

Detection and Diagnosis of Melanoma using Computer Vision

Objective

The objective of the project is to accurately identify melanoma, from a dataset of images of a person's skin lesions. The datasets contain several images of the same patient, but also several different patients, with different skin textures, skin colors and so on. The goal is to identify which of the lesions are benign, and which are malignant. A benign tumor is a tumor that will not invade its surrounding tissue or spread around the body. A malignant tumor, on the other hand, is a tumor that may invade its surrounding tissue and spread to other parts of the body. Using patient-level contextual information may help the development of image analysis tools, which could better support clinical dermatologists.

Motivation

The motivation behind developing a Computer Vision system for Melanoma diagnosis is to improve the accuracy and speed of diagnosis, which has a great potential to save many people's lives. However, diagnosing melanoma can be challenging, even for experienced dermatologists. With the aid of AI, we can leverage the power of Deep Learning and Neural Network algorithms to analyze skin lesion images within the clinical frame of reference and provide an objective and hopefully consistent diagnosis.

Additionally, an AI system for melanoma diagnosis can help address the shortage of dermatologists in many parts of the world, particularly in rural or remote areas, where access to specialized medical care may be limited or inexistent. Computer Vision can also help address the shortage of dermatologists in many parts of the world by providing a scalable and accessible tool for melanoma diagnosis.

Methodology

- Gathering a dataset of images** : The first step was to gather a large enough dataset of skin lesion images that are labeled as either melanoma or non-melanoma. There are several publicly available datasets, such as the ISIC dataset and the HAM10000 dataset, that are available for this purpose. The ISIC Archive contains the largest publicly available collection of quality-controlled dermoscopic images of skin lesions. This archive was used as the dataset for my project, and was screened to achieve the goal.
- Preprocessing the data** : Preprocessing can involve resizing the images, normalizing the pixel values, and augmenting the data by applying random rotations, flips, and other transformations to increase the size of the dataset. All my transformations and augmentations were a part of this process.
- Training the model** : I started with a normal CNN to train the model, and then increased complexity by training with ResNET50 and EffNET to improve the performance of my model. My training set contained 33,126 observations.
- Evaluating the model** : After training the model, I had to evaluate its performance on a held-out test set. This helped give me an estimate of the model's accuracy and helped me identify areas where it may be making mistakes. My testing set contained 10,982 observations. This, along with some improvisations helped me get the best results for the model.

