

# MACHINE LEARNING

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100% IMPLEMENTATION

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# Title

Image Segmentation for Brain Tumor Detection

## Abstract

In image related analysis and tasks such as image segmentation, image classification, image generation etc, deep convolutional neural networks have been proven to be very effective. We make use of a convolution neural network architecture that consists of a contracting path to capture context and a symmetric expanding path that enables precise localization. This type of architecture is capable of image segmentation with very high efficacy. This type of architecture provides several advantages for segmentation tasks: first, this model allows for the use of global location and context at the same time. Second, it works with very few training samples and provides better performance for segmentation tasks. We intend to apply this novel deep learning architecture to automate nucleus detection. By automating brain tumour detection, it enables us to help unlock cures faster. On top of detecting the tumours, our project will also be able to segment the tumour from the image.

## Introduction

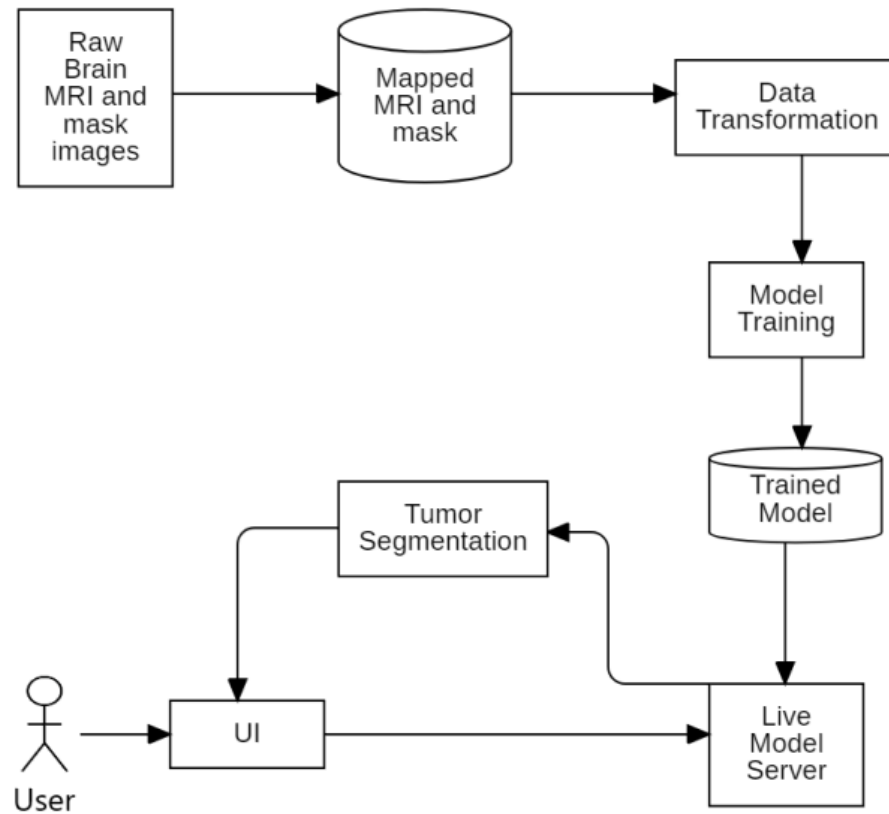
Several conventional computer vision techniques have been outperformed by deep learning in areas such as image classification, segmentation, tracking etc. Convolutional Neural Networks (CNN) is one of the most famous deep learning architectures. Its true effectiveness came to the surface when it is trained on more powerful machines with GPUs and leveraging large amount of training data. We generally use deep CNN models for image classification. But in the medical field, image segmentation has its own significance. For example, image segmentation is widely used in the localization of cancerous and defected regions in MRI and CT scans.

Segmentation of brain tumors allows visualization of the size and position of a tumor within the brain, and also provides for comparison of pre-operative and post-operative images or visualization of changes in a tumor's size and shape through a treatment time period. CNN models are used along with cross entropy loss as a pixel-wise measure in medical image segmentation

The most popular deep CNN architectures for medical image segmentation is based on an encoder-decoder architecture. The widely used models in this domain is U-Net and V-Net architectures. We will be using U-Net architecture to detect and localize brain tumors.

