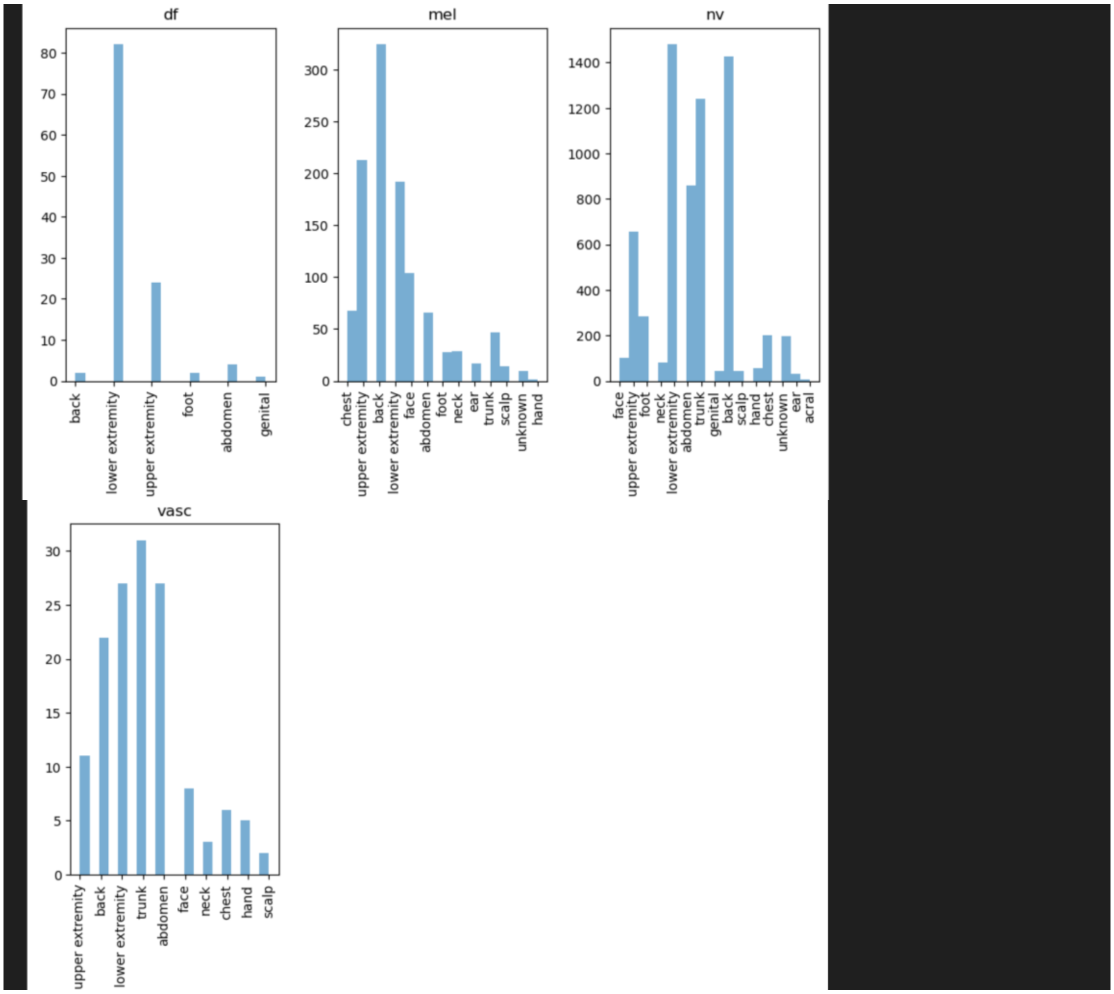
```
## CHECK WHAT ARE THE MOST BODY AFFECTED AREAS
data[LOCALIZATION].value_counts().plot(kind='barh', figsize=(5, 5), colormap='Paired',
                                        title='Samples per localization')
```

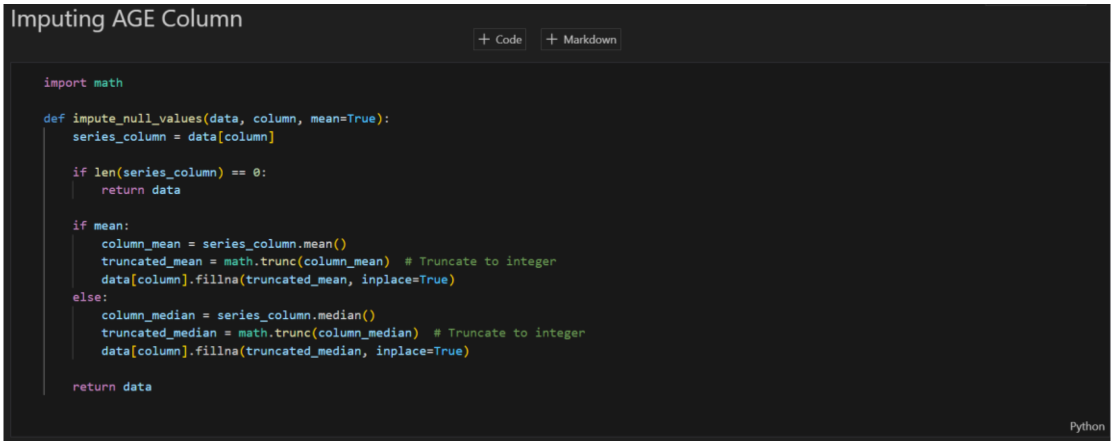
```
<Axes: title={'center': 'Samples per localization'}, ylabel='localization'>
```

```
## AFFECTED BODY AREAS BY CLASS
data[LOCALIZATION].hist(by=data[DX], bins=20, alpha=0.6, figsize=(10, 20))
```