Working of the Project – Block Diagram

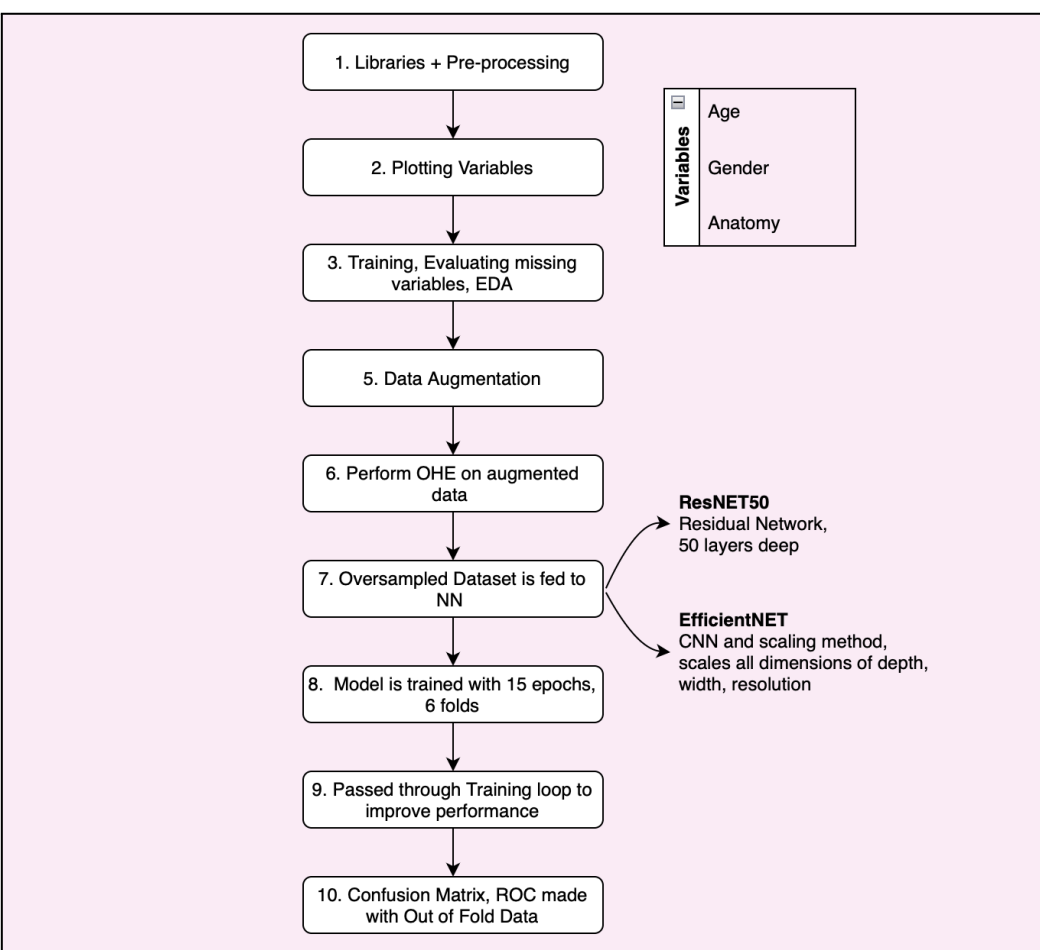


Fig 1 : Block Diagram for the execution of the project

Results and Analysis

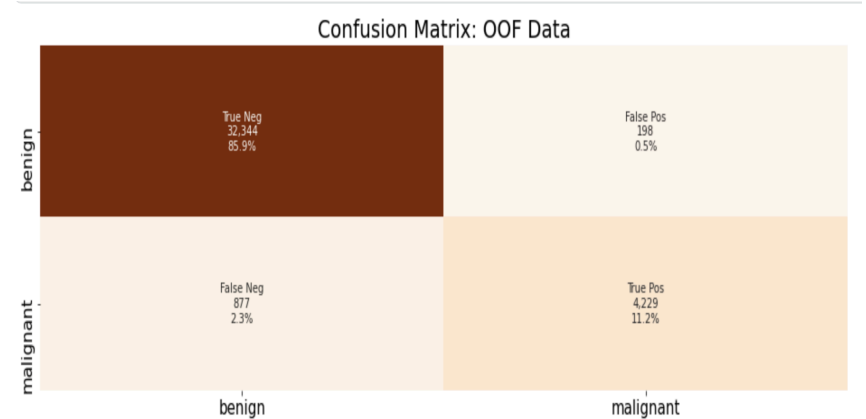


Fig 2 : Confusion Matrix, for Out of Fold data

```
[29]: # Import OOF (pretrained)
oof = pd.read_csv('../input/siim-melanoma-prep-data/oof_v7.csv')

# ROC on full Training data
print('OOF ROC: {:.3f}'.format(roc_auc_score(train_df['target'], oof)))

OOF ROC: 0.976
```

Fig 3 : ROC value to show how efficient model is

The confusion matrix with OOF data shows that the model correctly identified 11.2% of melanomas as malignant (TP) and incorrectly classified 0.5% of benign lesions as malignant (FP). This means that the model has a high precision (ratio of TP to all predicted positives), indicating that it is good at correctly identifying melanomas when they are present, with a relatively low FP rate.

In the context of melanoma detection, this confusion matrix suggests that the model has some limitations, particularly in terms of correctly identifying all cases of melanoma. The relatively high FN rate indicates that the model may miss some melanomas, which could be a serious issue in a medical setting where timely and accurate diagnosis is crucial. However, the high precision and relatively low FP rate suggest that the model is generally reliable when it comes to correctly identifying malignant lesions.

The Out-of-Fold ROC (Receiver Operating Characteristic) is 0.976, this means that the model has a high degree of accuracy in distinguishing between the positive and negative classes in the data. ROC is a curve that shows the relationship between the TP rate and the FP rate for different classification thresholds. An ROC value of 0.5 represents a random model, whereas an ROC value of 1 represents a perfect model.

Conclusion / Summary

The use of deep learning models such as ResNet50 and EfficientNet has allowed me to use feature extraction and classification of skin lesions at a high level of granularity, improving the overall performance of the model. With further refinement and optimization, this model has the potential to serve as a very valuable tool for dermatologists in improving early detection and treatment of melanoma, ultimately leading to improved patient outcomes and survival rates. By using these large datasets and applying various data augmentation techniques to balance class imbalance, the model has been able to achieve a high degree of accuracy in identifying melanoma lesions, while reducing the number of false positives.

References

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