Bacteria Classification using Image Processing and Deep Learning

A PROJECT REPORT

submitted By

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CERTIFICATE

This is to certify that the report entitled **Bacteria Classification using Image processing and Deep Learning** submitted by **Bronwin C Raj** to the APJ Abdul Kalam Technological University in partial fulfillment of the requirements for the award of the Degree of Master of Computer Applications is a bonafide record of the project work carried out by him under my guidance and supervision. This report in any form has not been submitted to any University or Institute for any purpose.

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ABSTRACT

An automizing process for bacteria recognition becomes attractive to reduce the analyzing time and increase the accuracy of diagnostic process. This research study possibility to use image classification and deep learning method for classify genera of bacteria. We propose the implementation method of bacteria recognition system using Python programing and the Keras API with TensorFlow Machine Learning framework. The implementation results have confirmed that bacteria images from microscope are able to recognize the genus of bacterium. The experimental results compare the deep learning methodology for accuracy in bacteria recognition standard resolution image use case. Proposed method can be applied the high-resolution datasets till standard resolution datasets for prediction bacteria type. However, this first study is limited to only two genera of bacteria.

ACKNOWLEDGEMENT

If words are considered as symbols of approval and tokens of acknowledgment, then let words play the heralding role of expressing my gratitude.

First of all, I would like to thank God for bestowing me with wisdom, courage and perseverance which had helped me to complete this project ***Bacteria classification using Image Processing and Deep Learning***. This project has been a reality as a result of the help given by a large number of personalities.

I would like to thank **Dr. Jiji C V** , Principal, College of Engineering Trivandrum, who helped us during the entire process of work.

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BRONWIN C RAJ

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Chapter 1

Introduction

Bacteria are single celled microbes. The cell structure is simpler than that of other organisms as there is no nucleus or membrane bound organelles. Instead their control centre containing the genetic information is contained in a single loop of DNA. Some bacteria have an extra circle of genetic material called a plasmid. The plasmid often contains genes that give the bacterium some advantage over other bacteria. For example it may contain a gene that makes the bacterium resistant to a certain antibiotic.Bacteria are classified into 5 groups according to their basic shapes: spherical (cocci), rod (bacilli), spiral (spirilla), comma (vibrios) or corkscrew (spirochaetes). They can exist as single cells, in pairs, chains or clusters.

The recognition of various genera and species of bacteria is useful diagnostic process. The classic techniques of bacteria recognition mainly use biological techniques such as gram staining and identify from contained specific metabolism of bacteria. This classical recognition of bacteria species is based on comparative analysis of the obtained samples with referential ones. Consequently, these methods are time-consuming process and require an expert knowledge and experience of worker. Therefore, automatizing the process of bacteria recognition is attractive to reduce the analyzing time and increase the accuracy of worker . The most important features of bacteria that can be recognized on the images is the color of gram stained and the shape of its cell.

The purpose of this research is to study possibility to use image classification and deep learning method for classify bacteria species by distinguish two basic shapes of long-rod and spherical. For this report, we researched to find the methodology to use deep learning to classify the standard resolution bacteria image for further research in mobile application or tablet use case. The aim of this project is to build a system that can classify bacteria through the images from the datasets with image processing using deep learning.

Chapter 2

Literature Review

Image-processing and pattern-recognition techniques combined with various types of classifiers are often used as an effective tools for recognition of the laboratory samples, occurring in the form of images. When taking those methods into consideration, we can state that there are many methods for automatic recognition of bacteria species and strains. There are, among others, statistical methods,the artificial neural networks or other machine learning classifiers .

In an algorithm proposed by Hiremath P.[1] identifies the species of bacteria based on their geometric features: circularity, compactness, eccentricity, tortuosity and length-to-width ratio. Moreover, because the shape of the bacillus is not a discriminant feature (due to the same morphology in different species of bacteria), it takes into consideration their color.

Ferero et al.[2] describes a method for automated recognition of tuberculosis. It is based not only on geometrical features but also on the average color of the images. In their research, authors tackles the issue of the deceptive similarities in bacterial morphology. He shows that the color of microorganisms is the key feature to improve the accuracy of recognition.

The other approach, presented in [3], applies two classifiers to the pre-segmented scanner images. It uses various measurement features to extract size and shape of the microorganisms and classify them into their appropriate morphotype. The first classifier uses single features to analyze relatively simple communities, containing only a few morphotypes (e.g., regular rods, cocci, and filaments). A second classifier is a hierarchical tree which uses an optimized subset of features to analyze significantly more complex communities, containing greater morphological diversity. Those classifiers automatically categorizes each cell into one of 11 predominant bacterial morphotypes, including cocci, spirals, curved rods, U-shaped rods, regular straight rods, unbranched filaments, ellipsoids, clubs, rods with extended prostheca, rudimentary branched rods, and branched filaments.

Ahmed et al.[4] proposes a method of identification and classification of foodborne pathogens, using colony scatter patterns. In the first step, big set of features are extracted, and then the Fisher's criterion is used for dimensionality reduction. In the final step, Support Vector Machine classifier is used. Similar approach, with

Random Forests instead of SVM, is presented in . Moreover, Ates et al. uses similar approaches to count the number of bacteria colonies, using the compactness ratio of the clusters for the particular species of bacteria. The overview paper concerning those methods was written by Sommer et al.

Most of the described methods are used to recognize very few species or strains (sometimes only one, e.g. tuberculosis). Moreover, in many cases the algorithms base on the morphological features combined with some classification method. Therefore, they are very limited.