Appendix 1.7 Data Exploration

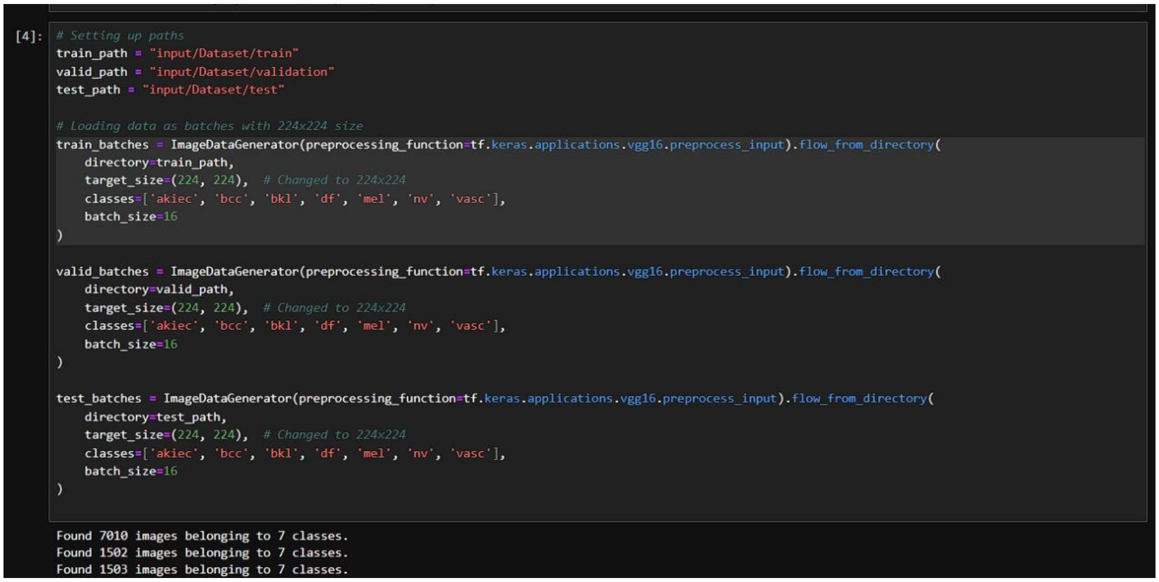




Imputing AGE Column

```python
import math

def impute_null_values(data, column, mean=True):
    series_column = data[column]

    if len(series_column) == 0:
        return data

    if mean:
        column_mean = series_column.mean()
        truncated_mean = math.trunc(column_mean)  # Truncate to integer
        data[column].fillna(truncated_mean, inplace=True)
    else:
        column_median = series_column.median()
        truncated_median = math.trunc(column_median)  # Truncate to integer
        data[column].fillna(truncated_median, inplace=True)

    return data
```

Appendix 1.7 Data Exploration

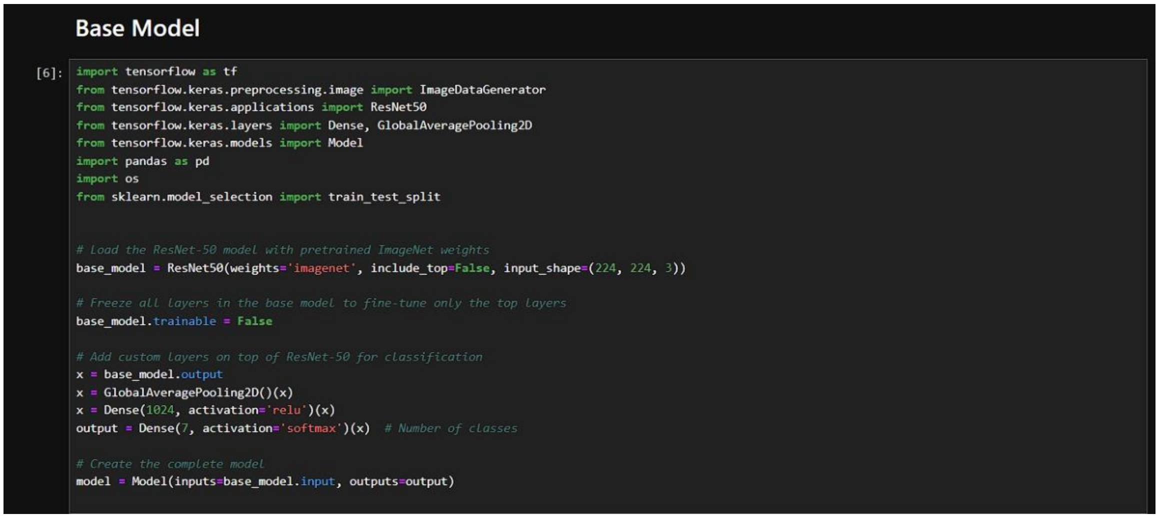


[4]:

```
# Setting up paths
train_path = "input/Dataset/train"
valid_path = "input/Dataset/validation"
test_path = "input/Dataset/test"

# Loading data as batches with 224x224 size
train_batches = ImageDataGenerator(preprocessing_function=tf.keras.applications.vgg16.preprocess_input).flow_from_directory(
    directory=train_path,
    target_size=(224, 224),  # Changed to 224x224
    classes=['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc'],
    batch_size=16
)

valid_batches = ImageDataGenerator(preprocessing_function=tf.keras.applications.vgg16.preprocess_input).flow_from_directory(
    directory=valid_path,
    target_size=(224, 224),  # Changed to 224x224
    classes=['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc'],
    batch_size=16
)

test_batches = ImageDataGenerator(preprocessing_function=tf.keras.applications.vgg16.preprocess_input).flow_from_directory(
    directory=test_path,
    target_size=(224, 224),  # Changed to 224x224
    classes=['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc'],
    batch_size=16
)
```

```
Found 7010 images belonging to 7 classes.
Found 1502 images belonging to 7 classes.
Found 1503 images belonging to 7 classes.
```