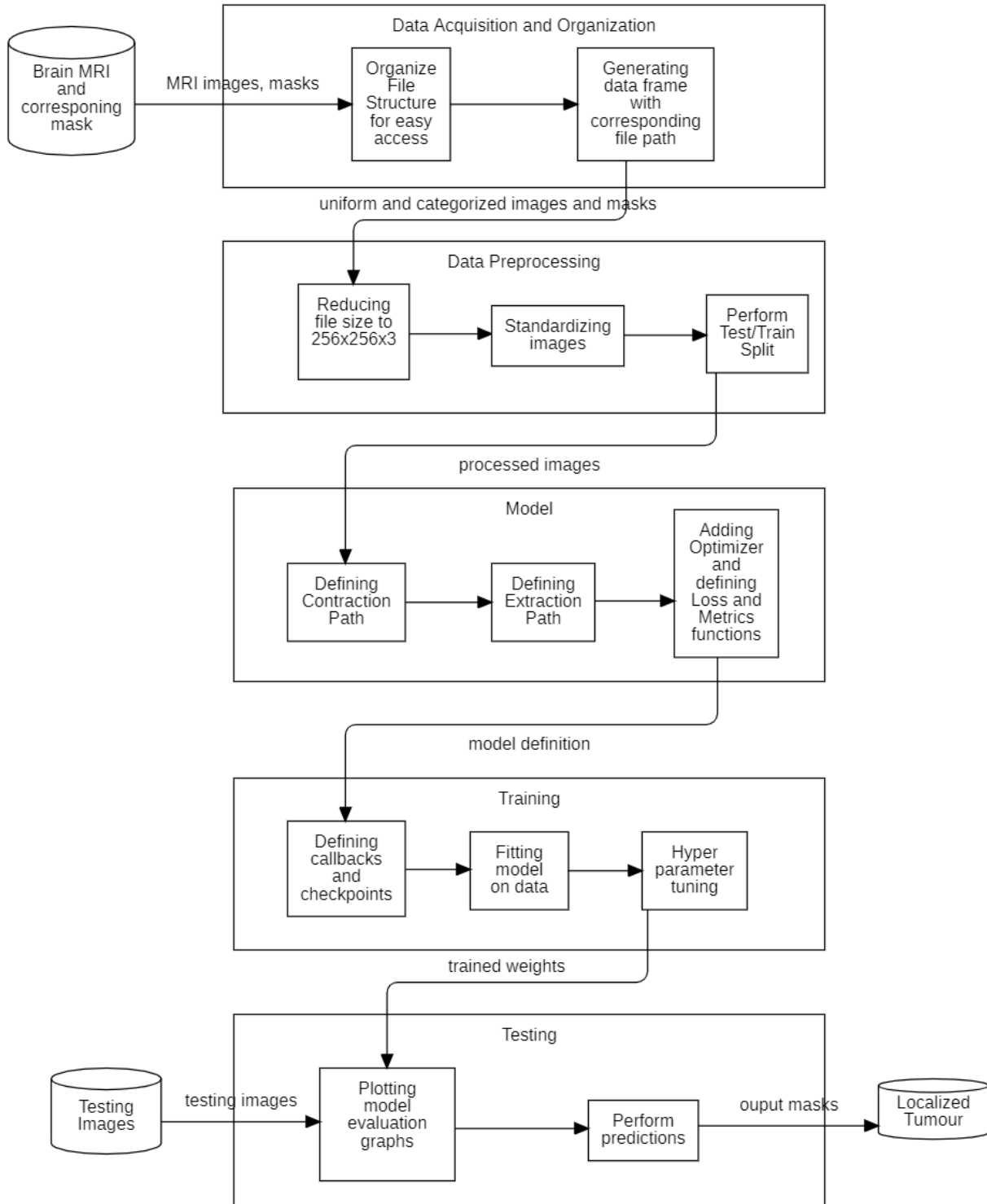
# Overall Architecture

## Project Architecture

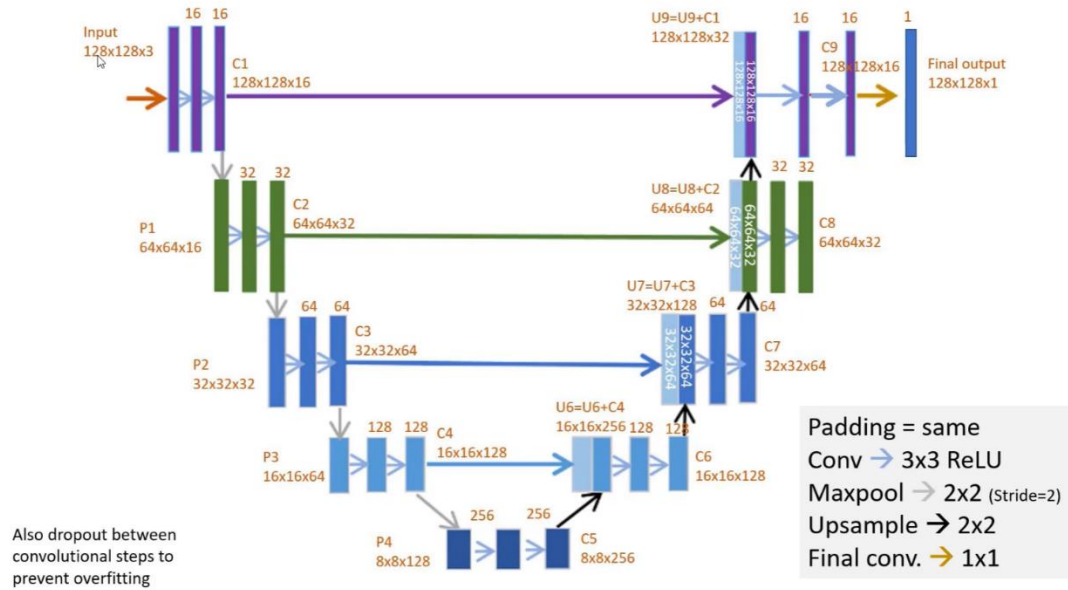


# Module Architecture

## Image Segmentation for Brain Tumor Detection



# Model Architecture



# Modules

**Input** - Images

**Output** - Masks

## **Module 1 - Data Acquisition and organization**

- First, we take messy and disorganized images and their corresponding training masks.
- Then we organize the file structure for easy access and efficient access.
- Data frame with corresponding file path is generated.

**Module Input** - Messy and disorganized images and training masks

**Module Output** - Uniform, categorized and refactored images and training masks

## **Module 2 - Data Preprocessing**

- Each of the images are read.
- Images are resized to 256x256x3.
- Then we standardize those images.
- After that we perform train/test split.

**Module Input** - Unprocessed images

**Module Output** - Processed Images in uniform size. Data is split into test and train

## **Module 3 – Model**

- Here we define the contraction path of the model architecture.
- Then we define the extraction path of the model architecture.
- And then we add optimizer and define loss and metric functions.

**Module Input** - Image size

**Module Output** - Defined model ready for training

### **Module 4 – Training**

- Callbacks and checkpoints are defined.
- Model is fitted on the data.
- Hyper parameter tuning is performed.

**Module Input** - Training images and defined model

**Module Output** - Trained weights

### **Module 5 – Testing**

- Here we plot model evaluation graphs.
- And then we perform predictions on test images.

**Module Input** - Testing images

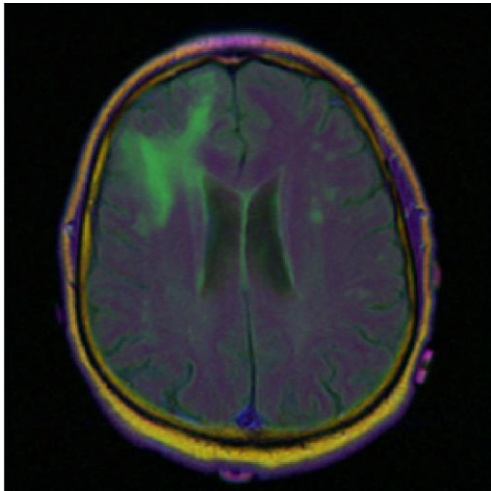
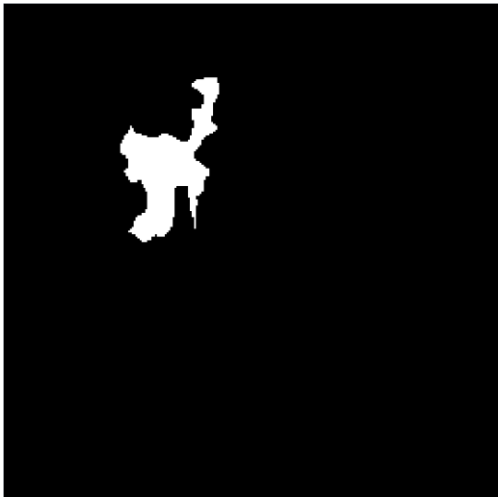
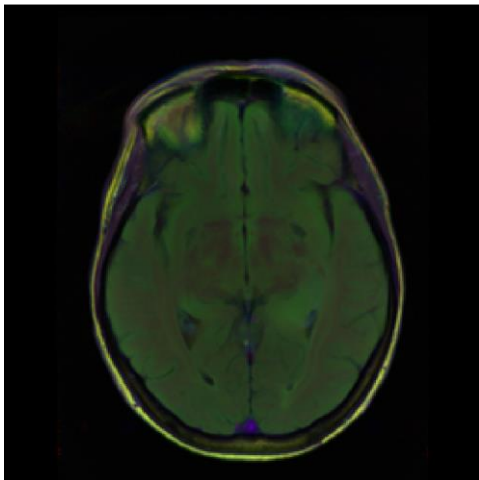

