A
Project Report
on
"Prostate Cancer Detection using Deep Learning"

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Under the guidance of

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388421 April2021

CHAROTAR UNIVERSITY OF SCIENCE AND TECHNOLOGY

CERTIFICATE

This is to certify that the report entitled "**Prostate Cancer Detection using Deep Learning**" is a bonafide work carried out by **Pankti Shah (17EC078)** under the guidance and supervision of **Dr. Amit V. Patel** for the subject **Project (EC448)** of 8th Semester of Bachelor of Technology in Electronics & Communication at Faculty of Technology & Engineering (C.S.P.I.T.) – CHARUSAT, Gujarat.

To the best of my knowledge and belief, this work embodies the work of candidate himself, has duly been completed, and fulfils the requirement of the ordinance relating to the B.Tech. Degree of the University and is up to the standard in respect of content, presentation and language for being referred to the examiner.

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ABSTRACT

Prostate cancer detection is the dangerous disease. It occurs in men mostly who are above 60. This disease is difficult to detect so, in most of the cases it is detected in the advanced state which leads to the severity and incurability. To overcome, this disease artificial intelligence has appeared in the context. Deep learning architecture such as MobileNet has been used in this for the modelling purpose. The dataset has been splitted in 75-25% ratio. We are able to attend approximately 75 % accuracy. With the help of this, we are able to detect the disease in its early stage and can save life.

INTRODUCTION

Prostate Cancer detection is the dangerous disease which has the highest rate of death in men because of this. The perspective of this project to train a machine with the prostate Gleason grade annotated data by the renowned pathologists. MobileNet architecture has been deployed. It works really well in comparison with the other neural networks such as the ResNet and VGG-16. It gains around 70-75% accuracy on the annotated data by the pathologists. Fine tune model and tissue mask image is used for the generation of the heatmaps and class activation maps on the model. Test results have been shown with the help of confusion matrix and diagrams.

OBJECTIVE

Objective of this project is to learn and explore the ongoing challenging topic in the field of deep learning. Deep learning is the emerging domain which outperforms on most of the dataset based on computer vision. Prostate cancer detection is the most novice task. Subsequently, I wish to explore this and understand clearly.

MOTIVATION

Motivation for taking this project was to work in the field of bio-medical image classification. Even, to work with the challenging data so that I can learn more. Work on Prostate Cancer is very less so, I have to explore more and understand eclectic topics for its implementation.

ACKNOWLEDGEMENT

I would like to express my sincere thanks to my internal guide **Dr. Amit V. Patel** for his valuable guidance, enthusiastic attitude and encouragement throughout the period of Project and Thesis work. His guidance, suggestion and very constructive appreciation have contributed immensely to the evolution of the project.

I would also like to express my sincere gratitude and sincere thanks to **Dr. Trushit Upadhyaya** HoD, Department of Electronics and Communication Engineering, Charotar University of Science and Technology, Changa for providing me the opportunity to undertake such a challenging and intellectual work.

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Abbreviations

PC	Prostate Cancer
PSA	Prostate Specific Antigen
DRE	Digital Rectal Examination
NN	Neural Network
CNN	Convolutional Neural Network
DCNN	Deep Convolutional Neural Network
WSI	Whole Slide Image
TCGA	The Cancer Genome Atlas
MRI	Magnetic Resonance Imaging

CHAPTER 1

INTRODUCTION TO PROSTATE CANCER

Prostate cancer is the deadliest disease which occurs only in men. This occurs due to the type of the food being consumed especially due to red meat and fat-based food. Weather also plays a vital role in this disease. It is usually detected in the advanced state which leads to the more chances of the incurability. Therefore, early detection with the help of artificial intelligence technology can help to detect the disease in the early stage.

1.1 DEFINITION OF PROSTATE

- The prostate is a gland which is about the size of the walnut and located below the bladder. It is present in men. Prostate helps in protecting the urinary tract from infections. Prostate produces prostate specific antigen (PSA) which is an enzyme to help liquefy the ejaculation process.

1.2 DEFINITION OF CANCER

- Mainly, it is uncontrolled growth of cells in the body.This abnormal growth is also sometimes known as tumour because there occurs a swelling without any inflammation, due to abnormal growth of tissue.

1.3 DEFINITION OF PROSTATE CANCER

- A small walnut-sized gland that produces seminal fluid which germinates cancerous cells in the man's prostate. Cells in the human body are normally tight and bound to the other cell in the core. After generation of the destructive cells in the body the pattern of the cells starts deforming which helps pathologists and experts to indicate the presence of the cancer in the prostate.

1.4 DEFINITION OF BENIGN PROSTATE HYPERPLASIA

- With respect to the elevation in the age of men, there is increase in the size of the prostate which is termed as BPH or benign prostatic hypertrophy. This non – cancerous enlargement may lead to difficulty in urination process and can be easily treated with medication or surgery. BPH is not cancerous and it does not indicate or play role in developing cancer.

1.5 TYPE OF PROSTATE CANCER

- Cancer is an Adenocarcinoma type of cancer.Adenocarcinomas develop in an organ or a gland.

1.6 MAIN CAUSE OF PROSTATE CANCER

- Prostate cancer development mainly depends on the type of food or beverages being consumed. In the present era, most of the edible items have higher rate of fats in it which in turn leads to the improper synthesis and obesity. Simulation of testosterone and other types of hormones elevates due to fats present in the body. Subsequently, this testosterone indirectly starts boosting the cancerous cells to activate at a speedy rate in the prostate.

Escalation in the quantity of testosterone leads to simulation of dormant prostate cancer cells into activity state.

1.7 SIGNS OF PROSTATE CANCER

- Burning sensation or pain during the urination or ejaculation process. Frequent call of urination especially at the night time. Even, sometimes there occurs difficulty in starting and stopping urination process. Withal, sudden erectile dysfunction takes place. Unexpected flow of blood occurs via the medium of urine or semen. Consequently, insufferable pain in the back, hips, rips and other bones happens.

1.8 TYPES OF FOOD WHICH TERMINATES THE GROWTH OF CELLS

- Mainly, the types of cruciferous vegetables help in languishing the growth of such deadly cells and the risk of advanced stage of cancer. These vegetables include broccoli, cauliflower, cabbage, brussels sprouts, bok choy, spinach and kale.

1.9 GENERAL AGE FOR OCCURANCE OF PROSTATE CANCER

- The chance of having or the development of prostate cancer in the men below the age of 40 is very rare however it jerkily inclines after the age of 50. On an average, 6 in 10 cases of this cancer are detected in the men who are elder than 65. Among 10000 men of age 40 or below, there is possibility that 1 man might get Prostate cancer. From 40 to 59 age, 1 in 38 have chances of getting it. Man with the age range of 60 to 69 have the highest chances of getting cancer and it is about 1 in 14. Coincidentally, it may transpire due to family history of prostate cancer such as a heredity (ethnicity).
- Chances of getting prostate cancer is highest in African American men and its lowest in Asian men. Even, the genes such as HOXB13, BRCA1, BRCA2, MSH2 and MLH1 plays vital role in its generation. The consumption of red meat at a higher rate and low in vegetables are highly prone to this.

1.10 TYPES OF GENES INVOLVED IN THE DEVELOPMENT

- Mutations which are inherited in specified genes such as HOXB13, BRCA1 and BRCA2 play major role for the development of heredity prostate cancer. Even, this mutation seldomly leads to various other types of cancer in man. Men who develop metastatic cancer have a higher rate of mutations in BRCA1 and BRCA2 or in other genes which help in DNA repair. So, around 10% of men have germline mutation and another 10% have somatic mutations.

1.11 RACES WHICH HAVE THE CHANCES OF DEVELOPMENT

- African and American men have maximum chances of developing Prostate cancer in comparison with Caucasian men. These North American and African men are nearly 2.5 times likely to die from this deadly disease. Asian men are at the lowest risk.

1.12 METHOD OF DIAGNOSIS

- Among multiple diagnosis and screening methodology, there are four most common methods. Firstly, there is Prostate Specific Antigen (PSA). It is blood test. In this test, protein is made by cells in the gland known as prostate gland with normal and cancerous

cells. Prostate based antigen is present in semen and sometimes also found in blood. It is measured in terms of nanograms per milliliter.Secondly, there is Digital Rectal Examination (DRE). This test examines human's lower rectum, lower belly and pelvis. This cancer can be detected with the presence of abnormal mass in the rectum or anus. Next is Biopsy based examination. Biopsy is a test where tissue sample such as a lesion, a mass or a tumor. Lastly, Multi parametric - MRI (MP-MRI). With the help of radio waves and large magnet to have a look at the organs and body structures inside the body.

1.13 TIMELINE OF DEVELOPMENT OF PROSTATE CANCER

- This diagram showcases the growth of the prostate cancer disease over time.Firstly, it is normal prostate epithelium and then, it prolongs to proliferative inflammatory atrophy and this prolongs to localized and finally to the metastatic cancer.

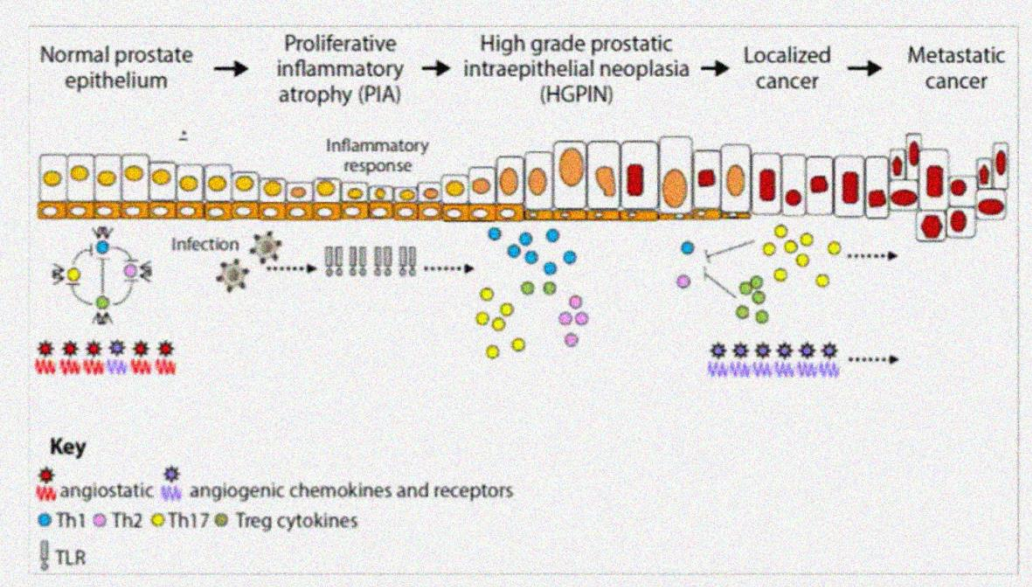


Fig 1. Timeline of development of PC

1.14 TYPES OF ANALYSIS STAGE OF CANCER

- The pathologist looking at the biopsy sample will assign one Gleason grade to the most predominant pattern in your biopsy and a second Gleason grade to the second most predominant pattern.
- For example: 3 + 4. The two grades will then be added together to determine your Gleason score.
- Theoretically, Gleason scores range from 2- 10.
- However, since Dr. Gleason's original classification, pathologists almost never assign scores 2-5, and Gleason scores assigned will range from 6 to 10, with 6 being the lowest grade cancer.

Fig 2. Gleason Pattern

Group 1	Gleason Score 6	5%
Group 2	Gleason Score 3+4=7	17%
Group 3	Gleason Score 4+3=7	35%
Group 4	Gleason Score 4+4=8	37%
Group 5	Gleason Score 9-10	76%

Fig 3. Gleason score of PC in terms of percentage

Risk Group*	Grade Group	Gleason Score
Low/Very Low	Grade Group 1	Gleason Score ≤ 6
Intermediate (Favorable/Unfavorable)	Grade Group 2	Gleason Score 7 (3 + 4)
	Grade Group 3	Gleason Score 7 (4 + 3)
High/Very High	Grade Group 4	Gleason Score 8
	Grade Group 5	Gleason Score 9-10

Fig 4. Gleason group intensity with its respective score

1.5 HISTOLOGICAL FEATURES

- It shows rudimentary necessary features which detects the specified disease by the biological features.
- From the image's (tissue) features, disease and its severity can be analysed.

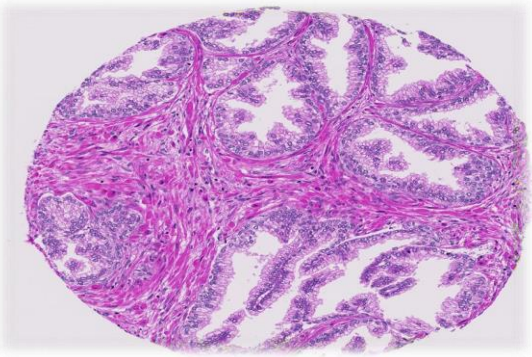


Fig 5. Histological features

CHAPTER 2

SOURCE OF DATASET

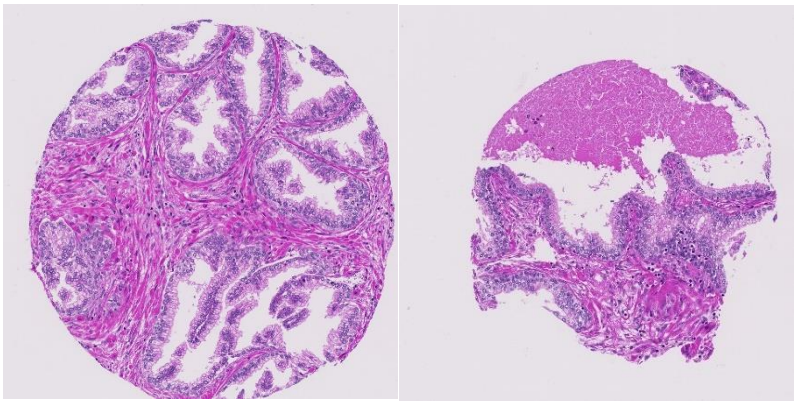
2.1 SOURCE OF DATA

- The prostate cancer data has been very rarely available on the online platform. In this project, I have taken the dataset from the Harvard data site [1]. In this dataset, there are various images available with the histological information available in it. It is available with certain group of tissue microarray such as ZTMA.
- This dataset has around 886 images in it.