Appendix 2.1 Dividing the data into batches

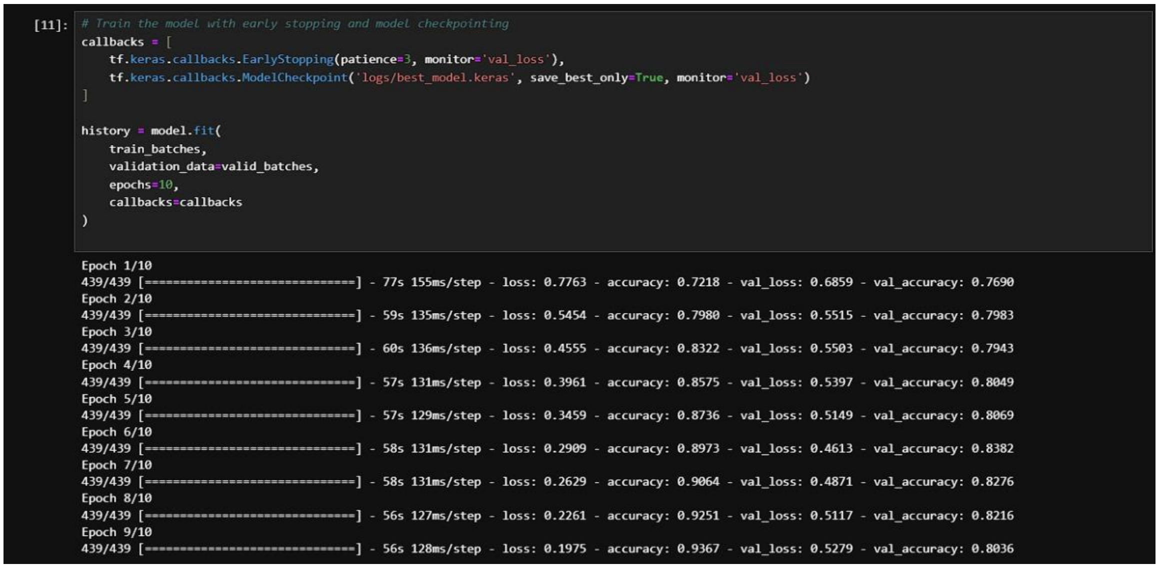


Base Model

[6]:

```
import tensorflow as tf
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.applications import ResNet50
from tensorflow.keras.layers import Dense, GlobalAveragePooling2D
from tensorflow.keras.models import Model
import pandas as pd
import os
from sklearn.model_selection import train_test_split


# Load the ResNet-50 model with pretrained ImageNet weights
base_model = ResNet50(weights='imagenet', include_top=False, input_shape=(224, 224, 3))

# Freeze all layers in the base model to fine-tune only the top layers
base_model.trainable = False

# Add custom layers on top of ResNet-50 for classification
x = base_model.output
x = GlobalAveragePooling2D()(x)
x = Dense(1024, activation='relu')(x)
output = Dense(7, activation='softmax')(x)  # Number of classes

# Create the complete model
model = Model(inputs=base_model.input, outputs=output)
```

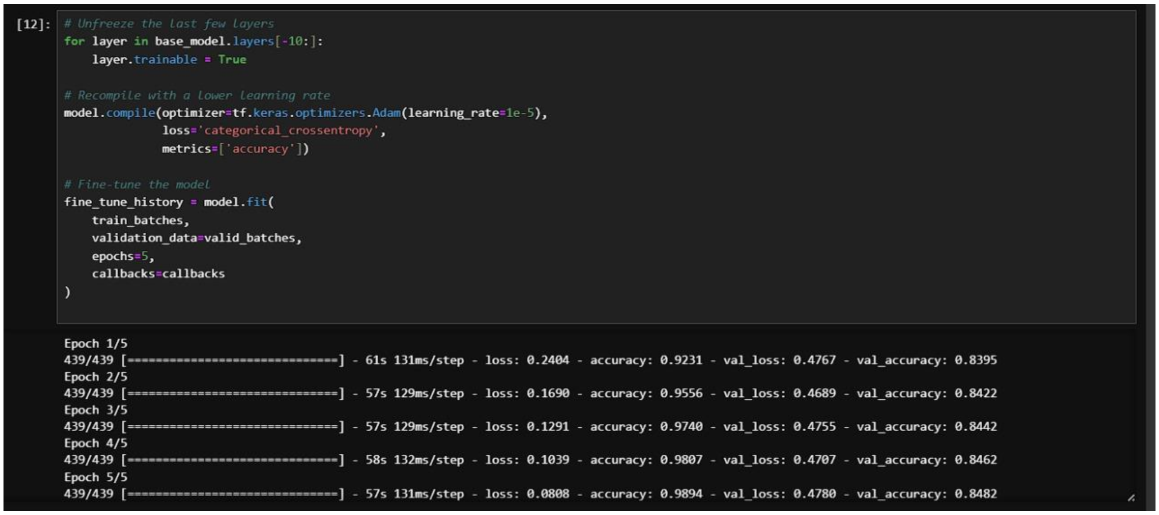
Appendix 2.2 Base Model (ResNet-50)



```
[11]: # Train the model with early stopping and model checkpointing
      callbacks = [
          tf.keras.callbacks.EarlyStopping(patience=3, monitor='val_loss'),
          tf.keras.callbacks.ModelCheckpoint('logs/best_model.keras', save_best_only=True, monitor='val_loss')
      ]

      history = model.fit(
          train_batches,
          validation_data=valid_batches,
          epochs=10,
          callbacks=callbacks
      )
```

```
Epoch 1/10
439/439 [==============================] - 77s 155ms/step - loss: 0.7763 - accuracy: 0.7218 - val_loss: 0.6859 - val_accuracy: 0.7690
Epoch 2/10
439/439 [==============================] - 59s 135ms/step - loss: 0.5454 - accuracy: 0.7980 - val_loss: 0.5515 - val_accuracy: 0.7983
Epoch 3/10
439/439 [==============================] - 60s 136ms/step - loss: 0.4555 - accuracy: 0.8322 - val_loss: 0.5503 - val_accuracy: 0.7943
Epoch 4/10
439/439 [==============================] - 57s 131ms/step - loss: 0.3961 - accuracy: 0.8575 - val_loss: 0.5397 - val_accuracy: 0.8049
Epoch 5/10
439/439 [==============================] - 57s 129ms/step - loss: 0.3459 - accuracy: 0.8736 - val_loss: 0.5149 - val_accuracy: 0.8069
Epoch 6/10
439/439 [==============================] - 58s 131ms/step - loss: 0.2909 - accuracy: 0.8973 - val_loss: 0.4613 - val_accuracy: 0.8382
Epoch 7/10
439/439 [==============================] - 58s 131ms/step - loss: 0.2629 - accuracy: 0.9064 - val_loss: 0.4871 - val_accuracy: 0.8276
Epoch 8/10
439/439 [==============================] - 56s 127ms/step - loss: 0.2261 - accuracy: 0.9251 - val_loss: 0.5117 - val_accuracy: 0.8216
Epoch 9/10
439/439 [==============================] - 56s 128ms/step - loss: 0.1975 - accuracy: 0.9367 - val_loss: 0.5279 - val_accuracy: 0.8036
```

