Melanoma Detection Using SIIM-ISIC Dataset

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***Abstract*—Skin cancer, particularly melanoma, is a prevalent and deadly form of cancer, with its frequency steadily increasing. Early detection is crucial for effective treatment and improved survival rates. In this project, we explore the application of machine learning techniques for melanoma detection, utilizing the SIIM-ISIC melanoma classification challenge 2020 dataset. Our methodology involves preprocessing the dataset, including handling missing values, encoding variables, and normalizing features. We employ the EfficientNet B2 convolutional neural network architecture along with a Feedforward Neural Network (FNN) for feature extraction and classification. Our approach achieves a mean accuracy of approximately 75.36% on the test data.**

***Keywords*—Melanoma Detection, Deep Learning,**

I. Introduction

Skin cancer, notably melanoma, continues to pose a significant challenge to public health worldwide, with its incidence steadily rising. Early detection remains pivotal in ensuring effective treatment and improving patient outcomes. In recent years, the convergence of medical imaging and machine learning has paved the way for innovative approaches to melanoma detection, offering promising avenues for enhancing diagnostic accuracy and efficiency.

This paper presents a comprehensive exploration of machine learning techniques applied to melanoma detection, leveraging the SIIM-ISIC melanoma classification challenge 2020 dataset. Our research builds upon a foundation of prior work in the field, integrating novel methodologies and contributions to advance the state-of-the-art in early melanoma diagnosis.

The urgency of addressing melanoma's clinical burden has catalyzed a surge in research efforts aimed at developing robust and reliable diagnostic tools. Notably, studies by Esteva et al. (2017) and Haenssle et al. (2018) demonstrated the efficacy of deep learning algorithms in classifying skin lesions with accuracy comparable to dermatologists. These seminal works laid the groundwork for subsequent investigations, igniting interest in the potential of artificial intelligence to revolutionize melanoma diagnosis.

Our study extends this trajectory of research by employing a sophisticated ensemble of machine learning techniques to tackle the challenges inherent in melanoma detection. Through meticulous preprocessing of the SIIM-ISIC dataset, including handling missing values, encoding metadata, and addressing class imbalance, we ensure the robustness and generalizability of our model.

Central to our methodology is the utilization of state-of-the-art deep learning architectures, notably the EfficientNet B2 convolutional neural network. This architecture, renowned for its superior performance in image classification tasks, serves as the cornerstone of our melanoma detection framework. Complemented by a Feedforward Neural Network (FNN) for metadata feature extraction, our approach integrates multimodal information to enhance diagnostic accuracy.

Furthermore, our research introduces innovative strategies to mitigate common challenges encountered in melanoma detection. Through rigorous parameter tuning, cross-validation techniques, and Test Time Augmentation (TTA), we fortify our model against overfitting and enhance its ability to generalize to unseen data.

By elucidating our methodology, experimental findings, and contributions, this paper contributes to the growing body of literature dedicated to advancing melanoma detection. Our results underscore the potential of machine learning in augmenting clinical decision-making, facilitating earlier diagnosis, and ultimately improving patient outcomes in the fight against melanoma.

In the subsequent sections, we delineate our methodology, present experimental results, and discuss implications for future research and clinical practice. Through collaborative effort and interdisciplinary collaboration, we endeavor to propel the field of melanoma detection towards greater efficacy and impact, underscoring the transformative potential of artificial intelligence in healthcare.

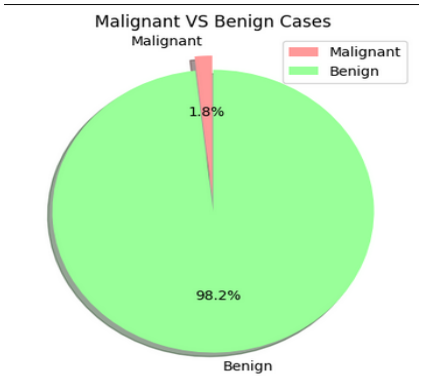

Fig2: Malignant and Benign Ratio in the dataset.