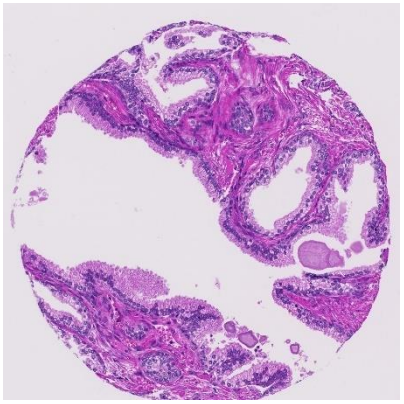
2.2 DETAILS OF DATASET

Name	Date modified	Type	Size
Gleason_masks_test	06-02-2021 20:56	File folder	
Gleason_masks_train	11-04-2021 10:45	File folder	
test_patches_750	06-02-2021 20:57	File folder	
tissue_masks	11-04-2021 10:53	File folder	
TMA_images	06-02-2021 20:58	File folder	
tma_info	06-02-2021 20:58	File folder	
train_validation_patches_750	11-04-2021 10:45	File folder	

Fig 6. Dataset content



(a) (b)



(c)

Fig 7. (a), (b) and (c) Original Image

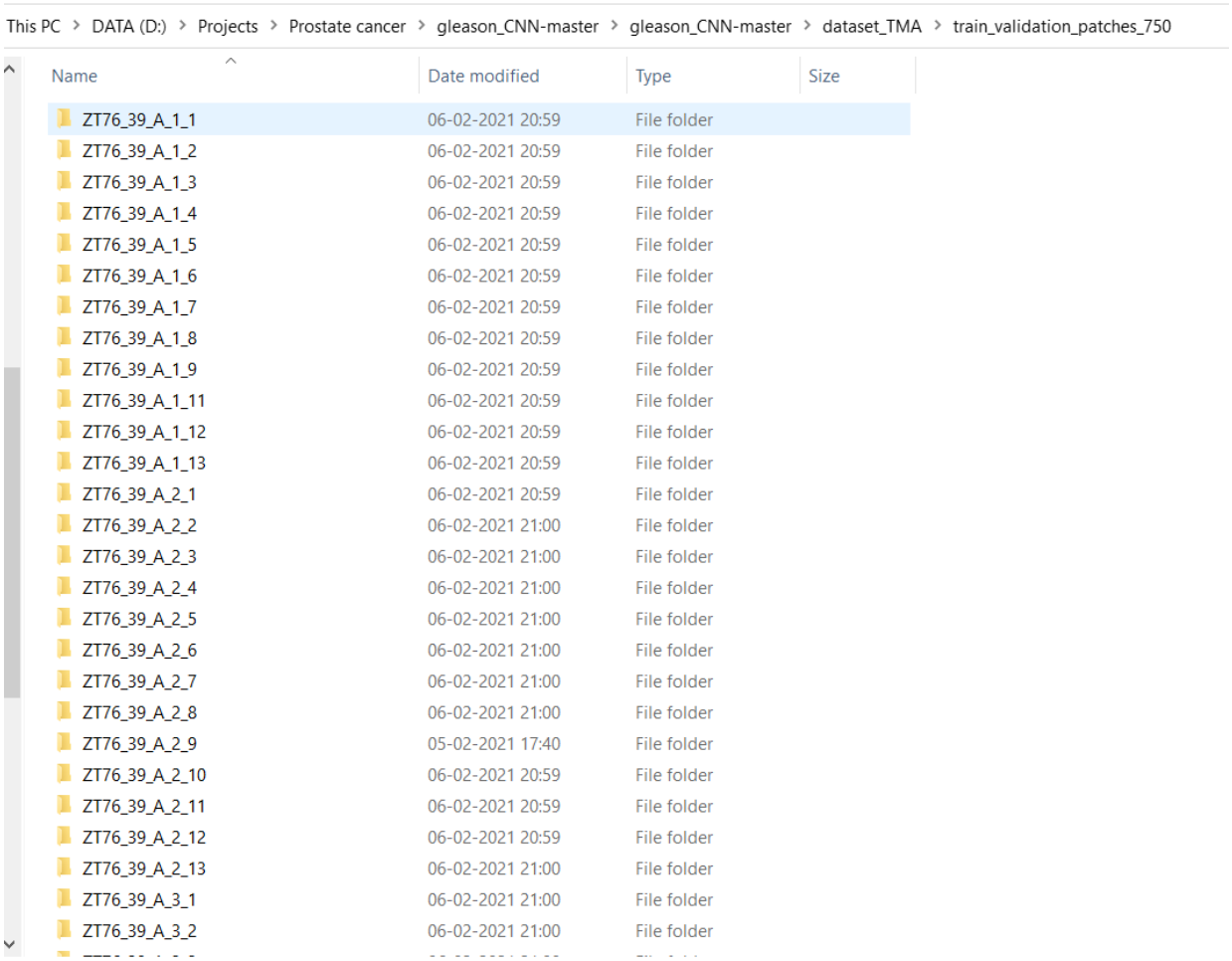


Fig 8. Image Patches of training validation data

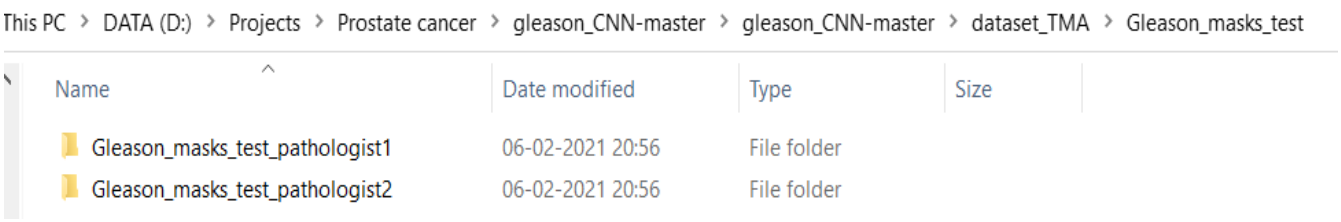


Fig 9. Image Mask by the pathologist on the testing data

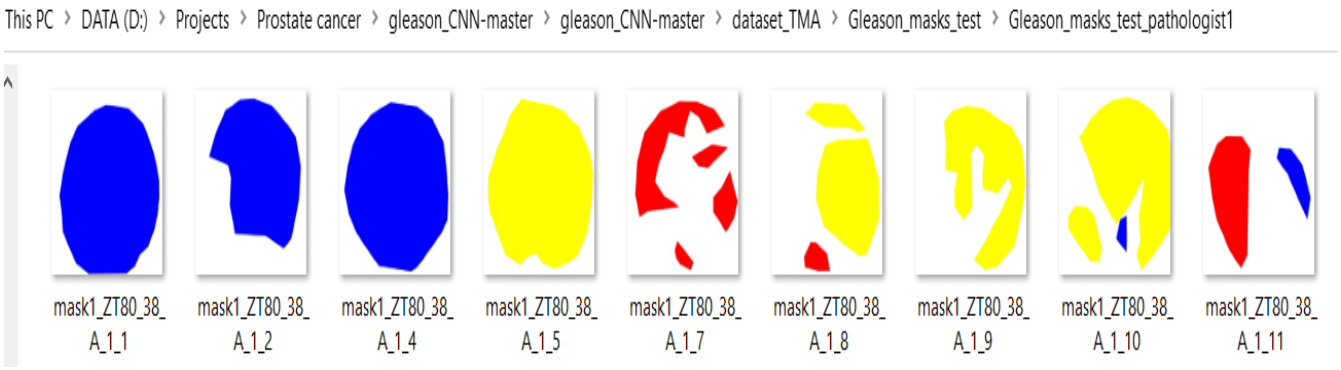


Fig 10. Image Mask by the pathologist1 on the testing data

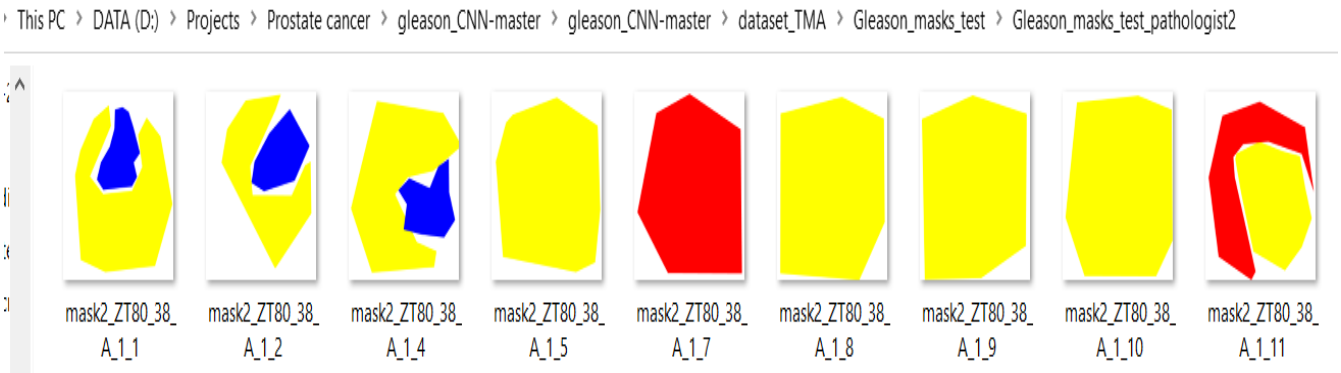


Fig 11. Image Mask by the pathologist2 on the testing data

CHAPTER 3

SUMMARY OF PYTHON LIBRARIES

3.1TENSORFLOW

- TensorFlow is the open-source library for the machine learning and deep learning applications. It allows to create dataflow of the model and delineates the details of how the data is systemically deployed through a processing node.

- TensorFlow is a tool which is flexible, comprehensive, combining bundles of libraries and its explanation. Even, model deployment is available.

- I have used many TensorFlow libraries and Keras based.

3.2 KERAS

- Keras is a deep learning library. Keras is a framework which is a neural network library whereas TensorFlow is the open-source library with machine learning based tasks.

- TensorFlow provides low-level and high-level APIs where Keras only provides high level APIs.

- It is used for generating a model with various packages such as

```
import keras.backend as K

from keras.preprocessing import image

from keras.models import Model, load_model

from keras.layers import AveragePooling2D, Conv2D, UpSampling2D

from keras.applications .mobilenet import MobileNet #,DepthwiseConv2D  #, relu6,

from keras.layers import DepthwiseConv2D

from keras.utils.generic_utils import CustomObjectScope

from keras.applications.mobilenet import MobileNet # DepthwiseConv2D #, relu6,

from keras.preprocessing import image

from keras.layers import AveragePooling2D, Conv2D, UpSampling2D
```

```
from keras.models import load_model, Model

from utils.keras_utils import preprocess_input_tf, center_crop

from keras.applications.densenet import DenseNet121

from keras.applications.vgg16 import VGG16

from keras.applications.resnet50 import ResNet50

from keras.applications.inception_v3 import InceptionV3

from keras.applications.mobilenet import MobileNet
```

3.3 GLOB

- Glob library is basically used for returning to a path that satisfies the mentioned pattern.
- It is built-in module in python.
- Linux and Unix also support it and it is present as system library in it.

```
import glob
glob.glob(pathname)
```

3.4NUMPY

- NumPy is the abbreviation of Numerical Python.
- NumPy works with arrays.
- It is used to create a matrix with ones or zeros or a random matrix.
- In this, we can generate2D, 3D matrix.

```
import numpy as np
```

3.5MATPLOTLIB

- Comprehensive library for generating interactive visualization plots.
- It is a plotting library.
- It's working is similar to MATLAB.
- Each pyplot function makes some change to a figure: e.g., creates a figure, creates a plotting

area in a figure, plots some lines in a plotting area, decorates the plot with labels, etc.

```
import matplotlib.pyplot as plt
```

3.6SEABORN

- Seaborn is a data visualization-based library.
- High level interfacing of data for plotting informative statistical data in an attractive way.

```
import seaborn as sns
```

3.7SCIPY

- SciPy is the abbreviation of Scientific Python.
- For analyzing of data

```
import scipy
```

3.8OS

- This library is used for interacting with the operating system.
- Also, for generating temporary files.

```
import os
```

3.9PANDAS

- Pandas is a library for data mining.
- For importing a file in terms of an object.
- For reading a file by using pd.read_csv command.

```
df = pd.read_csv(csv_path, sep='\t', index_col=0)
```

3.10 PICKLE

- It keeps tracks of an object.
- It is a process in which a python object channel is converted into a stream of byte.

```
import pickle
```

CHAPTER 4

DATA PRE-PROCESSING TECHNIQUES

Dataset is the most important thing in the model making process. It must be of the perfect size and without noise for the précised prediction. Feature selection and extraction is the rudimentary process for training the model. While data augmentation is the second most important procedure for perfect modelling because it helps in removing noise and rotating and shifting images as per the need. This helps in augmenting the size of the data. Segmentation is used for pointing out specific pattern or an area for feature extraction whereas masking is a prototype of a filter for pixel enhancement for dedicated pattern. Transfer learning is the approach where trained network is being used and fine tuning is the technique where final tuning of the model takes place. In this manner, data pre-processing is the intermediate process in every project. Detail description of every method is being provided below.

4.1 FEATURE SELECTION AND EXTRACTION

➔ Feature Selection

- Feature selection technique is used for reducing the number of input variables for specified targeted values. In feature selection, a wrapper is used which evaluates a specific model using subset of features which works well. Cost is very high and there are chances of over fitting with the good chance of success in prediction.
- Filtering process is the faster method of choice for ranking the features with the specified task or the problem. Feature selection process can be used by the Sklearn package.
- In embedded layer, there is usage of technique such as LASSO or L1 regularization.

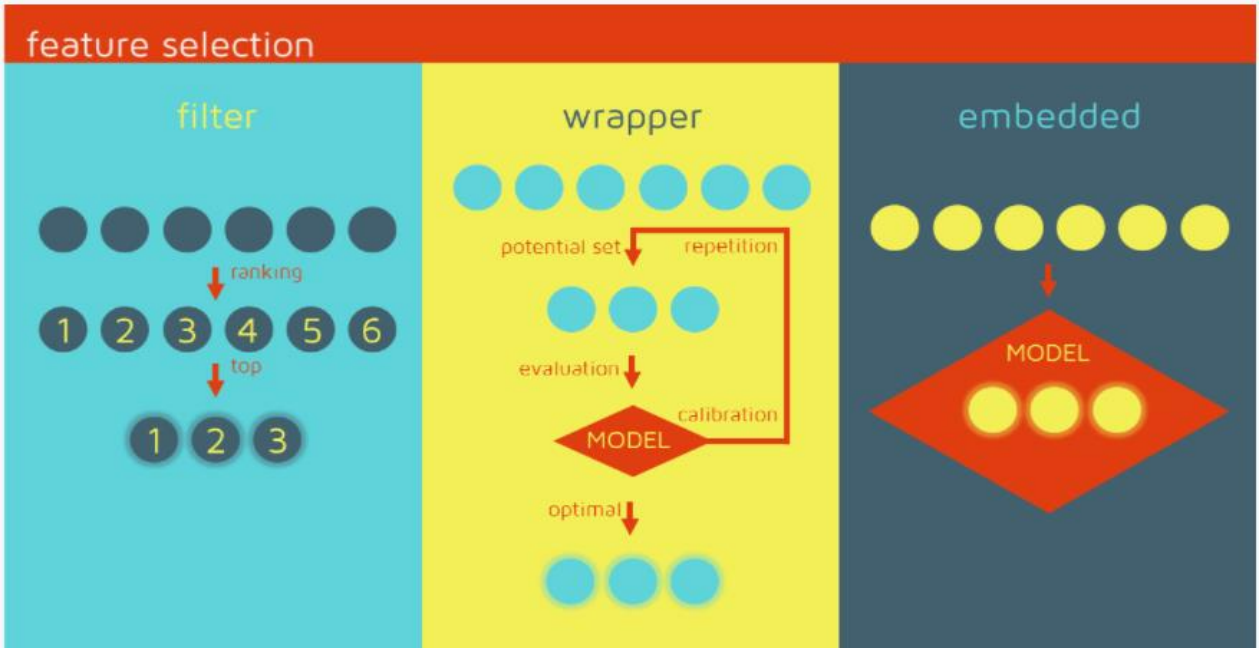


Fig 12. Feature selection

➔ Feature extraction

❖ Feature extraction is a pipelining process which changes with the help of basic data and algorithm to be used. This turns into something complex. Dimensionality reduction is a type of feature extraction with a huge number of pixels of the data consisting of an image with proper cauterization of important features.