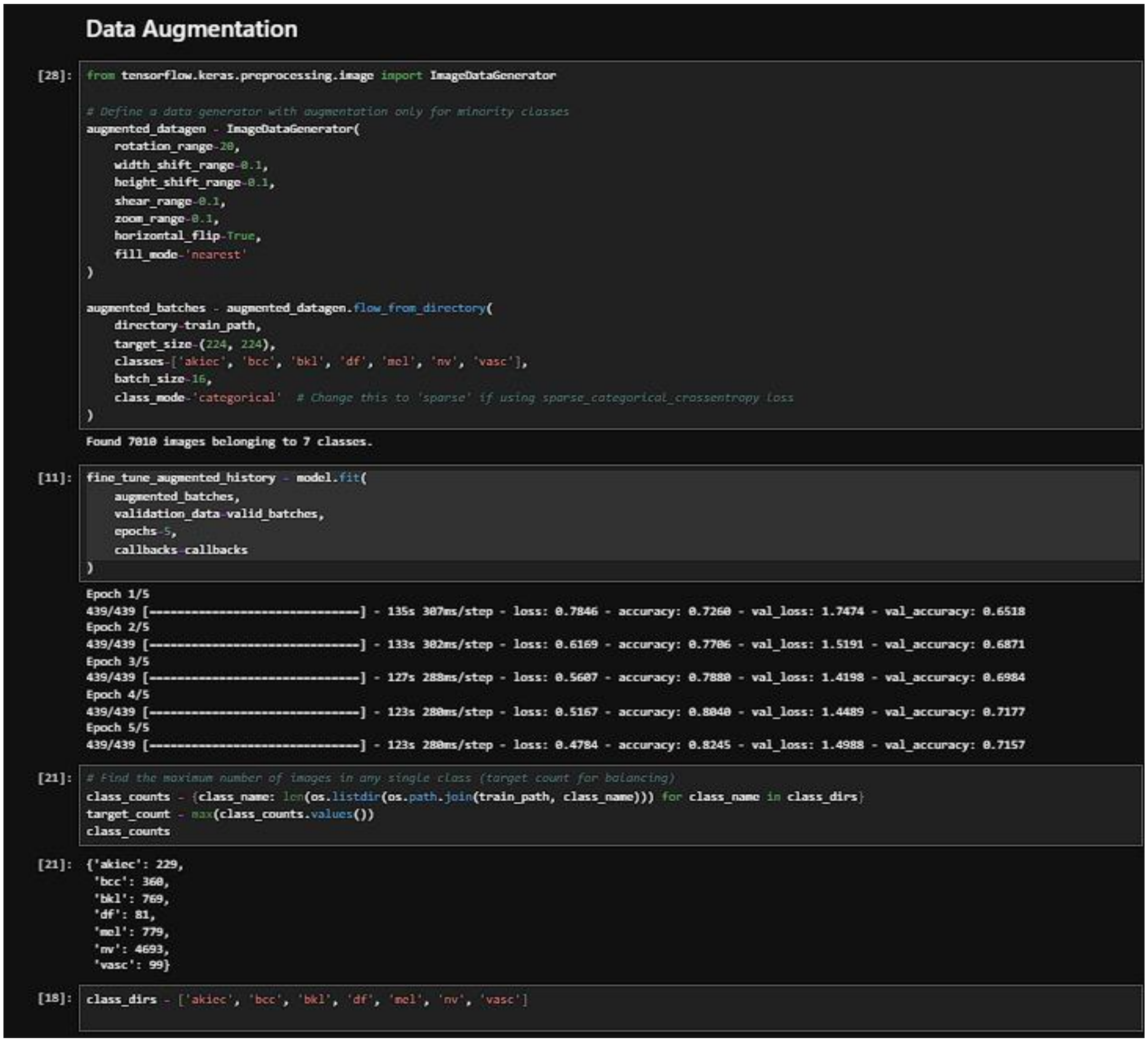
Appendix 2.3 Training



```
[12]: # Unfreeze the last few layers
      for layer in base_model.layers[-10:]:
          layer.trainable = True

      # Recompile with a lower learning rate
      model.compile(optimizer=tf.keras.optimizers.Adam(learning_rate=1e-5),
                    loss='categorical_crossentropy',
                    metrics=['accuracy'])

      # Fine-tune the model
      fine_tune_history = model.fit(
          train_batches,
          validation_data=valid_batches,
          epochs=5,
          callbacks=callbacks
      )
```

```
Epoch 1/5
439/439 [==============================] - 61s 131ms/step - loss: 0.2404 - accuracy: 0.9231 - val_loss: 0.4767 - val_accuracy: 0.8395
Epoch 2/5
439/439 [==============================] - 57s 129ms/step - loss: 0.1690 - accuracy: 0.9556 - val_loss: 0.4689 - val_accuracy: 0.8422
Epoch 3/5
439/439 [==============================] - 57s 129ms/step - loss: 0.1291 - accuracy: 0.9740 - val_loss: 0.4755 - val_accuracy: 0.8442
Epoch 4/5
439/439 [==============================] - 58s 132ms/step - loss: 0.1039 - accuracy: 0.9807 - val_loss: 0.4707 - val_accuracy: 0.8462
Epoch 5/5
439/439 [==============================] - 57s 131ms/step - loss: 0.0808 - accuracy: 0.9894 - val_loss: 0.4780 - val_accuracy: 0.8482
```