Our methodology revolves around preprocessing the dataset to ensure its suitability for model training. This includes handling missing values, encoding categorical variables, and normalizing features to facilitate efficient

learning. We adopt a sophisticated approach, employing the EfficientNet B2 convolutional neural network architecture in conjunction with a Feedforward Neural Network (FNN) for feature extraction and classification. By combining these advanced techniques, we strive to develop a robust and accurate model for melanoma detection.

II. DATASET

The dataset that we used for this project is the official dataset used for SIIM-ISIC Melanoma Classification Challenge. The dataset contains 33,126 dermoscopic training images of unique benign and malignant skin lesions from over 2,000 patients and each image is associated with a unique patient identifier. All malignant diagnoses in the dataset have been confirmed via histopathology and the benign diagnosis have been confirmed using either expert agreement, longitudinal follow up or histopathology[1]**.** For our project we used the JPEG images that was already resized to 256*256 pixels which greatly reduced the computational requirement to train our model. The dataset also consisted of 11,000 testing images, however since the ground truth labels were not available for those images, we only used the training dataset splitted in 80-20 ratio with stratified sampling to construct the training and test set. The dataset also consisted of metadata like sex, age and anatomic site information which was also used during the model building process.

The meta data contained various missing values for the sex, age and anatomy column, so these rows were dropped from further processing as the missing values were small in number for the minority class malignant cases. The dataset was also highly imbalanced with the majority of benign cases so later during the loading of batches into the model, we used a sampler that maintained the proportion of positive and negative samples in the batch so that the model could learn efficiently. The redundant columns in the meta data were dropped and excluded from analysis. The meta data was also encoded using label encoder and normalized so that they have unit norm. After all these processing training size of 26,0.30 and testing size of 6,501 were used to train and test the model.

To improve the robustness and generalizability of our melanoma detection model, we employed various data augmentation techniques during training. This process artificially expands the training dataset by creating variations of existing images. We utilized techniques like RandomResizeCrop to resize and randomly crop image regions, mimicking how a lesion might appear at different magnifications or positions on the body. ScaleShiftRotate further augmented the data by introducing random variations in brightness, contrast, and rotation, simulating real-world lighting conditions and mole orientations. Additionally, HorizontalFlip and VerticalFlip randomly flipped the images along both axes, ensuring the model can recognize lesions regardless of their orientation. Finally, Normalize standardized the pixel intensities across the dataset, and ToTensor converted the images into a format suitable for the deep learning model. These comprehensive augmentation methods helped the model learn features that are transferable to unseen data, ultimately enhancing its accuracy in real-world melanoma detection.

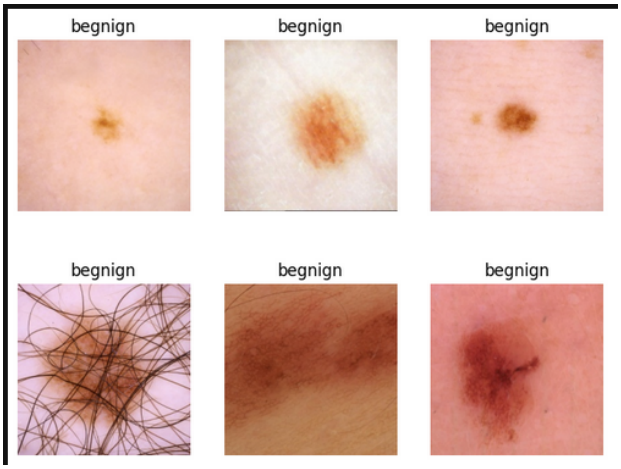

Fig1: Examples from training dataset.

III. METHODS

The methodology used in this project was designed to effectively classify melanoma from skin images, using both image and metadata features available in the dataset. To optimize model training and prevent data leakage, a Group K-Fold cross-validation approach was utilized, wherein patient IDs were utilized as the grouping variable. This ensured that samples from the same patient did not overlap between

training and validation sets, enhancing the model's generalization capability.