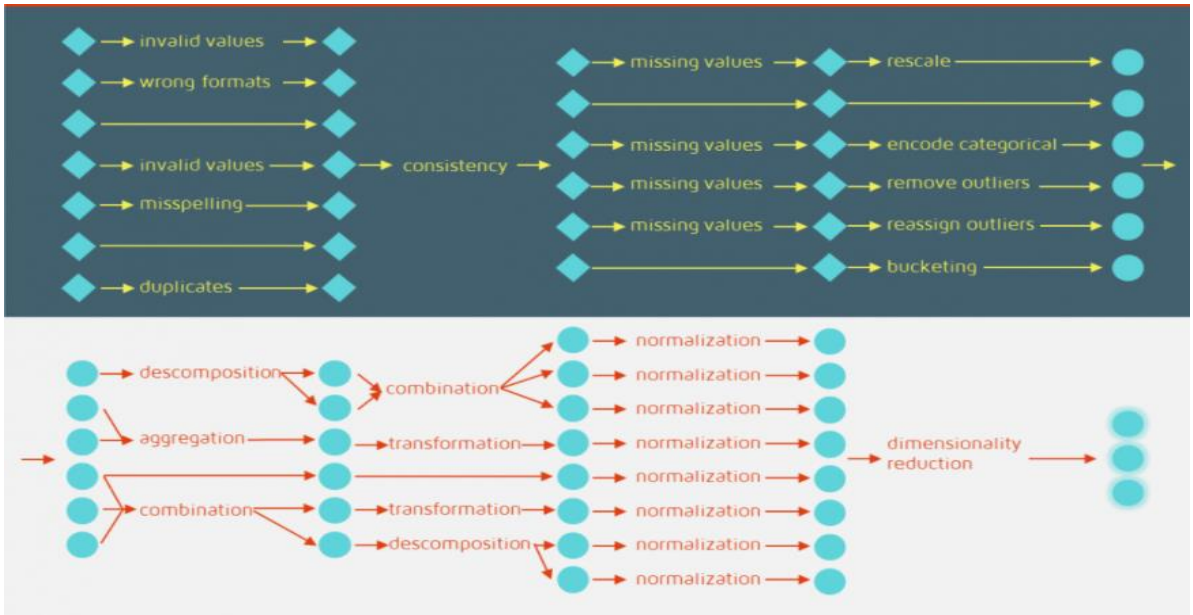


Fig 13. Feature extraction

4.2 DATA AUGMENTATION

- Data augmentation is the methodology in which it enables the combination and diversity of the data for the models of training and validating with the necessary modifications of the available data. It can help neural network have a special kind of performance with proper generalization.
- I have performed data augmentation with certain practical analysis.
- Such as we can use

```
import numpy as np
from skimage.io import imread, imsave
import matplotlib.pyplot as plt
from skimage import transform
from skimage.transform import rotate, AffineTransform
from skimage.util import random_noise
from skimage.filters import gaussian
from scipy import ndimage
```

- Input image was given as

Fig 14. Image for data augmentation

- Image rotation can be done with the help of

skimage.transformation.rotate.

rotate30 = rotate(img, angle=30)

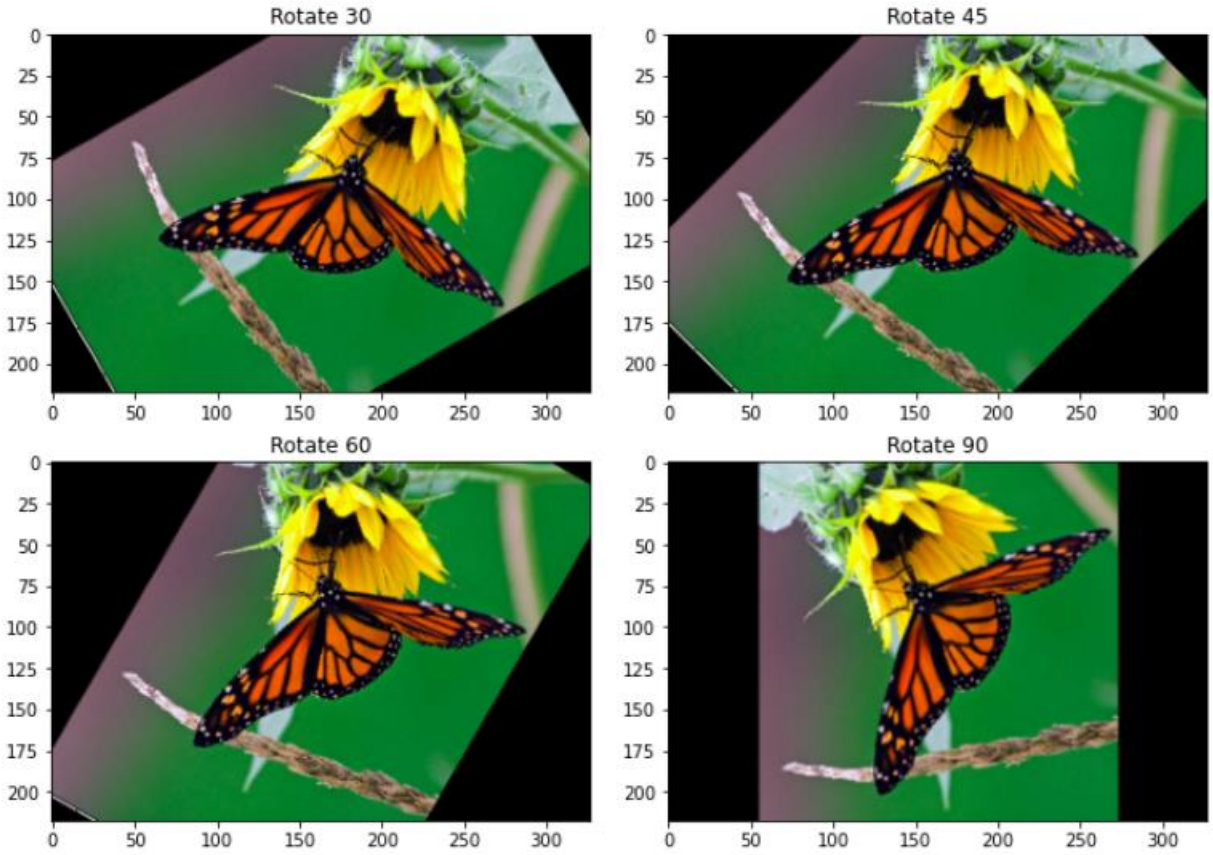


Fig 15. Rotated Image by data augmentation

❖ Image shearing

```
tf = AffineTransform(shear=-0.5)
sheared = transform.warp(img, tf, order=1, preserve_range=True, mode='wrap')
sheared_fig = plot_side_by_side(img, sheared, 'Original', 'Sheared')
```

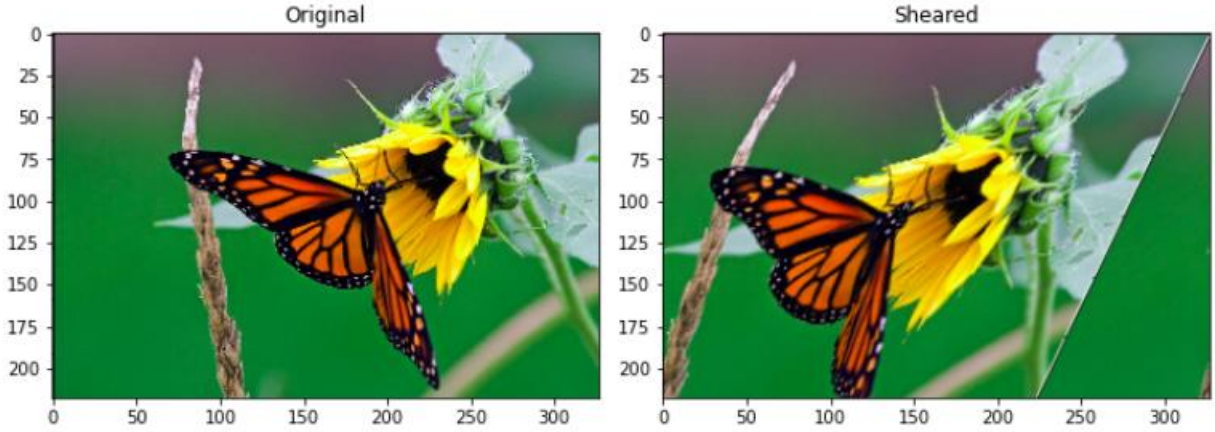


Fig 16. Sheraed Image by data augmentation

❖ Image rescaling

rescaled = transform.rescale(img, 1.1)

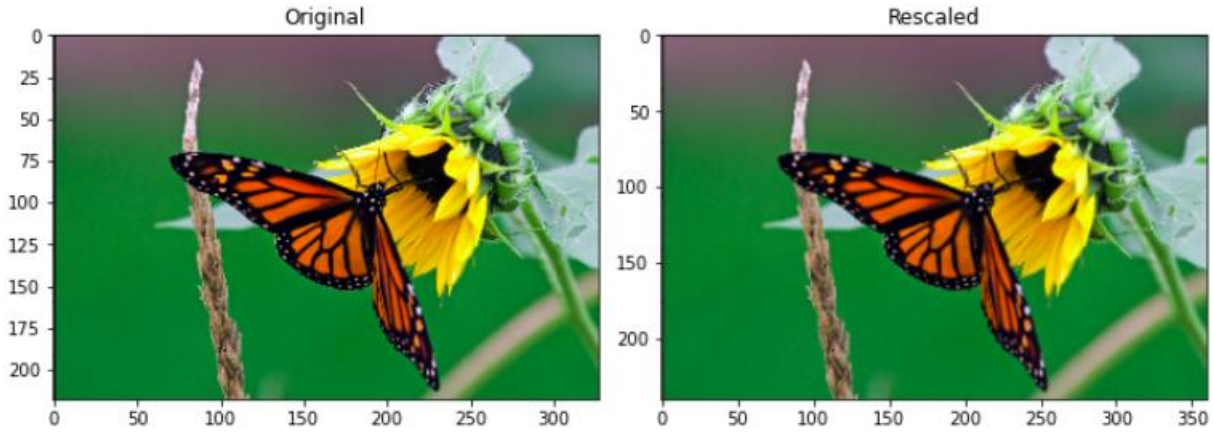


Fig 17. Rescaled Image by data augmentation

❖ Flipping of an Image

up_down = np.flipud(img)

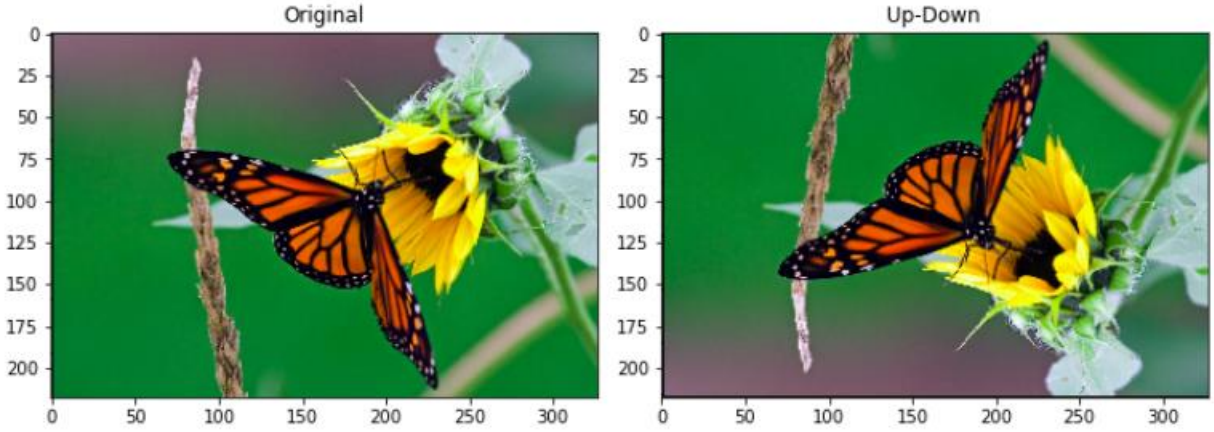


Fig 18. Flipped Image by data augmentation

❖ Applying random noise

noised = random_noise(img, var=0.1**2)

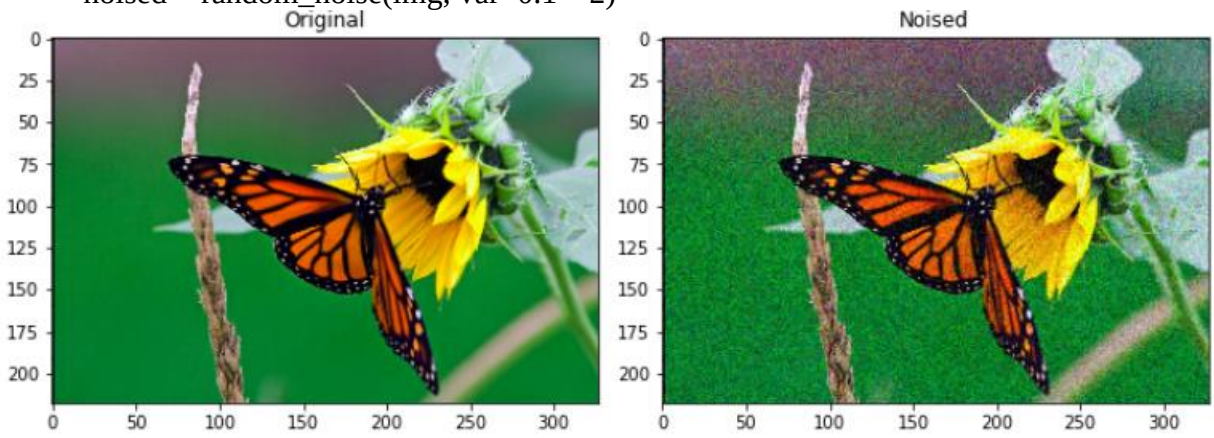


Fig 19. Image after applying random noise by data augmentation

❖ Brightness of an Image

highB = img + (100/255)

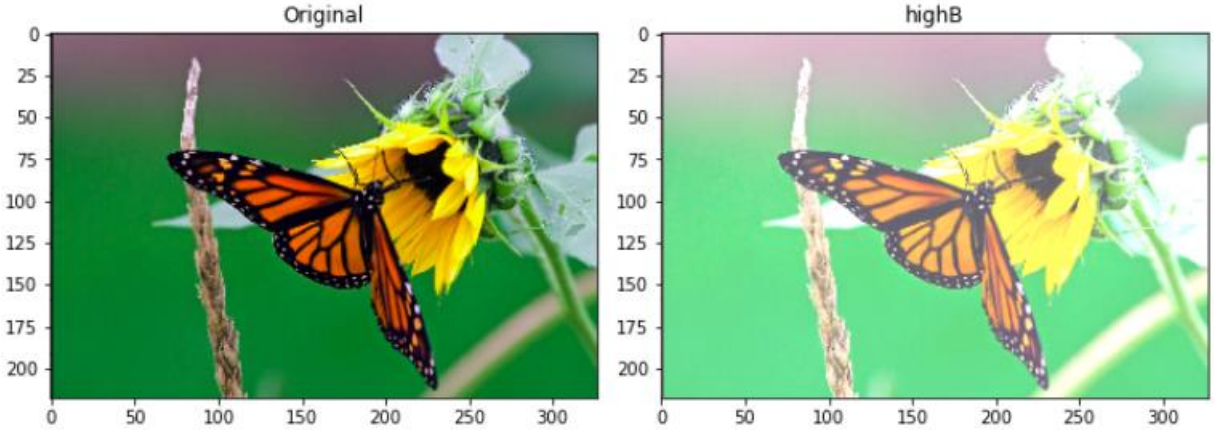


Fig 20. Image after applying brightness by data augmentation

❖ Contrasting of an Image

highC = img * 1.5

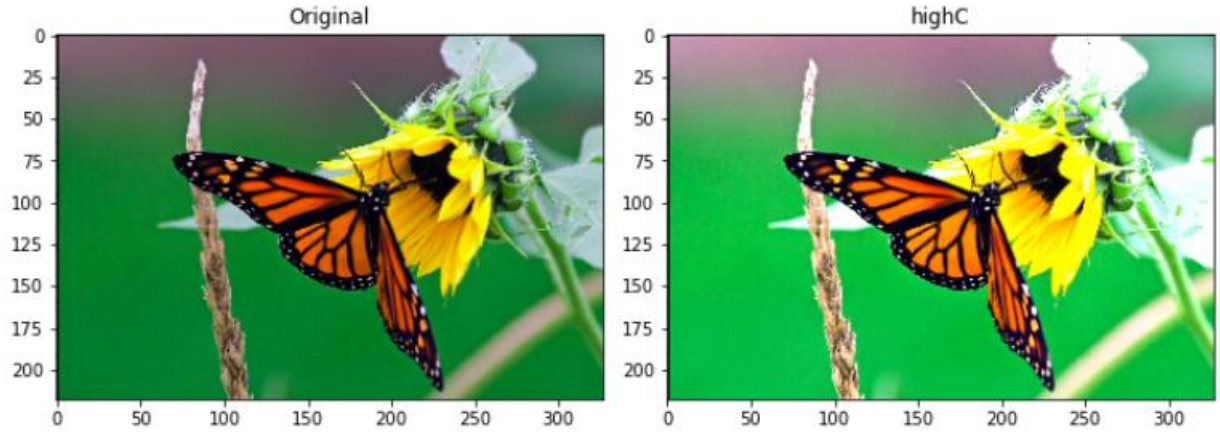


Fig 21. Image after applying contrast by data augmentation

4.3 IMAGE SEGMENTATION

Image segmentation used for detecting boundaries and extracting features from the pixel values of an image.