The approach used in this survey study is much more robust and can be used with any genera and species of bacteria.

Chapter 3

Background

3.1 Problem Definition

Bacteria, which are prokaryotic microorganisms, are the most abundant and simplest organisms in the world as we know it.

Bacteria identification is very important in microbiology and pathology as it serves a basis of understanding diseases. Bacteria classification plays important role in yielding information for disease control. Due to this, various types of methods have been introduced to classify bacteria in microbiology. Bacterial species are usually sub-grouped to different types and is used for many crucial pathogenic bacteria such as Salmonellae, E Coli, and Vibriones.

Traditional techniques of bacterial classification rely on phenotypic identification using gram staining, biochemical process as well as culture methods. However, these techniques of bacterial identification have two major problems. They can be used only for organisms which are cultivated in vitro and show unique biochemical attributes that are not suitable for patterns that have been used as a characteristic of any known groups of microorganism. Real time PCR and microarrays is also among of the most commonly used molecular methods.

One of the most important features that can be recognized on the images is the shape of a bacteria cell. We distinguish three basic shapes: cylindrical, spherical and spiral. However, the process of recognizing bacteria based solely on the shape would be a difficult one because many bacteria share very similar shapes. Second most differentiating feature is the shape and the size of the colonies formed by the bacteria. Some of them live solitary, some live in colonies which are very characteristic in terms of structure and spatial arrangement.

These methods are time-consuming process and require an expert knowledge and experience of worker. Using the traditional method which is hard to extract the features of an image of different bacteria. It is difficult to classify the bacterias from the datasets.

In this project ResNet CNN model is used to classify bacteria.It is a pre-trained model.It extracts all important features of an image and gives better result.It saves time , memory and cost and it performance high accuracy than other models.

3.2 Motivation

- The traditional methods are time-consuming process
- It require an expert knowledge and experience of worker.
- The manual procedures are susceptible to inconsistency and are a tedious and complicated work which needs abundant correlative data.
- These procedures also consume a lot of time and energy and are of great cost.
- The classical laboratory methods of bacteria recognition require an expert knowledge and experience. It is a time-consuming process.
- The traditional methods like gram staining, biochemical process, pattern recognition are gives less accuracy than the CNN model.
- The machine learning methods are SVM , Random Forest, Bayesian theory ,Naive-Bayes Classifier, Decision tree classifier, and other Neural networks are also classify the bacteria .But the deep learning with Convolutional Neural Network (CNN) model perform high accuracy.
- Artificial Neural Network (ANN) loses the spatial feature of an image. The spatial feature refer to the arrangement of the pixels in an image.
- ANN cannot capture sequential information in the input data which is required for dealing with sequence data.
- Recurrent Neural Network (RNN) follows drawback which is vanishing and exploding gradient associated with back propagation algorithm.
- Image classification is the task of classifying a given image into one of the predefined categories. Traditional pipeline for image classification involves two modules: viz. feature extraction and classification. These steps consumes lot of time.

3.3 Objectives and Contribution

- Deep learning is a subset of machine learning in artificial intelligence (AI) that has networks capable of learning unsupervised frThese steps need to

  om data that is unstructured or unlabeled.
- Deep learning with CNN method is used to bacteria classification.

- A Convolutional Neural Network (CNN, or ConvNet) are a special kind of multi-layer neural networks, designed to recognize visual patterns directly from pixel images with minimal preprocessing.
- Residual Neural Network (ResNet) CNN model gives better accuracy than other models. So this ResNet model is used for this classification.
- It is a pre-trained model and easy to implement.
- ResNets were learned with network depth of as large as 152. It is able to train a neural network with 152 layers while still having lower complexity than VGGNet.
- It achieves a top-5 error rate of 3.57percent which beats human-level performance on this dataset.
- It achieves better accuracy than VGGNet and GoogLeNet while being computationally more efficient than VGGNet. ResNet-152 achieves 95.51 top-5 accuracies.
- It resolve the problem of vanishing and exploding problem by skip connections.
- It gives better accuracy than the other CNN model ,Machine learning classifiers and traditional methods.

Chapter 4

Requirement Analysis

4.1 Purpose

As CNNs currently have been shown an impressive performance on recognizing patterns in digital images, it is well-suited to classify bacteria from the datasets. This project aims at optimizing the array of layers in CNN architecture to better learn a classifier to extract high level features of bacteria from datasets.It will determine how high of accuracy and recall that the model can achieve on bacteria classification with CNN ResNet model. In addition to creating a ResNet CNN model, other publicly available CNN model will be applied to the same dataset to evaluate the performance of the proposed model.

4.2 Overall Description

Bacteria classification plays important role in yielding information for disease control. At the moment, dataset is used as a diagnosis tool to accurately classify the bacteria. However,bacteria classification is difficult as it requires extensively trained specialists. As a result, deep learning models such as CNNs are currently deployed for automatic classification from images of dataset. These existing CNN architectures have used different types of convolutional architectures and various techniques for classification with varying classification accuracy. Therefore, the problem being studied in this work is to create a convolutional architecture in such a way that can extract useful features from images for high-accuracy bacteria classification. This study proposes a ResNet model based on deep CNNs to classify bacteria.

4.2.1 Product Functions

The main functions of the proposed product includes:

- Data Collection- Dataset is obtained from kaggle website.
- Data Acquisition- Detrmines which objects will be used as project objects.