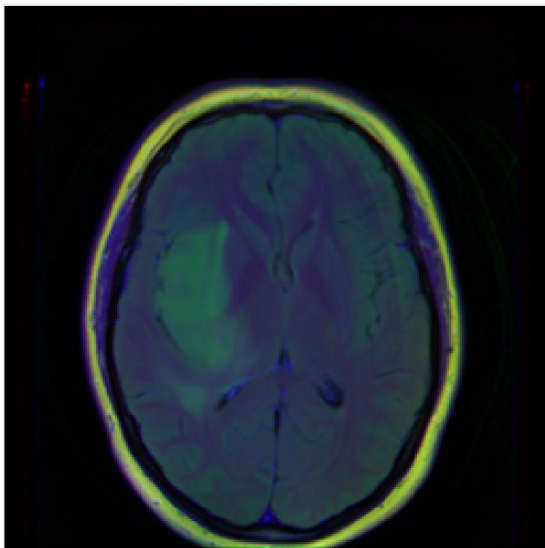

**Module Output** - Output masks

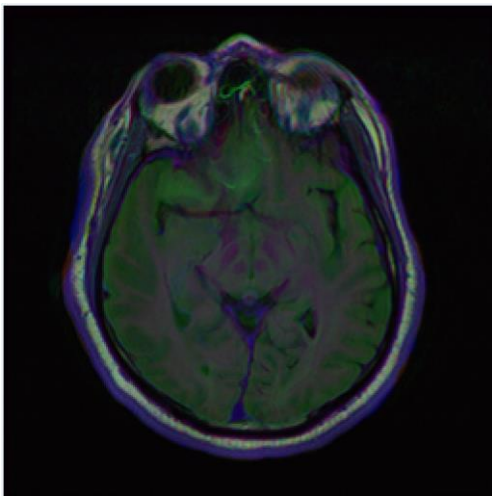
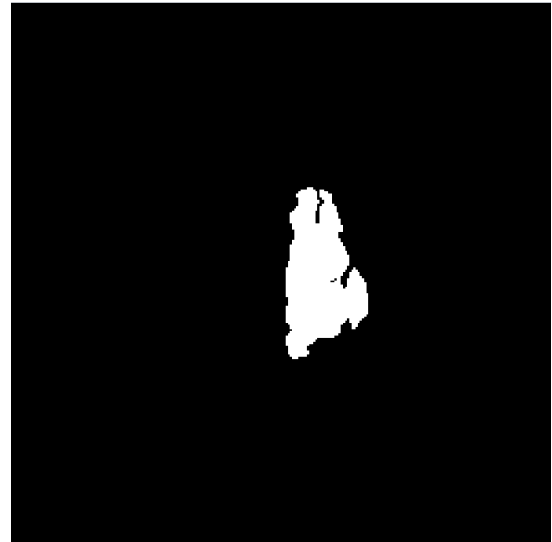
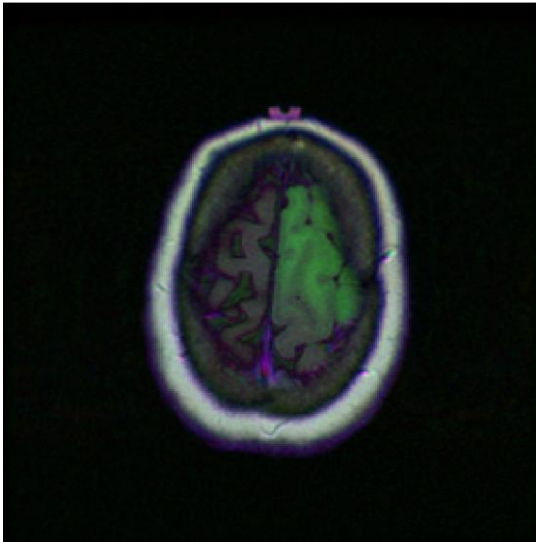
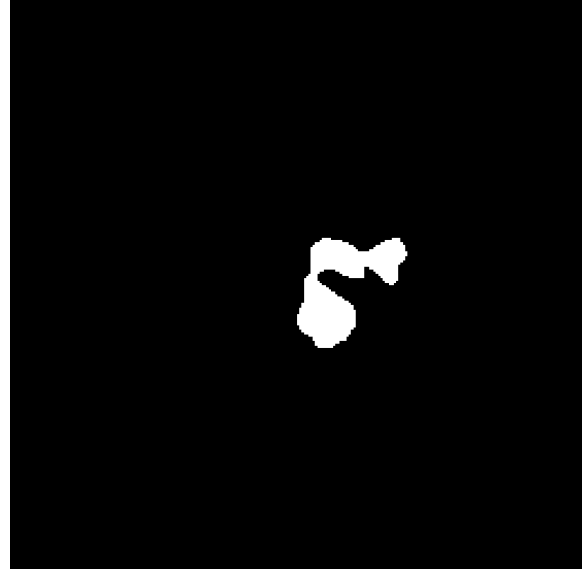
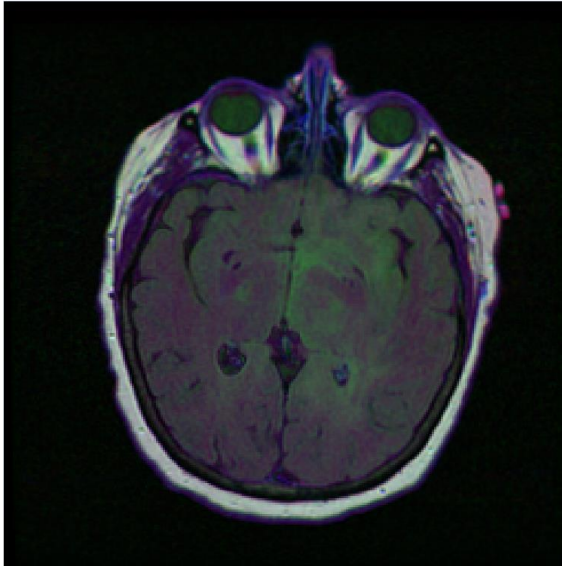
## **Dataset and Implementation Details**

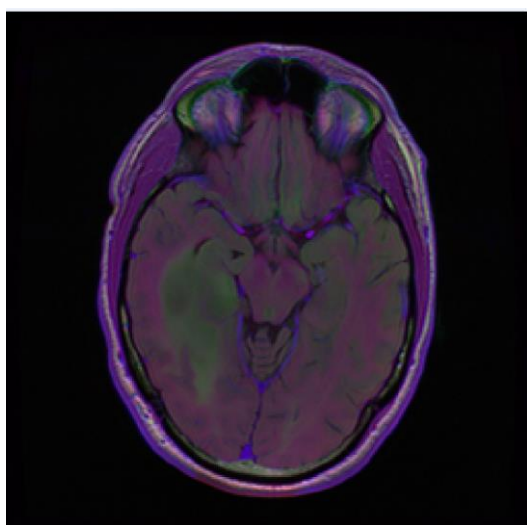
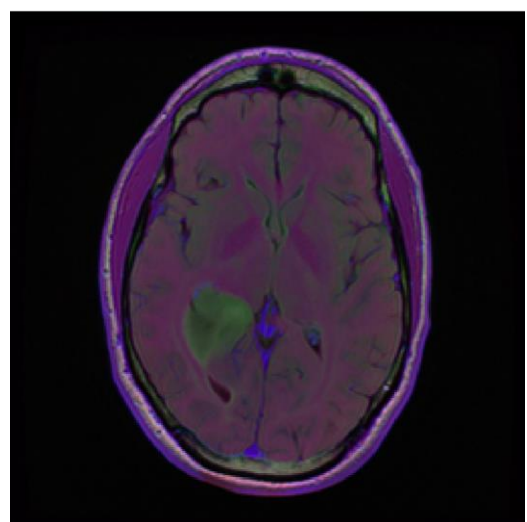
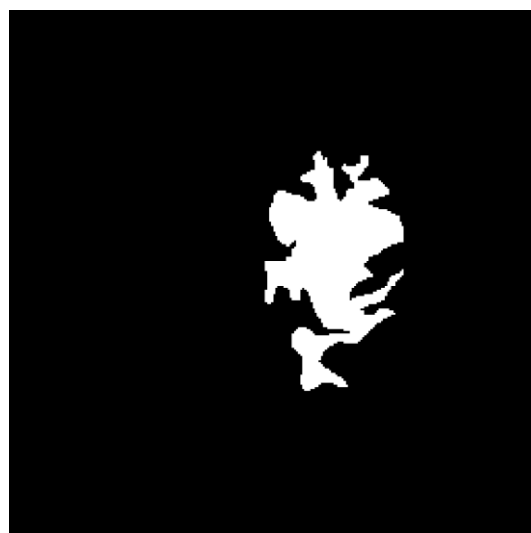
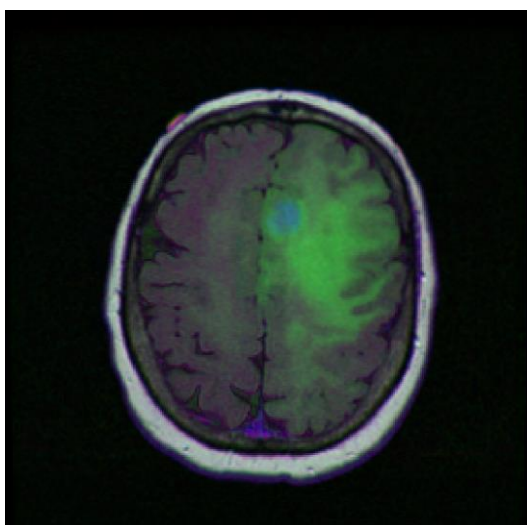
The Brain MRI dataset that we have considered has 3929 brain MRI images. Each of the brain MRI image has a corresponding mask image associated with it. Thus, the total number of images in the data set is 7858 images. The dataset comprises of brain MRI images that have a tumor and also contains brain MRI images that do not have a tumor. If a particular brain MRI image has a tumor, the corresponding mask has the tumor segmented with white pixels. Whereas if the brain MRI image does not have a tumor, the corresponding mask is a plain black image.