➔ **SEMANTIC SEGMENTATION**

❖ In semantic segmentation, there is detection based on group.

❖ Such as, if there is a group of people then it would be bounded with the same cluster.

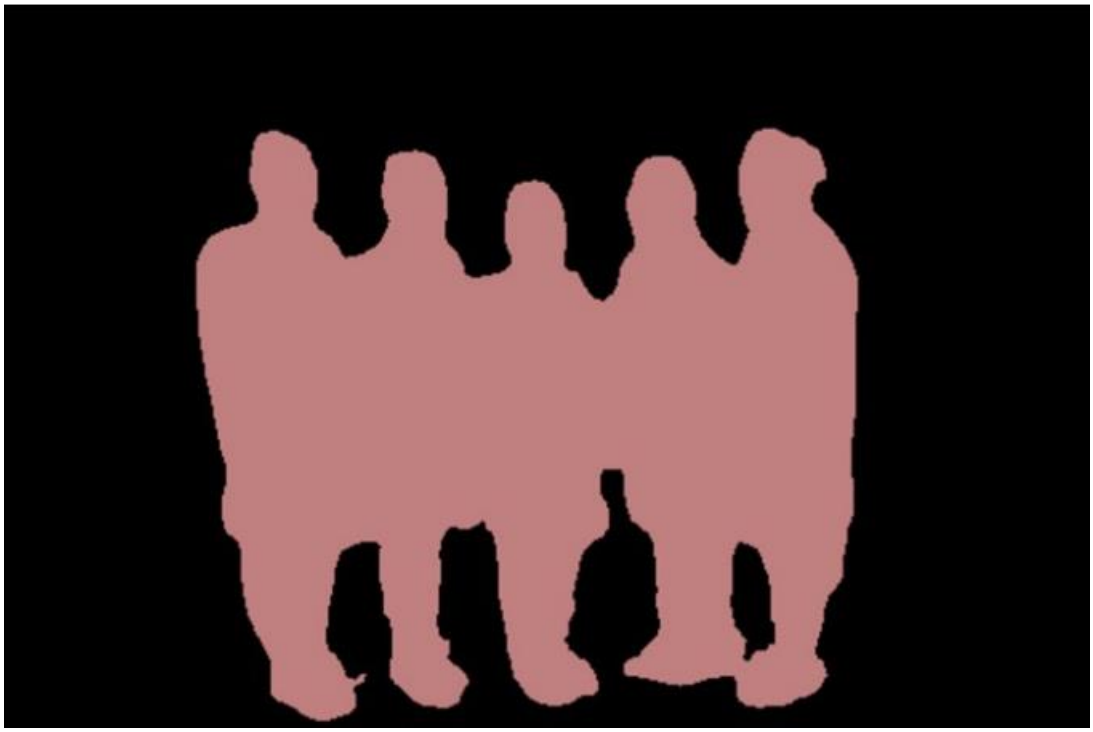


Fig 22. Semantic Segmentation

➔ **INSTANCE SEGMENTATION**

- In instance segmentation, there is detection based on individual and its indexing..
- Such as, if there is a group of people then it would be detected individually within the same cluster so, it becomes easy to detect.

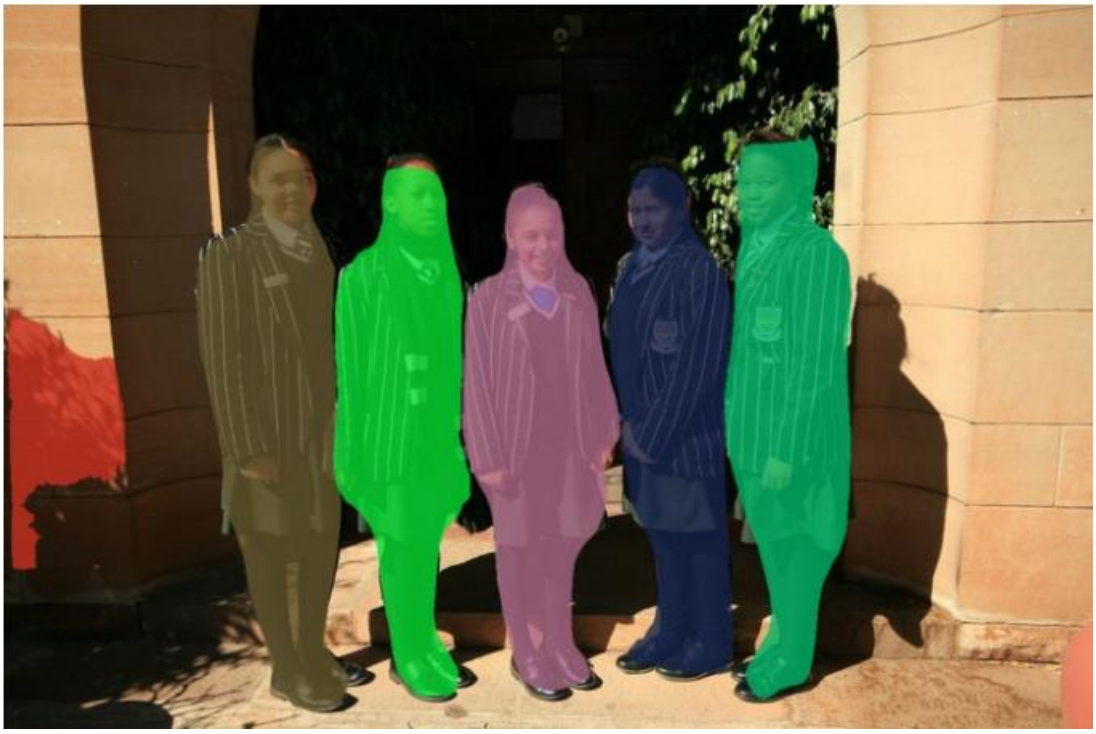


Fig 23. Instance Segmentation

4.4 IMAGE MASKING

- Image masking is used for processing and editing which is used to detect the specified area with the help of a mask.
- Masking an area of an image protects that area from being altered by changes made to the rest of the image.
- Mask is similar as a filter.
- The way we wish to extract data the same way we make the mask.

4.5 TRANSFER LEARNING

- Transfer learning is the approach in which the developed model for specified task is being deployed in other model as per the necessity.
- In transfer learning , there are two models such as

1. Approach of Develop Model

  - In this approach, a model is developed with the designed task which is able to work properly on that model.
  - Then, that source model with the specified selected architecture is being deployed.
  - Model fitting is done on the main model and then, deployed on the other task for gaining accuracy with good results.

- Finally, the tuning of the model comes as per the refined input-output data of the other specified task.

2. Approach of Pre-trained Model

- Many institutes develop model on the basis of the dataset available such as by the ImageNet model.
- Then, that developed model such as MobileNet is deployed into other datset which is the reusing of the model
- Finally, the tuning of the model comes as per the refined input-output data of the other specified task.

4.6 FINE TUNING

- In this, the model is tuned as per the necessity of the task.
- Making certain adjustments as per the need.
- To gain good output.
- It has good result in image classification task.

CHAPTER 5

DEEP LEARNING ALGORITHMS

Deep learning is the subset of artificial intelligence which is the replica of the human brain. It deploys the model and training with the amalgamation of the different size layers, pooling such as max or global average pooling. Usage of filter is also important in the processing of the model. There are many networks which is able to successfully deploy many models.

The Image Net Challenge is an annual competition helped between 2010 and 2017 in which

challenge tasks use subsets of the ImageNet dataset.

The goal of the challenge was to both promote the development of better computer vision techniques and to benchmark the state of the art.

So, in that architectures were proposed such as DenseNet, ResNet, GoogleNet, Inception Model and many more.

5.1NEURAL NETWORK

- Neural network is the rudimentary model of the human brain. Here, the dot shown the neurons which transfers the data through the pipeline which is the same model as the synapse of the brain.

- Supposedly the green dot shown are the input nodes of the network.

- Subsequently, the feature extraction takes place as per the assigned hidden layers.

- As we make the dense layer, the same way deeper the network becomes and more accurate.

- The red dot is considered the final layer.

- In each node, activation function is used such as ReLU or Sigmoid.Even, the optimization function such as Adam or Stochastic Gradient Descent is used.

- The equation of neural network is: y = w*x + b where y=output, w=weights, x= input and b= bias.

- The weights are adjusted as per the need of the network by seeing the condition of underweight or the overweight.

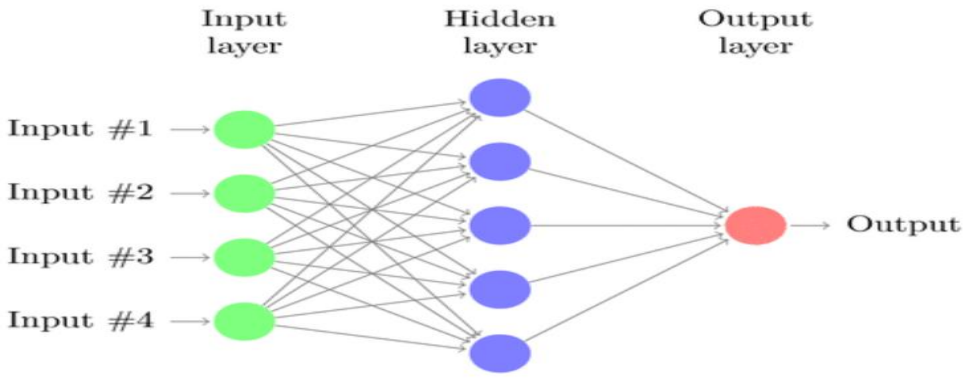


Fig 24. NN

5.2 CONVOLUTIONAL NEURAL NETWORK

- Convolutional neural network has much filtering process.
- Pixel multiplication with each filter takes place in every n x m image.
- Pooling is used for the matrix size reduction and in proper way of feature extraction.
- In this project, I have used global average pooling.
- In every layer, feature reduction takes place without feature loss.
- In final layers, fully connected layers are made which are actually one-hot matrix.

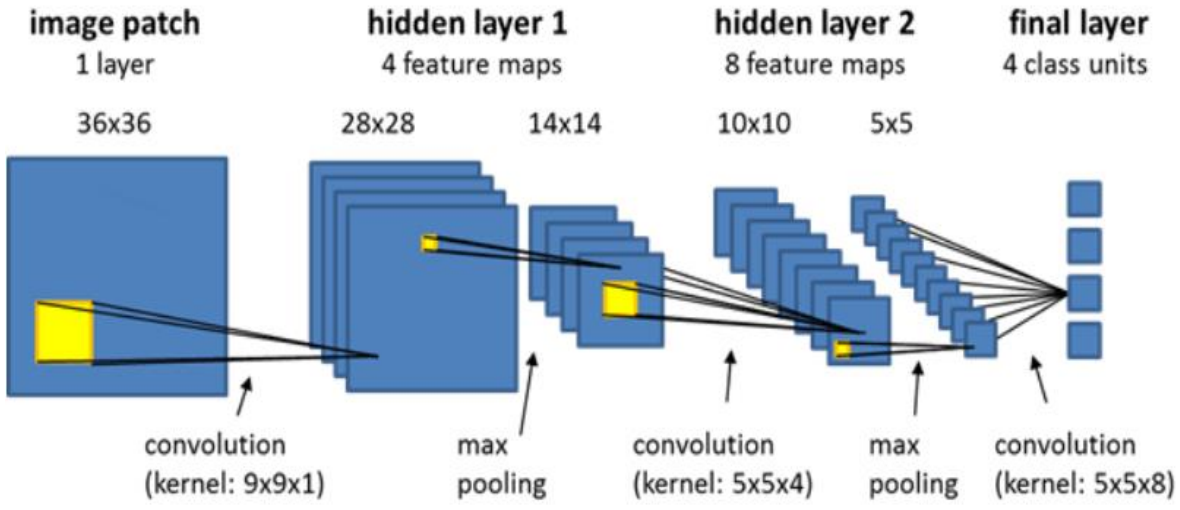


Fig 25. CNN

5.3 VGG 16

- In VGG 16, there are 13 convolutional layers.
- Max pooling is used in the model.
- There are 3 fully connected layers in it.
- It is mainly used for image classification task.

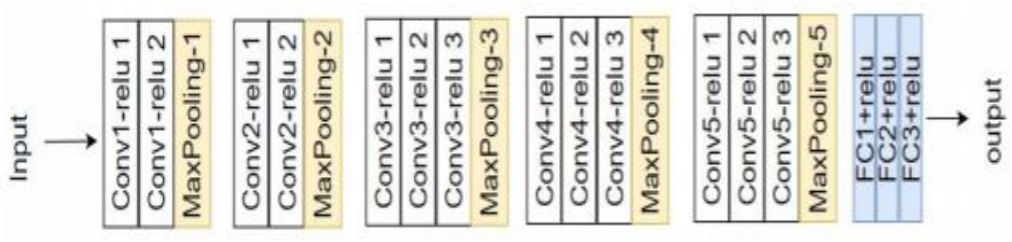


Fig 26. VGG 16

5.4 VGG 19

- In VGG 19, there are 16 convolutional layers.
- Max pooling is used in the model.
- There are 3 fully connected layers in it.
- It is mainly used for image classification task.
- This is the revised model of the VGG 16.

Fig 27. VGG 19

5.5 RESNET

- This network has the concept of skip connections, in order to solve the issue of vanishing gradient.

- The approach behind this network is instead of layers learn the underlying mapping, we allow network fit the residual mapping. So, instead of say H(x), initial mapping, let the network fit, $F(x) := H(x) - x$ which gives $H(x) := F(x) + x$.

- There are 34 plain layers and 34 residual layers.

