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Chapter 1

Introduction

CHAPTER 1

Introduction

Problem overview

Cancer is a leading cause of death worldwide, according to research by the World Health Organization (WHO), which has shown that nearly 10 million deaths in 2020, or nearly one in six deaths.

Cancer spread in the world, affecting 197.9 per 100,000 people, and men were more likely to have 218.6 infections per 100,000 people, compared to 182.6 cases per 100,000 people, and these statistics are according World Cancer Research Fund.

Cancer is a leading cause of death worldwide, accounting for nearly 10 million deaths in 2020. The most common in 2020 (in terms of new cases of cancer) were:

*breast (2.26 million cases);

*lung (2.21 million cases);

*colon and rectum (1.93 million cases);

*prostate (1.41 million cases);

*skin (non-melanoma) (1.20 million cases); and

*stomach (1.09 million cases).



1.2 Definitions and History

Definitions

Cancer is a disease in which some of the body's cells grow uncontrollably and spread to other parts of the body. Cancer can start almost anywhere in the human body, which is made up of trillions of cells. Normally, human cells grow and multiply (through a process called cell division) to form new cells as the body needs them. Sometimes this orderly process breaks down, and abnormal or damaged cells grow and multiply when they shouldn't. These cells may form tumors, which are lumps of tissue. Tumors can be cancerous or not cancerous (benign).

History:

History of Cancer :18th Century to Present

During the 18th century, 3 important observations launched the field of cancer epidemiology (epidemiology is the study of causes, distribution, and control of diseases):

In 1713, Bernardino Ramazzini, an Italian doctor, reported the virtual absence of cervical cancer and relatively high incidence of breast cancer in nuns and wondered if this was in some way related to their celibate lifestyle. In 1775, Percival Pott of Saint Bartholomew's Hospital in London described an occupational cancer in chimney sweeps, cancer of the scrotum, which was caused by soot collecting in the skin folds of the scrotum.

Thomas Venner of London was one of the first to warn about tobacco dangers in his *Via Recta*, published in London in 1620. He wrote that "immoderate use of tobacco hurts the brain and the eye and induces trembling of the limbs and the heart." And 150 years later, in 1761, only a few decades after recreational tobacco became popular in London, John Hill wrote a book entitled *Cautions Against the Immoderate Use*. These first observations linking tobacco and cancer led to epidemiologic research many years later (in the 1950s and early 1960s) which showed that smoking causes lung cancer and led to the US Surgeon General's 1964 report *Smoking and Health*.

How Does Cancer Develop?

Cancer is a genetic disease—that is, it is caused by changes to genes that control the way our cells function, especially how they grow and divide.

Genetic changes that cause cancer can happen because:

- of errors that occur as cells divide.

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- of damage to DNA caused by harmful substances in the environment, such as the chemicals in tobacco smoke and ultraviolet rays from the sun
- they were inherited from our parents

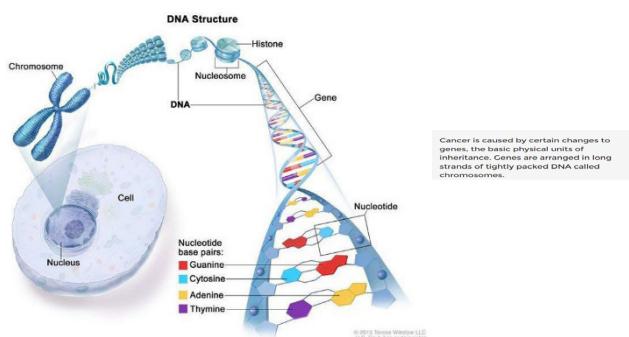
Types of Genes that Cause Cancer:

the genetic changes that contribute to cancer tend to affect three main types of genes—proto-oncogenes, tumor suppressor genes, and DNA repair genes. These changes are sometimes called “drivers” of cancer.

Proto-oncogenes: are involved in normal cell growth and division. However, when these genes are altered in certain ways or are more active than normal, they may become cancer-causing genes (or oncogenes), allowing cells to grow and survive when they should not.

Tumor suppressor: genes are also involved in controlling cell growth and division. Cells with certain alterations in tumor suppressor genes may divide in an uncontrolled manner.

DNA repair gene: are involved in fixing damaged DNA. Cells with mutations in these genes tend to develop additional mutations in other genes and changes in their chromosomes, such as duplications and deletions of chromosome parts. Together, these mutations may cause the cells to become cancerous.



Cancer prevention:

Since cancer most commonly occurs for genetic reasons, there are some external factors and exposure to a lot of these factors causes this disease

These factors are the following:

- Smoking (either type)
- drinking alcohol
- Exposure to air polluted environment
- Too much sun exposure

To avoid getting cancer, you must follow the general guidelines from the World Health Organization, which are represented in the figure shown

Ways to reduce your cancer risk



Do not smoke or use any form of tobacco



Make your home smoke-free



Breastfeeding reduces the mother's cancer risk



Vaccinate your children against Hepatitis B and HPV



Avoid too much sun, use sun protection



Reduce indoor and outdoor air pollution



Be physically active



Limit alcohol intake



Take part in organized cancer screening programmes

This project deals with cancer in general, especially hereditary and most common cancers, so we studied breast cancer and brain cancer.

Breast cancer:

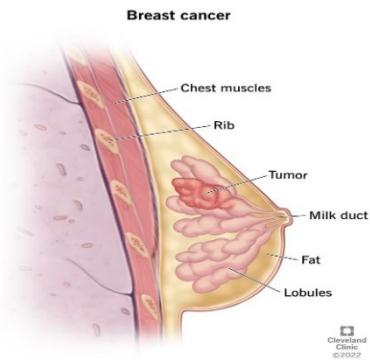
Breast cancer arises in the cells lining (the epithelium) of the ducts (85%) or the lobules (15%) of the glandular breast tissue. Initially, the cancerous growth is limited to the duct or lobule, where it generally does not cause symptoms and its spread diminishes. Over time, these cancers may develop *in situ* (stage 0) and invade surrounding breast tissue (invasive breast cancer) and then spread to nearby lymph nodes (metastasis near the end). tumor) or to other organs in the body (distant metastases). If a woman dies of breast cancer, it is attributed to widespread metastases.

Breast cancer is the most common type of cancer with more than 2.2 million cases in 2020. About 1 in 12 women will develop breast cancer in their lifetime. Breast cancer is the number one cause of cancer death among women, with approximately 685,000 women dying from it in 2020. The incidence ranges from high-income countries to low- and middle-income countries. Survival after infection in high-income countries is 90%, and in low-income countries, survival rates range from 40% to 66%.

CHAPTER 1

SYMPTOMS:

- a lump or thickening in the breast;
- a change in its size, shape or appearance;
- or other alteration of the skin;
- a change in the appearance of the nipple or a change in the skin of the nipple (areola)



Brain cancer:

A brain tumor is an abnormal growth^[1] of tissue in the brain or central spine that can disrupt proper brain function. Doctors refer to a tumor based on where the tumor cells originated, and whether they are cancerous (malignant) or not (benign).

Benign: The least aggressive type of brain tumor is often called a benign brain tumor. They originate from cells within or surrounding the brain, do not contain cancer cells, grow slowly, and typically have clear borders that do not spread into other tissue.

Malignant: Malignant brain tumors contain cancer cells and often do not have clear borders. They are considered to be life threatening because they grow rapidly and invade surrounding brain tissue.

Primary: Tumors that start in cells of the brain are called primary brain tumors. Primary brain tumors may spread to other parts of the brain or to the spine, but rarely to other organs.

Metastatic: Metastatic or secondary brain tumors begin in another part of the body and then spread to the brain. These tumors are more common than primary brain tumors and are named by the location in which they begin.

SYMPTOMS:

- Recurrent headaches

- Issues with vision
- Seizures
- Changes in personality
- Short-term memory loss
- Poor coordination
- Difficulty speaking or comprehending



1.3 Problem definitions:

Cancer is a deadly disease and diagnosing it is not simple because it costs a lot of money. For example, breast cancer tests in Egypt in some cases amount to more than tens of thousands of pounds. In addition, tests for some types of cancer need a difficult method, and there are some cases that cannot tolerate these methods

Late diagnosis of cancer reduces the chance of survival, especially in low- and middle-income countries

The wide spread of cancer in general, and especially breast and brain cancer around the world, has shifted the attention of countries to establishing institutions and organizations responsible for raising awareness, facilitating early diagnosis and detection, and increasing investment in scientific research in order to access new treatments. One such treatment, to name a few, is therapy. With genes, this method depends on a complete and detailed genetic analysis to know the most accurate functions of the gene and its impact on the formation of cancer cells and to identify the functional units in the gene for the purpose of trying to reach a means that enables dealing with these units and repairing them to fight cancer, whether by curbing cancer or limiting its spread.

Chapter 2

Our Genes

2.1 introduction

In this chapter, we will talk about genes that are responsible for the breast and ovarian cancer and brain cancer. Through it, we determined the definition of the gene, its location, and the mutations that occur in the gene that cause cancer of the gene.

2.2 BRCA

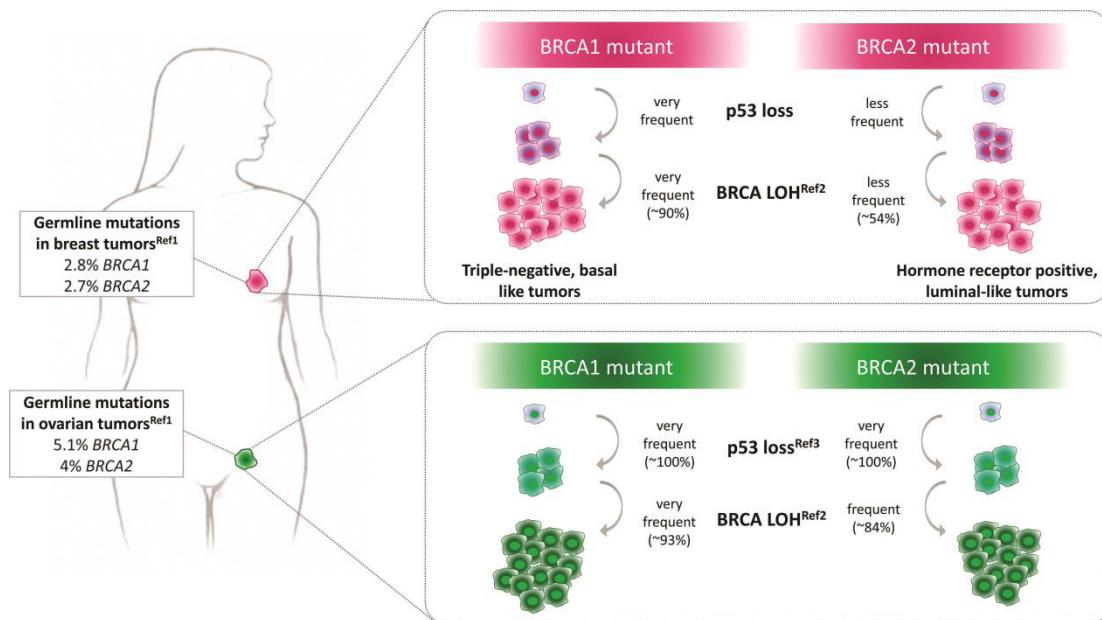
The genes most commonly affected in hereditary breast and ovarian cancer are the *breast cancer type 1 (BRCA1)* and *breast cancer type 2 (BRCA2)* genes. About 5% of breast cancers (about 5,000 women per year) and 10% of ovarian cancers (about 1,000 women per year) result from inherited mutations in the *BRCA1* and *BRCA2* genes.

Both two genes are tumor suppressor genes and that means the *BRCA1* and *BRCA2* genes protect you from getting certain cancers. But some mutations in the *BRCA1* and *BRCA2* genes prevent them from working properly, so that if you inherit one of these mutations, you are more likely to get breast, ovarian, and other cancers. However, not everyone who inherits a *BRCA1* or *BRCA2* mutation will get breast or ovarian cancer.

Everyone has two copies of the *BRCA1* and *BRCA2* genes, one copy inherited from their mother and one from their father. Even if a person inherits a *BRCA1* or *BRCA2* mutation from one parent, they still have the normal copy of the *BRCA1* or *BRCA2* gene from the other parent. Cancer occurs when a second mutation happens that affects the normal copy of the gene, so that the person no longer has a *BRCA1* or *BRCA2* gene that works properly. Unlike the inherited *BRCA1* or *BRCA2* mutation, the second mutation would not be present throughout the person's body, but would only be present in the cancer tissue. Breast and ovarian cancer can also be caused by inherited mutations in genes other than *BRCA1* and *BRCA2*. This means that in some families with a history of breast and ovarian cancer, family members will not have mutations in *BRCA1* or *BRCA2*, but can have mutations in one of these other genes. These mutations might be identified through [genetic testing](#) using multigene panels, which look for mutations in several

different genes at the same time.

You and your family members are more likely to have a *BRCA1* or *BRCA2* mutation if your family has a strong history of breast or ovarian cancer. Family members who inherit *BRCA1* and *BRCA2* mutations usually share the same mutation. If one of your family members has a known *BRCA1* or *BRCA2* mutation, other family members who get [genetic testing](#) should be checked for that mutation.



