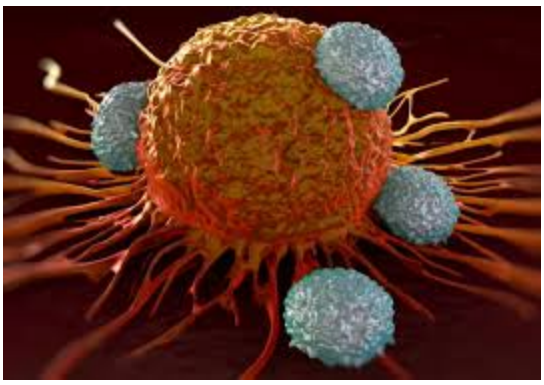
OPEN SOURCE TECHNOLOGY

Project link :

https://github.com/arunroxx33/Skin-Cancer-App

Skin Cancer Classification (Malign or Benign) Using Transfer Learning



- Arun Kumar
(2017UCO1603)

Abstract

As specified by the World Health Organization, the occurrence of Skin Cancer has been growing over the past decades. At present, **2-3 million non-melanoma skin** cancers and **132,000 melanoma skin cancers** arise worldwide annually. The **detection** and classification of skin cancer in the **early stage** of development allow patients to have **proper diagnosis** and **treatment**. Similar to other cancers, skin cancers **initiate** as **non-cancerous lesions**. These lesions are modifications in the skin that are **not cancerous** but could **convert** to **cancer** over time.

Artificial intelligence and cancer diagnosis are gaining attention as a way to define better diagnostic tools.

An **automated** framework would be **helpful** for doctors and patients to **identify** the type of Skin **Cancer** using lesion images.

Introduction

Cancer is the **leading cause** of **deaths** worldwide. Both researchers and doctors are facing the challenges of fighting cancer According to the American cancer society, **96,480 deaths** are expected due to **skin** cancer, **142,67**0 from **lung** cancer, **42,260** from **breast** cancer, **31,620** from **prostate** cancer, and **17,760** deaths from **brain** cancer in 2019 (American Cancer Society, new cancer release report 2019). **Early detection** of **cancer** is the top **priority** for **saving** the **lives** of many. Typically, **visual examination** and manual **techniques** are used for these types of cancer **diagnosis**. This manual **interpretation** of medical **images** demands high **time** consumption and is highly **prone** to **mistakes**.

Similar to other cancers, **Skin** Cancers initiate as **non-cancerous lesions**. These lesions are **modifications** in the **skin** that are **not cancerous** but could **convert** to **cancer** over time.
There can be two types of skin lesions: **Benign** and **Malignant**.

In order to reduce **computational complexity** and achieve **higher accuracy**, the theory of **transfer learning** has been introduced which enhances the performance of individual **pre-trained CNN architectures**.

Dataset

Dataset provided by the ISIC(**International Standard Industrial Classification**) challenge 2019 hosted on **Kaggle**, has been used for **testing** and **training**.