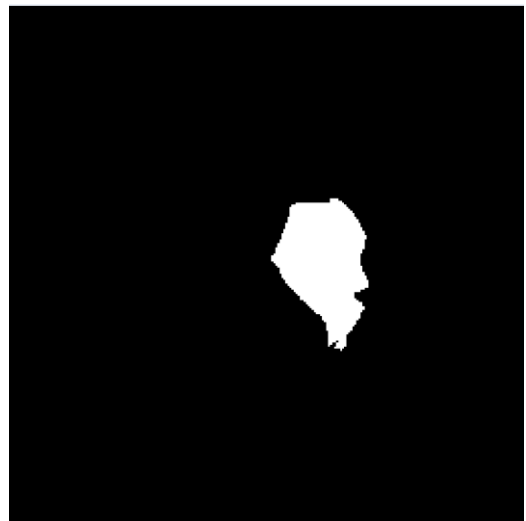
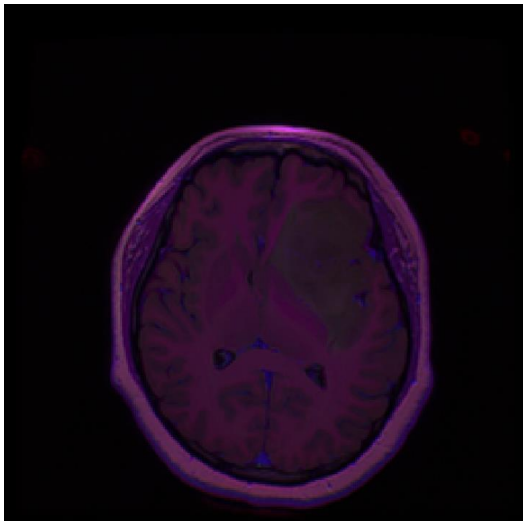
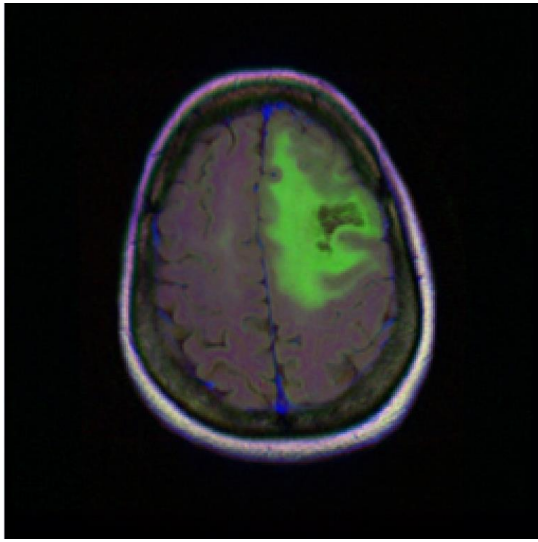
<https://www.kaggle.com/mateuszbeda/lgg-mri-segmentation>



Brain MRI Image	Mask Image
	
	
	







## Implementation Details

### Packages

**Numpy** – used to work with arrays

**Pandas** – used to analyze data and structure them into dataframes

**Matplotlib** – used to create interactive visualizations

**Seaborn** – provides high level interface or statistical graphs

**cv2** – used to work with images

**Tensorflow** – used to build, train and deploy machine learning models

**Tensorflow.keras** – high level tensorflow api which is used to define and train neural network models

**Random** – used to generate random numbers

**Sklearn.model\_selection.train\_test\_split** – used to split train and test data

### Algorithm

Input image is reshaped into a 256x256x3 matrix

#### Contraction Path:

- Convolution and max pool layers are applied numerous times on the input image which will result in extracted features
- At the end of this, our model will be able to detect nuclei in the image
- The results of the contraction path is now fed into the expansion path

### Expansion path:

- The matrix is fed into numerous Transposed Convolution layers and upsampling layers
- At the end of this, the model will result in a 128x128x16 matrix

Dimensionality reduction is applied on the matrix which results in a 128x128x1 image which corresponds to the output masks which contain the segmentation for the nuclei.

Trained is performed for several epochs and in batches, until the model converges and results in minimum loss.

## Screenshots

### MODULE 1 - Data Acquisition and Organization

#### Importing Libraries and Dataset

```
In [1]: import os
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import cv2
from skimage import io

import tensorflow as tf
import tensorflow.keras.backend as K

import random
import glob
from IPython.display import display

from sklearn.model_selection import train_test_split
```

```
In [2]: #Loading Dataset
data = pd.read_csv('../input/lgg-mri-segmentation/kaggle_3m/data.csv')
data.info()
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 110 entries, 0 to 109
Data columns (total 18 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   Patient                               110 non-null    object
1   RNASeqCluster                         92 non-null     float64
2   MethylationCluster                   109 non-null    float64
3   miRNACluster                         110 non-null    int64
4   CNCluster                           108 non-null    float64
5   RPPACluster                         98 non-null     float64
6   OncosignCluster                     105 non-null    float64
7   COCCluster                          110 non-null    int64
8   histological_type                    109 non-null    float64
9   neoplasm_histologic_grade            109 non-null    float64
10  tumor_tissue_site                    109 non-null    float64
11  laterality                           109 non-null    float64
12  tumor_location                       109 non-null    float64
13  gender                               109 non-null    float64
14  age_at_initial_pathologic             109 non-null    float64
15  race                                 108 non-null    float64
16  ethnicity                            102 non-null    float64
17  death01                              109 non-null    float64
dtypes: float64(15), int64(2), object(1)
memory usage: 15.6+ KB

```

```

In [3]: #Displaying dataset
        data.head(10)

```

Out[3]:

	Patient	RNASeqCluster	MethylationCluster	miRNACluster	CNCluster	RPPACluster	OncosignCluster	COCCluster
0	TCGA_CS_4941	2.0	4.0	2	2.0	NaN	3.0	2
1	TCGA_CS_4942	1.0	5.0	2	1.0	1.0	2.0	1
2	TCGA_CS_4943	1.0	5.0	2	1.0	2.0	2.0	1
3	TCGA_CS_4944	NaN	5.0	2	1.0	2.0	1.0	1
4	TCGA_CS_5393	4.0	5.0	2	1.0	2.0	3.0	1
5	TCGA_CS_5395	2.0	4.0	2	2.0	NaN	3.0	2
6	TCGA_CS_5396	3.0	3.0	2	3.0	2.0	2.0	3
7	TCGA_CS_5397	NaN	4.0	1	2.0	3.0	3.0	2
8	TCGA_CS_6186	2.0	4.0	1	2.0	1.0	3.0	2
9	TCGA_CS_6188	2.0	4.0	3	2.0	3.0	3.0	2