BRCA1

BRCA1 Mutation

Responsible for approximately 35% of hereditary breast cancer

Increased risk of developing breast cancer by age 70 to 44% to 78%

Increased risk of developing ovarian cancer by age 70 to 18% to 54%

Increased risk of developing male breast cancer by age 70 to 0.22 to 2.8%

BRCA1 Location

This gene is located on chr 17 (NC_000017.11)

CHAPTER 2

BRCA2

BRCA 2 Mutation

Responsible for approximately 25% of hereditary breast cancer

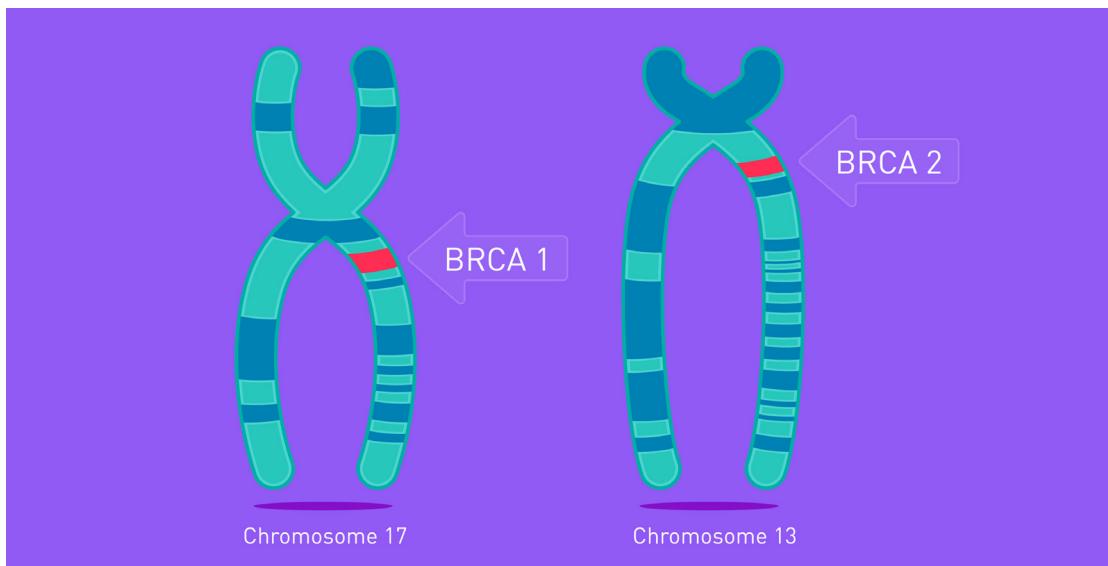
Increased risk of developing breast cancer by age 70 to 31% to 56%

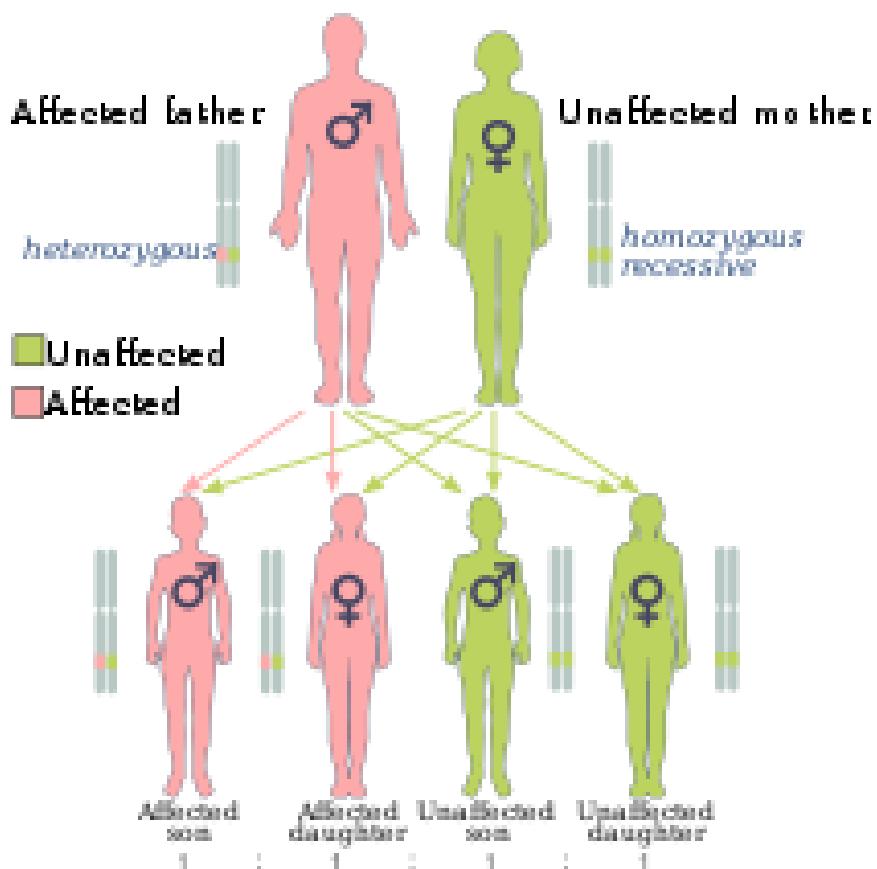
Increased risk of developing ovarian cancer by age 70 to 2.4% to 19%

Increased risk of developing male breast cancer by age 70 to 3.2% to 12%

BRCA2 Location

This gene is located on chr 13 (NC_000013.11)





2.3 TP53

And finally, we'll talk about another gene called TP53. This gene makes a protein that is found inside the nucleus of cells and plays a key role in controlling cell division and cell death. Mutations (changes) in the p53 gene may cause cancer cells to grow and spread in the body. These changes have been found in a genetic condition called Li-Fraumeni syndrome and in many types of cancer. The p53 gene is a type of tumor

suppressor gene. Also called TP53 gene and tumor protein p53 gene.

The p53 tumor suppressor gene (TP53) is the most frequently altered gene in human cancer and is also found mutated in several types of brain tumors. Loss of p53 function plays a central role in the development of cancer.

Chapter 3

Proposed Application

3.1 introduction

In this chapter we will talk about our website and why we chose website and our system analysis with details.

3.2 website

What is website?

A website, as a collection of web pages; Such as HTML pages or PHP pages, which are formed with each other and linked through hypertext links, and uploaded to the server service provider, and the ability to access them within a single website on the Internet.

Benefits of website

- Online Presence
- Credibility
- It Cuts Costs
- Market Expansion
- Competitors Online
- Customer Service Online
- Growth Opportunity

Why we chose website?

The decision to rely on the website was linked to several reasons, including:

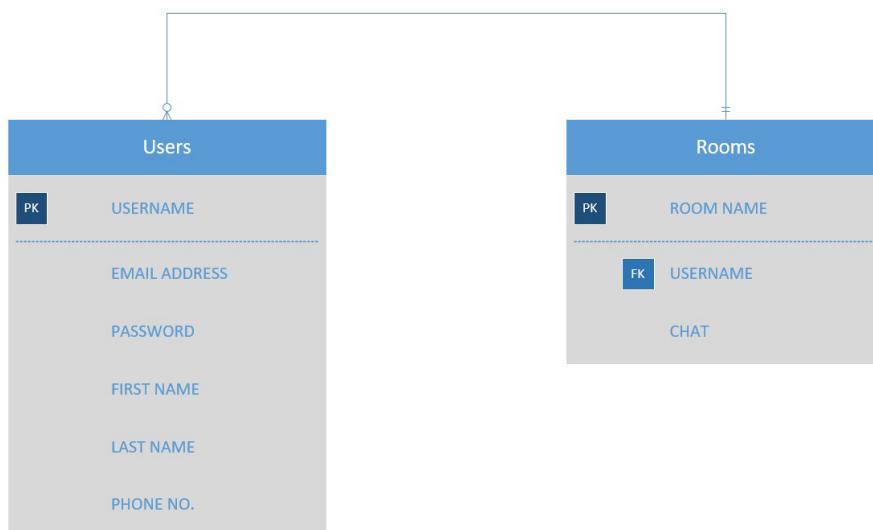
- 1 - Researchers and those interested in genetics, especially mutagenesis, rely on the Internet to obtain information.
- 2- The availability of gene banks on the Internet and the presence of websites for them.
- 3- Research papers and laboratory experiments circulated on the Internet.
- 4- Diversity of genetic mutations associated with cancer and the desire to build a site that helps in conducting many operations to understand the mutation.

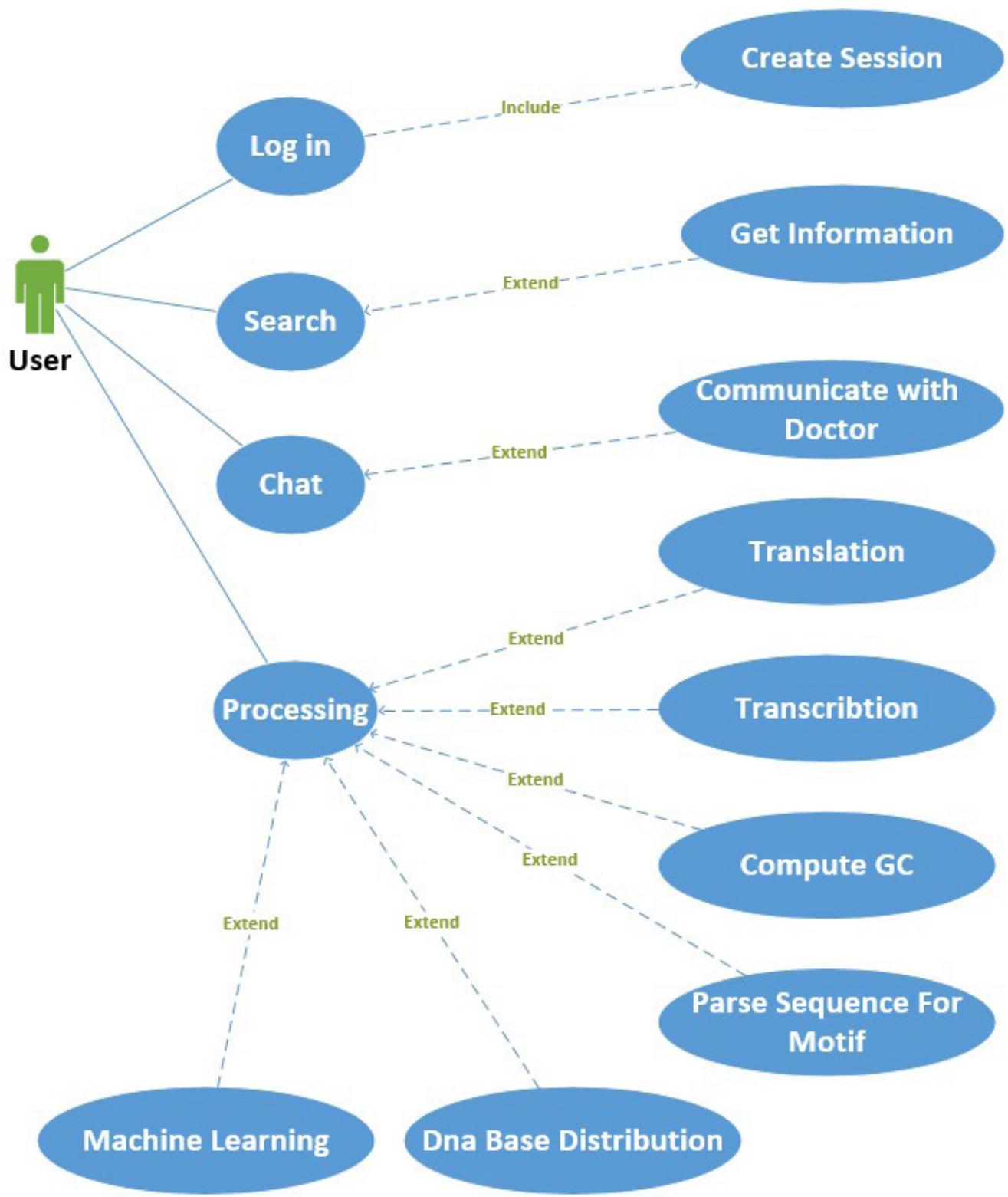
3.3 system analysis

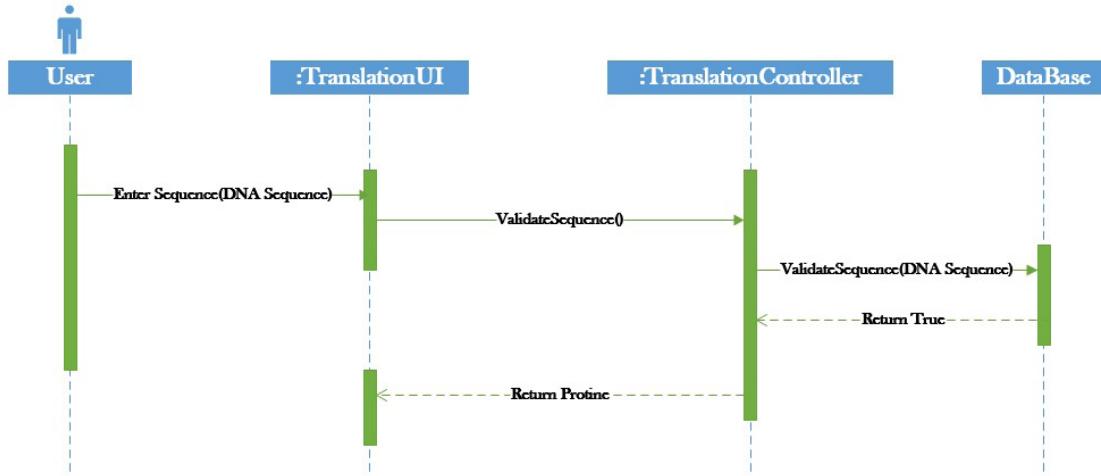
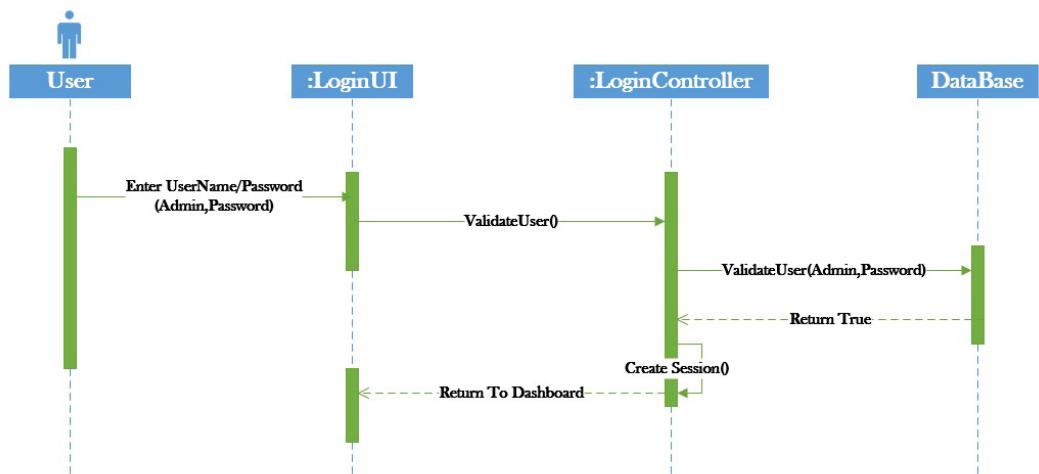
It is the process of examining and studying all parts of the system, and how they perform their work. The concept of the system in this context includes individuals, machines, and elements that collectively make up the system, and have an effective role in achieving the desired goal for a specific job.