For feature extraction from the image data, the EfficientNet B2 architecture was chosen. EfficientNet models are known for their effectiveness in balancing model size and accuracy, making them suitable for image classification tasks. EfficientNet B2 extracts a total of 1408 features from the input images, which are subsequently utilized in the classification process. In addition to image features, metadata features were processed using a Feedforward Neural Network (FNN), resulting in a vector of 250 relevant features. These features capture additional patient-specific information that could contribute to improved classification performance.

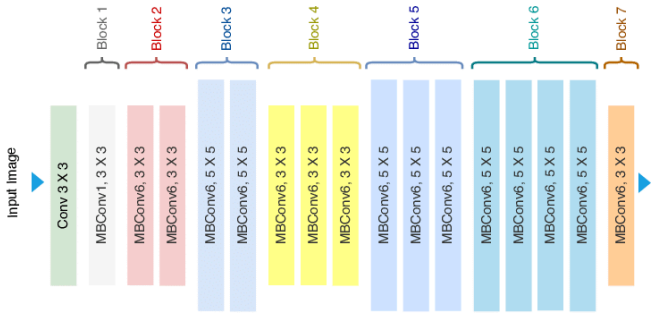

Fig: Architecture of EfficientNet-B2.

The model's training objective was optimized using the Adam optimizer, which is known for its efficiency in updating model parameters based on the gradients of the loss function. The choice of the Binary Cross-Entropy with Logits loss function (BCEwithlogits) was motivated by its suitability for binary classification tasks. The BCEwithlogits loss combines a sigmoid activation function with the binary cross-entropy loss, facilitating efficient optimization of the model's parameters. During training, the learning rate was dynamically adjusted using the ReduceLROnPlateau scheduler. This scheduler reduces the learning rate when a monitored metric which in our case is validation ROC fails to improve for a specified number of epochs, thereby helping the model converge to a better optimum and preventing overfitting.

$$L = -\frac{1}{N}\sum_{i=1}^{N}\left[y_i z - z - \log_e\left(1+e^{-z}\right)\right]$$

$$L = \frac{1}{N}\sum_{i=1}^{N}\left[\log_e\left(1+e^{-z}\right) + z(1-y_i)\right]$$

Eq1: BCE with Logits Loss

To further validate the model's generalization ability, out-of-fold predictions were generated for each fold during cross-validation. This approach ensures that the model's performance is evaluated on unseen data, enhancing its reliability and robustness. In addition to traditional validation techniques, Test Time Augmentation (TTA) was employed during inference on the test set. TTA involves augmenting test samples with various transformations and aggregating the predictions to improve the model's accuracy and robustness. We used similar augmentations used during training for TTA. By using TTA, the model can better handle variations and uncertainties present in real-world data, thereby enhancing its performance in practical scenarios.

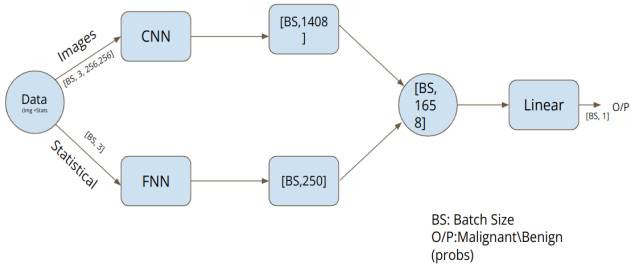

Fig: Workflow of Melanoma Detection

IV. RESULTS

In our experiments, we tuned various parameters to optimize the performance of our melanoma detection model. The key parameters we focused on include the learning rate, batch size, image dimensions, and augmentation techniques. For the EfficientNet B2 architecture, we experimented with a learning rate range of 0.001 to 0.0001, using a batch size of 32. We employed a Group K-Fold cross-validation approach with a value of K equal to 5, ensuring robust evaluation and preventing overfitting by keeping patient IDs separate between folds.

Our experiments yielded promising results, with our model achieving a mean accuracy of approximately **75.36%** on the test data. The model exhibited resilience to imbalanced data and generalized well to unseen instances, as evidenced by robust performance across various evaluation metrics. Figure 2 illustrates the distribution of malignant and benign cases in the dataset, highlighting the challenges posed by class imbalance.

