DEEP LEARNING TECHNIQUES FOR MELANOMA CLASSIFICATION

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ABSTRACT

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1 Introduction

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2 Related Work

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3 Background

3.1 Dataset

There are few skin lesion image datasets available to the public which are of adequate size for a machine learning algorithm to train on. There are even fewer datasets specific to melanoma. We considered multiple different datasets, such as:

- HAM10000
- •

The dataset used was the ISIC 2020 Challenge Dataset generated by the International Skin Imaging Collaboration (ISIC) using images from Hospital Clínic de Barcelona, Medical University of Vienna, Memorial Sloan Kettering Cancer Center, Melanoma Institute Australia, The University of Queensland, and the University of Athens Medical School. The ISIC 2020 Challenge Dataset consists of skin lesion images, patient ID, gender, age, anatomical site, and lesion diagnosis. Each image is classified as either benign or malignant melanoma. Examples of various images in the dataset are included in (Fig.1).

3.1.1 Inputting the Dataset

4 Methodology

4.1 Metadata Preprocessing

In order to correct gaps in the data and convert it into an interpretable format, we first remove rows with missing values in the gender column and convert the gender values into binary (0 for female, 1 for male). To correct the age variances in the metadata, we normalized the age to a [0,1] range. Age is normalized by dividing all the ages by the max age,

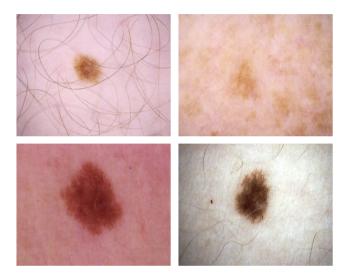


Figure 1: Examples of skin lesion images in the dataset

90. In addition, the anatomical site of the skin lesion is encoded into one hot vector's of either 0 (not the lesion site) or 1 (lesion site). There were seven possible anatomical sites- head/neck, lower extremity, oral/genital, palms/soles, torso, upper extremity, and NaN. In total, we created a feature vector of size nine with the characteristics of gender, age, and anatomical site. For example, the feature vector of [1, 0.277777777777778, 0, 0, 0, 0, 1, 0, 0] represents an approximate 25 year old male with a skin lesion on the torso.

There is a massive data imbalance between the number of benign and malignant images. The original dataset contains 32542 benign images and 584 malignant images, so approximately 82.4% of the data is benign. To combat the data imbalance, we take a sample of size 1461 from the benign images. We then split this data into a train set and a validation set, with 291 malignant and 194 benign images in the validation. For the train set, we started out with 1170 malignant images and 390 benign photos. However, by performing hair image augmentation twice, we were able to triple the number of malignant images in the train set, bringing us to an even 1170 benign and 1170 malignant images. While augmenting each malignant image, we needed to ensure that the feature vector for the image was also kept with the newly augmented image. We handled this by adding a separate column in the feature vector csv file to distinguish augmented from non-augmented images (0 represented non-augmented images and 1 or 2 represented augmented).

	Missing Values	% of Total Values
anatom_site_general_challenge	527	1.6
age_approx	68	0.2
sex	65	0.2

Figure 2: Missing Values of the Dataset

4.2 Image Augmentation

The malignant images are augmented to increase image diversity and to decrease the data imbalance between benign and malignant images. However, when dealing with medical images the safety of image augmentation must be taken into account[1]. For example, using methods that change the color pigmentation of the images will endanger the image's target label; an image previously classified as melanoma transformed by color pigmentation might give out a false positive. Therefore, the melanoma images are augmented using a safe form of image augmentation, and augmentation methods such as transformations are avoided to avoid risking the label's integrity.

• Hair Augmentation: The melanoma images are augmented by concatenating melanoma images with predefined hair strand images (Fig. 3). The size/width of each hair strand is randomly resized, the number of hairs being added to each augmented image is randomly chosen, and the position of the hairs onto the skin lesion are randomly placed. This approach increases the diversity of the dataset while being safe, thus resulting in higher accuracy and reduced overfitting.

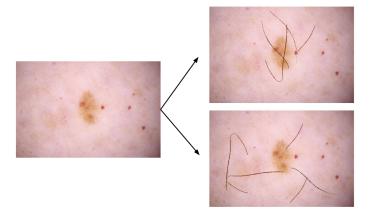


Figure 3: Malignant Image Hair Augmentation

4.3 Model

We implemented two models, one where we predicted melanoma classification based only on the images, and a second where we created a multimodal model by combining the images and the image's metadata. A structure of the model used when only images were inputted is given below.

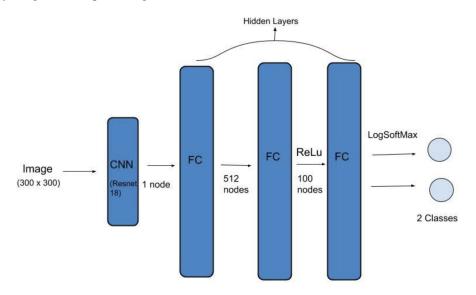


Figure 4: CNN only

The loss function used for the images only CNN model was Cross Entropy Loss, and is given by

$$-(y\log(p) + (1-y)\log(1-p)). (1)$$

Our loss function for the multimodal model was a Binary Cross Entropy with Logits Loss, which combines the Sigmoid layer and the Binary Cross Entropy loss. This method of combining the Sigmoid layer and the BCE loss into one layer is much more numerically stable than separating the Sigmoid and BCE loss into separate layers. The loss function was defined as

$$\ell(x,y) = L = \{l_1, l_2, ..., l_N\}^{\top},\tag{2}$$

$$l_n = -w_n[y_n \cdot \log \sigma(x_n) + (1 - y_n) \cdot \log(1 - \sigma(x_n))]$$
(3)

where N is the batch size. The log sum exp trick can be advantageously used for this loss function to provide numerical stability.

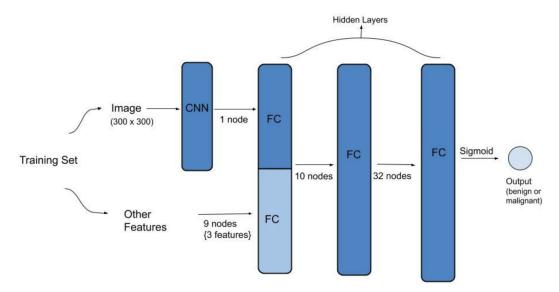


Figure 5: CNN with additional features

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5 Results

6 Conclusion

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7 Division of Labor

We divided the work as follows:

- Inputting the Dataset Minnie Liang and Isabelle Hu
- Preprocessing the Dataset Preeti Gomathinayagam and Mohammad Masoud
- Modeling
- Performance Metric
- Visualizations
- Saliency Maps/GradCAMs

8 Acknowledgements

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References

[1] Connor Shorten and Taghi M Khoshgoftaar. A survey on image data augmentation for deep learning. *Journal of Big Data*, 6(1):60, 2019.