The importance of system analysis:

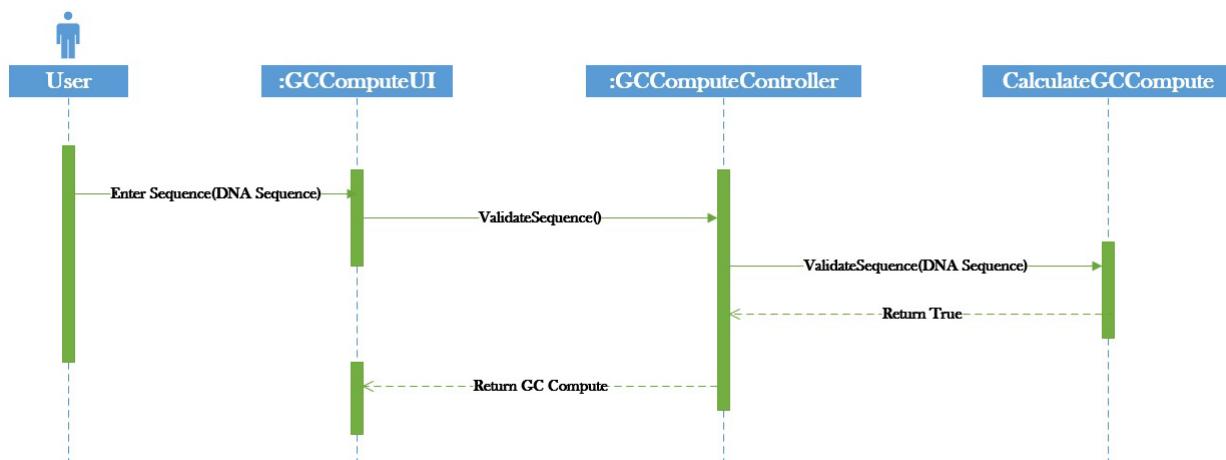
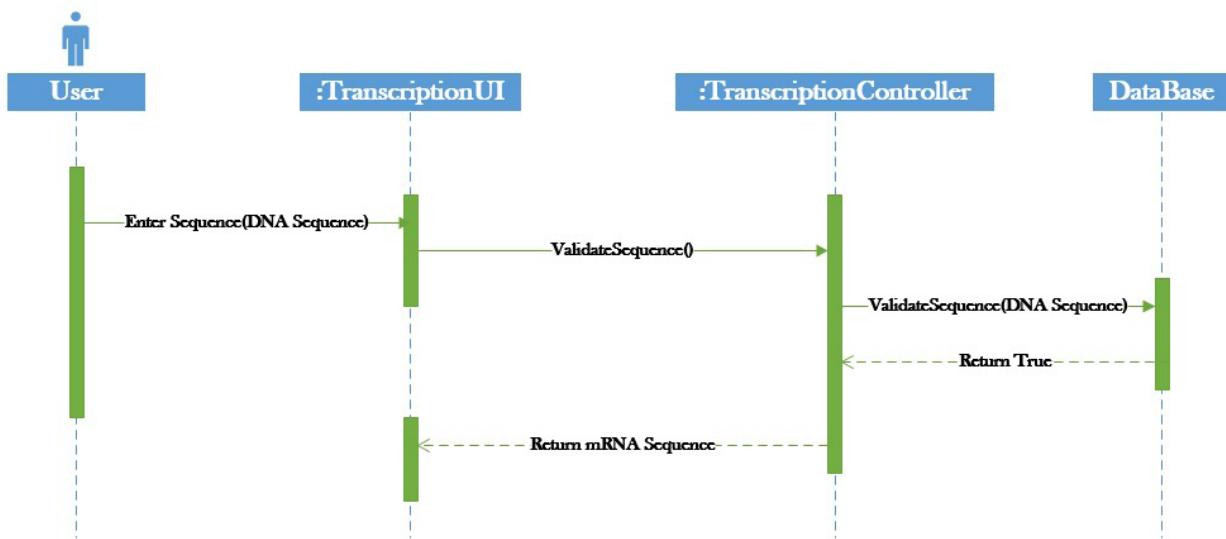
- The importance of systems analysis is to break down a complex system in its structure into its main components in a logical manner.
- The data analysis entrance is concerned with all individuals involved in the system analysis process and the roles assigned to them, in addition to the devices, documents and reports used in the systems.

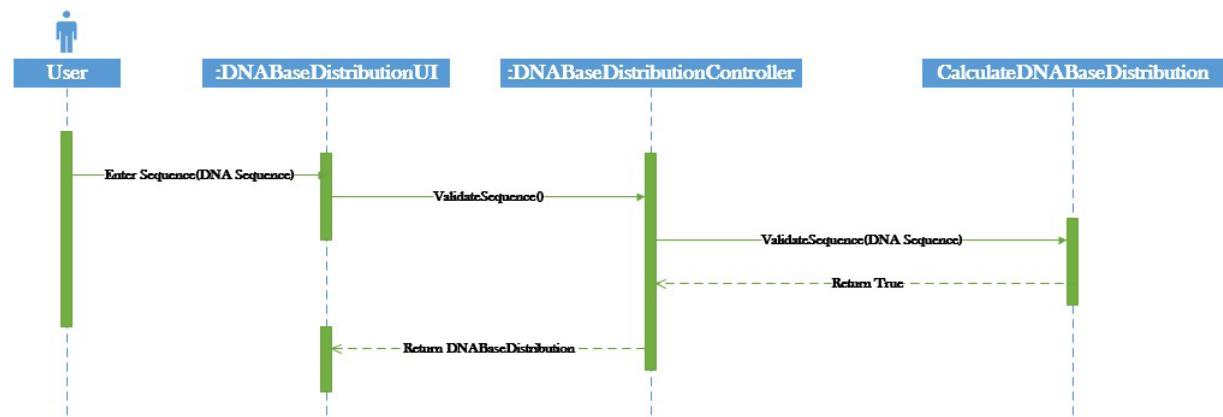
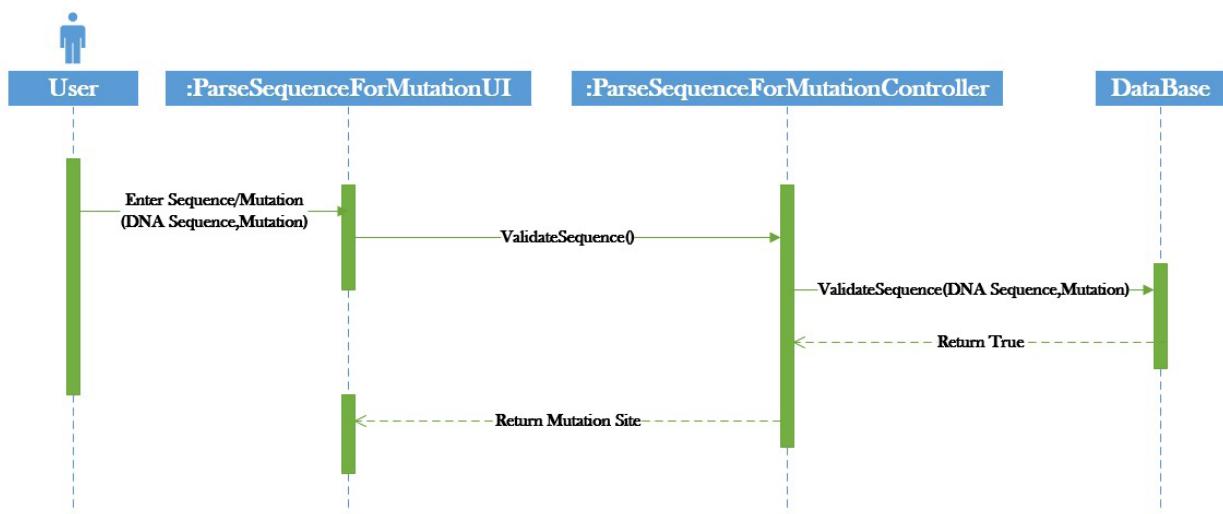




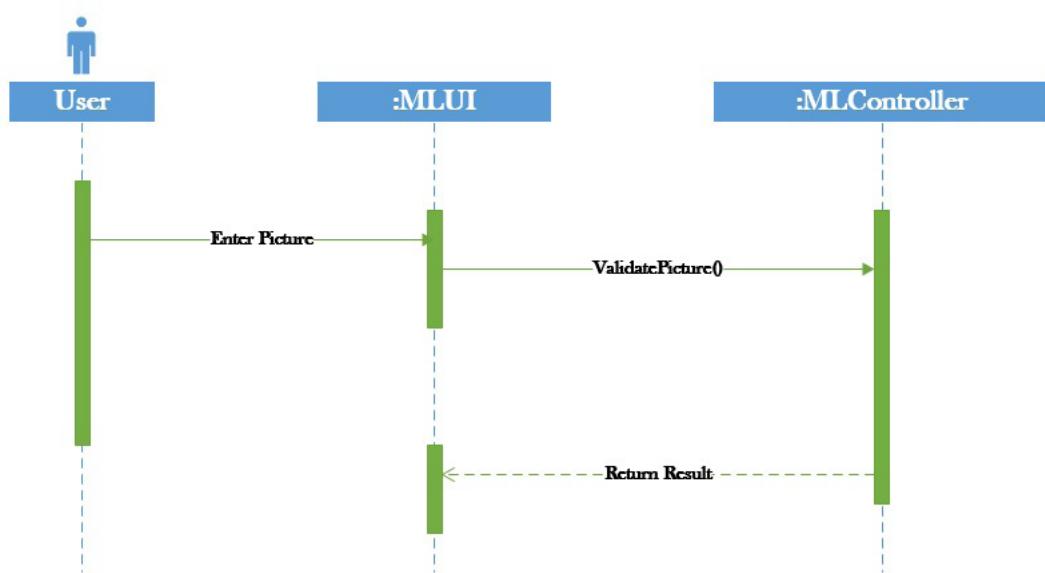
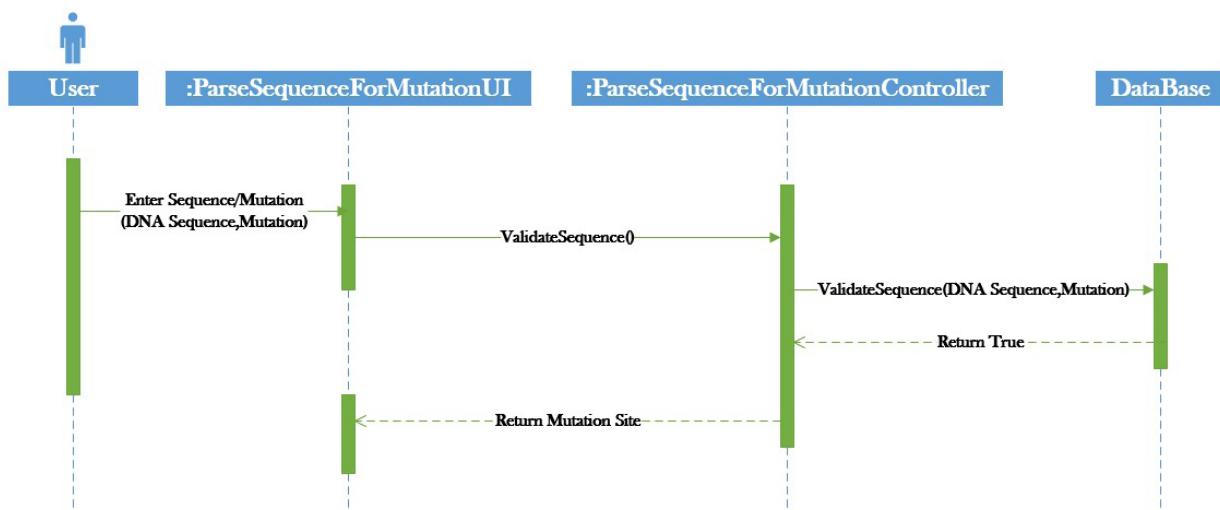


CHAPTER 3





CHAPTER 3



Chapter 4

Implementation and Results

sours code

first we show the implement for All processing to analysis DNA and protein

Translation DNA sequence:

translate DNA to protein depend on codon table show below post function in view.py to show result in template

```
def post(self, request):

    # Define the form
    form = HomeForm(request.POST)

    # Validate input
    if form.is_valid():
        posted = form.cleaned_data['post']
        result = translate(posted)
        form = HomeForm()

    # Render the page
    args = {
        'form': form,
        'posted': posted,
        'result': result,
    }
    return render(request, self.template_name, args)
```

CHAPTER 4

```
def translate(seq):

    # Handle both DNA and RNA
    sequence = seq.replace('U', 'T').upper()

    # use regular expressions to parse codons from sequence
    codons = re.findall('...', sequence)
    res = []

    # Iterate through the codons
    for codon in codons:
        res.append(codonTable[codon])
    result = ''.join(res)

    return result
```

```
codonTable = {
    'TTT': 'F', 'TTC': 'F', 'TTA': 'L', 'TTG': 'L', 'CTT': 'L', 'CTC': 'L', 'CTA': 'L', 'CTG': 'L',
    'ATT': 'I', 'ATC': 'I', 'ATA': 'I', 'ATG': 'M', 'GTT': 'V', 'GTC': 'V', 'GTA': 'V', 'GTG': 'V',
    'TCT': 'S', 'TCC': 'S', 'TCA': 'S', 'TCG': 'S', 'CCT': 'P', 'CCC': 'P', 'CCA': 'P', 'CCG': 'P',
    'ACT': 'T', 'ACC': 'T', 'ACA': 'T', 'ACG': 'T', 'GCT': 'A', 'GCC': 'A', 'GCA': 'A', 'GCG': 'A',
    'TAT': 'Y', 'TAC': 'Y', 'TAA': 'L', 'TAG': 'L', 'CAT': 'H', 'CAC': 'H', 'CAA': 'Q', 'CAG': 'Q',
    'AAT': 'N', 'AAC': 'N', 'AAA': 'K', 'AAG': 'K', 'GAT': 'D', 'GAC': 'D', 'GAA': 'E', 'GAG': 'E',
    'TGT': 'C', 'TGC': 'C', 'TGA': 'S', 'TGG': 'W', 'CGT': 'R', 'CGC': 'R', 'CGA': 'R', 'CGG': 'R',
    'AGT': 'S', 'AGC': 'S', 'AGA': 'R', 'AGG': 'R', 'GGT': 'G', 'GGC': 'G', 'GGA': 'G', 'GGG': 'G',
}
```

Transcription DNA to mRNA:

process of copying a segment of DNA into RNA. The segments of DNA transcribed into RNA molecules that can encode proteins are said to produce messenger RNA function to transcript DNA to mRNA second function in view.py to show result in template

```
def transcribe(seq):  
  
    result = seq.replace('T', 'U')  
  
    return result
```

```
def post(self, request):  
  
    # Define the view  
    form = HomeForm(request.POST)  
  
    # Validate input  
    if form.is_valid():  
        posted = form.cleaned_data['post']  
        result = transcribe(posted)  
        form = HomeForm()  
  
    # Render the page  
    args = {  
        'form': form,  
        'posted': posted,  
        'result': result,  
    }  
    return render(request, self.template_name, args)
```

```
def post(self, request):  
  
    # Define the form  
    form = HomeForm(request.POST)  
  
    # Validate input  
    if form.is_valid():  
  
        # Store cleaned input data  
        posted = form.cleaned_data['post']  
  
        # Process data  
        result = computeGC(form.cleaned_data['post'])  
  
        # Clear text field  
        form = HomeForm()  
  
        # Render the page with form and result data  
  
        args = {'form': form, 'posted': posted, 'result': result}  
  
        return render(request, self.template_name, args)
```