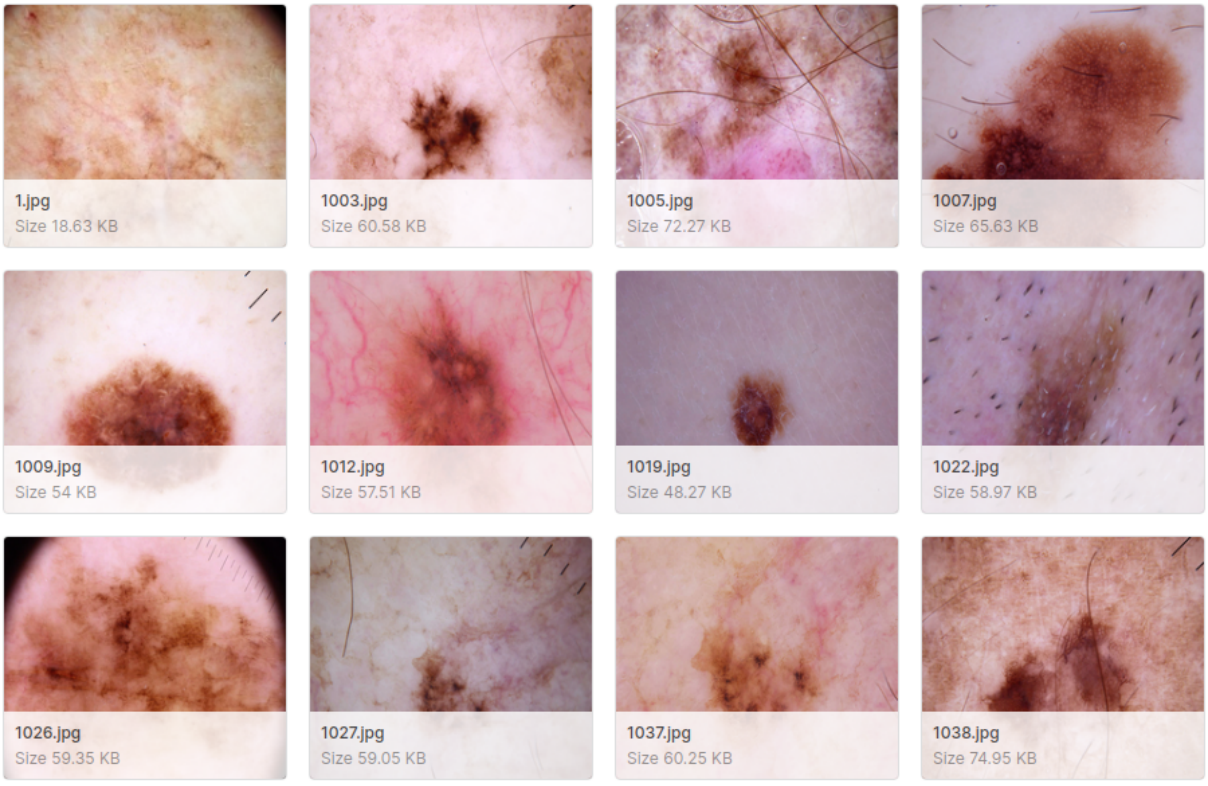
This dataset contains a **balanced** dataset of **images** of **benign** skin moles and **malignant** skin **moles**.
The data consists of two folders with every **1800 pictures (224x244)** of the two types of moles.

The lesion is chosen as Malign lesion if the prediction value is less than 0.5 otherwise the lesion is chosen as Benign lesion.

The dataset is made available as a Kaggle dataset and therefore the **dataset** is chosen **precisely** by Kaggle.
The **best** set of **lesions** is **picked** to add a certain amount of **noise** in the dataset.

Benign Lesions

Malign Lesions



Related Work

2015 (First Time)

Sumithra R.[5] proposed an image processing based method to segment and classify different skin lesions.
Maximum Classification Accuracy of 61%.

2017

D. B. Mendes and Nilton Correia da Silva[6] used a pre-trained deep learning architecture ResNet-152 to classify 12
different kinds of skin lesions
1. AUC for Melanoma - 97%
2. AUC for BCC - 96%
3. DrawBack: Due to the large ResNet - 152 model the training time was huge.

2018

Muhammad Nasir et al.[8] used feature selection based method to classify the skin lesions
using SVM on PH2 dataset.
1. Accuracy : 97.5%.
2. Drawback: PH2 dataset is small and thus SVM might have produced a wrong separation line for different classes.

2019

Sameena Pathan et al.[11] proposed an ensemble technique to classify and detect
malignant skin lesions.
1. Accuracy: 97% on PH2 dataset.

Methodology

The pre-trained **CNN architectures** like **InceptionV3**, **VGG19** and **VGG16** are used for extraction of low-level features from the image set.

These features are fed into dense and fully connected softmax layer of the network for classification of different skin cancer cell types.

Now, it’s clear that there is noise in the dataset as the dataset is taken from Kaggle competition. Therefore,
a network should not be overtrained at all as it would give false results and often the results provided would all be useless.

As we can see the images are crystal clear and all the images are (224 x 224) there is no need for any techniques to be applied as to make the images clearer.

Data Augmentation

Techniques like cropping, padding, and horizontal flipping are applied to increase the size of data-set.

Model Architecture

We are using transfer learning-based approaches in deep learning in order to detect the type of Skin Cancer Benign or Malign given the skin lesions. We have employed **Convolutional Neural Networks** [1], a type of **Deep Learning** techniques which involves Convolutional Units, which have proven to be highly **successful** in **image processing** and **computer vision** tasks.

We have tested several Convolutional Network Architecture with weights **pre-trained** on **ImageNet** (ILSVRC) dataset. Hence, making use of **Transfer Learning**, in order to get good results on the dataset. The architectures we will be testing for this datasets are as follows:

- **VGG19**[2]
- **VGG16**[3]
- **InceptionV3**[4]

The best CNN selected from the above given according to the accuracy of predicting the skin lesions accurately was **VGG19** which gave an **accuracy** of **93%** on **train** data and **87%** on **test** data.