## Mapping patient id to filepath

```
In [4]: #Creating arrays of filename with its path
data_map = []
for sub_dir_path in glob.glob("/kaggle/input/lgg-mri-segmentation/kaggle_3m/*"):
    #if os.path.isdir(sub_dir_path):
    try:
        dir_name = sub_dir_path.split('/')[-1]
        for filename in os.listdir(sub_dir_path):
            image_path = sub_dir_path + '/' + filename
            data_map.extend([dir_name, image_path])
    except Exception as e:
        print(e)
```

```
[Errno 20] Not a directory: '/kaggle/input/lgg-mri-segmentation/kaggle_3m/README.md'
[Errno 20] Not a directory: '/kaggle/input/lgg-mri-segmentation/kaggle_3m/data.csv'
```

```
In [5]: #Converting array to a dataframe
df = pd.DataFrame({"patient_id" : data_map[:,2],
                  "path" : data_map[1::2]})

df.head()
```

Out[5]:

	patient_id	path
0	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...
1	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...
2	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...
3	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...
4	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...



## Mapping brain MRI image to corresponding mask

```
In [6]: #Sorting and mapping Brain MRI to corresponding mask
df_imgs = df[~df['path'].str.contains("mask")]
df_masks = df[df['path'].str.contains("mask")]

# File path line length images for later sorting
BASE_LEN = 89 # len(/kaggle/input/lgg-mri-segmentation/kaggle_3m/TCGA_DU_6404_19850629/TCGA_DU_6404_19850629_<-!!!43.tif)
END_IMG_LEN = 4 # len(/kaggle/input/lgg-mri-segmentation/kaggle_3m/TCGA_DU_6404_19850629/TCGA_DU_6404_19850629_43 !!!->.tif)
END_MASK_LEN = 9 # (/kaggle/input/lgg-mri-segmentation/kaggle_3m/TCGA_DU_6404_19850629/TCGA_DU_6404_19850629_43 !!!->_mask.tif)

# Data sorting
imgs = sorted(df_imgs["path"].values, key=lambda x : int(x[BASE_LEN:-END_IMG_LEN]))
masks = sorted(df_masks["path"].values, key=lambda x : int(x[BASE_LEN:-END_MASK_LEN]))
```

## Feature Extraction of presence/absence of tumor

### Final dataset - Segregating Brain MRI by Presence/Absence of Tumor

```
In [7]: #Final Dataset with groudtruth labels of whether tumor exists or not
#Final dataframe
brain_df = pd.DataFrame({"patient_id": df_imgs.patient_id.values,
                        "image_path": imgs,
                        "mask_path": masks
                        })

def pos_neg_diagnosis(mask_path):
    #/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...
    value = np.max(cv2.imread(mask_path))
    if value > 0 :
        return 1
    else:
        return 0

brain_df['mask'] = brain_df['mask_path'].apply(lambda x: pos_neg_diagnosis(x))
brain_df
```

Out[7]:

	patient_id	image_path	mask_path	mask
0	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
1	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
2	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
3	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
4	TCGA_DU_7010_19860307	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
...	...	...	...	...
3924	TCGA_DU_7306_19930512	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
3925	TCGA_DU_7306_19930512	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
3926	TCGA_DU_7306_19930512	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
3927	TCGA_DU_7306_19930512	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0
3928	TCGA_DU_7306_19930512	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	0

3929 rows × 4 columns

## Performing Data Visualization

In [8]:

```
#Visualization of number of images with and without tumors
class_count = brain_df['mask'].value_counts()
class_count
```

Out[8]:

```
0    2556
1    1373
Name: mask, dtype: int64
```

In [9]:

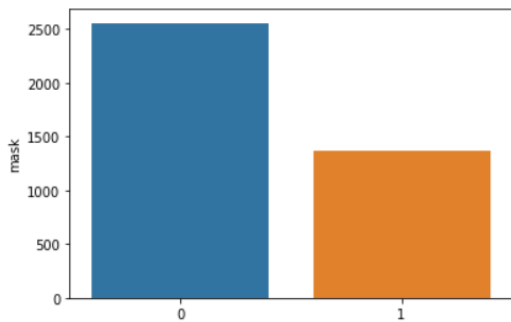
```
class_count = class_count.to_frame()
class_count
```

Out[9]:

	mask
0	2556
1	1373

```
In [10]: sns.barplot(x=class_count.index ,y='mask', data=class_count)
```

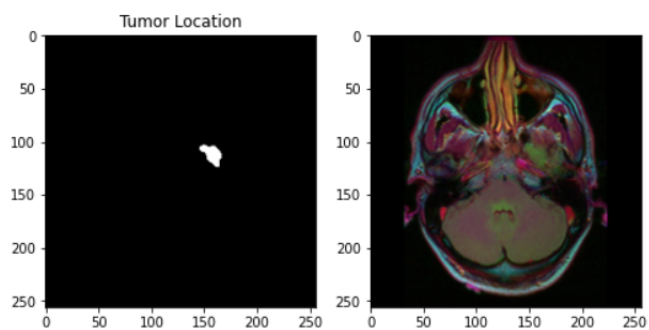
```
Out[10]: <AxesSubplot:ylabel='mask'>
```



```
In [11]: #Plotting Single Brain MRI image and mask with tumour
for i in range(len(brain_df)):
    if cv2.imread(brain_df.mask_path[i]).max() > 0:
        break

plt.figure(figsize=(8,8))
plt.subplot(1,2,1)
plt.imshow(cv2.imread(brain_df.mask_path[i]));
plt.title('Tumor Location')

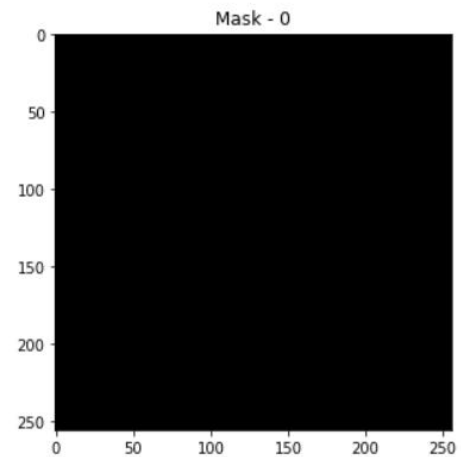
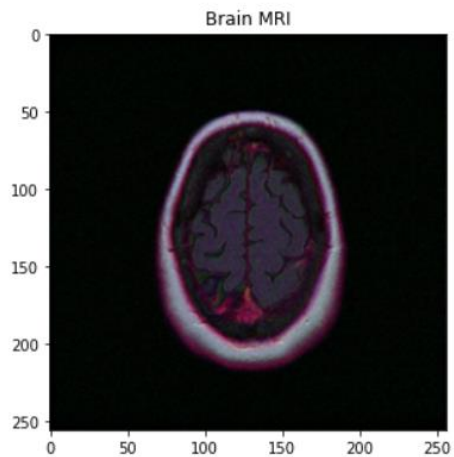
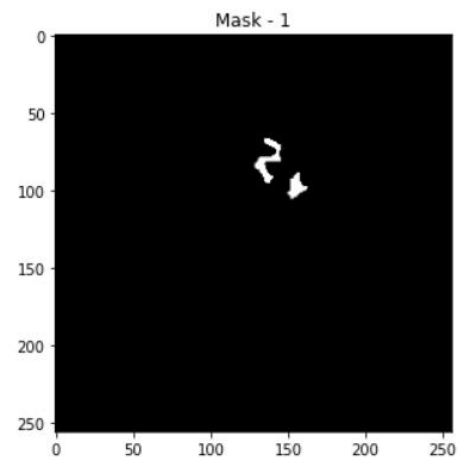
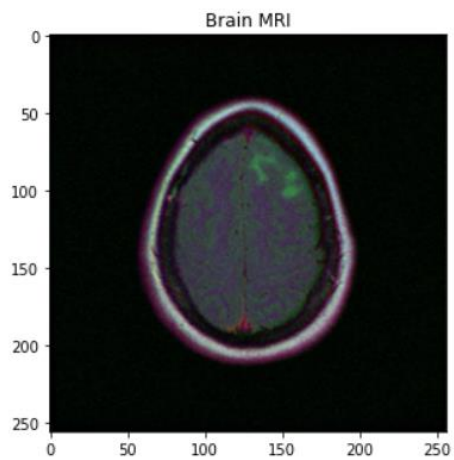
plt.subplot(1,2,2)
plt.imshow(cv2.imread(brain_df.image_path[i]));
```