- Pre-Processing- Rescale all the images to 32 x 32 pixels for this deep learning network.
- Training Data Process

4.2.2 Operating Environment

The operating environment required are:

- **Hardware Requirements**
  Processor : Intel Core i5
  Memory : 8 GB RAM
- **Software Requirements**
  Libraries used:
  Keras
  Numpy
  Matplotlib
  Tensorflow
  OpenCV
  ResNet
  Scikit-learn

4.3 Functional requirements

Functional requirements represent the intended behavior of the system. This behavior may be expressed as services, tasks or functions that the specified system is required to perform. The following functional requirements have been identified for this project.

The proposed system consists of the following steps:

4.3.1 Data Collection :

For this project it needs collection of cell images which are contains bacteria and absence of bacteria cell images. So that here used two datasets : Training and Tesing dataset and in each dataset contains five classes
Training Dataset - 670 images belonging to two classes.
Testing Dataset - 660 images belonging to five classes.

4.3.2 Image Pre-Processing :

The quality of cell images had to be enhance by filtered to remove unwanted noises. This noises may cause inaccuracies in classification process .The CNN learns the filters automatically without mentioning it explicitly.

4.3.3 Automatic Feature Extraction :

Once the bacteria has been determining, in consequence of colour, texture and shape are related. Therefore, the features are ready to be extracted

4.3.4 Classifier :

Once the features have been obtained, we have had to use CNN classifier for classify images of bacteria.

4.3.5 Prediction :

After building the classifier and training and actual prediction happens.

4.4 Non Functional requirements

Non-Functional requirements define the general qualities of the software product. Non-functional requirement is in effect a constraint placed on the system or the development process.

4.4.1 Performance Requirements

- Classification Accuracy : It is the ratio of number of correct classification to the total number of input samples.
- Speed: The system must be capable of offering speed.

4.4.2 Quality Requirements

- Scalability: The software will meet all of the functional requirements.
- Maintainability: The system should be maintainable. It should keep backups to atone for system failures, and should log its activities periodically.

- Reliability: The acceptable threshold for down-time should be long as possible. i.e.mean time between failures should be large as possible. And if the system is broken, time required to get the system back up again should be minimum.

Chapter 5

Design And Implementation

5.1 Methodology

An automizing process for bacteria recognition becomes attractive to reduce the analyzing time and increase the accuracy of diagnostic process. This project is a Deep Learning application that is used to classify which bacteria is found. CNN consists of one or more convolutional layers followed by one or more fully-connected layers. As CNNs assume that the inputs are images, we can encode certain properties into the architecture. Another advantage of convolutional neural networks over full-connected networks is easiness to train the model. ResNet CNN model is used to classify bacteria from dataset and it gives high accuracy than other models.

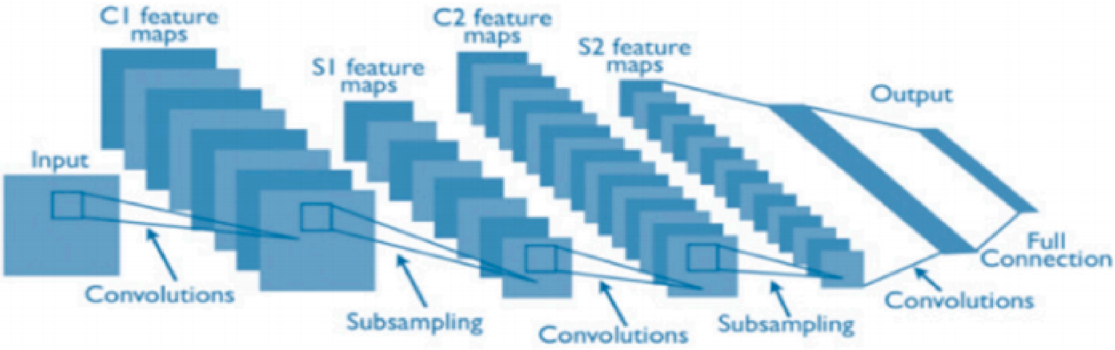

Figure 5.1: A typical CNN architecture

The ResNet CNN model is useful for this classification . CNNs are contained three sorts of layers. These are convolutional layers pooling layers and completely associated layers. At the point when these layers are stacked, a CNN technique has been framed. The working of the CNN model has been categorized into four main functions as given below:

1. Firstly, there is an input layer which is used for holding the pixel values of the image.

2. Then, the convolution layer is there which helps in determining the output of several neurons and these neurons are being connected to the local regions. Then,

the further calculation is being done by scalar product between their weights and with the regions which is connected to the input volume. After this the Rectified Linear Unit (ReLu) is there which has a function of applying an activation function which is done element wise like sigmoid function to the output which is produced by the activation of the previous layer.

3. Then, the pooling layer is there which is used to down sample the spatial dimensionality of the input and then it reduces the vario us parameters and shorten the image s ometimes to its half within that activation.

4. The fully connected layers help in producing the various scores obtained from the activations. The main aim of this layer is that it takes the results from the convolution or pooling layer and then us that result to classify the image into a form of label. After this they pass the obtained result to the output layer, where each neuron will represent a classification label.

5.2 Overall Design

Deep learning is a type of Machine Learning using deep layered structure Convolutional Neural Network (CNN) implemented the ReSNet CNN architecture. It automatically detects the important features without any human supervision. It uses special convolution and pooling operations. And perform parameter sharing,feature learning and weight sharing. ResNet CNN model is a pre-trained model which only train the classifier at the end of the labels. ResNets were learned with network depth of as large as 152. It is able to train a neural network with 152 layers while still having lower complexity than VGGNet. It resolve the problem of vanishing and exploding gradient using skip connections in a Residual block.