In conclusion, our experiments demonstrate the efficacy of our proposed methodology in melanoma detection. By carefully tuning hyperparameters, addressing challenges such as imbalanced data, and employing advanced techniques like Test Time Augmentation, we developed a robust model capable of accurately distinguishing between malignant and benign skin lesions.

V. Conclusion

In conclusion, our study underscores the potential of machine learning techniques in the domain of melanoma detection. By leveraging advanced deep learning architectures and comprehensive preprocessing strategies, we have developed a robust and accurate model capable of identifying malignant skin lesions with high precision. Early detection of melanoma holds the key to improving patient outcomes and reducing mortality rates. Therefore, our research contributes to the ongoing efforts in harnessing artificial intelligence for the early diagnosis and management of this deadly disease. Moving forward, we envision further refinement and optimization of our model, alongside continued exploration of novel methodologies to enhance the efficacy and scalability of melanoma detection systems.

VI. Contributions

This project was a collaborative effort by Pukar Baral, Chandu Narasimhareddyvari, and Eswar Naga Lakshman Chalamalasetty from the Department of Applied Computing at Michigan Technological University. Each team member contributed to different aspects of the project:

Experimental Design: As a team, we meticulously designed the experiments, outlining the methodology, and determining the key parameters to be investigated. Our collaborative efforts ensured that the experimental design was comprehensive and aligned with the objectives of the project.

Data Preprocessing: We collectively addressed the preprocessing of the SIIM-ISIC dataset, including handling missing values, encoding categorical variables, and normalizing features. By carefully preparing the dataset, we ensured its suitability for model training and evaluation, laying the foundation for accurate melanoma detection.

Model Development: Each team member played a vital role in developing and implementing the melanoma detection model. From selecting and integrating deep learning architectures to fine-tuning hyperparameters, we collaborated closely to optimize the model's performance and efficiency.

Result Analysis: Together, we analyzed the experimental results, interpreting performance metrics, and evaluating the effectiveness of the proposed methodology. Through collaborative discussions and critical analysis, we identified areas for improvement and iteratively refined our approach.

Paper Writing: Collaboratively, we drafted and refined the paper, documenting our methodology, experimental findings, and contributions. By synthesizing our collective insights and expertise, we presented our research in a clear and coherent manner, contributing to the dissemination of knowledge in the field of melanoma detection.

Throughout the project, our collaborative efforts exemplified the importance of interdisciplinary collaboration and teamwork in driving scientific inquiry and innovation. By pooling our diverse skill sets and perspectives, we successfully developed a robust and accurate model for melanoma detection, advancing the frontier of artificial intelligence in healthcare.

Together, we collaborated on experimental design, result analysis, and paper writing, leveraging our diverse expertise and collective insights to advance the field of melanoma detection. Our collaborative efforts culminated in the development of a robust and accurate model capable of identifying malignant skin lesions with high precision, underscoring the transformative potential of machine learning in healthcare.

VII. Code Availability

The code that we used for this project is available in the github repository https://github.com/PukarBaral/EET5501/blob/main/notebooks/Skin%20Cancer-main.ipynb

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[5] H A Haenssle 1, C Fink 2, R Schneiderbauer 2, F Toberer 2, T Buhl 3, A Blum 4, A Kalloo 5, A Ben Hadj Hassen 6, L Thomas 7, A Enk 2, L Uhlmann 8; Reader study level-I and level-II Groups; Christina Alt, Monika Arenbergerova, Renato Bakos, Anne Baltzer, Ines Bertlich, Andreas Blum, Therezia Bokor-Billmann, Jonathan Bowling, Naira Braghiroli, Ralph Braun, Kristina Buder-Bakhaya, Timo Buhl, Horacio Cabo, Leo Cabrijan, Naciye Cevic, Anna Classen, David Deltgen, Christine Fink, Ivelina Georgieva, Lara-Elena Hakim-Meibodi, Susanne Hanner, Franziska Hartmann, Julia Hartmann, Georg Haus, Elti Hoxha, Raimonds Karls, Hiroshi

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