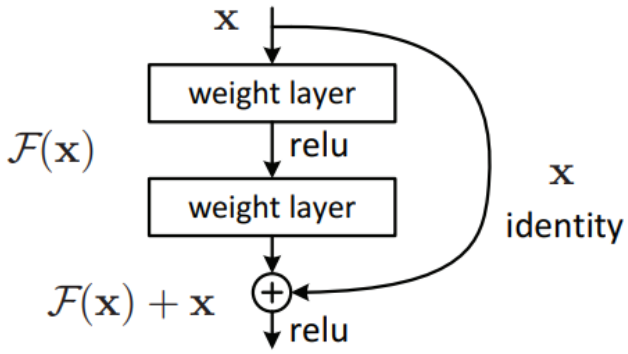


Fig 28. Skip connection

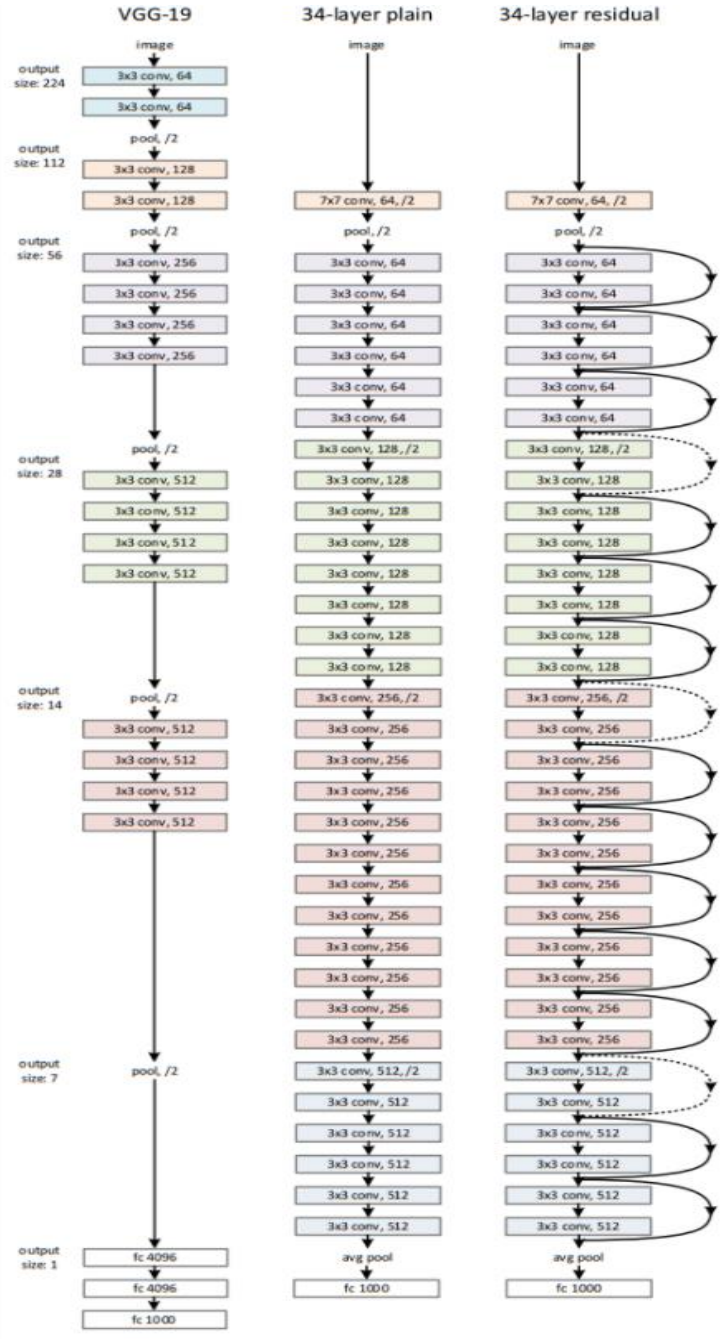


Fig 29. Resnet

5.6 MOBILENET

- MobileNet uses depthwise separable convolutions. It significantly reduces the number of parameters when compared to the network with regular convolutions with the same depth in the nets. This results in lightweight deep neural networks.

- In depthwise convolution, there is m x n convolution result which leads to more feature extraction.

- In pointwise, there is one column similar to fully connected layer.

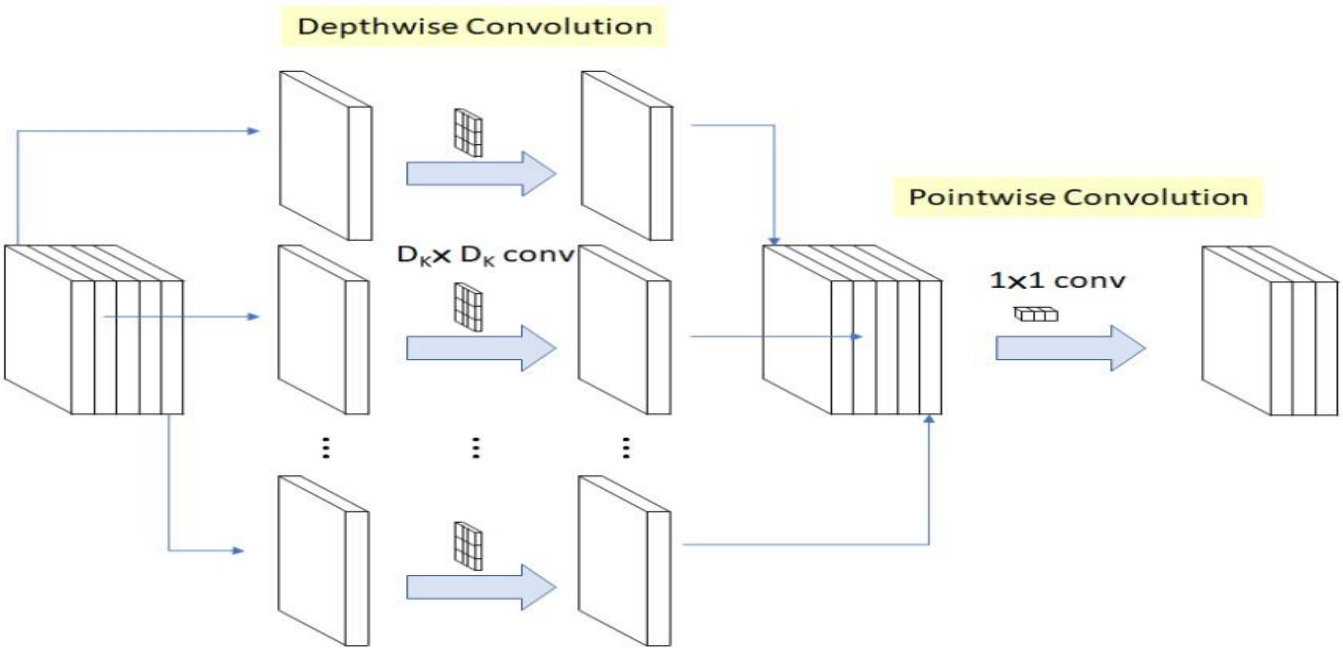


Fig 30. MobileNet

CHAPTER 6

IMPLEMENTATION OF PROSTATE CANCER DETECTION USING DEEP LEARNING

➔ Prostate Cancer detection is being modelled in this project.

➔ As mentioned above in chapter 2, the dataset has been properly arranged in the folder dataset_TMA.

	Benign	6 (3+3)	7 (3+4, 4+3)	8 (4+4, 5+3, 3+5)	9 (4+5, 5+4)	10 (5+5)	Total
TMA 76	42	35	25	15	2	14	133
TMA 80	12	88	38	91	3	13	245
TMA 111	0	95	39	69	16	8	227
TMA 199	61	69	17	26	2	1	176
TMA 204	0	1	2	25	8	69	105

Fig 31. Dataset Summary

➔ Masked image by pathologist1 on mask1_ZT80_38_A_1_1:

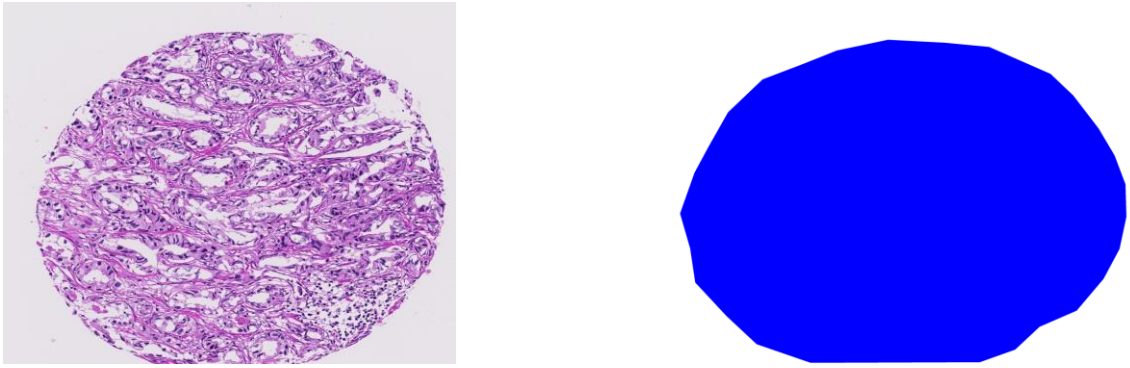


Fig 32. Masking by pathologist1

➔ Masked image by pathologist2 on mask1_ZT80_38_A_1_1:

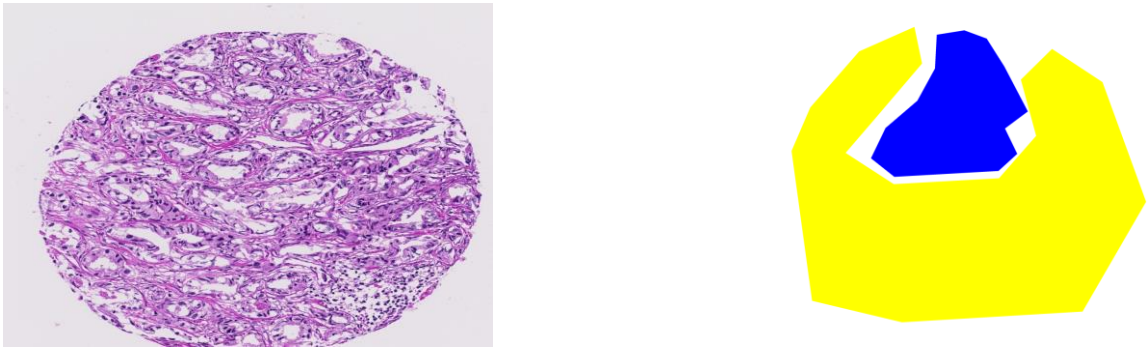


Fig 33. Masking by pathologist2

➔ In this first phase, tissues were generated from that image's patches.

Image tissue conversion to patches example of ZT76_39_A_1_1:

From:

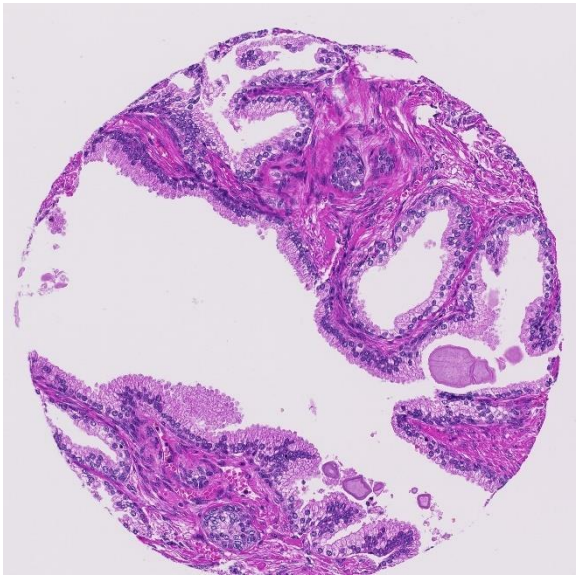
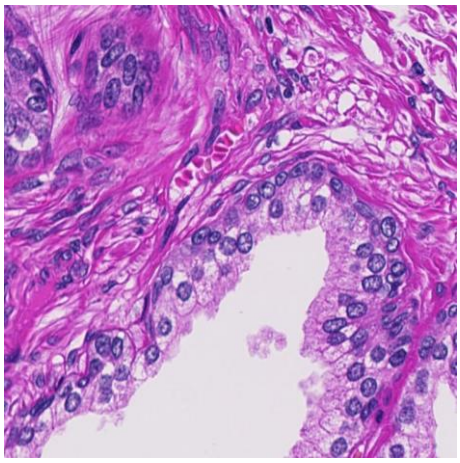
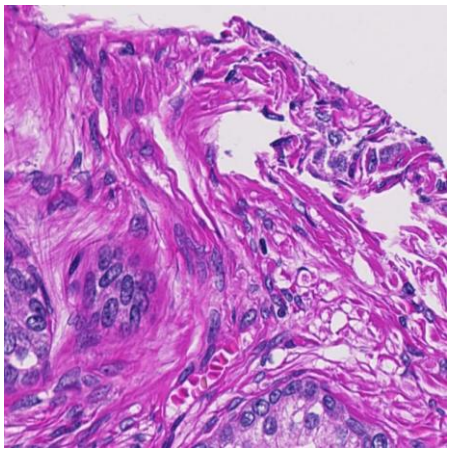
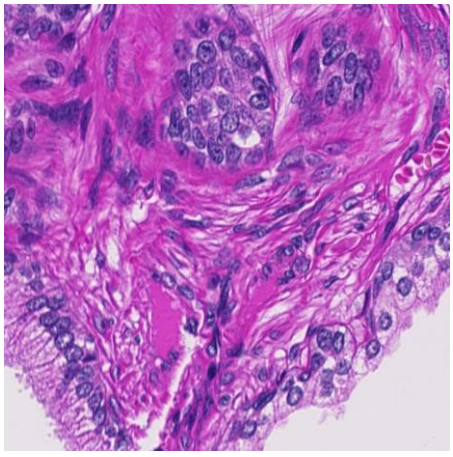


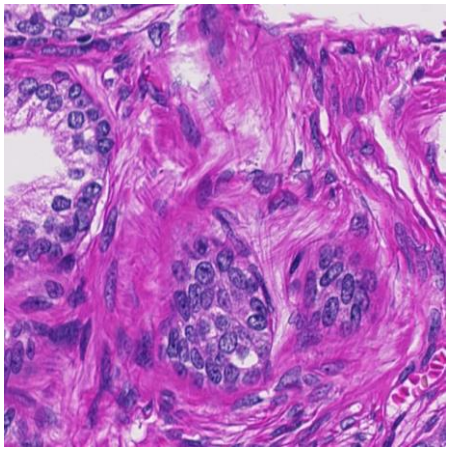
Fig 34. Original Image

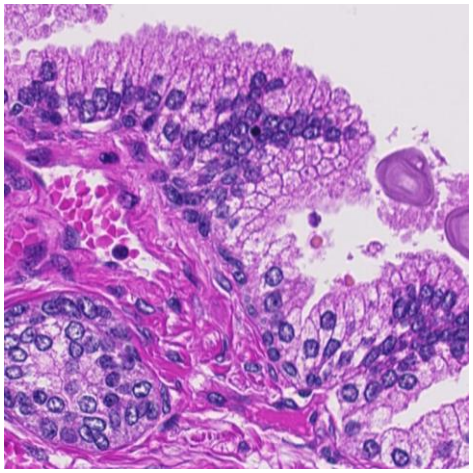
To:

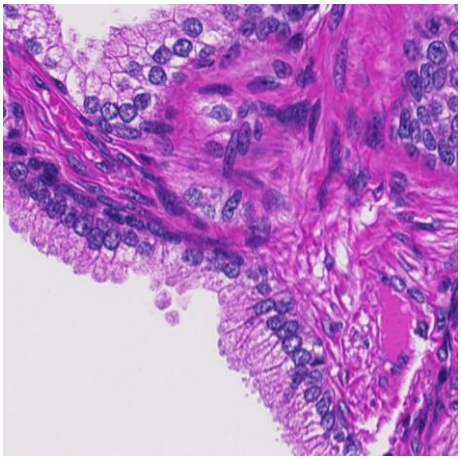












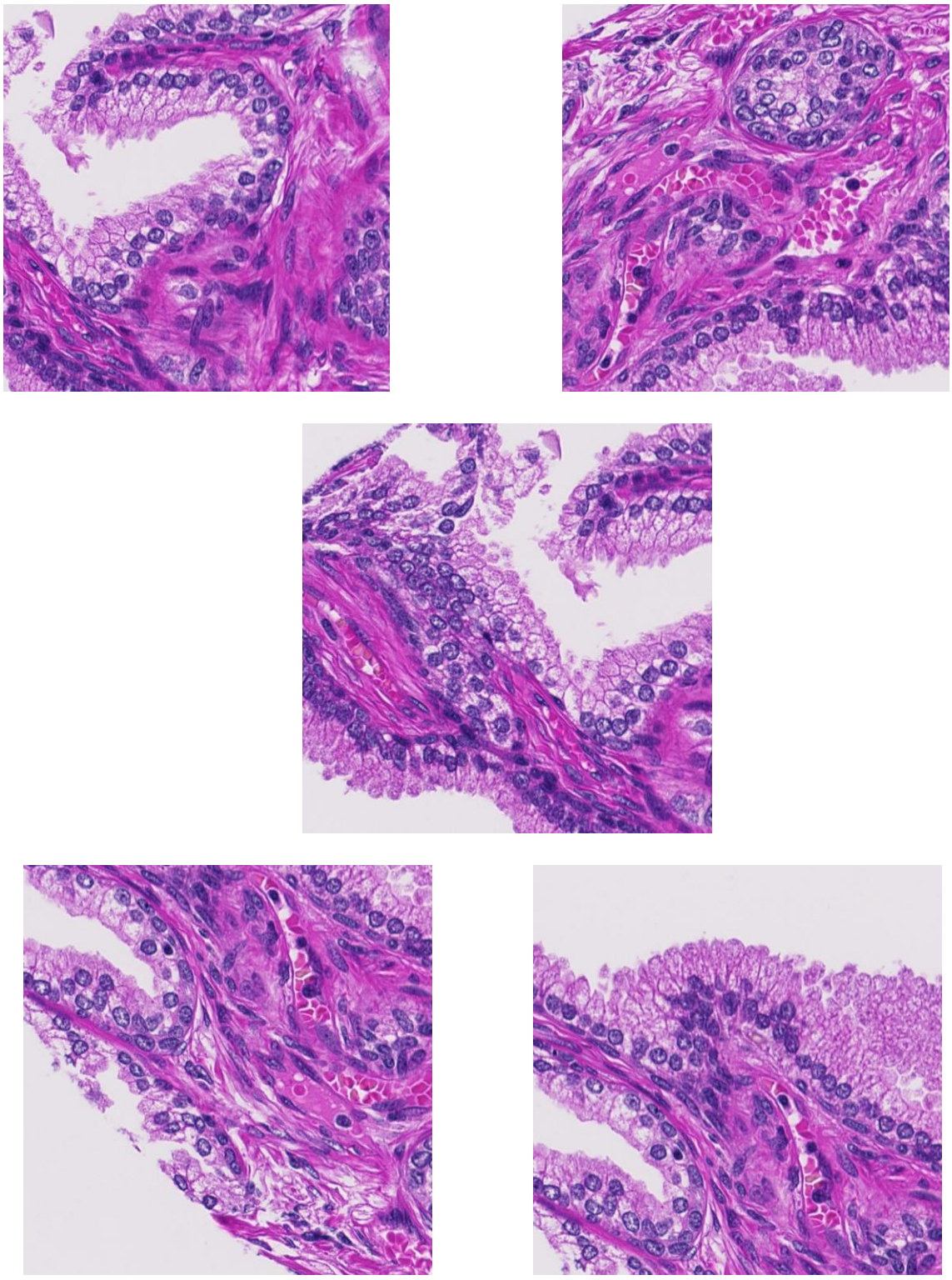


Fig 35. All images are the patches of the fig. 34.

➔ Continuing with the finetuning, the model was tuned with the MOBILENET_50 architecture.

➔ Furthermore, in the create tissue masks the image patches were trained with the patches of tissue and the respective mask with the mentioned colour palette.

my_palette = [0, 255, 0, # benign is green

0, 0, 255, # Gleason 3 is blue

255, 255, 0, # Gleason 4 is yellow

255, 0, 0, # Gleason 5 is red

255, 255, 255] # ignore class is white

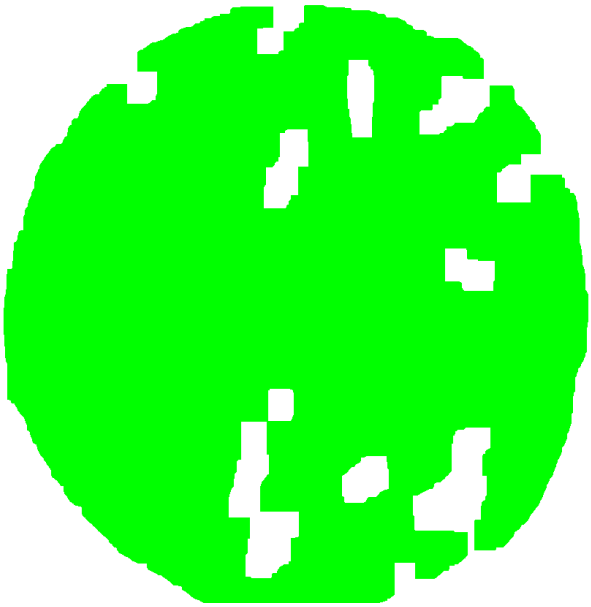


Fig 36. Mask on mask_ZT76_39_A_1_1

Fig 37. Mask on mask_ZT76_39_A_1_2

Fig 38. Mask on mask_ZT76_39_A_1_3

Fig 39. Mask on mask_ZT76_39_A_1_2

➔ Then, that .h5 model was deployed in the heatmap and CAM file with the masking data available.

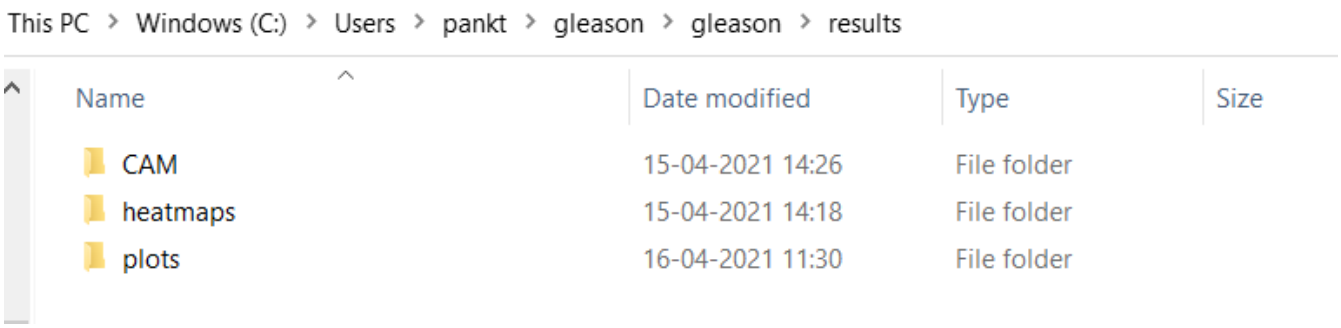


Fig 40. Image of result folder

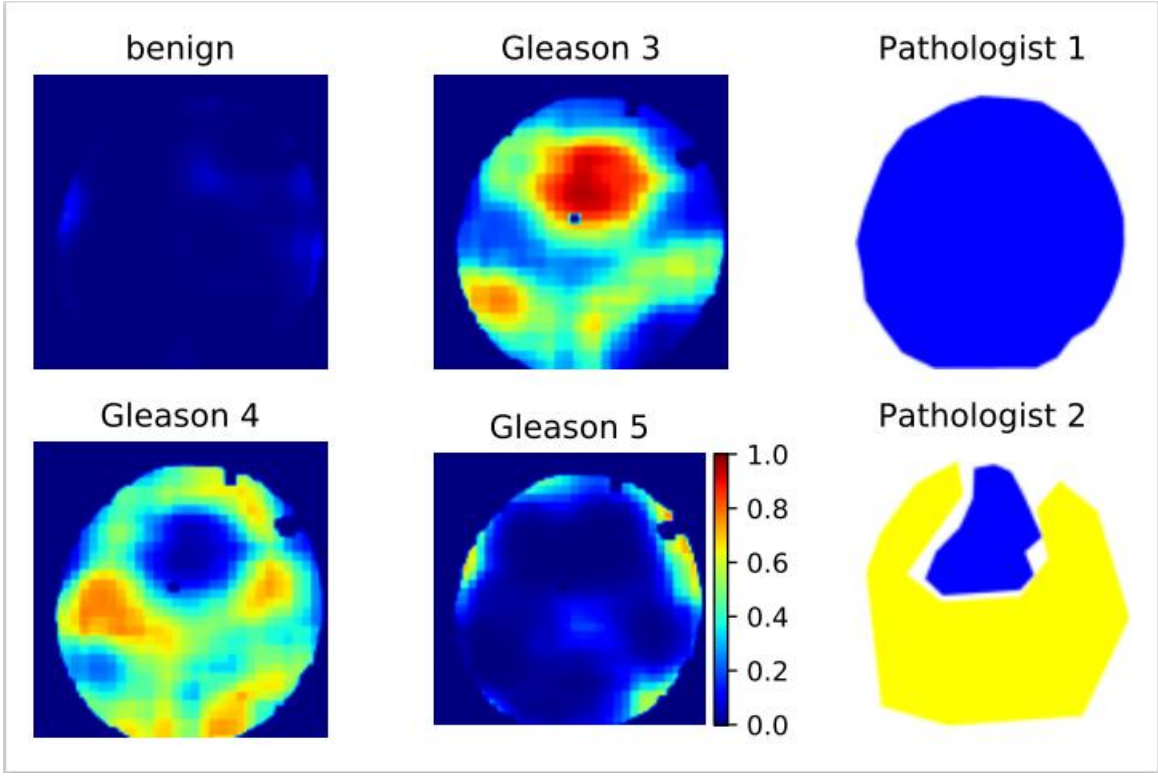


Fig 41. Image of ZT80_38_A_1_1_heatmap_output

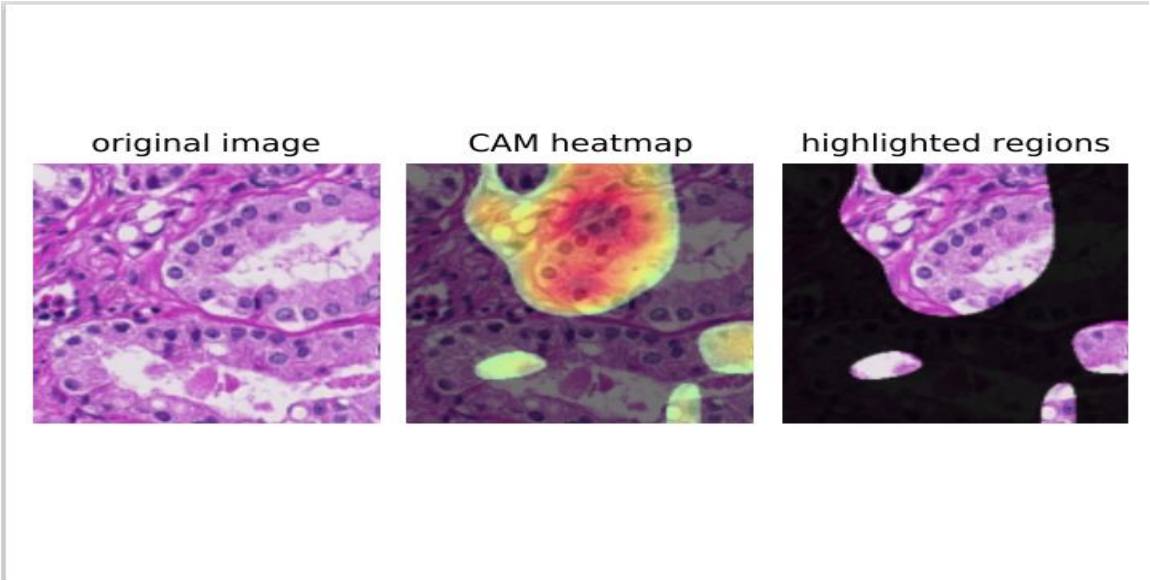


Fig 42. Image of cam_ZT80_38_A_1_2_patch_29_class_1

➔ Finally, the .h5 model with the gleason weights is deployed in the final result visualization file with the amalgamation of the all files and its respective outputs.

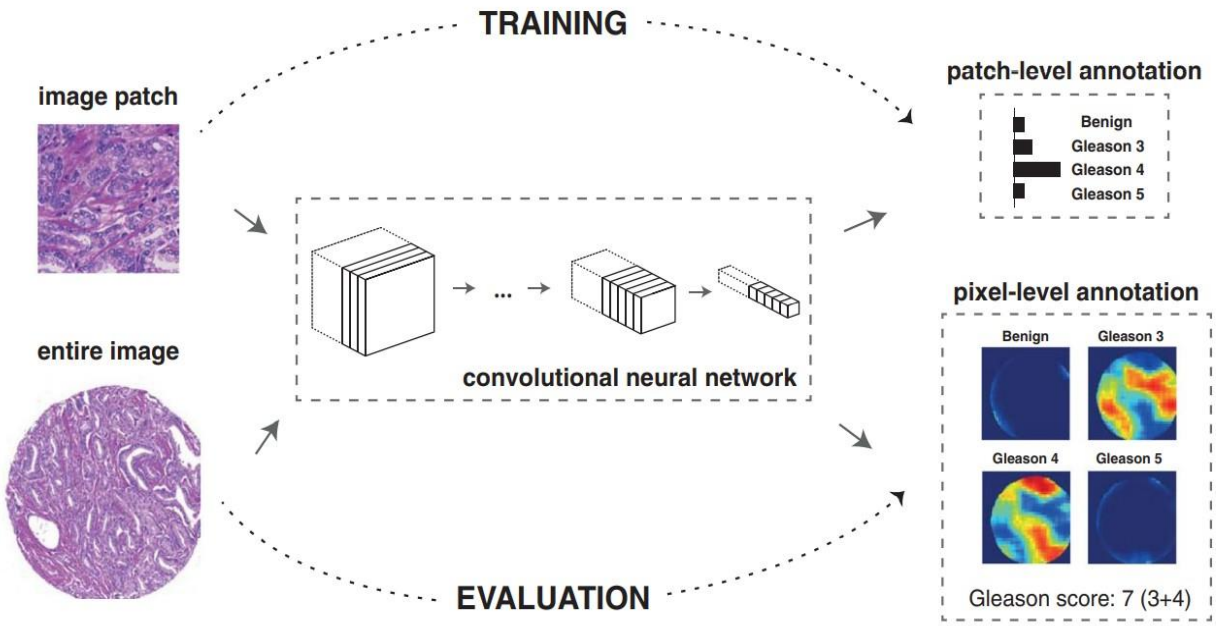
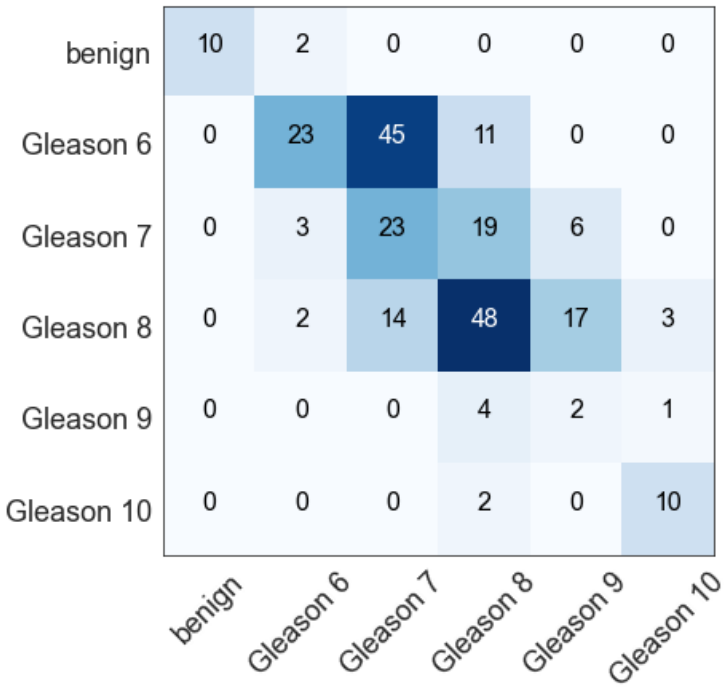
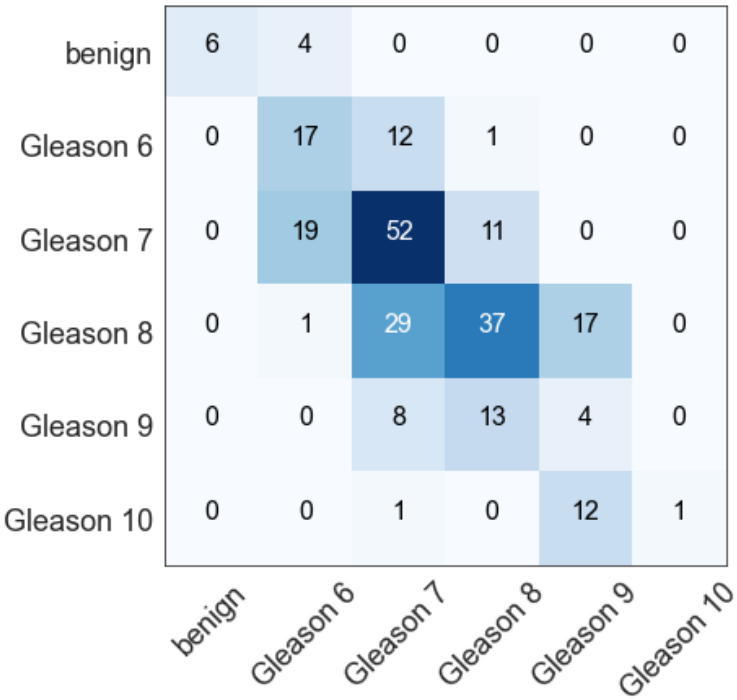