GC-content of short oligonucleotides known as primers is often used to predict their annealing temperature to the template DNA. A higher GC-content level indicates a relatively higher melting temperature computeGC function compute GC content value and post function in views.py to show result in template

```
def computeGC(seq):  
  
    # Initialize count to 0  
    n = 0  
  
    # Iterate through the sequence  
    for char in seq:  
        if char == 'G':  
            n += 1  
        elif char == 'C':  
            n += 1  
        else:  
            pass  
    test=float(n) / float(len(seq))  
  
    # Convert numbers to floats, carry out division, and return result  
    return str(float(n) / float(len(seq)))
```

sequence Motify

sequence motif is a nucleotide or amino-acid sequence pattern that is widespread and has, or is conjectured to have, a biological significance. Function parsemotif to compare between to sequence post function in view.py to show result in template

```
def parseMotif(motif, seq):

    # Stringify inputs from DOM HTML input
    motif, seq = str(motif), str(seq)

    # Initialize result to an empty list
    result = []

    # Iterate through each frame among those where motif occurs
    for frame in re.finditer(motif, seq):
        # Append the indices of occurrence to result
        result.append([frame.start(), frame.end()])

    return result
```

```
def post(self, request):

    # Define the form
    form = HomeForm2(request.POST)

    # Validate input
    if form.is_valid():
        posted = form.cleaned_data['post']
        against = form.cleaned_data['against']
        result = parseMotif(posted, against)
        form = HomeForm2()

    # Render page with results
    args = {
        'form': form,
        'posted': posted,
        'against': against,
        'result': result,
    }
    return render(request, self.template_name, args)
```

DNA Base Distribution

Function post to show the result of DNA Base distribution this function in view.py

```
def post(self, request):
    # Define the form
    form = HomeForm(request.POST)
    # Validate input
    if form.is_valid():
        # Store data from input field
        posted = form.cleaned_data['post']

        # Calculate results
        result = baseDistribution(posted)
        total = sum(result)
        distribution = []
        for i in range(0, len(result)):
            distribution.append(str(round(result[i] / total*100), '%', 'Base Pairs'))
        # clear text field
        form = HomeForm()
    # Render the page with new args
    args = {
        'form': form,
        'posted': posted,
        'result': result,
        'distribution': distribution
    }
    return render(request, self.template_name, args)
```

ML Model:

Pre-processing Module: The images of the dataset are of varying sizes. During the pre processing stage we resize the images of the dataset so that all the images in the entire dataset will be of the same size.

Feature extraction Module: During this phase, pre-trained model VGG16 is used to get 4096

deep features. The reason for the poor performance of any machine learning model could be

the improper bias and variance. One way to avoid model over-fitting is by reducing the number of dimensions of the data. After extracting deep features from VGG16

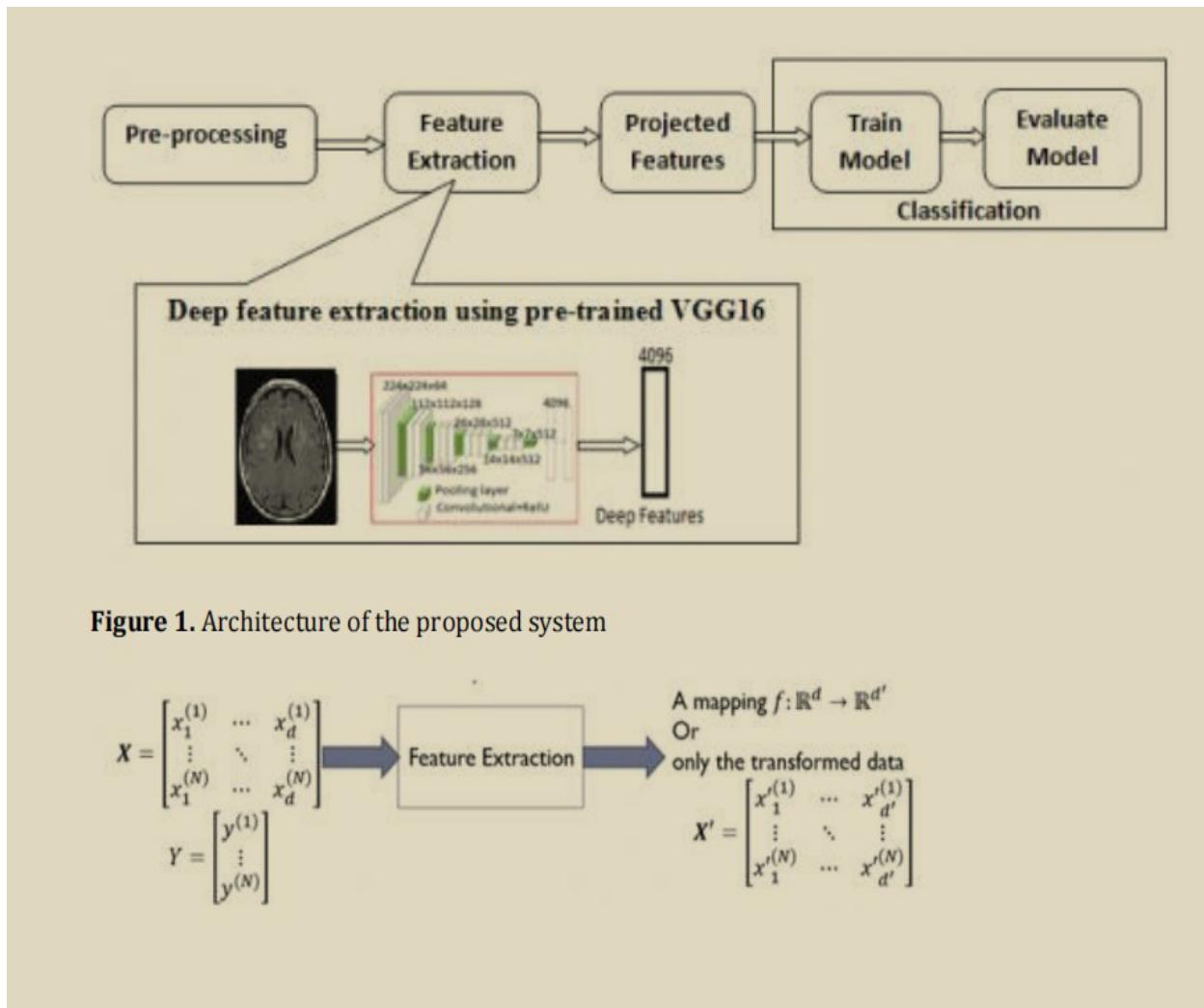


Figure 1. Architecture of the proposed system

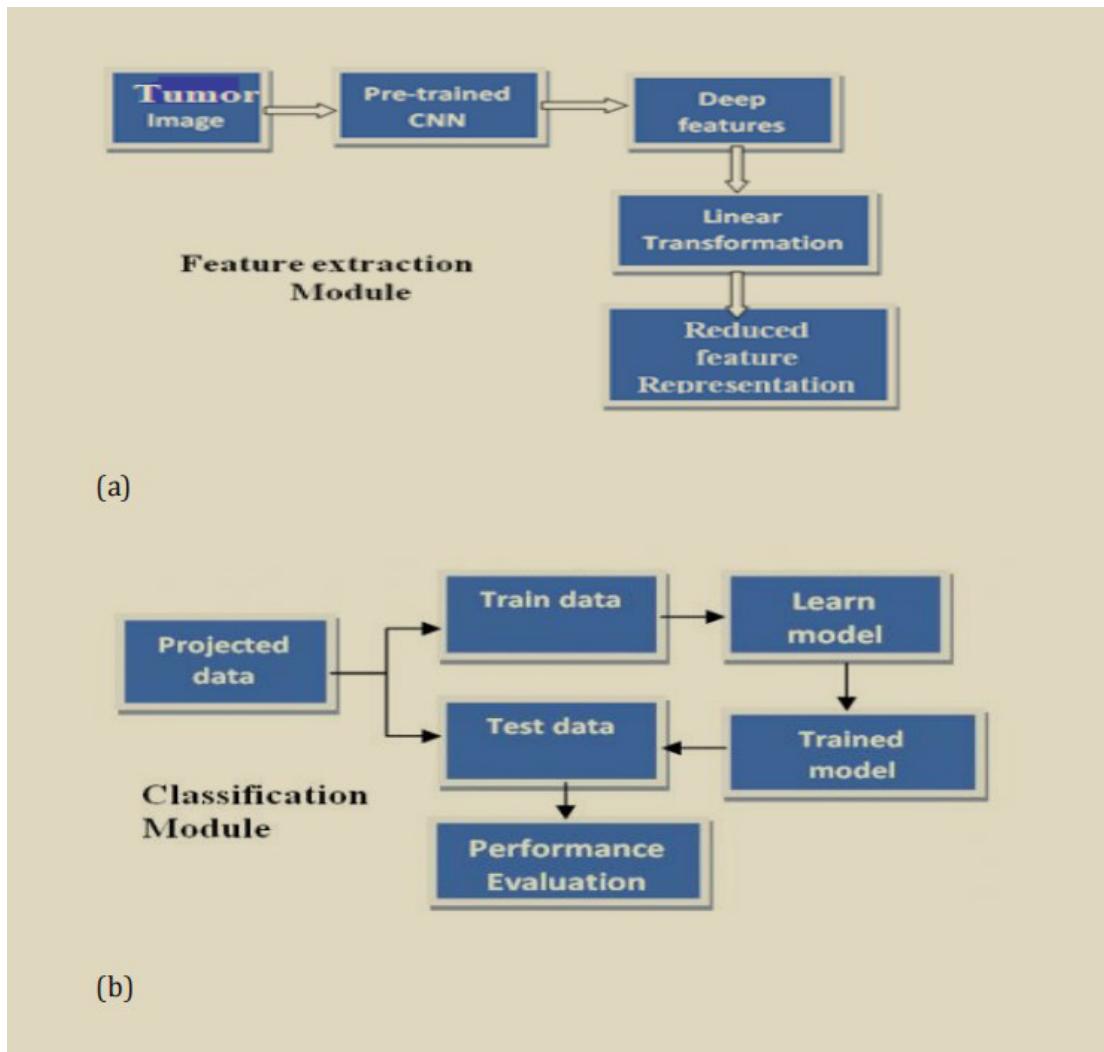
$$\begin{aligned}
 X &= \begin{bmatrix} x_1^{(1)} & \dots & x_d^{(1)} \\ \vdots & \ddots & \vdots \\ x_1^{(N)} & \dots & x_d^{(N)} \end{bmatrix} \xrightarrow{\text{Feature Extraction}} \begin{array}{l} \text{A mapping } f: \mathbb{R}^d \rightarrow \mathbb{R}^{d'} \\ \text{Or} \\ \text{only the transformed data} \end{array} \\
 Y &= \begin{bmatrix} y^{(1)} \\ \vdots \\ y^{(N)} \end{bmatrix}
 \end{aligned}$$

Model training and evaluation module:

During this phase, we train the model on trained

data that is formed using the features in the transformed space, apply the model on test data,

evaluate the model performance on test data. Figure 3(b) shows the details of this module.



Data Set Description:

The image data that was used for this problem is Brain MRI Images for Brain Tumor Detection. It consists of MRI scans of two classes:

NO - no tumor, encoded as 0

YES - tumor, encoded as 1

Setting up the Environment

Import all function and packages we used to implement machine learning model VGG16

```
import numpy as np
from tqdm import tqdm
import cv2
import os
import shutil
import itertools
import imutils
import matplotlib.pyplot as plt
from sklearn.preprocessing import LabelBinarizer
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, confusion_matrix

import plotly.graph_objs as go
from plotly.offline import init_notebook_mode, iplot
from plotly import tools

from keras.preprocessing.image import ImageDataGenerator
from keras.applications.vgg16 import VGG16, preprocess_input
from keras import layers
from keras.models import Model, Sequential
from keras.optimizers import Adam, RMSprop
from keras.callbacks import EarlyStopping

init_notebook_mode(connected=True)
RANDOM_SEED = 123
```

3. Data Import and Preprocessing

```
TRAIN_DIR = 'TRAIN/'  
TEST_DIR = 'TEST/'  
VAL_DIR = 'VAL/'  
IMG_SIZE = (224,224)  
  
# use predefined function to load the image data into workspace  
X_train, y_train, labels = load_data(TRAIN_DIR, IMG_SIZE)  
X_test, y_test, _ = load_data(TEST_DIR, IMG_SIZE)  
X_val, y_val, _ = load_data(VAL_DIR, IMG_SIZE)
```

```
100%|██████████| 2/2 [00:00<00:00,  4.76it/s]  
100%|██████████| 2/2 [00:00<00:00, 93.17it/s]  
100%|██████████| 2/2 [00:00<00:00, 21.17it/s]
```

193 images loaded from TRAIN/ directory.

10 images loaded from TEST/ directory.

50 images loaded from VAL/ directory.

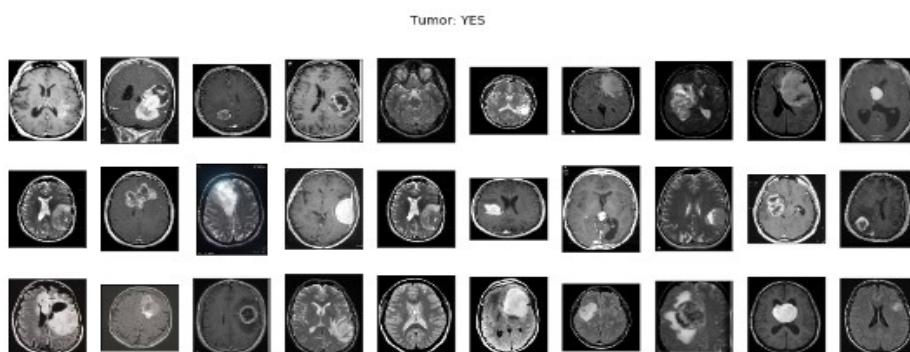
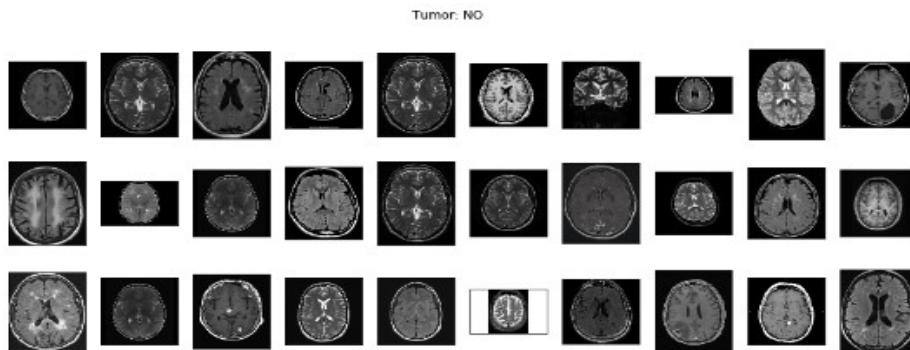
CHAPTER 4

Digital image processing:

In our project we will use python as programming language to preprocessing data , we need to remove noise and remove addition part in image.