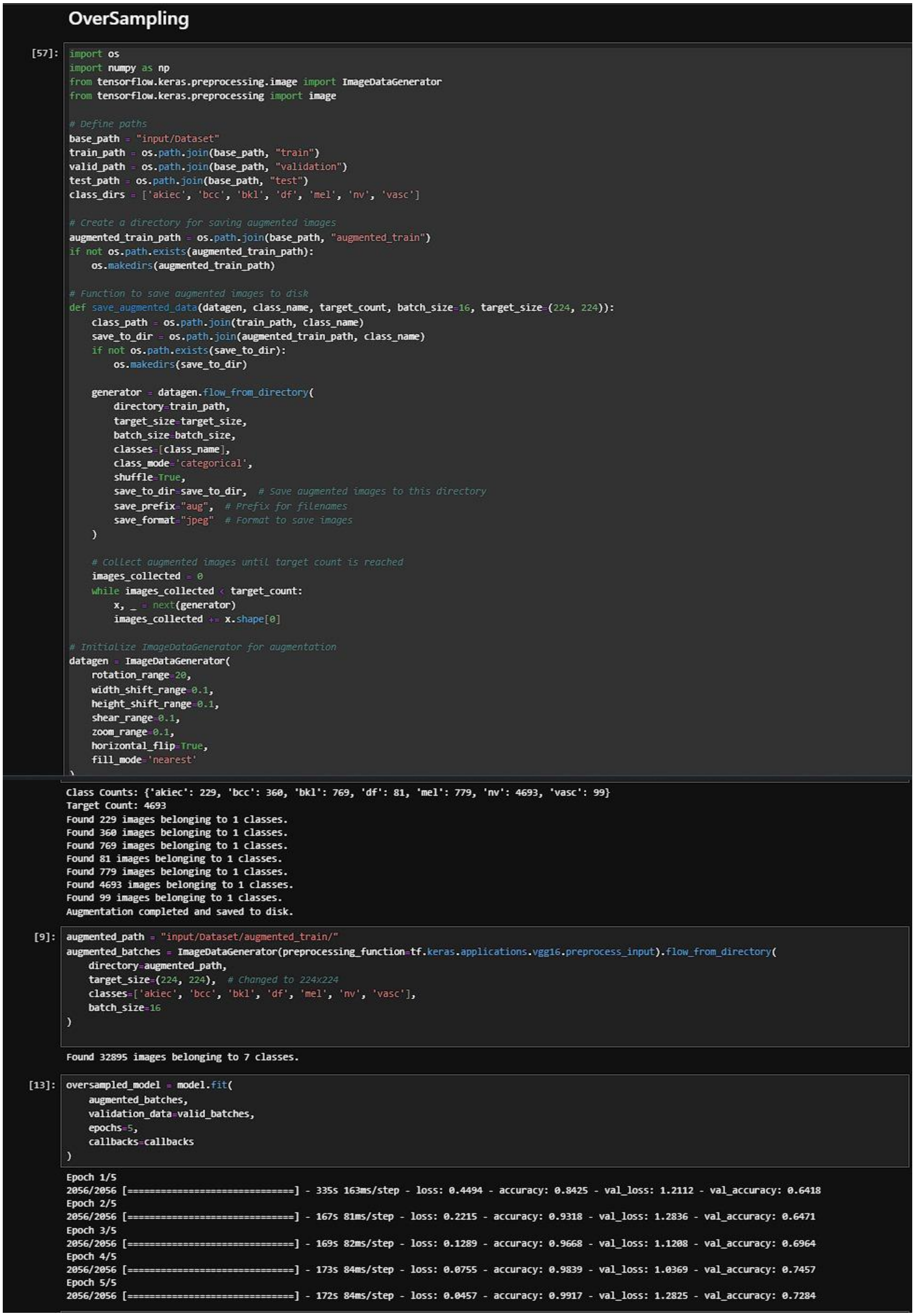
Appendix 2.4 Fine Tuned Model (10 layers)