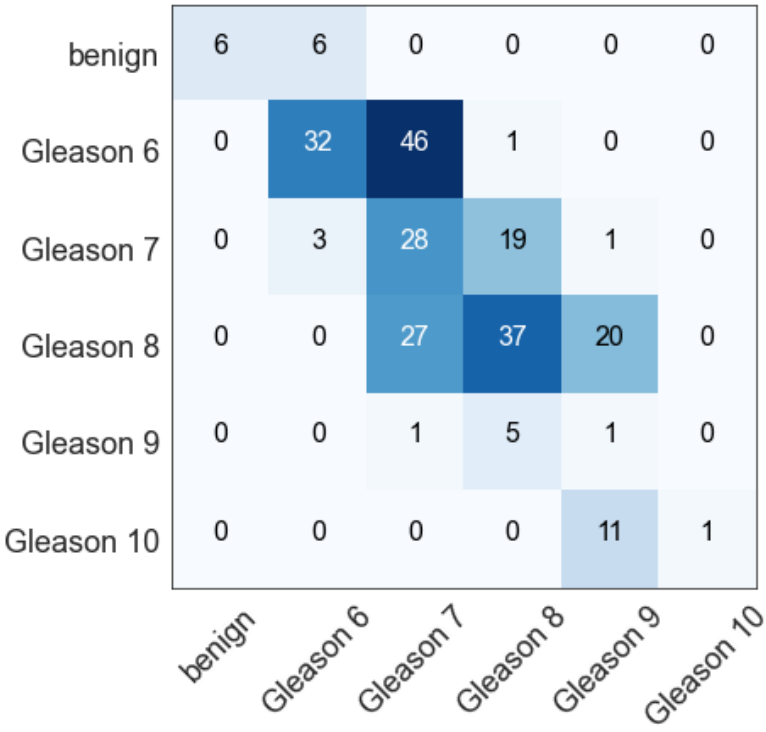
Fig 43. Whole training process diagram


benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10
10 2 0 0 0 0
0 23 45 11 0 0
0 3 23 19 6 0
0 2 14 48 17 3
0 0 0 4 2 1
0 0 0 2 0 10
benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10

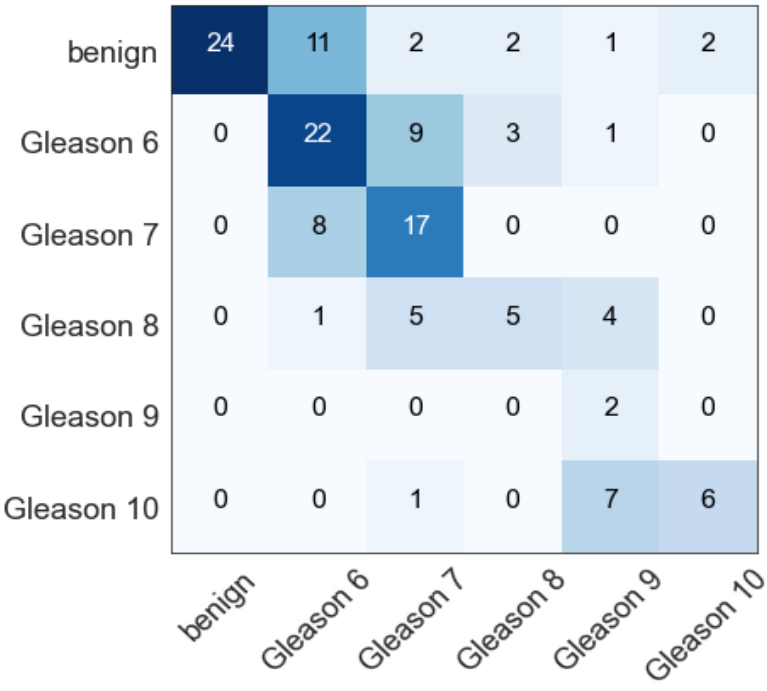
(a)


benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10
6 4 0 0 0 0
0 17 12 1 0 0
0 19 52 11 0 0
0 1 29 37 17 0
0 0 8 13 4 0
0 0 1 0 12 1
benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10

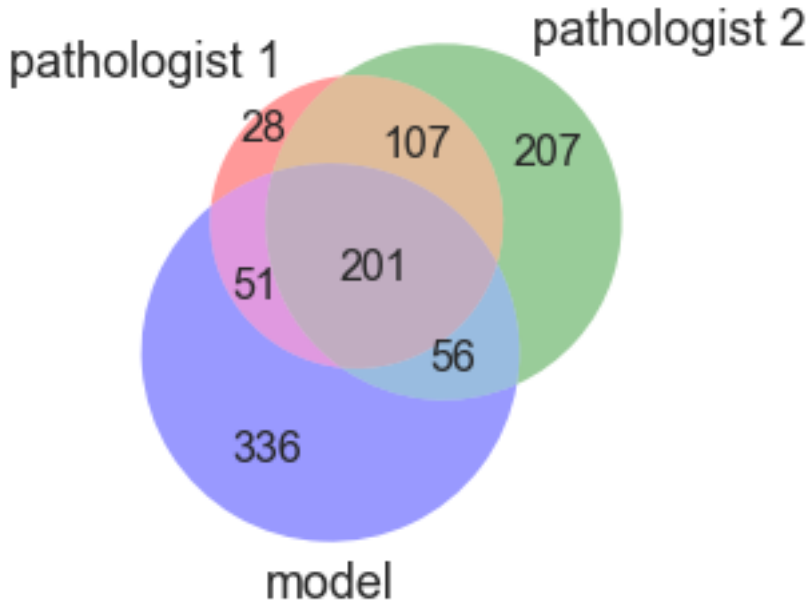
(b)


benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10
6 6 0 0 0 0
0 32 46 1 0 0
0 3 28 19 1 0
0 0 27 37 20 0
0 0 1 5 1 0
0 0 0 0 11 1
benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10

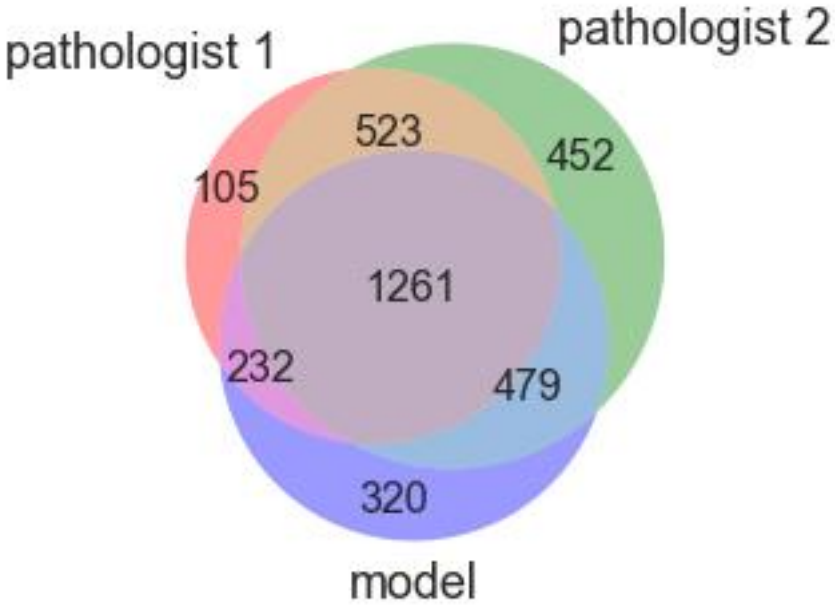
(c)


benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10
24 11 2 2 1 2
0 22 9 3 1 0
0 8 17 0 0 0
0 1 5 5 4 0
0 0 0 0 2 0
0 0 1 0 7 6
benign
Gleason 6
Gleason 7
Gleason 8
Gleason 9
Gleason 10

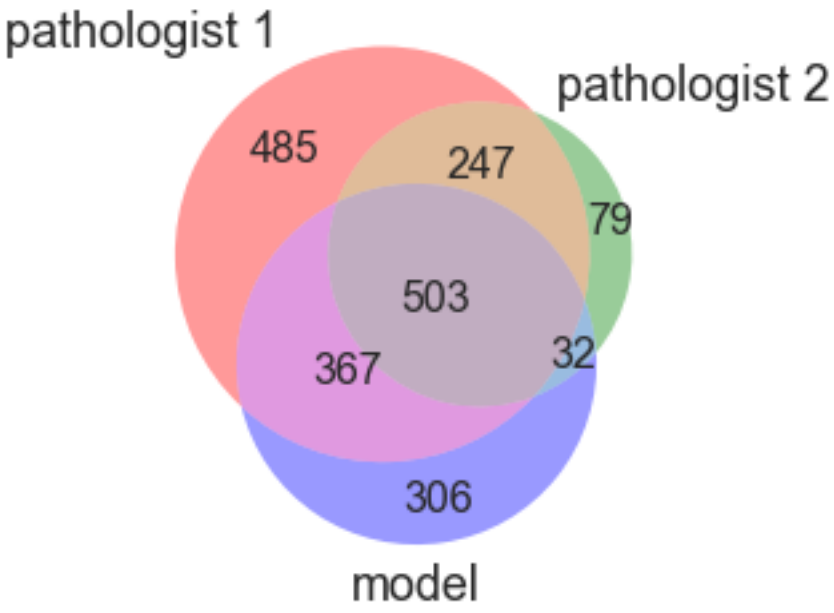
(d)


pathologist 1
pathologist 2
28
107
207
201
51
56
336
model

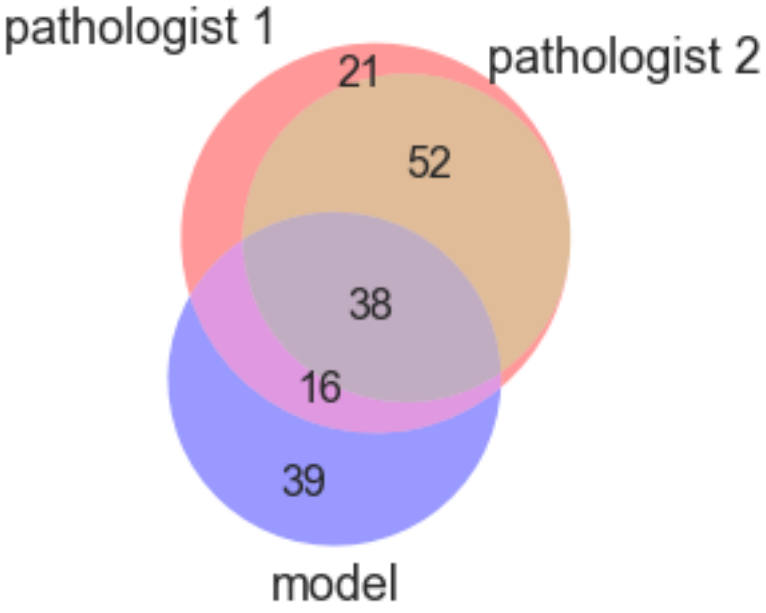
(e)


pathologist 1
pathologist 2
523
452
105
1261
232
479
320
model

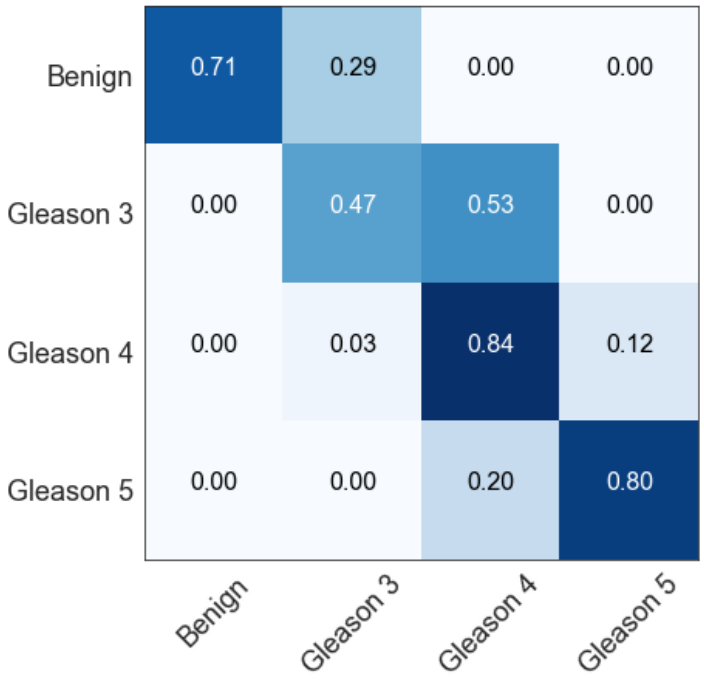
(f)


pathologist 1
pathologist 2
485
247
79
503
367
32
306
model

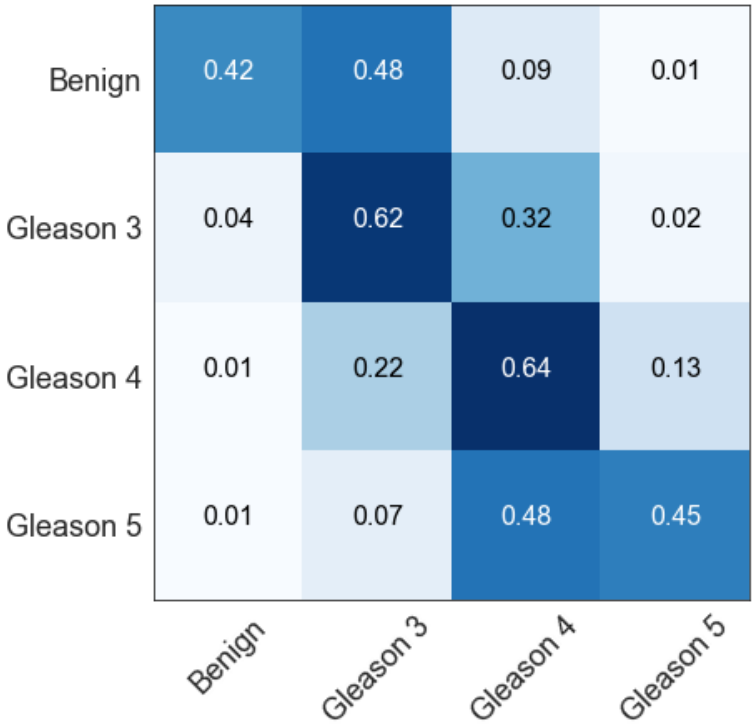
(g)


pathologist 1
pathologist 2
21
52
38
16
39
model

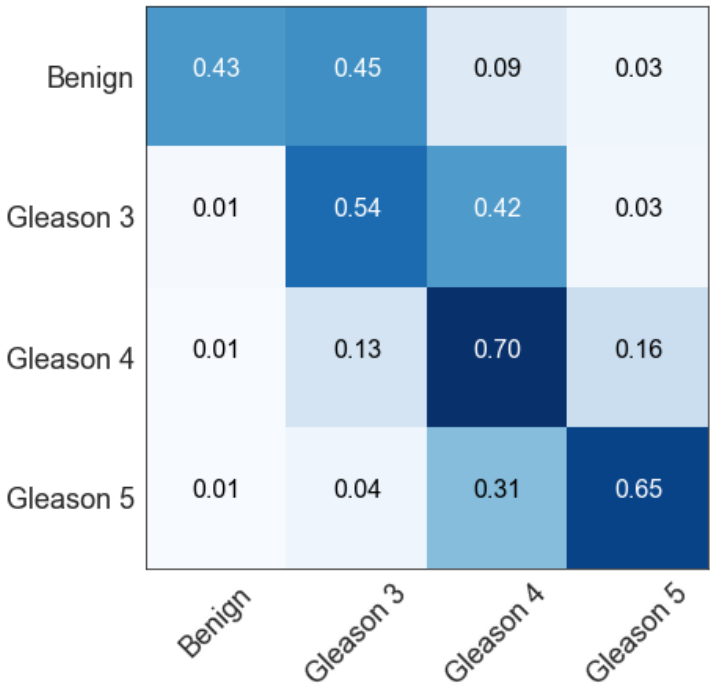
(h)