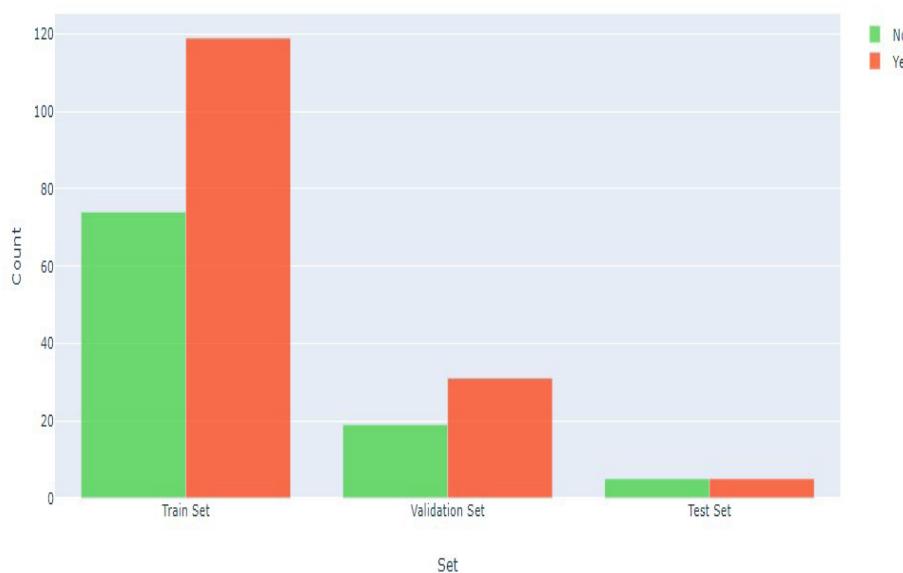
```
import numpy as np
import cv2
import imutils
RANDOM_SEED = 123
def crop_imgs(set_name, add_pixels_value=0):
    set_new = []
    for img in set_name:
        gray = cv2.cvtColor(img, cv2.COLOR_RGB2GRAY)
        gray = cv2.GaussianBlur(gray, (5, 5), 0)
        # threshold the image, then perform a series of erosions +
        # dilations to remove any small regions of noise
        thresh = cv2.threshold(gray, 45, 255, cv2.THRESH_BINARY)[1]
        thresh = cv2.erode(thresh, None, iterations=2)
        thresh = cv2.dilate(thresh, None, iterations=2)
        # find contours in thresholded image, then grab the largest one
        cnts = cv2.findContours(thresh.copy(), cv2.RETR_EXTERNAL, cv2.CHAIN_APPROX_SIMPLE)
        cnts = imutils.grab_contours(cnts)
        c = max(cnts, key=cv2.contourArea)
        # find the extreme points
        extLeft = tuple(c[c[:, :, 0].argmin()][0])
        extRight = tuple(c[c[:, :, 0].argmax()][0])
        extTop = tuple(c[c[:, :, 1].argmin()][0])
        extBot = tuple(c[c[:, :, 1].argmax()][0])
        ADD_PIXELS = add_pixels_value
        new_img = img[extTop[1]-ADD_PIXELS:extBot[1]+ADD_PIXELS, extLeft[0]-ADD_PIXELS:extRight[0]+ADD_PIXELS].copy()
        set_new.append(new_img)
    return np.array(set_new)
```

Let's take a look at the distribution of classes among sets:

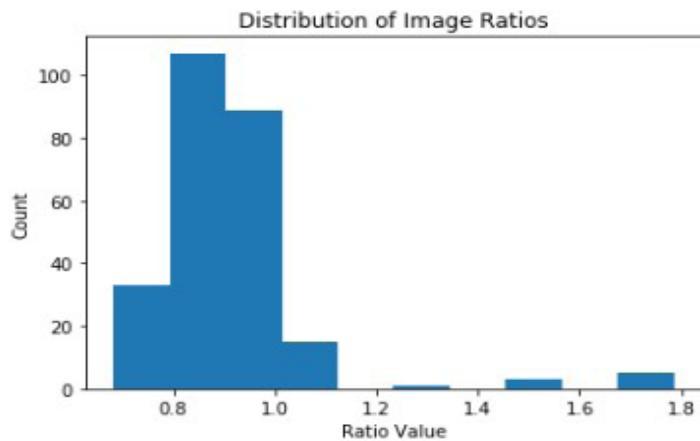


```
plot_samples(X_train, y_train, labels, 30)
```

Count of classes in each set



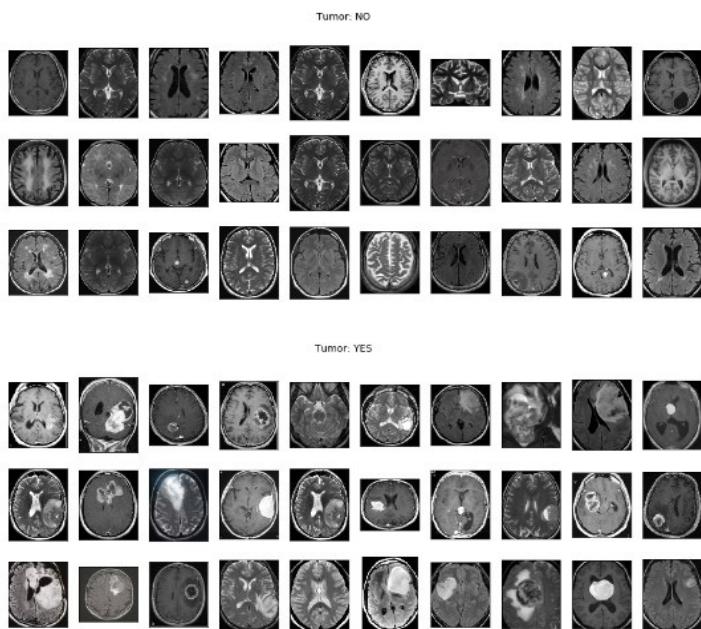
As you can see, images have different width and height and different size of “black corners”. Since the image size for VGG-16 input layer is (224,224) some wide images may look weird after resizing. Histogram of ratio distributions (ratio = width/height):



The first step of “normalization” would be to crop the brain out of the images. I used technique which was perfectly described in pyimagesearch blog and I highly suggest to looks deeper into it.

Images after doing digital image processing

```
In [15]: plot_samples(X_train_crop, y_train, labels, 30)
```



Now start train a model and there is some view result while it training Epoch 1/30

50/50 [=====] - 342s 7s/step - loss: 5.1453 - accuracy: 0.5770

- val_loss: 0.3496 - val_accuracy: 0.7437

Epoch 2/30

50/50 [=====] - 338s 7s/step - loss: 3.4533 - accuracy: 0.6642

- val_loss: 0.8502 - val_accuracy: 0.8956

Epoch 3/30

50/50 [=====] - 336s 7s/step - loss: 2.4265 - accuracy: 0.7419

- val_loss: 0.2249 - val_accuracy: 0.9241

CHAPTER 4

Epoch 4/30

50/50 [=====] - 352s 7s/step - loss: 2.2433 - accuracy: 0.7617

- val_loss: 2.4419e-07 - val_accuracy: 0.8775

Epoch 5/30

50/50 [=====] - 339s 7s/step - loss: 2.1873 - accuracy: 0.7833

- val_loss: 1.3205 - val_accuracy: 0.9367

Epoch 6/30

50/50 [=====] - 336s 7s/step - loss: 1.4051 - accuracy: 0.8163

- val_loss: 0.2334 - val_accuracy: 0.8987

Epoch 7/30

50/50 [=====] - 348s 7s/step - loss: 1.4480 - accuracy: 0.8243

- val_loss: 0.0526 - val_accuracy: 0.9399

Epoch 8/30

50/50 [=====] - 330s 7s/step - loss: 0.9705 - accuracy: 0.8800

- val_loss: 1.8374 - val_accuracy: 0.9404

29 Epoch 9/30

50/50 [=====] - 346s 7s/step - loss: 1.1262 - accuracy: 0.8402

- val_loss: 0.3801 - val_accuracy: 0.8987

Epoch 10/30

50/50 [=====] - 350s 7s/step - loss: 1.2723 - accuracy: 0.8691

- val_loss: 0.3088 - val_accuracy: 0.9177

Epoch 11/30

50/50 [=====] - 336s 7s/step - loss: 0.9026 - accuracy: 0.8691

- val_loss: 1.4465 - val_accuracy: 0.9399

Epoch 12/30

50/50 [=====] - 341s 7s/step - loss: 1.0098 - accuracy: 0.8894

- val_loss: 5.2724e-05 - val_accuracy: 0.9404

Epoch 13/30

50/50 [=====] - 333s 7s/step - loss: 1.1503 - accuracy: 0.8988

- val_loss: 0.3767 - val_accuracy: 0.9399

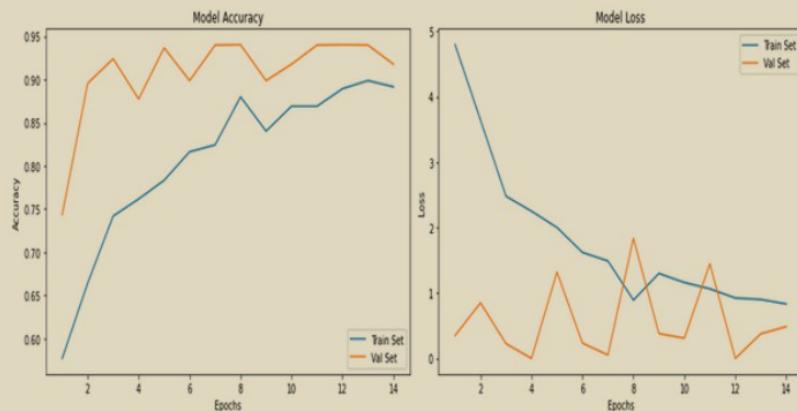
Epoch 14/30

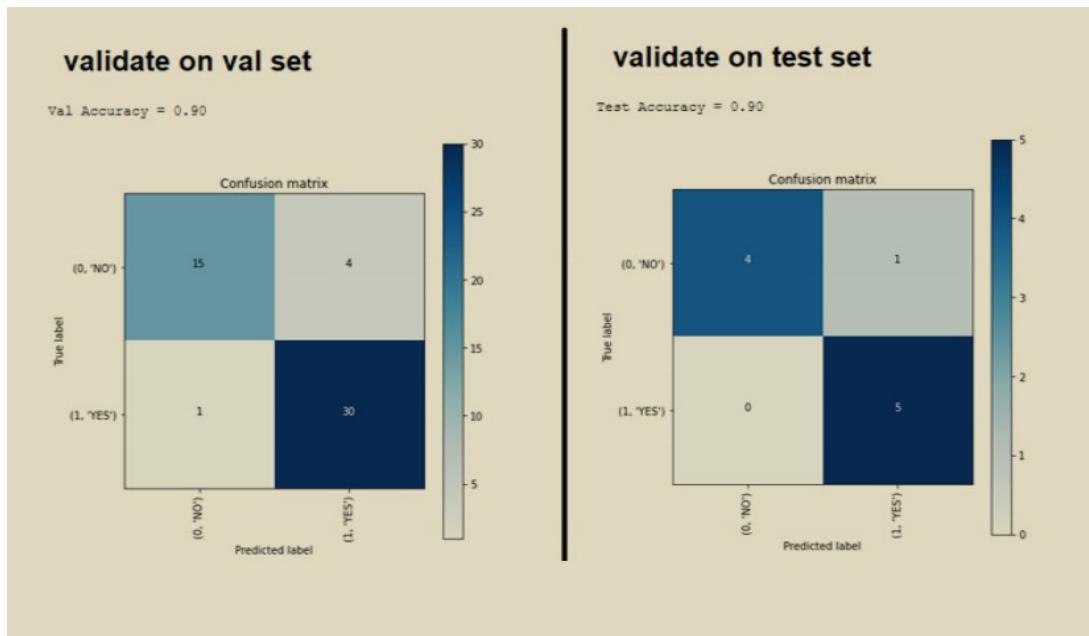
50/50 [=====] - 337s 7s/step - loss: 0.7633 - accuracy: 0.8915

- val_loss: 0.4861 - val_accuracy: 0.9177

We notice that model stop after epoch 14 that is because early stoping

Model accuracy and loss





We have a model with accuracy reach to 90 %

Model: "sequential_1"	Layer (type)	Output Shape	Param #
	conv2d_1 (Conv2D)	(None, 150, 150, 64)	1664
	max_pooling2d_1 (MaxPooling2D)	(None, 75, 75, 64)	0
	dropout_1 (Dropout)	(None, 75, 75, 64)	0
	conv2d_2 (Conv2D)	(None, 75, 75, 128)	73856
	max_pooling2d_2 (MaxPooling2D)	(None, 37, 37, 128)	0
	dropout_2 (Dropout)	(None, 37, 37, 128)	0
	conv2d_3 (Conv2D)	(None, 37, 37, 128)	147584
	max_pooling2d_3 (MaxPooling2D)	(None, 18, 18, 128)	0
	dropout_3 (Dropout)	(None, 18, 18, 128)	0
	conv2d_4 (Conv2D)	(None, 18, 18, 128)	65664
	max_pooling2d_4 (MaxPooling2D)	(None, 9, 9, 128)	0
	dropout_4 (Dropout)	(None, 9, 9, 128)	0
	conv2d_5 (Conv2D)	(None, 9, 9, 256)	131328
	max_pooling2d_5 (MaxPooling2D)	(None, 4, 4, 256)	0
	dropout_5 (Dropout)	(None, 4, 4, 256)	0
	flatten_1 (Flatten)	(None, 4096)	0
	dense_1 (Dense)	(None, 1024)	4195328
	dropout_6 (Dropout)	(None, 1024)	0
	dense_2 (Dense)	(None, 4)	4100
<hr/>			
Total params: 4,619,524			
Trainable params: 4,619,524			
Non-trainable params: 0			