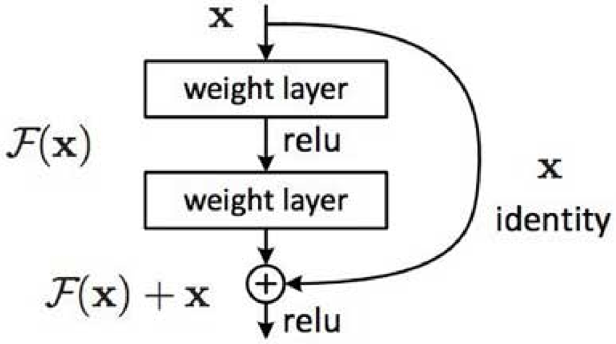
x
weight layer
$\mathcal{F}(\mathbf{x})$
relu
weight layer
x
identity
$\mathcal{F}(\mathbf{x}) + \mathbf{x}$
relu

Figure 5.2: Residual Block

ResNet, short for Residual Networks is a classic neural network used as a backbone for many computer vision tasks. The fundamental breakthrough with ResNet was it allowed us to train extremely deep neural networks with 150+layers successfully. Prior to ResNet training very deep neural networks was difficult due to the problem of vanishing gradients.Deep networks are hard to train because of the notorious vanishing gradient problem — as the gradient is back-propagated to earlier layers, repeated multiplication may make the gradient extremely small. As a result, as the network goes deeper, its performance gets saturated or even starts degrading rapidly.ResNet is a powerful backbone model that is used very frequently in many computer vision tasks ResNet uses skip connection to add the output from an earlier layer to a later layer. This helps it mitigate the vanishing gradient problem.

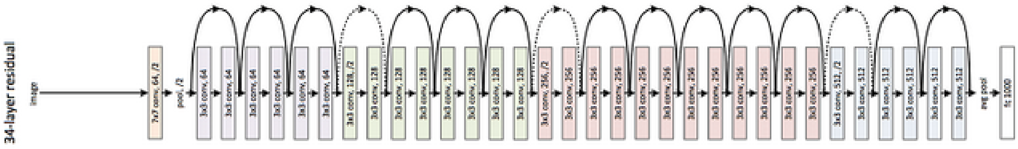

Figure 5.3: A typical ResNet CNN model Architecture

The main operations of the convolutional network layers are folows:

5.2.1 Convolutional layer

Convolution is the first layer to extract features from an input image.It constitute the core building block of the convolutional network . Parameters of convolutional layers are made of learnable filters, which are sometimes referred to as kernels. Every filter consists of a small area of an image, and this area is called a receptive field. The filter extends to a depth that is similar to the full depth of the input volume. Convolution preserves the relationship between pixels by learning image features using small squares of input data. It is a mathematical operation that takes two inputs such as image matrix and a filter or kernel.

5.2.2 Pooling Layer

Generally, a pooling layer is inserted in between successive convolutional layers in convolutional network. It reduces the spatial size of the representation in order to reduce the parameters used in the network.A pooling layer operates independently on every depth slice of the input and resizes it partially using the MAX operation.

5.2.3 Dense Layer

A dense layer represents a matrix vector multiplication. (assuming your batch size is 1) . The values in the matrix are the trainable parameters which get updated during backpropagation. A dense layer thus is used to change the dimensions of your vector. Mathematically speaking, it applies a rotation, scaling, translation transform to your vector.

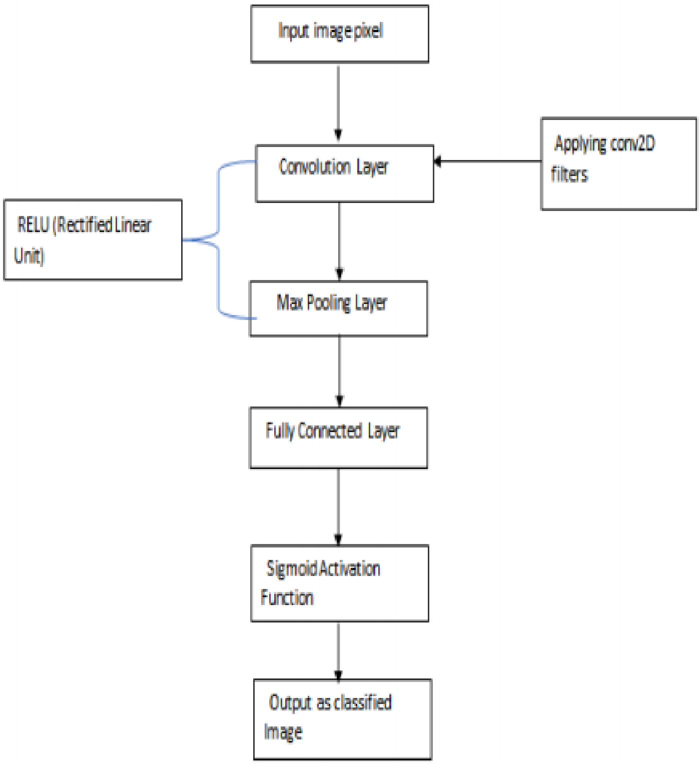

Figure 5.4: Flowchart of CNN model

5.2.4 Dropout Layer

A dropout layer is used for regularization where you randomly set some of the dimensions of your input vector to be zero with probability keep_prob. A dropout layer does not have any trainable parameters i.e. nothing gets updated during backward pass of backpropagation. To ensure that expected sum of vectors fed to this layer remains the same if no dropout was applied, the remaining dimensions which are not set to zero are scaled by 1 keep_prob.