Data Augmentation

```
[28]: from tensorflow.keras.preprocessing.image import ImageDataGenerator

      # Define a data generator with augmentation only for minority classes
      augmented_datagen = ImageDataGenerator(
          rotation_range=20,
          width_shift_range=0.1,
          height_shift_range=0.1,
          shear_range=0.1,
          zoom_range=0.1,
          horizontal_flip=True,
          fill_mode='nearest'
      )

      augmented_batches = augmented_datagen.flow_from_directory(
          directory=train_path,
          target_size=(224, 224),
          classes=['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc'],
          batch_size=16,
          class_mode='categorical'  # Change this to 'sparse' if using sparse_categorical_crossentropy loss
      )

      Found 7010 images belonging to 7 classes.

[11]: fine_tune_augmented_history = model.fit(
          augmented_batches,
          validation_data=valid_batches,
          epochs=5,
          callbacks=callbacks
      )

      Epoch 1/5
      439/439 [==============================] - 135s 307ms/step - loss: 0.7846 - accuracy: 0.7260 - val_loss: 1.7474 - val_accuracy: 0.6518
      Epoch 2/5
      439/439 [==============================] - 133s 302ms/step - loss: 0.6169 - accuracy: 0.7706 - val_loss: 1.5191 - val_accuracy: 0.6871
      Epoch 3/5
      439/439 [==============================] - 127s 288ms/step - loss: 0.5607 - accuracy: 0.7880 - val_loss: 1.4198 - val_accuracy: 0.6984
      Epoch 4/5
      439/439 [==============================] - 123s 280ms/step - loss: 0.5167 - accuracy: 0.8040 - val_loss: 1.4489 - val_accuracy: 0.7177
      Epoch 5/5
      439/439 [==============================] - 123s 280ms/step - loss: 0.4784 - accuracy: 0.8245 - val_loss: 1.4988 - val_accuracy: 0.7157

[21]: # Find the maximum number of images in any single class (target count for balancing)
      class_counts = {class_name: len(os.listdir(os.path.join(train_path, class_name))) for class_name in class_dirs}
      target_count = max(class_counts.values())
      class_counts

[21]: {'akiec': 229,
       'bcc': 360,
       'bkl': 769,
       'df': 81,
       'mel': 779,
       'nv': 4693,
       'vasc': 99}

[18]: class_dirs = ['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']
```

Appendix 2.5 Data Augmentation



OverSampling

[57]:
```
import os
import numpy as np
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.preprocessing import image

# Define paths
base_path = "input/Dataset"
train_path = os.path.join(base_path, "train")
valid_path = os.path.join(base_path, "validation")
test_path = os.path.join(base_path, "test")
class_dirs = ['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']

# Create a directory for saving augmented images
augmented_train_path = os.path.join(base_path, "augmented_train")
if not os.path.exists(augmented_train_path):
    os.makedirs(augmented_train_path)

# Function to save augmented images to disk
def save_augmented_data(datagen, class_name, target_count, batch_size=16, target_size=(224, 224)):
    class_path = os.path.join(train_path, class_name)
    save_to_dir = os.path.join(augmented_train_path, class_name)
    if not os.path.exists(save_to_dir):
        os.makedirs(save_to_dir)

    generator = datagen.flow_from_directory(
        directory=train_path,
        target_size=target_size,
        batch_size=batch_size,
        classes=[class_name],
        class_mode='categorical',
        shuffle=True,
        save_to_dir=save_to_dir,  # Save augmented images to this directory
        save_prefix="aug",  # Prefix for filenames
        save_format="jpeg"  # Format to save images
    )

    # Collect augmented images until target count is reached
    images_collected = 0
    while images_collected < target_count:
        x, _ = next(generator)
        images_collected += x.shape[0]

# Initialize ImageDataGenerator for augmentation
datagen = ImageDataGenerator(
    rotation_range=20,
    width_shift_range=0.1,
    height_shift_range=0.1,
    shear_range=0.1,
    zoom_range=0.1,
    horizontal_flip=True,
    fill_mode='nearest'
)
```

```
Class Counts: {'akiec': 229, 'bcc': 360, 'bkl': 769, 'df': 81, 'mel': 779, 'nv': 4693, 'vasc': 99}
Target Count: 4693
Found 229 images belonging to 1 classes.
Found 360 images belonging to 1 classes.
Found 769 images belonging to 1 classes.
Found 81 images belonging to 1 classes.
Found 779 images belonging to 1 classes.
Found 4693 images belonging to 1 classes.
Found 99 images belonging to 1 classes.
Augmentation completed and saved to disk.
```

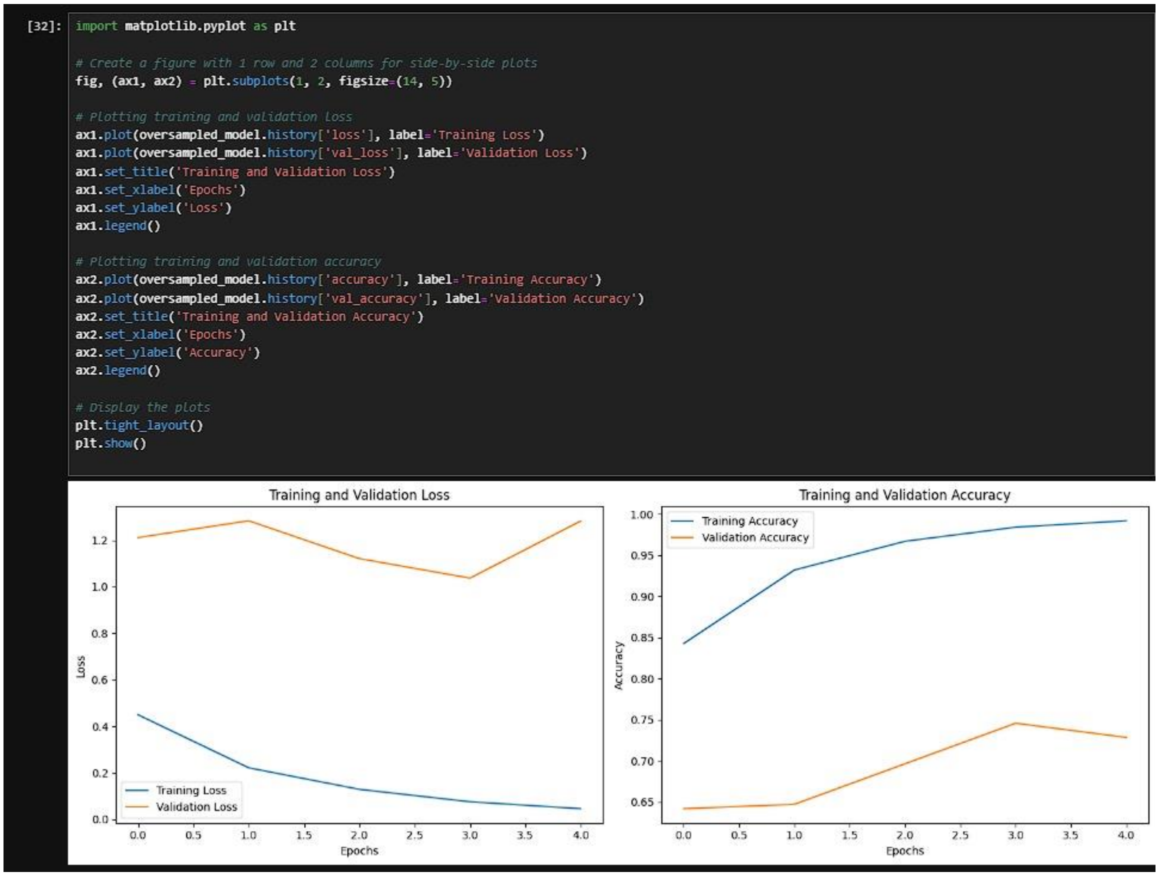
[9]:
```
augmented_path = "input/Dataset/augmented_train/"
augmented_batches = ImageDataGenerator(preprocessing_function=tf.keras.applications.vgg16.preprocess_input).flow_from_directory(
    directory=augmented_path,
    target_size=(224, 224),  # Changed to 224x224
    classes=['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc'],
    batch_size=16
)
```

```
Found 32895 images belonging to 7 classes.
```