And start train the model

CHAPTER 4

second model

Here is some of steps of training the model

Epoch 1/50

57/57 [=====] - 122s 2s/step - loss: 1.3707 - accuracy: 0.2620

- val_loss: 1.3442 - val_accuracy: 0.2770

Epoch 2/50

57/57 [=====] - 121s 2s/step - loss: 1.2494 - accuracy: 0.3932

- val_loss: 1.3464 - val_accuracy: 0.3467

Epoch 3/50

57/57 [=====] - 120s 2s/step - loss: 1.1515 - accuracy: 0.4410

- val_loss: 1.3030 - val_accuracy: 0.3815

Epoch 4/50

57/57 [=====] - 120s 2s/step - loss: 1.0314 - accuracy: 0.5412

- val_loss: 1.1559 - val_accuracy: 0.4355

Epoch 5/50

57/57 [=====] - 122s 2s/step - loss: 0.9597 - accuracy: 0.5882

- val_loss: 0.9586 - val_accuracy: 0.5714

Epoch 6/50

57/57 [=====] - 121s 2s/step - loss: 0.8350 - accuracy: 0.6538

- val_loss: 0.9292 - val_accuracy: 0.6272

Epoch 7/50

3457/57 [=====] - 122s 2s/step - loss: 0.7931
- accuracy: 0.6835
- val_loss: 0.8482 - val_accuracy: 0.6603

Epoch 8/50

57/57 [=====] - 122s 2s/step - loss: 0.6932 - accuracy: 0.7237
- val_loss: 0.8166 - val_accuracy: 0.6394

Epoch 9/50

57/57 [=====] - 138s 2s/step - loss: 0.6330 - accuracy: 0.7392
- val_loss: 0.8620 - val_accuracy: 0.6272

Epoch 10/50

57/57 [=====] - 169s 3s/step - loss: 0.6327 - accuracy: 0.7482
- val_loss: 0.8533 - val_accuracy: 0.6359

Epoch 11/50

57/57 [=====] - 170s 3s/step - loss: 0.5747 - accuracy: 0.7757
- val_loss: 0.7128 - val_accuracy: 0.6864

Epoch 12/50

57/57 [=====] - 156s 3s/step - loss: 0.5587 - accuracy: 0.7806
- val_loss: 0.7343 - val_accuracy: 0.6934

Epoch 13/50

57/57 [=====] - 121s 2s/step - loss: 0.5292 - accuracy: 0.7957

CHAPTER 4

- val_loss: 0.8167 - val_accuracy: 0.6463

Epoch 14/50

57/57 [=====] - 121s 2s/step - loss: 0.5058 - accuracy: 0.8032

- val_loss: 0.7298 - val_accuracy: 0.6812

35 Epoch 15/50

57/57 [=====] - 122s 2s/step - loss: 0.4457 - accuracy: 0.8338

- val_loss: 0.8028 - val_accuracy: 0.6655

Epoch 16/50

57/57 [=====] - 120s 2s/step - loss: 0.4717 - accuracy: 0.8248

- val_loss: 0.7082 - val_accuracy: 0.7056

Epoch 17/50

57/57 [=====] - 121s 2s/step - loss: 0.4695 - accuracy: 0.8156

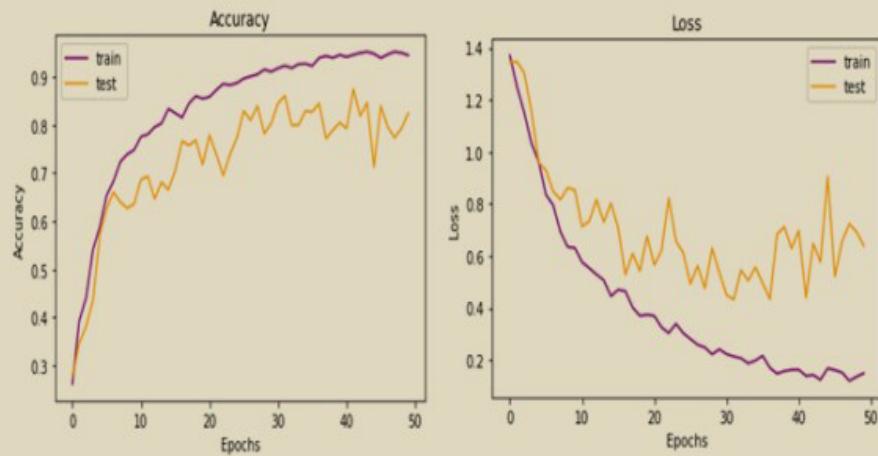
- val_loss: 0.5283 - val_accuracy: 0.7666

Epoch 18/50

57/57 [=====] - 123s 2s/step - loss: 0.4015 - accuracy: 0.8449

- val_loss: 0.6098 - val_accuracy: 0.7578

Model accuracy and loss



- Accuracy = 82 %

We have a model with accuracy reach to 82 % and that is not a good for us And as we all know that misdiagnosing these diseases can only lead to very big consequences, so we came up with a method which is the possibilities that we make the two models work at the same time

CHAPTER 4

```
def predict_tumor(img):
    model = tf.keras.models.load_model('scane/models/2019-06-07_VGG_model.h5')
    predictions = model.predict(convert_img_to_batch_opencv(img))
    predictions = [1 if x > 0.67 else 0 for x in predictions]
    return predictions[0]

def compafe_2_model(res2, res1):
    CATEGORIES = ["glioma", "meningioma", "no_tumor", "pituitary"]
    if (res2 == 2 and res1 == 1):
        return 1
    if (res2 == 0 and res1 == 0):
        return 2
    if (res2 == 1 and res1 == 0):
        return 3
    if (res2 == 2 and res1 == 0):
        return 0
    if (res2 == 3 and res1 == 0):
        print("pituitary")
        return 4
    else:
        return CATEGORIES[res2]
```

implement function to predict type of brain tumor

```
def Radiology_Diagnostics(request):
    try:
        if request.method == 'POST' and request.FILES['myfile']:
            try:
                my_f = request.FILES["myfile"].read()
                image = Image.open(io.BytesIO(my_f))
                opencvImage_model_1 = cv2.cvtColor(numpy.array(image), cv2.COLOR_RGB2BGR)
                res1 = predict_tumor(opencvImage_model_1)
                opencvImage_model_2 = cv2.cvtColor(numpy.array(image), cv2.COLOR_RGB2GRAY)
                X = cv2.resize(opencvImage_model_2, (150, 150))
                X = X.reshape((150, 150, 1))
                X = X / 255.0
                X = np.array([X])
                mymodel = tf.keras.models.load_model('scane/models/mod2.h5')
                predictions = mymodel.predict_classes(X)
                res2 = predictions[0]
                fin_res = compafe_2_model(res2, res1)
                print(fin_res)
                context = { "fin_re": fin_res, "test": "testy" }
                return render(request, 'scane/show_res.html', context)
            except:
                print("error accur")
        except:
            pass
    return render(request, 'scane/Radiology_Diagnostics.html')
```

```
def show_res(request):
    return render(request, 'scane/show_res.html')
```

Show result in template

Build system

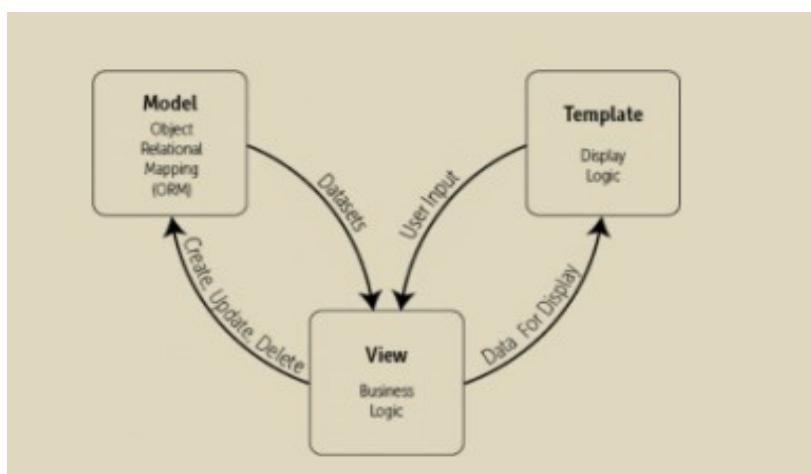
Website consist of(back end and front end)

backend(Django,ajax)

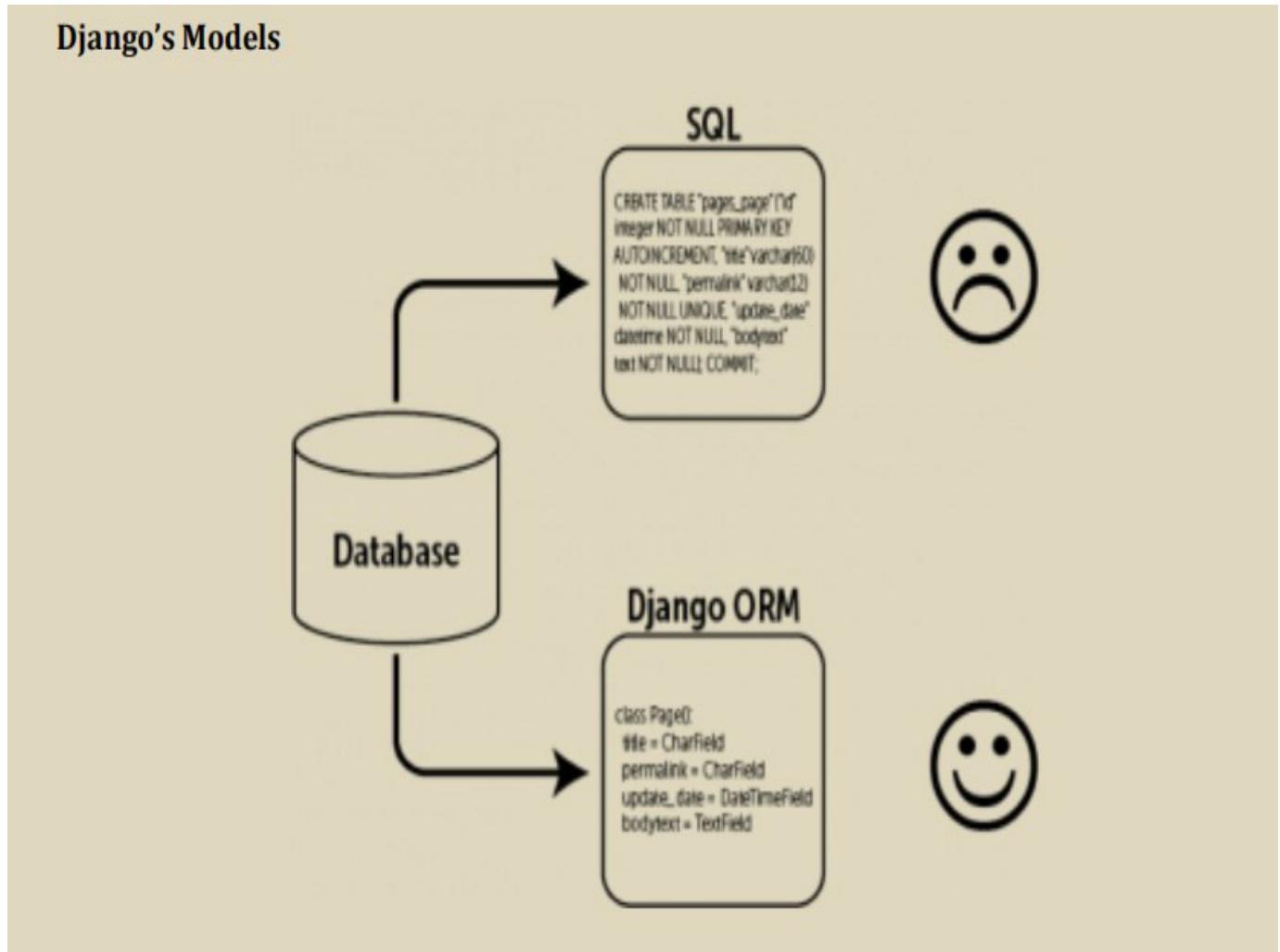
#Django

What is Django?

Django is an MVT web framework used to build web applications. It defines itself as a “batteries included” web framework, with robustness and simplicity to help web developers write clean, efficient and powerful code. It is among the most famous web frameworks out there in the world and it’s one of the most used frameworks as well. It’s used by Instagram, Youtube, Google and even NASA for their website. So let’s break it down even further to learn more about it. The Structure



Django follows an MVT architecture which stands for Model-View-Template. MVT is a Django variation of the famous MVC structure, that's why you'll feel it's quite analogous to how other frameworks work. When the Django server receives a request, the URL router maps the request to the appropriate view. The view then fetches the data through the models, fill the template and send it back to the user.



What is Django Used for?

Without Object-Relational-Mapping, developers would have to create the tables themselves and define the queries or procedures which sometimes translates to the hefty amount of SQL that is prone to be complex and hard to track. The ORM layer lets you write all the table definitions in simple python code, and it takes care of translating that to the appropriate query language chosen, and it also facilitates the CRUD operations.

In fact, the developer doesn't necessarily need to know the complex SQL altogether or what it translates to, though, it's worth noting that understanding SQL would allow you to write better and faster queries and also make your website more secure.

Unlike other frameworks, the models are all placed in one file, conventionally, `models.py`, which might make it feel

crowded for bigger projects. Django supports many database systems. SQLite is really good for testing and development

because it could be used right out of the box without having to install further software. For

production, you can go for MySQL or PostgreSQL, and if you're looking for a NoSQL database,

you can use MongoDB with Django, and here's a further read on the topic.