Benign
Gleason 3
Gleason 4
Gleason 5
0.71
0.29
0.00
0.00
0.00
0.47
0.53
0.00
0.00
0.03
0.84
0.12
0.00
0.00
0.20
0.80
Benign
Gleason 3
Gleason 4
Gleason 5

(i)


Benign
Gleason 3
Gleason 4
Gleason 5
0.42
0.48
0.09
0.01
0.04
0.62
0.32
0.02
0.01
0.22
0.64
0.13
0.01
0.07
0.48
0.45
Benign
Gleason 3
Gleason 4
Gleason 5

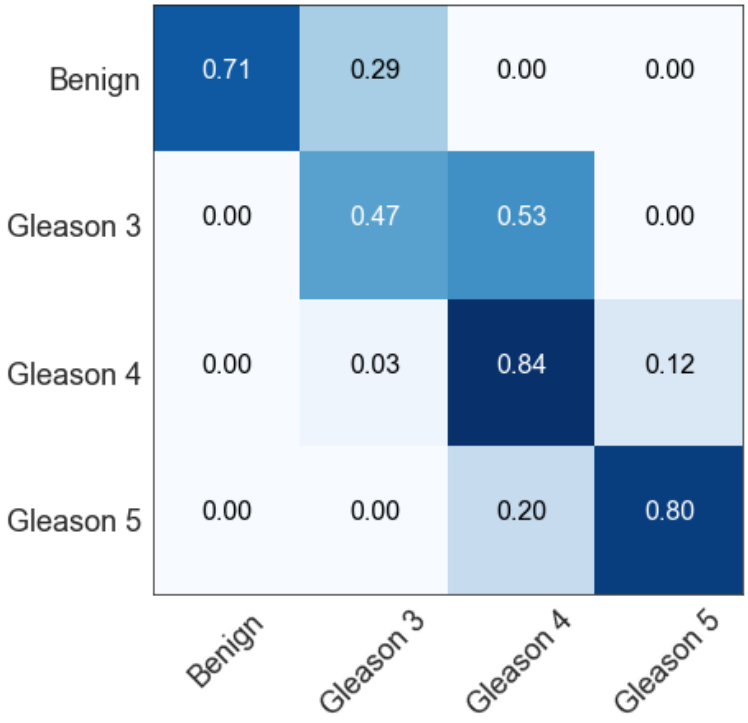
(j)


Benign
Gleason 3
Gleason 4
Gleason 5
0.43
0.45
0.09
0.03
0.01
0.54
0.42
0.03
0.01
0.13
0.70
0.16
0.01
0.04
0.31
0.65
Benign
Gleason 3
Gleason 4
Gleason 5

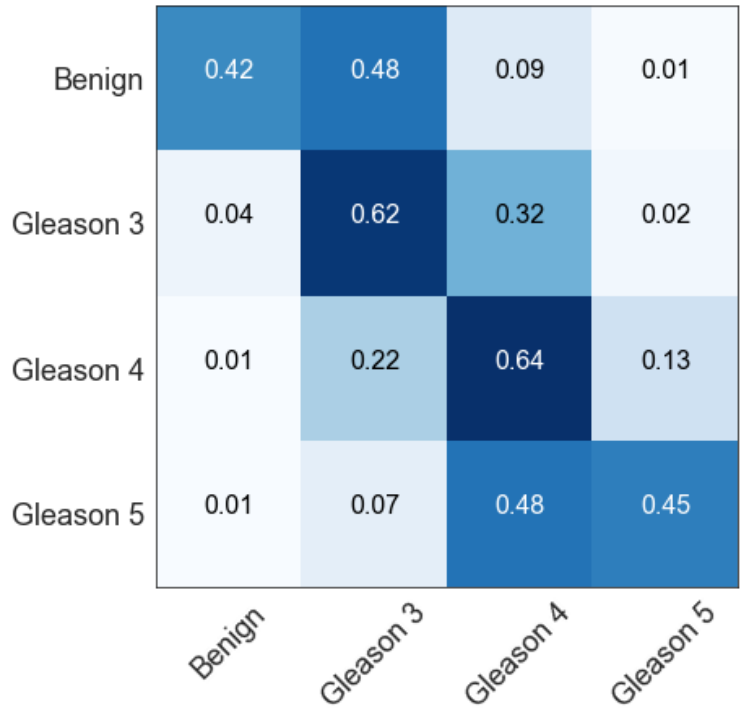
(k)


Benign
Gleason 3
Gleason 4
Gleason 5
0.63
0.17
0.11
0.10
0.03
0.72
0.23
0.02
0.01
0.24
0.58
0.17
0.02
0.01
0.09
0.88
Benign
Gleason 3
Gleason 4
Gleason 5

(l)


Benign
Gleason 3
Gleason 4
Gleason 5
0.71
0.29
0.00
0.00
0.00
0.47
0.53
0.00
0.00
0.03
0.84
0.12
0.00
0.00
0.20
0.80
Benign
Gleason 3
Gleason 4
Gleason 5

(m)


Benign
Gleason 3
Gleason 4
Gleason 5
0.42
0.48
0.09
0.01
0.04
0.62
0.32
0.02
0.01
0.22
0.64
0.13
0.01
0.07
0.48
0.45
Benign
Gleason 3
Gleason 4
Gleason 5

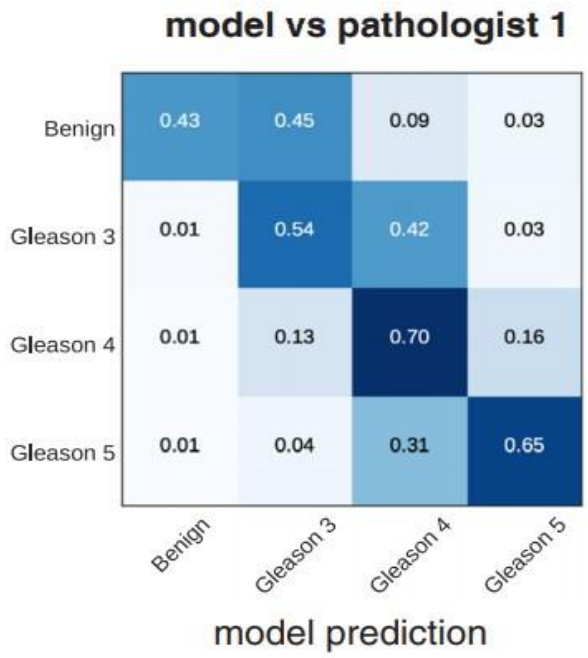
(n)


Benign
Gleason 3
Gleason 4
Gleason 5
0.43
0.45
0.09
0.03
0.01
0.54
0.42
0.03
0.01
0.13
0.70
0.16
0.01
0.04
0.31
0.65
Benign
Gleason 3
Gleason 4
Gleason 5

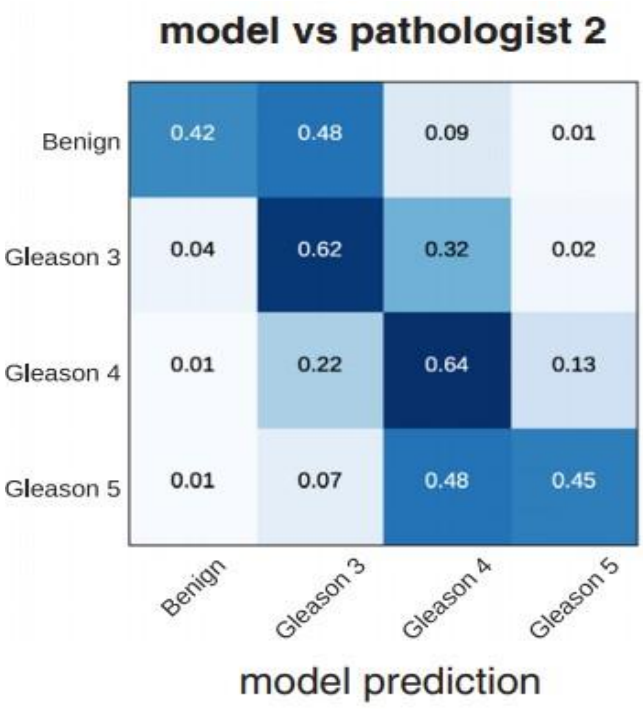
(o)


Benign
Gleason 3
Gleason 4
Gleason 5
0.63
0.17
0.11
0.10
0.03
0.72
0.23
0.02
0.01
0.24
0.58
0.17
0.02
0.01
0.09
0.88
Benign
Gleason 3
Gleason 4
Gleason 5

(p)



(q)



(r)

Fig 44. A- R is the output confusion matrix and other diagrams

CHAPTER 7

LITERATURE REVIEW

[2] Deep neural network is complex in terms of architecture. Layers have been designed such that the gain accuracy elevates from considerably increased depth. They have utilised the ImageNet model with VGG nets. Ensemble residual net lowers the complexity. An analysis on CIFAR dataset has been provided with 100 and 1000 layers. Deep Residual networks is the proposed model of COCO 2015 competition for detection and segmentation. In this they have used pre-designed VGG-19 architecture and continuing with 34 layers plain and 34 residual layers with global average pooling. This network works well with PASCAL and MS COCO dataset. Detection of objects with VGG and ResNet based model is very high.

[3] In this paper, they have provided comparison of disparate architectures such as DNN, CNN, RNN, Deep CNN Extreme learning machine, Deep Boltzman Machine and many more with their advantages and disadvantages. In medical imaging, maximum use of CNN architecture is being applied. Furthermore, summary of diabetic retinopathy has been provided with different layers of neural network. Even, the analysis of tumour detection, cardiac imaging has been provided. With the help of GoogLeNet, LeNet-5 and AlexNet they are able to gain 98.66%, 96.18% and 95.79% accuracy respectively for tumour detection. In Alzheimer disease detection, they have received 100% accuracy for malaria with the DCNN. With the help of GoogLeNet, LeNet-5 and AlexNet they are able to gain 98.66%, 96.18% and 95.79% accuracy respectively.

[4] Digitization has accelerated in two consecutive decades. Tissue regions identification in WSI. Tissues like alveolar, fatty and poor staining are difficult to detect. In this, they have performed practical analysis on U-net architecture with disparate backbone network. Comparison of backbone network on MobileNet, ResNet50, ResNet101, EfficientNet-B3 and DenseNet121. TCGA dataset has been used for modelling with labelled subset. Tissue segmentation is the main motive in this. 0.99 sensitivity and specificity has been achieved with the MobileNet and EfficientNet-B3 architecture. Lowest specificity has been received with VGG16 and lowest sensitivity has been received when implemented with the Otsu Algorithm. Performance measure is given in terms of dice co-efficient also.

[5] In this paper, they have majorly emphasised on data augmentation method on PC dataset. They have used five most commonly used techniques such as random rotation, horizontal flip, vertical flip, random crop and translation on MRI dataset which has 217 patient's data. Augmentation algorithms were applied on CNN with different augmented data and also tested it on 95 patients and validated on 102 data. Shallow network worked well with 2D slice data with 85% accuracy. Furthermore, detailed analysis of augmentation methods has been provided in this paper with mathematical equations. In shallow network, they have taken 4 convolutional layers and 3 fully connected layers whereas in deep network, they have taken 10 convolutional layers and 4 fully connected layers. Max pooling is used in both the network. Accuracy with deep network is about 80.23 and 74.81 on validation and test dataset respectively.

[6] HyperDense Net has been designed for the segmentation process on the MRI images. It has taken 6- month infant data and images of an adult for training purpose. It has received 90% accuracy on the data.

[7] In this paper, they have done classification on PC MRI data. With SVM, they have achieved median of 0.91 whereas on linear discriminant analysis they have received 0.74. Thorough discussion has been provided in there with the discrimination statistics. This is a systematic review with the PC classification with machine and deep learning algorithms. It points out that methods for validation is lacking.

[8] The Gleason score is the most important thing in the analysing part. The system was developed using 1243 patients with 5834 biopsies. They have used U-net model for training purpose and it showcases that it outperforms 10 out of 15 pathologists.

[9] This paper is the best paper I have found on the prostate cancer. It has worked on the Harvard dataverse as taken in this project. It works on the tissue microarrays. Automated annotation procedures constitute a viable solution to remedy these limitations. In this study, we present a deep learning approach for automated Gleason grading of prostate cancer tissue microarrays with Hematoxylin and Eosin (H&E) staining. Our system was trained using detailed Gleason annotations on a discovery cohort of 641 patients and was then evaluated on an independent test cohort of 245 patients annotated by two pathologists. On the test cohort, the inter-annotator agreements between the model and each pathologist, quantifed via Cohen's quadratic kappa statistic, were 0.75 and 0.71 respectively, comparable with the inter-pathologist agreement (kappa=0.71).

[10] Totally, 191 patients were taken for MRI and systematic and targeted fusion biopsy was made. Models were scrutinized and marked with the use of repeated 5-fold cross-validation and a special independent test cohort. In the test cohort, an ensemble model with the combination of a radiomics model, with models for PI-RADS, PSAD and DRE recieved high predictive AUCs for the differentiation of (i) malignant from benign prostatic lesions (AUC = 0.889) and of (ii) clinically significant (csPCa) from clinically insignificant PCa (cisPCa) (AUC = 0.844).

[11] Biomedical Image classification is the most novice domain in the field of artificial intelligence. A new modelled named, c-net was designed for this purpose. It was applied on the two histological based datasets namely BreakHis and Osteosarcoma. It outperforms on both with zero misclassification.

[12] This prostate cancer detection was made with the help of the transfer learning. Robust CNN is deployed using this approach. Results are compared with the machine learning classifiers. Highest accuracy was received on GoogLeNet.

[13] There are 136 patients among with 73 patients with PC and remaining without PC. For predicting the presence of PCa, the AUCs of clinical independent risk factors model, mp-MRI model, and mixed model were 0.81, 0.93, and 0.94 in training sets, and 0.74, 0.92, and 0.93 in validation sets, respectively.

CONCLUSION

The prostate cancer is the deadliest disease which occurs only in men. Mostly, it is detected in the advanced state of that cancer. It cells has much variance in its histological patches which leads to critical thinking for its examination. So, early and accurate detection can help in its proper treatment before time. As of now, artificial intelligence is playing a vital role in the biological domain. Examination of prostate cancer with the help of Gleason grading system is most accurate till now. Therefore, the dataset has been used which has graded patches with Gleason grade. In this pattern, there is two types of grade annotation which leads to the complexity in prediction. With the usage of deep learning algorithm such as MobileNet architecture, I have deployed the code with good prediction rate. Application of deep learning in this disease leads to early detection in most of the cases.

In future, I will try to implement with other algorithms and make an ideal model with high true positive rate. Thus, the trained model can be framed into a handy application for easy and worthy usage.

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