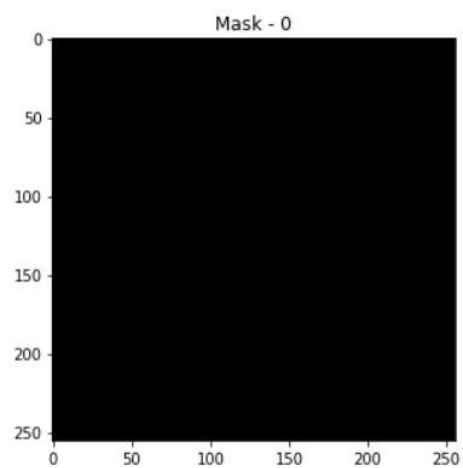
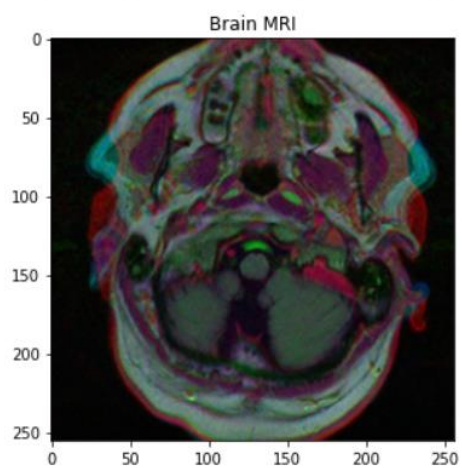
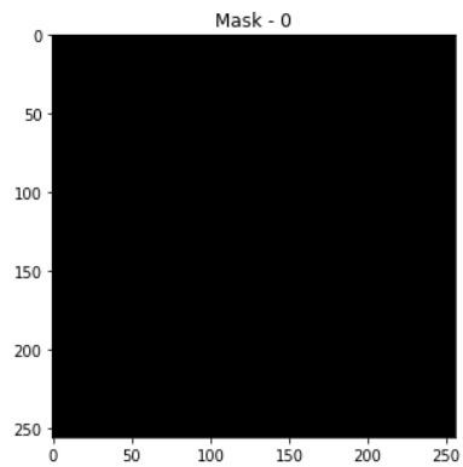
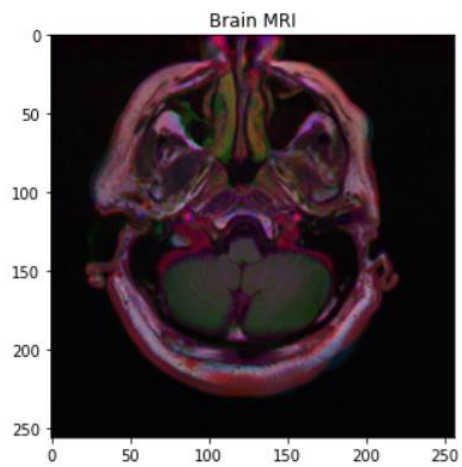


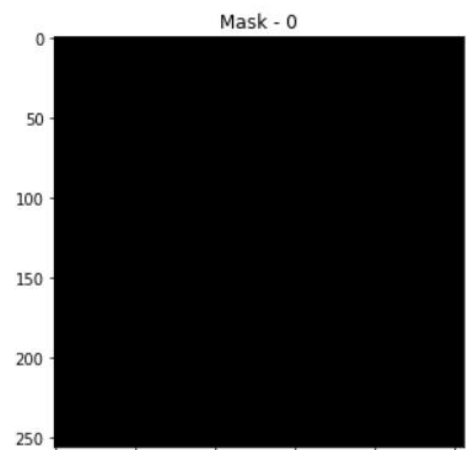
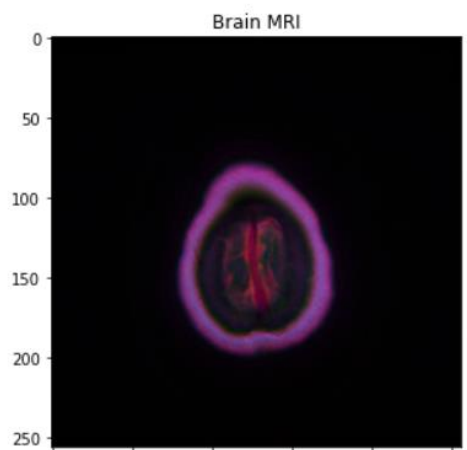
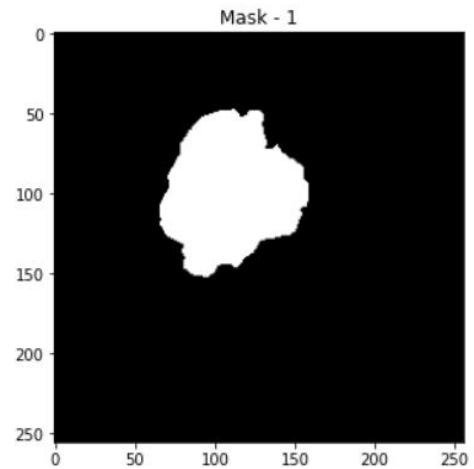
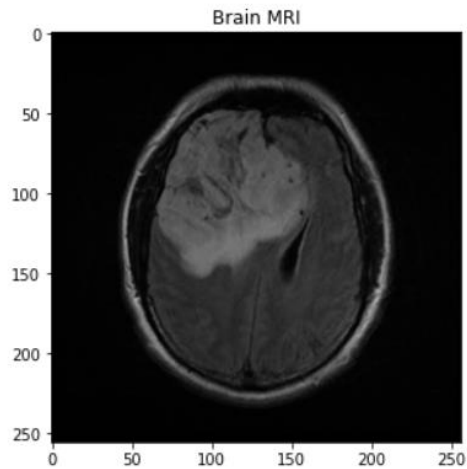
In [12]:

```
# More Plot examples
fig, axes = plt.subplots(6,2, figsize=(16,26))
count = 0
for x in range(6):
    i = random.randint(0, len(brain_df)) # select a random index
    axes[count][0].title.set_text("Brain MRI") # set title
    axes[count][0].imshow(cv2.imread(brain_df.image_path[i])) # show MRI
    axes[count][1].title.set_text("Mask - " + str(brain_df['mask'][i])) # plot title on the mask (0
    or 1)
    axes[count][1].imshow(cv2.imread(brain_df.mask_path[i])) # Show corresponding mask
    count += 1

fig.tight_layout()
```