Django's Templates

The template layer is used to separate the data from the way it's actually presented and

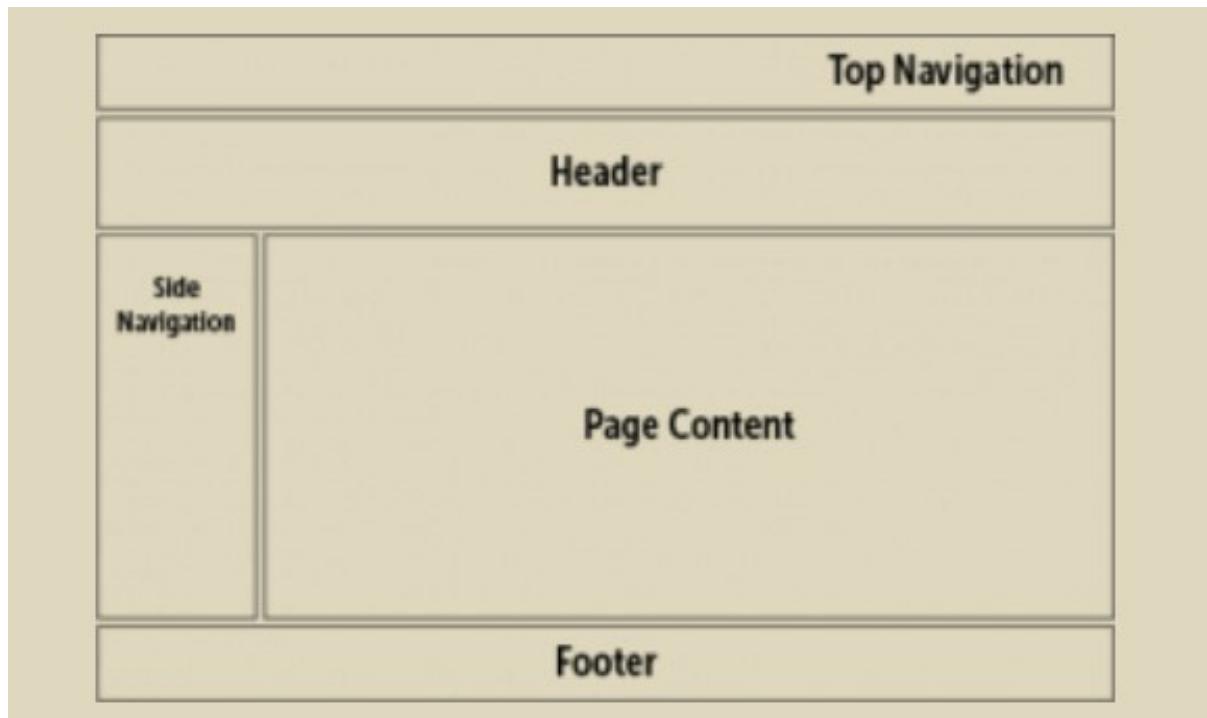
viewed by the user. The template layer is similar to the MVC's View layer. If you're familiar

with templating in other languages, it's kind of the same in Django; you use an HTML like

syntax that is later compiled to HTML with all the respective data injected. Of course, there are

CHAPTER 4

formats for templates other than HTML, if you want to generate XML documents or JSON files, etc...



DRY is one of Django's core template design principles and it's a design pattern that stands for Don't-Repeat-Yourself. It's exactly what it sounds like, it means that you shouldn't, at least in

most cases, by copying and pasting the code. Instead, your template, for example, should be divided into reusable components such as the side navigation bar, the main navigation bar, the

header of the page, the footer of the page and so on. This minimizes repetition and makes for writing efficient and cleaner code.

One of the things that Django makes distinct of itself is how seriously it considers security. This indeed affects the writing of the template.

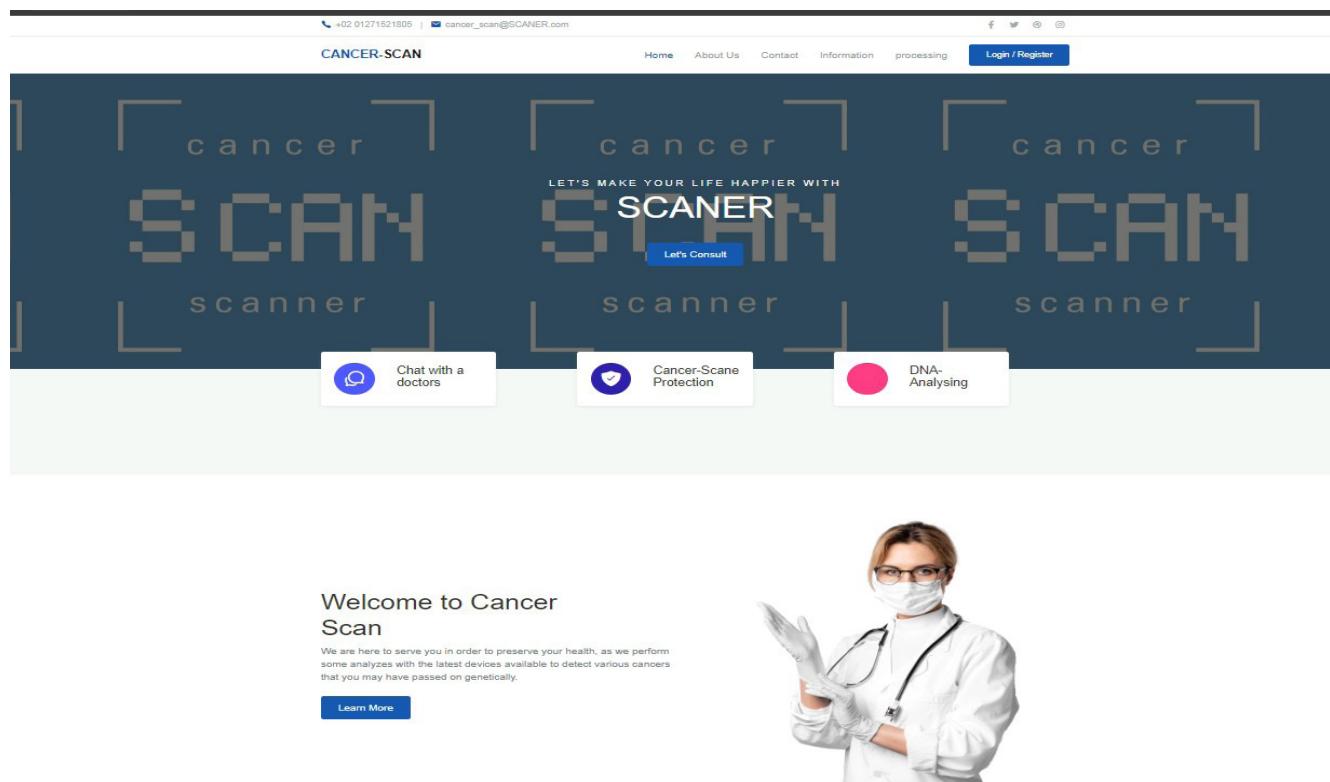
AJAX:

- Update a web page without reloading the page.
- Request data from a server - after the page has loaded.
- Receive data from a server - after the page has loaded.
- Send data to a server - in the background.

frontend

We used many different languages and libraries.: These three main front-end coding languages are HTML, CSS and JavaScript, BOOTSTRAP, JQUERY

website pages



home page



Dr.youssef
Surgical oncologists



Dr.Ali
Neuro-oncologists



Dr.Mohamed
Medical oncologists



Genomics News



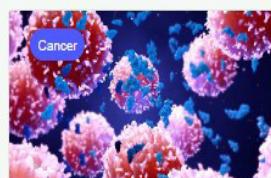
Using Analytics to Improve Cancer Diagnosis and Therapy Selection

Roger Adams · 22/5/2021



Actionable Genome Consortium to guide NGS in cancer Four major cancer institutes have joined Illumina

Antonella Teramo · 11/5/2014



You, Your Family and Cancer: How Genetic Counseling Works
By Robert Preidt HealthDay

Robert Simmons · 12/6/2022

about us

We provide some special services for you and your health by using the best and latest equipment in the field of bioinformatics and modern medicine. Gene therapy is a technique that modifies a person's genes to treat or cure disease. Gene therapies can work by several mechanisms: Replacing a disease-causing gene with a healthy copy of the gene. Inactivating a disease-causing gene that is not functioning properly.

Welcome to Your SCANER Center

We provide some special services for you and your health by using the best and latest equipment in the field of bioinformatics and modern medicine. Gene therapy is a technique that modifies a person's genes to treat or cure disease. Gene therapies can work by several mechanisms: Replacing a disease-causing gene with a healthy copy of the gene. Inactivating a disease-causing gene that is not functioning properly.

The researcher can also analyze the DNA with various processes provided by the site. DNA analysis is the name given to the interpretation of genetic sequences, and can be used for a wide variety of purposes. It can be used to identify a species, but can also differentiate individuals within a species.

Our Doctors



Dr.Mohammed
Medical oncologists



Dr. Youssef
Neuro-oncologists

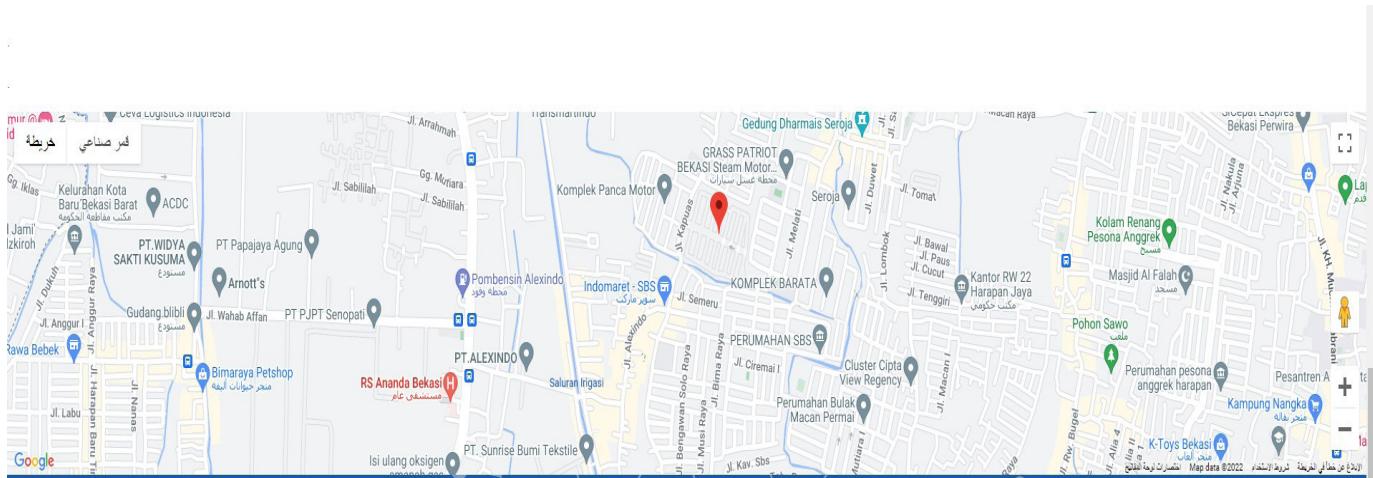


Dr.Ali
General Health

CHAPTER 4

Contact

User can contact with our doctors with chat room for each doctor can user choice



Our Doctors



Dr.youssef
Cardiology



Dr.Ali
Dental



Dr.Mohamed
General Health



Get in Touch

Name

Email

Doctor Name

Username

Enter Room



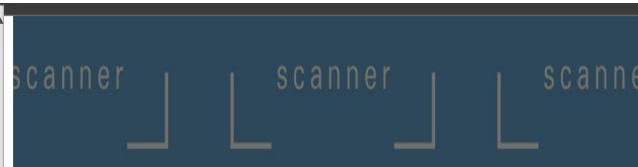
DR.ALi welcomes you How i can Help you?

Enter your Message

Send



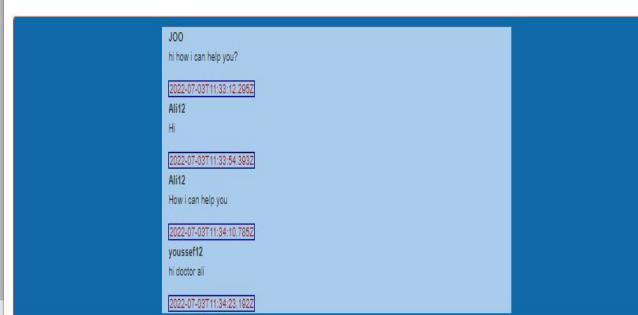
Our Doctors



DR.ALi welcomes you How i can Help you?

Enter your Message

Send



Our Doctors



CHAPTER 4

02 01271521805 | cancer_scan@SCANER.com

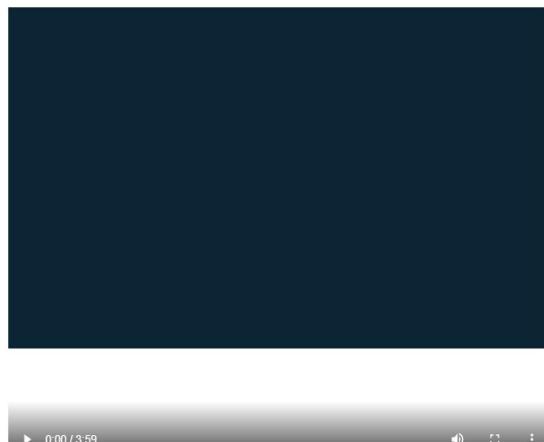


CANCER-SCAN

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Introduction to Next Generation Sequencing (NGS)



▶ 0:00 / 3:59

Search for any Gen on NCBI and EMPL Databases

Search...

NGS Platforms

Illumina

Ion Torrent

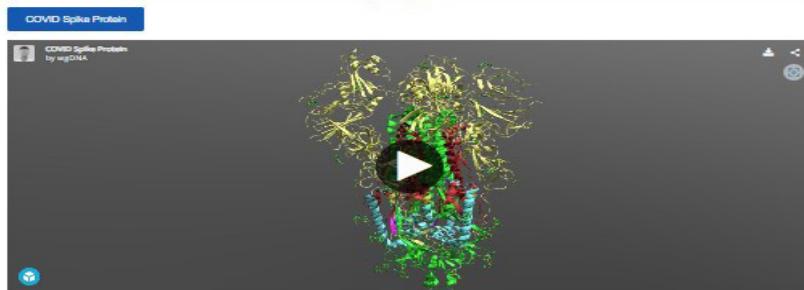
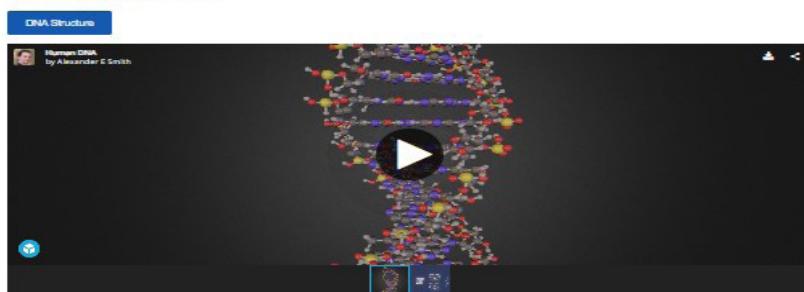
Complete Genomics Technology.

Information :

TOW Models to View DNA structure and Protein 3D structure

DNA bases pair up with each other, A with T and C with G, to form units called base pairs. Each base is also attached to a sugar molecule and a phosphate molecule. Together, a base, sugar, and phosphate are called a nucleotide. Nucleotides are arranged in two long strands that form a spiral called a double helix.

Protein tertiary structure is the three dimensional shape of a protein. The tertiary structure will have a single polypeptide chain "backbone" with one or more protein secondary structures, the protein domains. Amino acid side chains may interact and bond in a number of ways. Programmes such as AlphaFold will exponentially increase our general understanding of different biological processes. As mentioned earlier, having a protein 3D structure is key to reveal the function of unknown proteins which would allow, for example, a better and accelerated understanding of diseases.



References

These are all the sources on which we based our idea of DNA analysis and its structure, as well as the study of protein structure



List of Countries without
Coronavirus case

Doctor.Joe 1 week ago



What is the impact of
eating too much sugar?