5.2.5 Fully connected layer

In a fully-connected layer, neurons are fully connected to all activations in the previous layer, whose structure is same as regular neural networks. The only difference between fully-connected layers and convolutional layers is, convolutional layers are connected to only a local region of the input. Fully-connected layer takes the input volume and outputs an N-dimensional vector. In an output layer, N is the number of classes in which one is trying to classify an image . A fully-connected layer that is also an output layer takes the output of the previous layer (a convolutional, layer of activation function or pooling layer), which represents the activation map of high-level features, and determines which features are associated to a particular class.

5.2.6 Activation Function

The activation function is the non linear transformation that we do over the input signal. This transformed output is then sent to the next layer of neurons as input.In this project uses two main activation functions

ReLU Function

ReLU function is the most widely used activation function in neural networks today. One of the greatest advantage ReLU has over other activation functions is that it does not activate all neurons at the same time. From the image for ReLU function above, we'll notice that it converts all negative inputs to zero and the neuron does not get activated. This makes it very computational efficient as few neurons are activated per time. It does not saturate at the positive region. In practice, ReLU converges six times faster than tanh and sigmoid activation functions. The equation of Relu function is max(0,x).

Sigmoid Function

The sigmoid activation function, also called the logistic function, is traditionally a very popular activation function for neural networks. The input to the function is transformed into a value between 0.0 and 1.0. Inputs that are much larger than 1.0 are transformed to the value 1.0, similarly, values much smaller than 0.0 are snapped to 0.0. The shape of the function for all possible inputs is an S-shape from zero up through 0.5 to 1.0. For a long time, through the early 1990s, it was the default activation used on neural networks. The equation of sigmoid function is $\sigma\left(x\right)=\frac{1}{1+e^{-x}}$

5.2.7 System Design

The DFD of the project include:

DataFlow Diagram

A data flow diagram (DFD) is a design tool to represent the flow of data through an information system. A context level DFD can be used to show the interaction between a system and outside entities; it can also show the internal data flows within a system. It often shows the information system as a single circular shape with no details of its inner working: what it shows is its relationships with the external entities. A data flow diagram graphically represents:

- Processes - jobs that are done with the data. A process transforms incoming data flow into outgoing data flow.

- Data stores - files, databases, archives. They can be manual, digital or temporary.

- External entities - other systems or people beyond the control of the current system.

- Connecting data flows - arrows show how data flows from one place to another.

Notations in a Data Flow Diagram

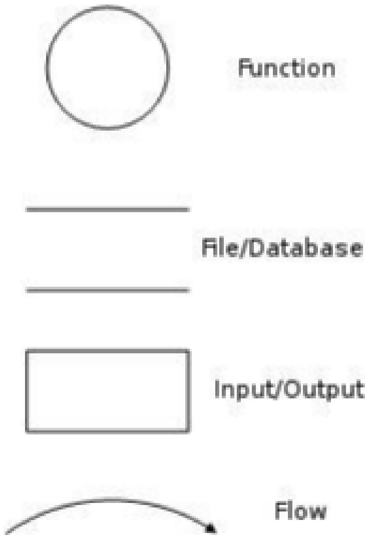

Figure 5.5: Notations in dataflow diagram

Context Diagram (Level 0)

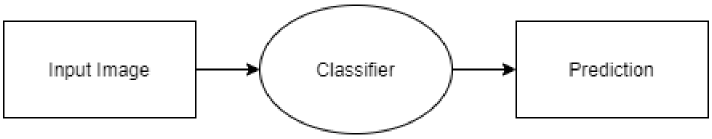

Figure 5.6: Level 0 DFD

Top Level DFD(Level 1)