This CNN was also connected with the dense layers later With the below structure:

X = L.MaxPool2D()(base_model.output)
X = L.GlobalMaxPool2D()(X)
X = L.Dense(1024, activation='relu')(X)
X = L.Dropout(0.5)(X)
X = L.BatchNormalization()(X)
X = L.Dense(512,activation = 'softmax')(X)
X = L.Dropout(0.3)(X)
X = L.BatchNormalization()(X)
X = L.Dense(256,activation = 'relu')(X)
X = L.BatchNormalization()(X)
X = L.Dense(1, activation='sigmoid')(X)

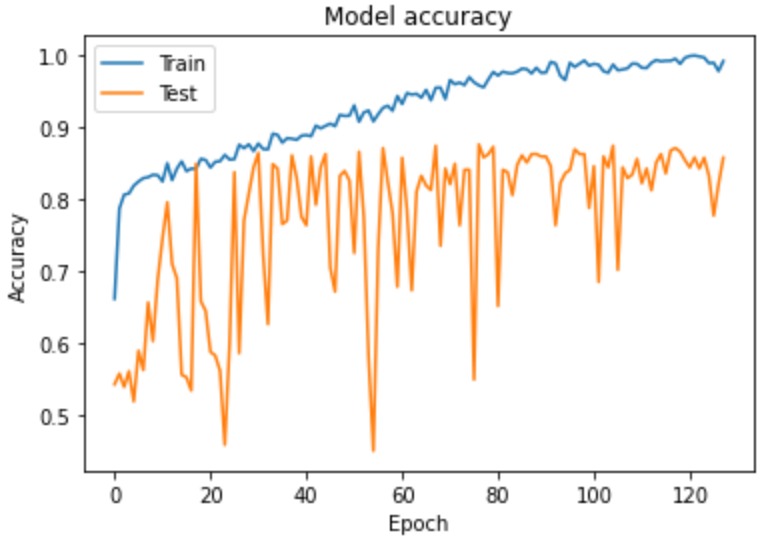
The final architecture consisted of a total of 30 layers.

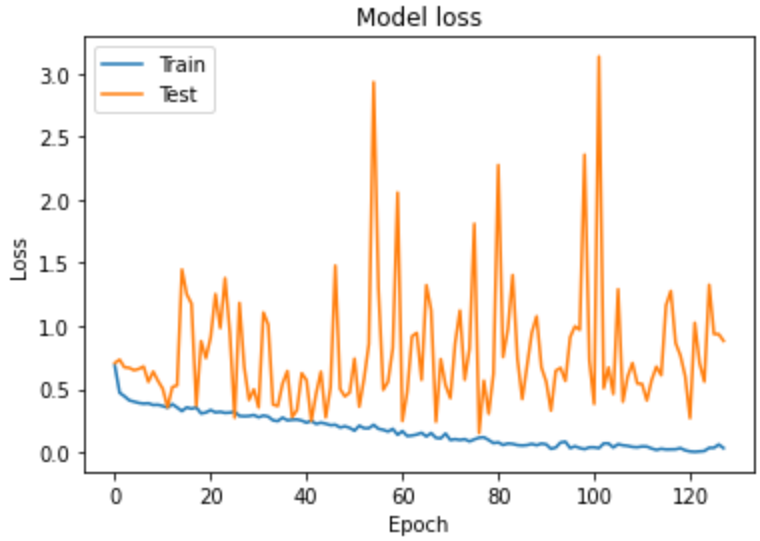
The **loss** function used was **Binary Crossentropy** and the **optimizer** as **adam**. The model was trained for a total of **200 epochs** which took a total of **24 minutes** to train and **ModelCheckpoint** from **Keras** was used to save the **best weights** of the model.

Results

The architecture gave the accuracy of **93%** on **training** data and **87%** on **test** data. The model was trained on the dataset provided by **Kaggle** which was originally from **ISIC** with a total of **1800 images** among which **1200** were used for **training** purpose and the remaining **600** for **testing**. This dataset contained a balanced dataset of images of **benign** skin moles and **malignant** skin moles. The model took **less time** as compared to **other models** to **train** and gave a **decent accuracy**.

The model output results are as shown below :





Future Work

1) Although the model was fast to train still the **accuracy** could be **improved** through a **large dataset** and a **more accurate** model could be built.
2) The model consisted of a CNN but with the coming generation, **artificial intelligence library** (**FastAI**) could be a given a shot too to **achieve** an even **more decent accuracy**.
3) The **Front - End** user **compatibility** could be increased with the latest technologies like **React**, **NodeJS**, etc.

References

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