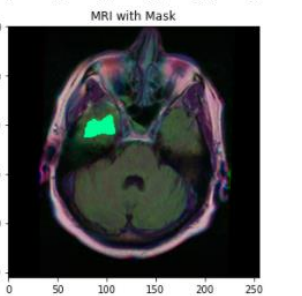
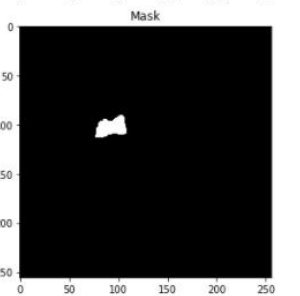
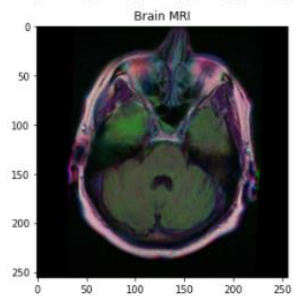
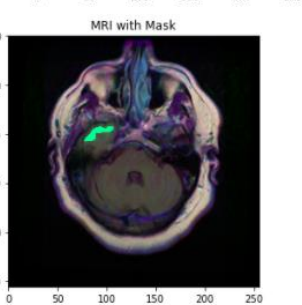
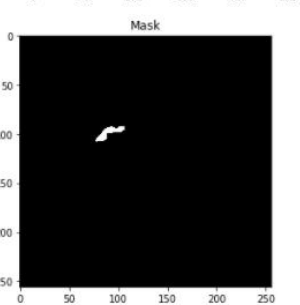
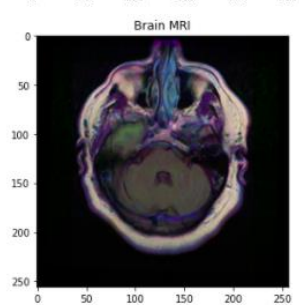
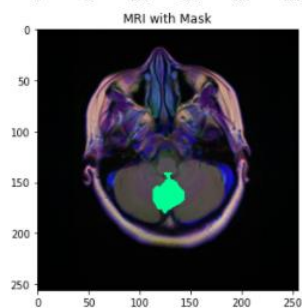
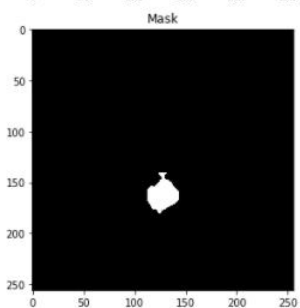
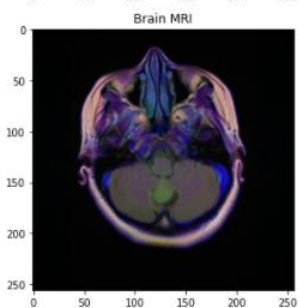
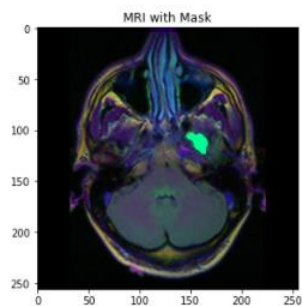
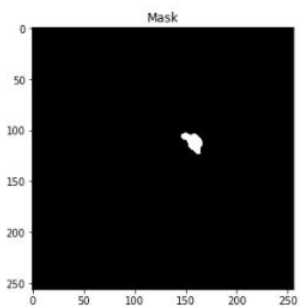
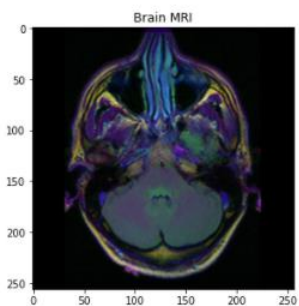