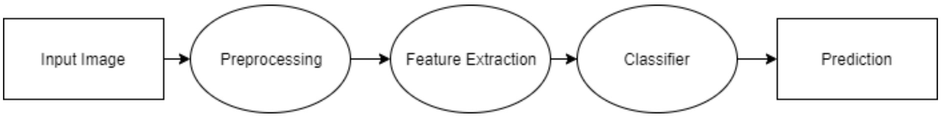

Figure 5.7: Level 1 DFD

Level 2

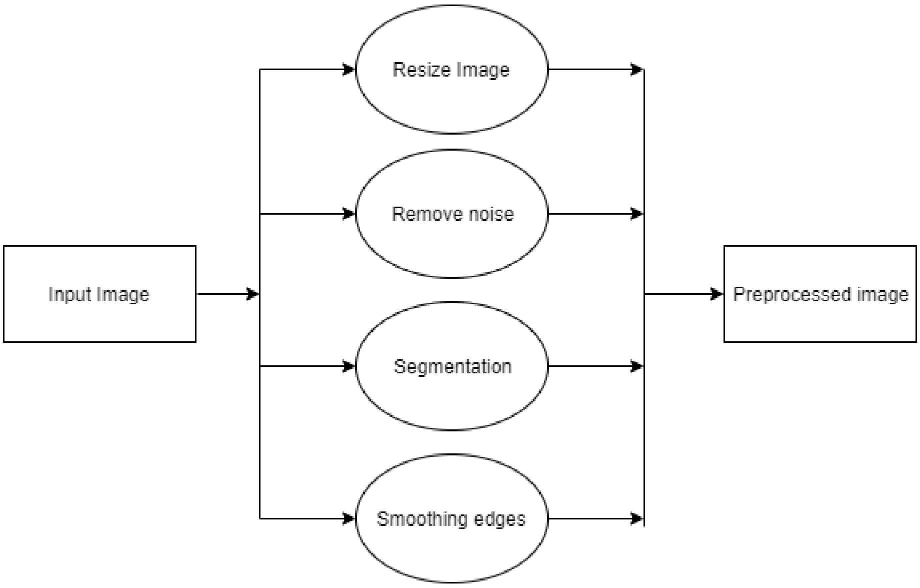

Figure 5.8: Level 2 DFD

Level 3

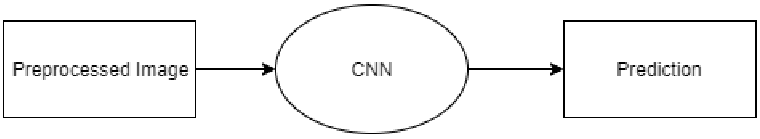

Figure 5.9: Level 3 DFD

Chapter 6

Coding

Convolutional Neural Network

A convolutional neural network (CNN, or ConvNet) is a class of deep neural networks.A convolutional neural network consists of an input and an output layer, as well as multiple hidden layers. The hidden layers of a CNN typically consist of a series of convolutional layers that convolve with a multiplication or other dot product. The activation function is commonly a RELU layer, and is subsequently followed by additional convolutions such as pooling layers, fully connected layers and normalization layers, referred to as hidden layers because their inputs and outputs are masked by the activation function and final convolution.

Algorithm 1 Algorithm for CNN is as follows:

- **Step 1(a) Convolutional operation:** The first building block in our project is convolution operation. In this step, we will touch on feature detectors, which basically serve as the neural network's filters. It will also discuss feature maps, learning the parameters of such maps, how patterns are detected, the layers of detection, and how the findings are mapped out.
- **Step1(b) ReLU layer** :The second part of this step will involve the Rectified Linear Unit or ReLU. We will cover ReLU layers and explore how linearity functions in the context of Convolutional Neural Networks.
- **Step2 Pooling:** In this step Pooling operation takes place and maxpooling is used.
- **Step3 Flattening:** Here flattening process occurs and how we move from pooled to flattened layers when working with Convolutional Neural Networks.
- **Step4 Dense Layer:**it used to represent matrix vector multiplication. Also it is used to change the dimensions of your vector.
- **Step5 Dropout Layer:**it is used for regularization where you randomly set some of the dimensions of your input vector to be zero with probability keep_prob.
- **Step6 Activation Function:**it determine the output of a deep learning model, its accuracy, and also the computational efficiency of training a model—which can make or break a large scale neural network.

Chapter 7

Experimental Results And Future Extensions

The experiment was conducted on 660 images of test data using a different number of training data (images) and epochs in the training process. The experiment obtained the highest accuracy of 99 percent in training result using 2637 images and 50 epochs. Meanwhile, in testing , result obtained 85 percent of accuracy for using 660 images and 50 epochs .

Model Evaluation :