Wisdom Jack 2/5/2022



Shifting goalposts:
Research in the time of
the coronavirus

Adams Collier 2/5/2022



What are the
nonmedical factors most
closely linked to death
risk?

Doctor.Joe 2/5/2022



Do out bacteria



The Recovery Room:

Data Bases

NCBI

DDJP

EMPL

UniProt

IHEC

Bioinformatics Researches



Even the all-
powerful Pointing
has no control

2/5/2022 Admin 19



Even the all-
powerful Pointing
has no control

2/5/2022 Admin 19



Even the all-
powerful Pointing
has no control

2/5/2022 Admin 19

CHAPTER 4

some genes related to cancer

BRCA1 BRCA2 TP53

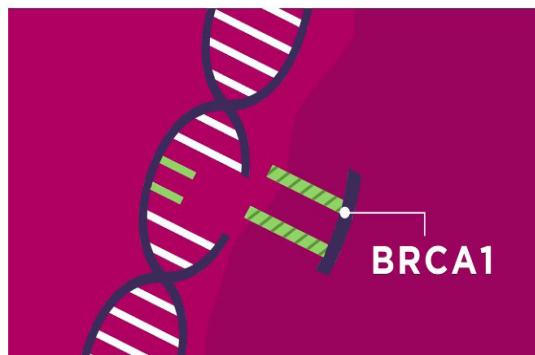
Analysis TOW DNA STRAND

We are here to serve you in order to preserve your health, as we perform some analyzes with the latest devices available to detect various cancers that you may have passed on genetically.

Convert of two DNA sequences
tow capital letters and count it

Sequence 1	Capital litter
GGAGTGAGGG GAGCAGTTGG CTGAAGATGG TCCCCGCCGA GGGACCGGTG GGGCACGGCG 60 AGCTGTGGCA GACCTGGCTT CCTAACACAG TCCGTGTTCT TCCGGCTCCG GGAGGGACTG 120	

Sequence 2	Capital litter
CGCATCGGGA GTGAGGGAG CAGTTGGAA CAGATGGTCC CCGCCGAGGG ACCGGTGGGC 60 GACGGCCAGC TGTGGCAGAC CTGGCTTCCT AACCACGGAA CGTTCTTCC GCTCCGGGAG 120	



Processing

All processes for DNA Analysis

Translation Transcription Compute GC Parse Sequence for Motif DNA Base Distribution ML
Hamming Distance Calculator

Translation :

DNA translation is the term used to describe the process of protein synthesis by ribosomes in the cytoplasm or endoplasmic reticulum.

Input Sequence:
(DNA or mRNA)

```
CCATTGCACTCC  
AGCCTGGCGACAGAGCGAGACTGTCTAAACAAAACAAAACAAAACAAAAAC  
ACCGGCTGGT  
ATGTATGAGAGGATGGGACCTTGTGGAAGAAGAGGTGCCAGGAATATGTCAGGGAGGGG  
AGGAGACAGG  
ATTTTGAGGGAGGAGAACTTAAGAACTGGATCCATTGCGCCATTGAGAAAGCGCAAGA  
GGGAAGTAGA
```

Submit

Output Protein

```
AETSWTGDRLWGFSDNWAPALRRLHPLLWVKVESRERDRGPKSCSGYWGRVDFRSSQMG  
LSRGVGANLRGVRRCEPWGGQFVGREGSARIRKGALSVRGGILVIGTICLEGTLCLLKRRLV  
RSGVPDQPDQRVKLRLYLYKNLPGVVPQLLRRSGRIARTREAEAVSRDRAIALSLGDRARL  
SQNKTQNKTKNTGWMYERMGPCGRRGARNMSGKRRQILWEGETKNWIHLRHSESARGKL
```

Copy

Transcription :

Transcription, as related to genomics, is the process of making an RNA copy of a gene's DNA sequence. This copy, called messenger RNA (mRNA), carries the gene's protein information encoded in DNA

Input Sequence
(DNA or mRNA)

```
CCATTGCACTCC  
AGCCTGGCGCACAGCGAGACTGTCTCAAAACAAAACAAAACAAAAC  
ACCGCGTGT  
ATGTATGAGAGATGGGACCTTGGAAGAGAGGTGCAGGAATATGTCGGAGGG  
AGGAGACAGG  
ATTTGTGGAGGGAGAACTTAAGAACCTGGATCCATTGCGCATTGAGAAAGCGAAGA  
GGGAAGTAGA
```

Submit

Output Protein

```
GCUGAGACUUCUUGACGGGGACAGCGUGUGGGGUUUUCACAUACUGGCC  
GGCGUCAGAGGC  
CUUCACCCUCUGCUUGGUAAAGGUAGUAGAGUCGGGAAAGGGACAGGGGCC  
AAGUGAUGUCUG  
GGGUACUGCGUGGGAGAGUGGUUUCGAAGCUGACAGAUGGGUAUUCUUGACGG  
GGGGUAGGGCGG  
AACCUAGAGGCCUAAGCCGUUGUGAACCCUGGGAGGGGGCAGTTGAGGTGCGC
```

Copy

content:

GC-content of short oligonucleotides known as primers is often used to predict their annealing temperature to the template DNA. A higher GC-content level indicates a relatively higher melting temperature.

Input:

```
GCTGAGACTCCTGGACGGGGACAGGCTGTGGGTTCTAGATAACTGGGCCCTGC  
GCTCAGGAGGC  
CTTCACCCCTGCTGGTAAAGGTAGTAGAGTCCCGGAAAGGGACAGGGGCCAA  
GTGATGCTCTG  
GGGTACTGGCGTGGGAGAGTGGATTCCGAAGCTGACAGATGGGTATTCTTGACGGGG  
GGTAGGGGCGG  
AACCTGAGAGGCCGAAGGCCTGAAACCCCTGGGAGGGGGCAGTTGAGGTGCGC
```

Submit

GC Content:

0.5417721518987342

DNA Parse Motif

A sequence motif is a nucleotide or amino-acid sequence pattern that is widespread and has, or is conjectured to have, a biological significance.

Motif Sequence:

Search Sequence:

```
GCTGAGACTTCCTGGACGGGGACAGGCTGTGGGTTCTAGATAACTGGGCCCTGC
GCTCAGGAGGC
CTTCACCCCTCTGCTCTGGTAAGGTAGTAGACTCCGGAAAGGGACAGGGGGCCAA
GTGATGCTCTG
GGGTACTGGCGTGGGAGAGTGGATTCCGAAGCTGACAGATGGTATTCTTGACGGG
GGTAGGGGGCGG
AACCTGAGAGGCCTAAGGCCTGTGAACCCCTGGGGAGGGGGCAGTTGAGGTCGCG
```

Submit

Search Result:
Start index: 91. End index: 95
Start index: 375. End index: 379
Start index: 450. End index: 454

Input Sequence:

```
CCATTGCACTCC
AGCCTGGCGACAGAGCGAGACTGTCTAAAACAAACAAAACAAAACAAAAAC
ACCGGCTGGT
ATGTATGAGAGGATGGGACCTTGGAAGAAGAGGTGCCAGGAATATGTCAGGGAGGG
AGGAGACAGG
ATTTGTGGGAGGGAGAACCTAAGAACTGGATCCATTGCCATTGAGAAAGCGCAAGA
GGGAAGTAGA
```

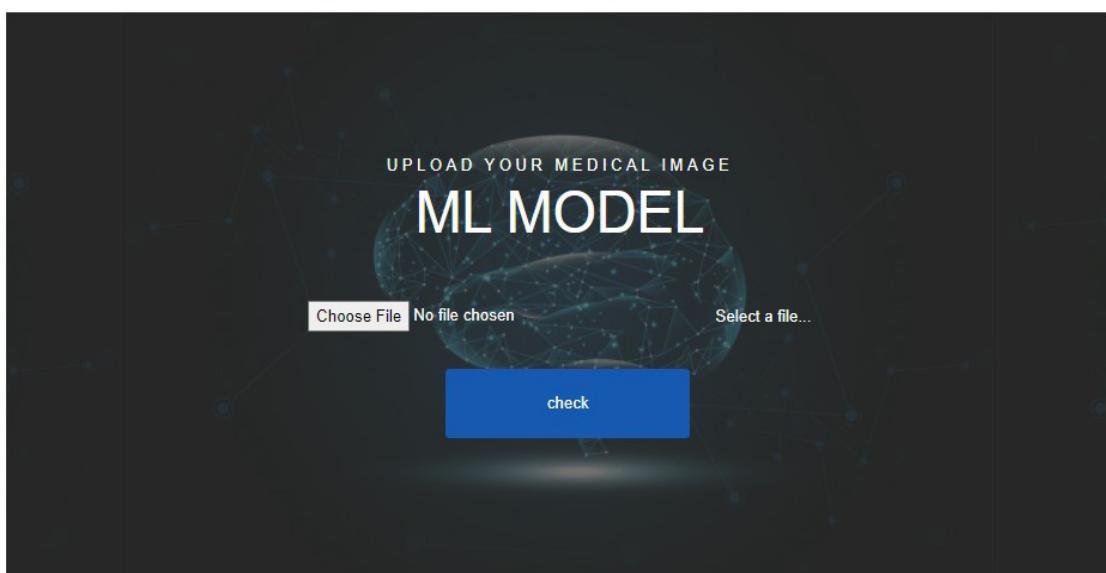
Submit

	A	T	C	G
Count	200	142	153	275

Distribution(26, '%', 'Base Pairs')(18, '%', 'Base Pairs')(20, '%', 'Base Pairs')(36, '%', 'Base Pairs')

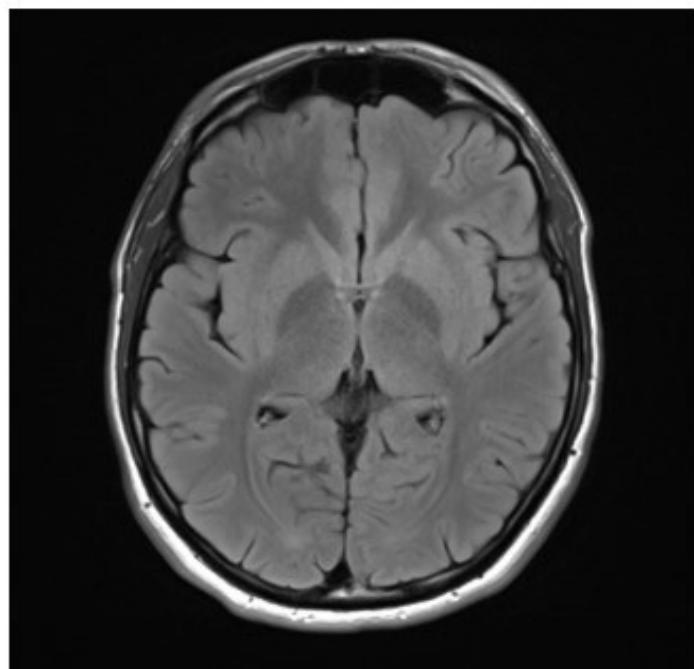
DNA Base Distribution

Machine learning model for image brain cancer recognition



- if the sample normal

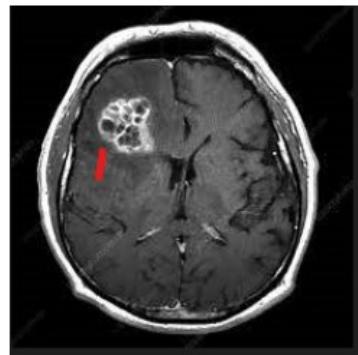
result of radiology diagnostics



you are well

-If the sample have tumor glioma

result of radiology diagnostics



Unfortunately, You Are Diagnosed With Glioma 😞

And You Should Consult The Doctor And Begin In Treatment

The treatment for a glioma depends on its grade. There are four grades of brain tumors; however, gliomas are most often referred to as "low grade" (grades I or II) or "high grade" (grades III or IV), based on the tumor's growth potential and aggressiveness.

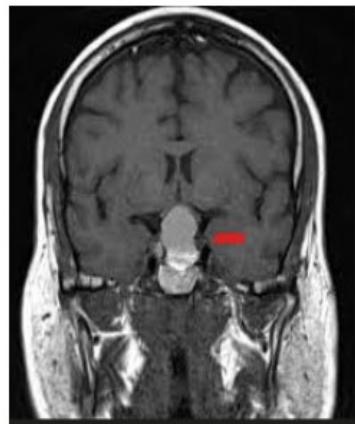
The best treatment for an individual patient takes into account the tumor location, potential symptoms, and potential benefits versus risks of the different treatment options (modalities).

Treatment for a glioma is customized to the individual patient and may include surgery, radiation therapy, chemotherapy or observation.

- **Surgery is the most common initial treatment for gliomas, and requires craniotomy (opening of the skull). It is sometimes performed with intraoperative MRI or intraoperative brain mapping if the tumor is near important areas of the brain.**

-If the sample have tumor PituitaryAdenoma

result of radiology diagnostics



Unfortunately, You Are Diagnosed With Pituitary Adenomas 😞

And You Should Consult The Doctor And Begin In Treatment

Pituitary adenomas are usually treated with surgery, medicine, radiation or a combination of these therapies.

- **Surgery:** Doctors can often remove the tumor with endoscopic surgery, reaching the pituitary using very small tools and a camera inserted in a small opening made through the nose and sinuses. This approach is called the transsphenoidal technique. In cases where this approach cannot be used, the doctor must open the skull to get to the pituitary and the adenoma.

-If the sample have tumor meningioma

result of radiology diagnostics



**Unfortunately, You Are Diagnosed With
Meningioma 😞**

**And You Should Consult The Doctor And Begin In
Treatment**

The decision of whether to, and how best to, treat a meningioma is based on multiple factors, including size and location of the tumor, symptoms, growth rate, and age of the patient (among others). In general, there are three basic options: observation, surgical removal, and radiation.

Conclusion

We have accomplished our goal of the project and successfully delivered it with all required features, the website is running now. We can do Development of the site to do more analyzes on biological sequences such as phylogenetic analysis And Develop the site to have an application on mobile phones with iOS and Android systems using FLUTTER.

References

- [1] nature nature biotechnology news article Published: 09 October 2014 Actionable
- [2] NIH Chelsea Toledo and Kirstie Saltsman Posted June 12, 2012
- [3] June 7, 2012 N Engl J Med 2012; 366:2207-2214 DOI: 10.1056/NEJMra1204479
- [4] Cancer Genetics Risk Assessment and Counseling (PDQ®)—Health Professional Version
- [5] Genetics of Breast and Gynecologic Cancers (PDQ®)—Health Professional Version
- [6] Genetic Testing for Inherited Cancer Susceptibility Syndromes
- [7]<https://www.who.int/news-room/fact-sheets/detail/breast-cancer>
- [8]<https://www.cancer.gov/about-cancer/understanding/what-is-cancer>