[13]:
```
oversampled_model = model.fit(
    augmented_batches,
    validation_data=valid_batches,
    epochs=5,
    callbacks=callbacks
)
```

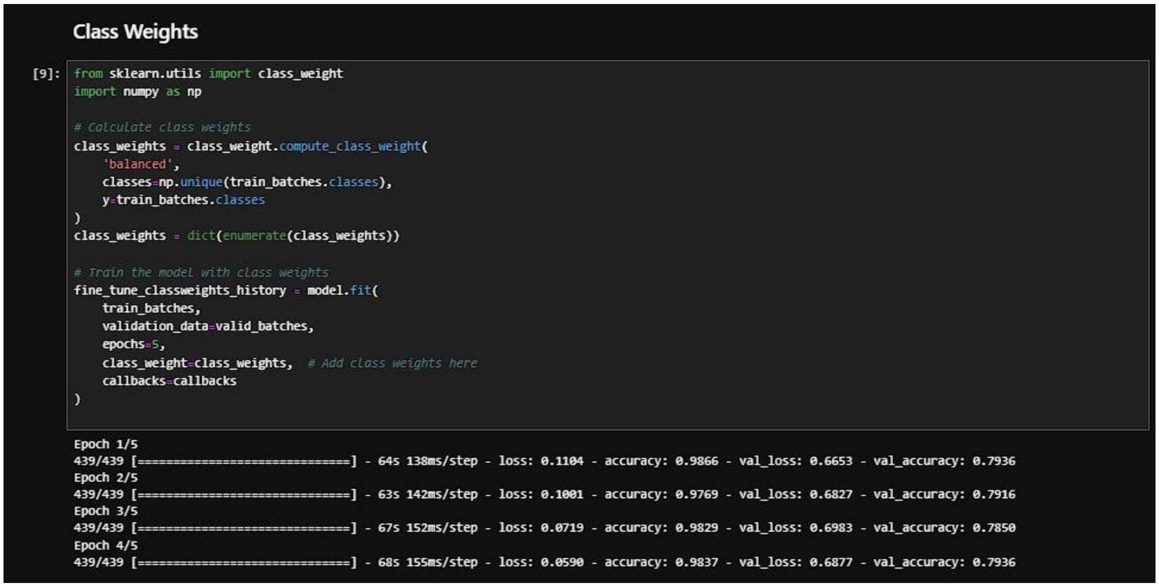
```
Epoch 1/5
2056/2056 [==============================] - 335s 163ms/step - loss: 0.4494 - accuracy: 0.8425 - val_loss: 1.2112 - val_accuracy: 0.6418
Epoch 2/5
2056/2056 [==============================] - 167s 81ms/step - loss: 0.2215 - accuracy: 0.9318 - val_loss: 1.2836 - val_accuracy: 0.6471
Epoch 3/5
2056/2056 [==============================] - 169s 82ms/step - loss: 0.1289 - accuracy: 0.9668 - val_loss: 1.1208 - val_accuracy: 0.6964
Epoch 4/5
2056/2056 [==============================] - 173s 84ms/step - loss: 0.0755 - accuracy: 0.9839 - val_loss: 1.0369 - val_accuracy: 0.7457
Epoch 5/5
2056/2056 [==============================] - 172s 84ms/step - loss: 0.0457 - accuracy: 0.9917 - val_loss: 1.2825 - val_accuracy: 0.7284
```

Appendix 2.6 OverSampling



```
[32]: import matplotlib.pyplot as plt

      # Create a figure with 1 row and 2 columns for side-by-side plots
      fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 5))

      # Plotting training and validation loss
      ax1.plot(oversampled_model.history['loss'], label='Training Loss')
      ax1.plot(oversampled_model.history['val_loss'], label='Validation Loss')
      ax1.set_title('Training and Validation Loss')
      ax1.set_xlabel('Epochs')
      ax1.set_ylabel('Loss')
      ax1.legend()

      # Plotting training and validation accuracy
      ax2.plot(oversampled_model.history['accuracy'], label='Training Accuracy')
      ax2.plot(oversampled_model.history['val_accuracy'], label='Validation Accuracy')
      ax2.set_title('Training and Validation Accuracy')
      ax2.set_xlabel('Epochs')
      ax2.set_ylabel('Accuracy')
      ax2.legend()

      # Display the plots
      plt.tight_layout()
      plt.show()
```