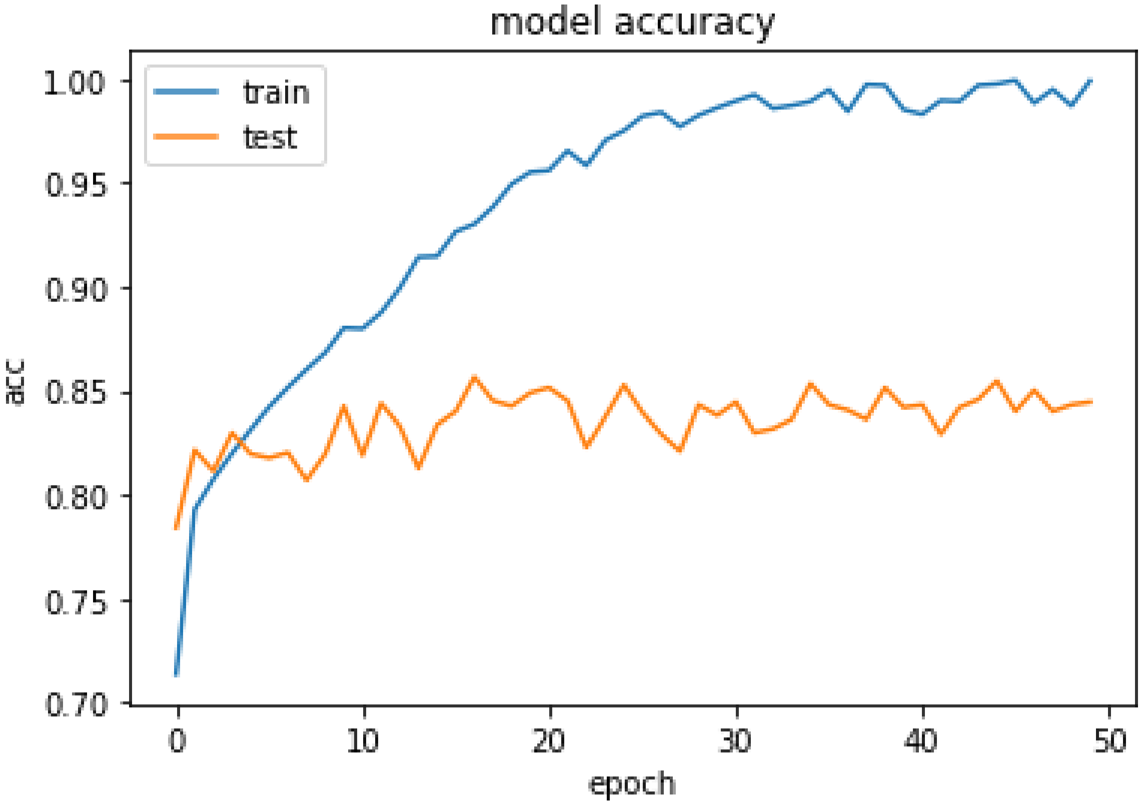

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Figure 7.1: Model Accuracy

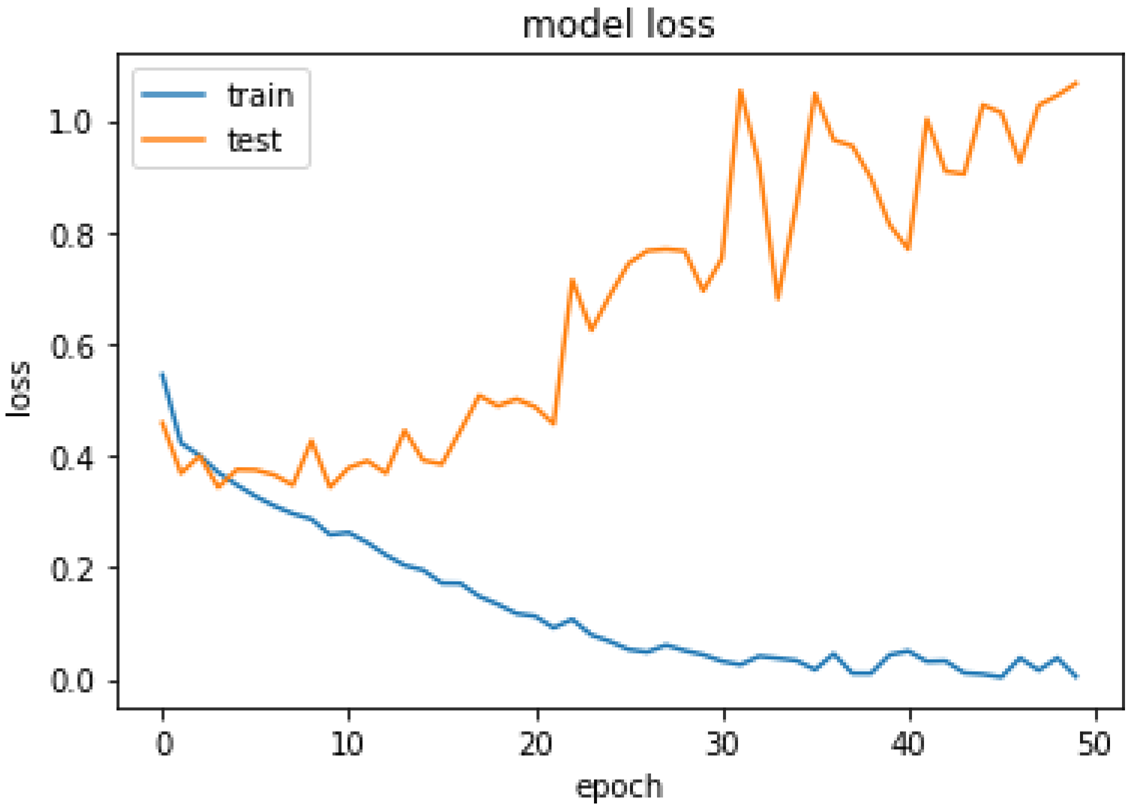

Figure 7.2: Model Loss

7.1 Future Extension

The idea is to generate a tool to predict the probability of a malign mole. So that the proposed system can be extended as :

- **Web App :** The web app will have the possibility that a user upload a high quality image of an specific mole. The results will be a prediction about the probability that the given mole be malign in terms of percentage.
- **Iphone App :** Our CNN model will be loaded into the iPhone to make local predictions. Advantages: The image data don't need to be uploaded to any server, because the model predictions can be done through the pre-trained model loaded into the iPhone.
- **Android App**

Chapter 8

Conclusion

Classification of melanoma cancer images is carried out in 2 stages; the first stage is training the dataset to produce a model. The second stage is the process of classification which the system takes the image data, then initializes the model from the results of the training and makes predictions using the model, then the system takes the prediction results along with their probabilities and display the prediction results along with the image.

The experiment was conducted on 660 images of test data using a different number of training data (images) and epochs in the training process. The experiment obtained the highest accuracy of 99 percent in training result using 2637 images and 50 epochs. Meanwhile, in testing result obtained 85 percent of accuracy for using 660 images and 50 epochs in testing.

The experiment results prove that the amount of training data and epochs used for training affects the level of accuracy in classifying melanoma cancer images. The more data that is trained, the better the test results will be produced .