Appendix 2.7 OverSampling Result

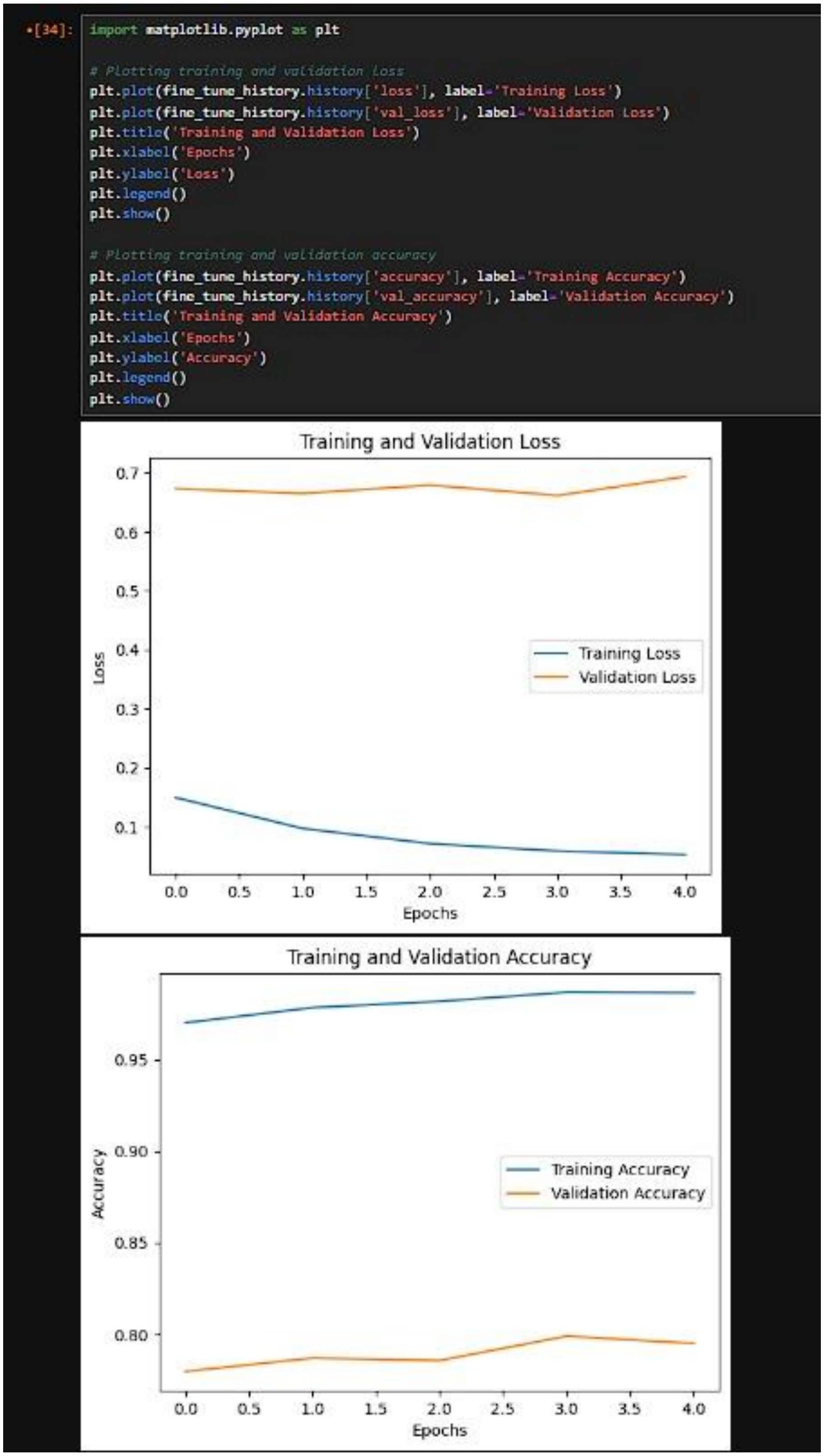


Class Weights

```
[9]: from sklearn.utils import class_weight
     import numpy as np

     # Calculate class weights
     class_weights = class_weight.compute_class_weight(
         'balanced',
         classes=np.unique(train_batches.classes),
         y=train_batches.classes
     )
     class_weights = dict(enumerate(class_weights))

     # Train the model with class weights
     fine_tune_classweights_history = model.fit(
         train_batches,
         validation_data=valid_batches,
         epochs=5,
         class_weight=class_weights,  # Add class weights here
         callbacks=callbacks
     )
```

```
Epoch 1/5
439/439 [==============================] - 64s 138ms/step - loss: 0.1104 - accuracy: 0.9866 - val_loss: 0.6653 - val_accuracy: 0.7936
Epoch 2/5
439/439 [==============================] - 63s 142ms/step - loss: 0.1001 - accuracy: 0.9769 - val_loss: 0.6827 - val_accuracy: 0.7916
Epoch 3/5
439/439 [==============================] - 67s 152ms/step - loss: 0.0719 - accuracy: 0.9829 - val_loss: 0.6983 - val_accuracy: 0.7850
Epoch 4/5
439/439 [==============================] - 68s 155ms/step - loss: 0.0590 - accuracy: 0.9837 - val_loss: 0.6877 - val_accuracy: 0.7936
```

Appendix 2.8 Class Weights



```
import matplotlib.pyplot as plt

# Plotting training and validation loss
plt.plot(fine_tune_history.history['loss'], label='Training Loss')
plt.plot(fine_tune_history.history['val_loss'], label='Validation Loss')
plt.title('Training and Validation Loss')
plt.xlabel('Epochs')
plt.ylabel('Loss')
plt.legend()
plt.show()

# Plotting training and validation accuracy
plt.plot(fine_tune_history.history['accuracy'], label='Training Accuracy')
plt.plot(fine_tune_history.history['val_accuracy'], label='Validation Accuracy')
plt.title('Training and Validation Accuracy')
plt.xlabel('Epochs')
plt.ylabel('Accuracy')
plt.legend()
plt.show()
```

Appendix 2.9 Class Weights Result