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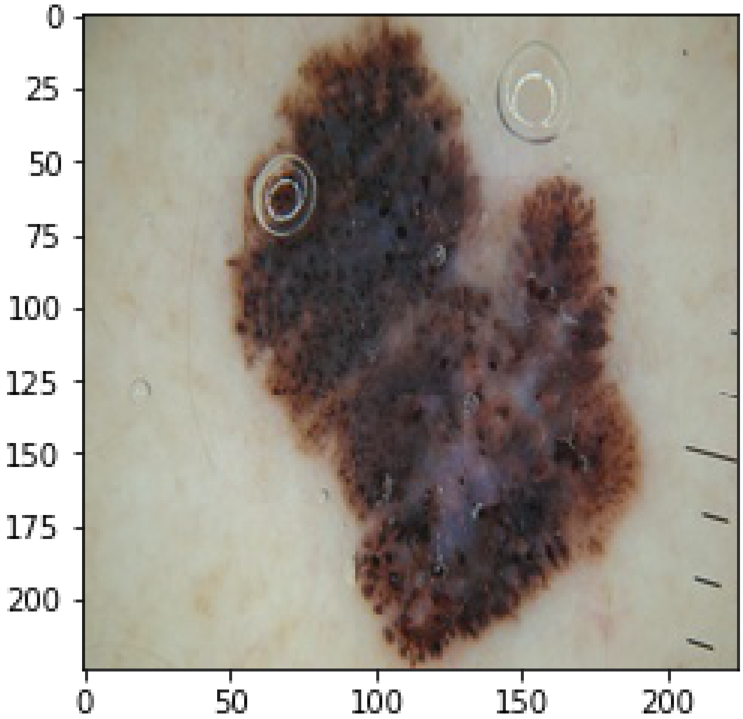
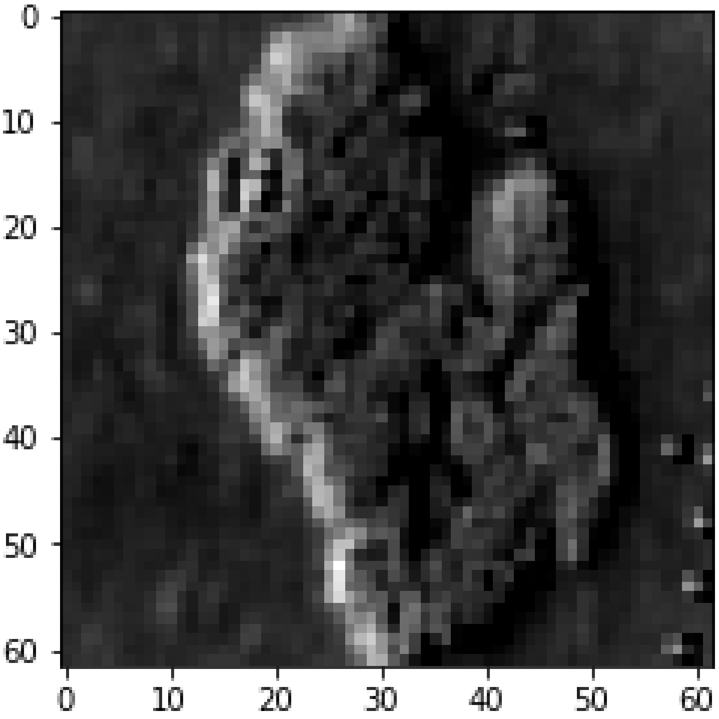
APPENDIX

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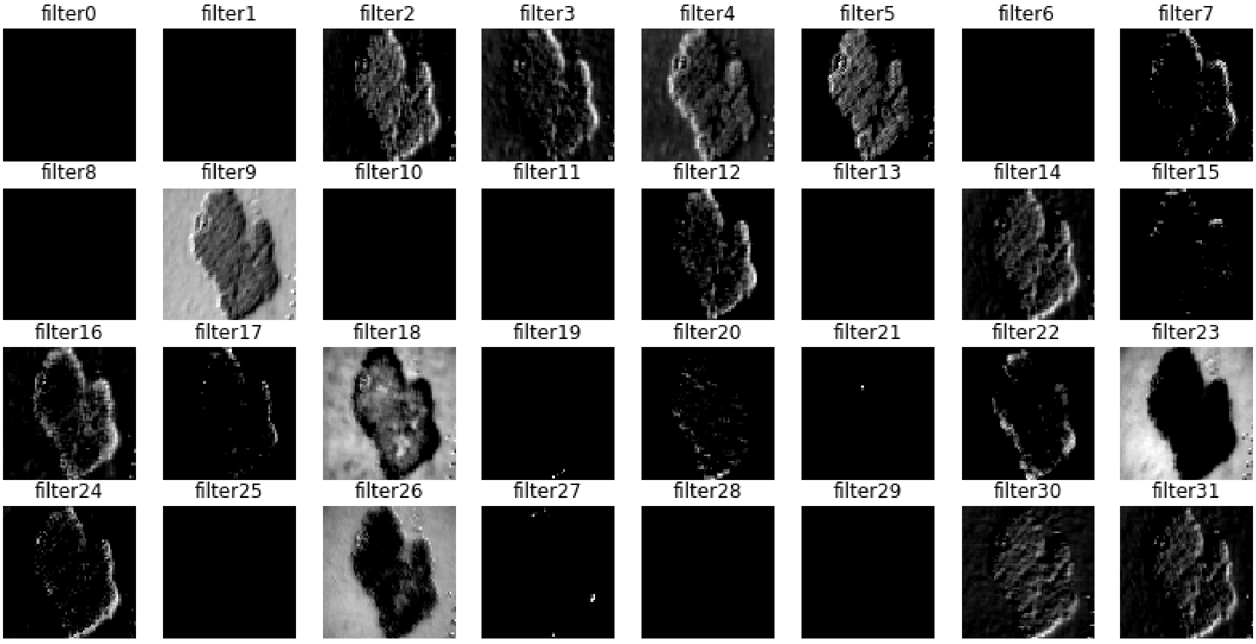
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