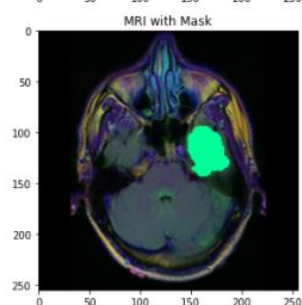
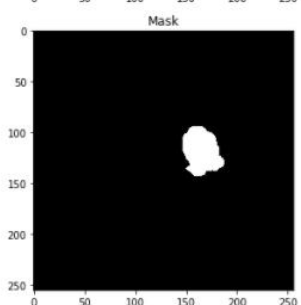
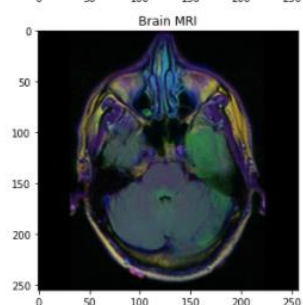
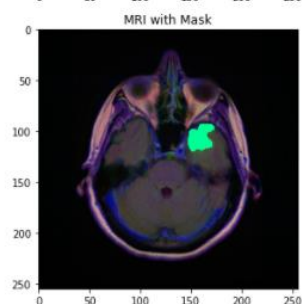
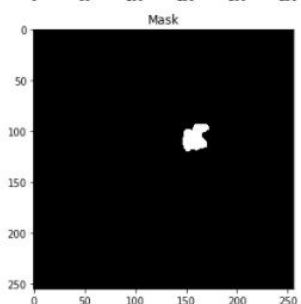
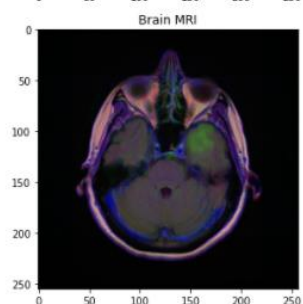
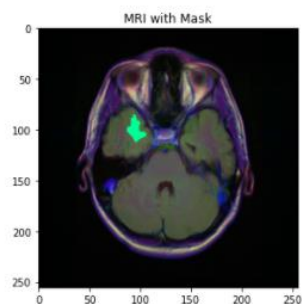
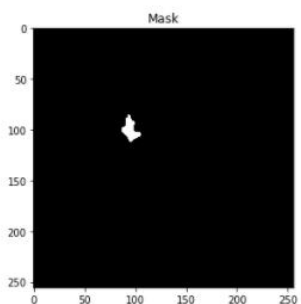
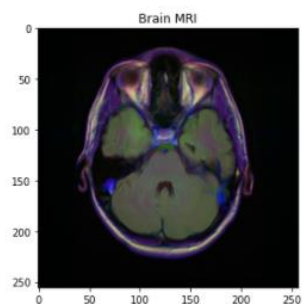
```
In [13]:
count = 0
i = 0
fig, axes = plt.subplots(12, 3, figsize=(20, 50))
for mask in brain_df['mask']:
    if (mask==1):
        img = io.imread(brain_df.image_path[i])
        axes[count][0].title.set_text("Brain MRI")
        axes[count][0].imshow(img)

        mask = io.imread(brain_df.mask_path[i])
        axes[count][1].title.set_text("Mask")
        axes[count][1].imshow(mask, cmap='gray')

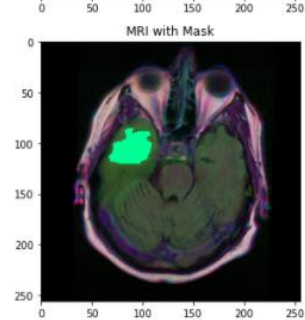
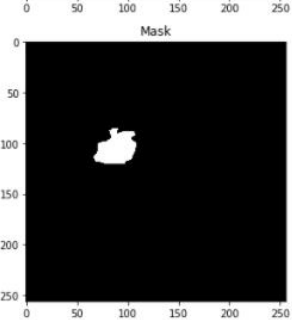
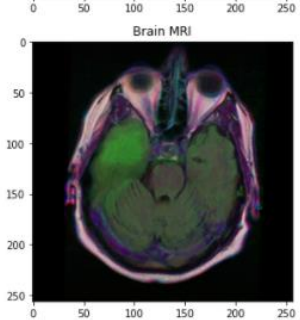
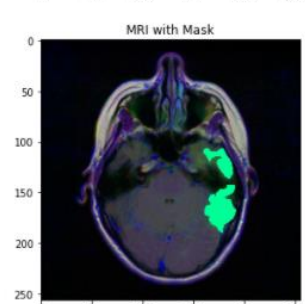
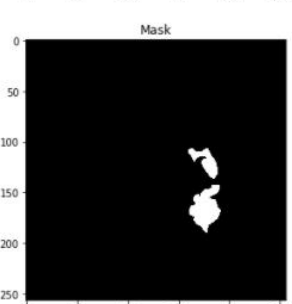
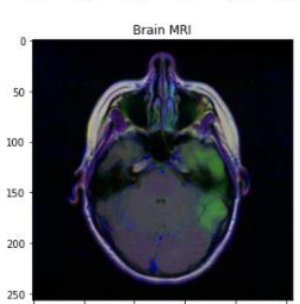
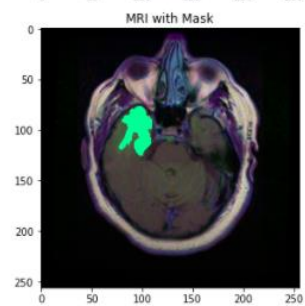
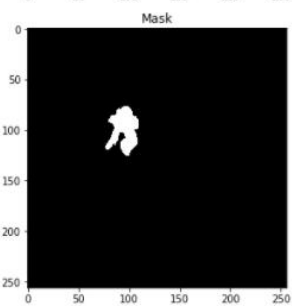
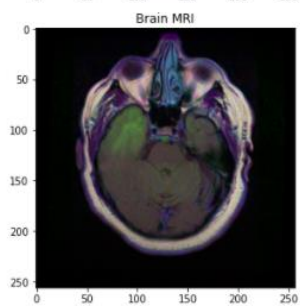
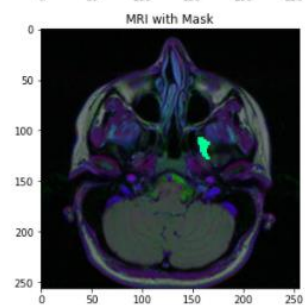
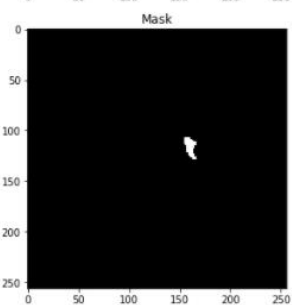
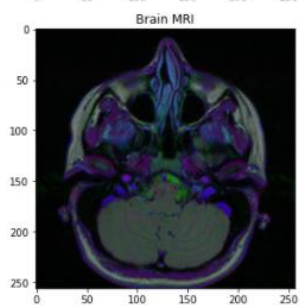
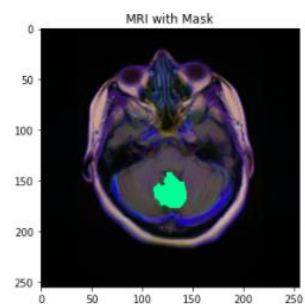
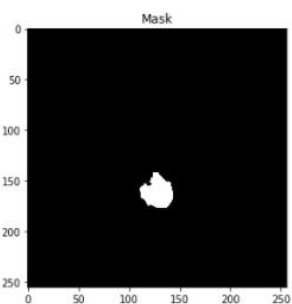
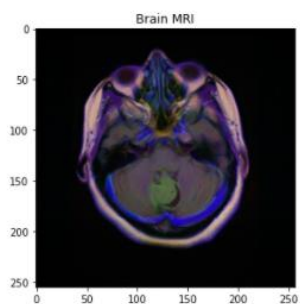
        img[mask==255] = (0, 255, 150) # change pixel color at the position of mask
        axes[count][2].title.set_text("MRI with Mask")
        axes[count][2].imshow(img)
        count += 1
    i += 1
    if (count==12):
        break

fig.tight_layout()
```









## MODULE 2 - Data Preprocessing

### Performing train and test split

```
In [14]: brain_df_train = brain_df.drop(columns=['patient_id'])
brain_df_train['mask'] = brain_df_train['mask'].apply(lambda x: str(x))
brain_df_train.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3929 entries, 0 to 3928
Data columns (total 3 columns):
#   Column      Non-Null Count  Dtype
---  ---
0   image_path  3929 non-null   object
1   mask_path   3929 non-null   object
2   mask        3929 non-null   object
dtypes: object(3)
memory usage: 92.2+ KB
```

```
In [16]: brain_df_mask = brain_df[brain_df['mask'] == 1]
brain_df_mask.shape
```

```
Out[16]: (1373, 4)
```

```
In [17]: brain_df_mask.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 1373 entries, 537 to 3802
Data columns (total 4 columns):
#   Column      Non-Null Count  Dtype
---  ---
0   patient_id  1373 non-null   object
1   image_path  1373 non-null   object
2   mask_path   1373 non-null   object
3   mask        1373 non-null   int64
dtypes: int64(1), object(3)
memory usage: 53.6+ KB
```

In [18]:

```
# Creating test, train and val sets
X_train, X_val = train_test_split(brain_df_mask, test_size=0.15)
X_test, X_val = train_test_split(X_val, test_size=0.5)
print("Train size is {}, valid size is {} & test size is {}".format(len(X_train), len(X_val), len(X_test)))

train_ids = list(X_train.image_path)
train_mask = list(X_train.mask_path)

val_ids = list(X_val.image_path)
val_mask = list(X_val.mask_path)
```

```
Train size is 1167, valid size is 103 & test size is 103
```

## Resizing and standardizing images

In [19]:

```
class DataGenerator(tf.keras.utils.Sequence):
    def __init__(self, ids, mask, image_dir = './', batch_size = 16, img_h = 256, img_w = 256, shuffle = True):

        self.ids = ids
        self.mask = mask
        self.image_dir = image_dir
        self.batch_size = batch_size
        self.img_h = img_h
        self.img_w = img_w
        self.shuffle = shuffle
        self.on_epoch_end()

    def __len__(self):
        'Get the number of batches per epoch'
        return int(np.floor(len(self.ids)) / self.batch_size)
```

```

def __getitem__(self, index):
    'Generate a batch of data'

    #generate index of batch_size length
    indexes = self.indexes[index* self.batch_size : (index+1) * self.batch_size]

    #get the ImageId corresponding to the indexes created above based on batch size
    list_ids = [self.ids[i] for i in indexes]

    #get the MaskId corresponding to the indexes created above based on batch size
    list_mask = [self.mask[i] for i in indexes]

    #generate data for the X(features) and y(label)
    X, y = self.__data_generation(list_ids, list_mask)

    #returning the data
    return X, y

```

```

def on_epoch_end(self):
    'Used for updating the indices after each epoch, once at the beginning as well as at the end of each epoch'

    #getting the array of indices based on the input dataframe
    self.indexes = np.arange(len(self.ids))

    #if shuffle is true, shuffle the indices
    if self.shuffle:
        np.random.shuffle(self.indexes)

def __data_generation(self, list_ids, list_mask):
    'generate the data corresponding the indexes in a given batch of images'

    # create empty arrays of shape (batch_size,height,width,depth)
    #Depth is 3 for input and depth is taken as 1 for output because mask consist only of 1 channel.
    X = np.empty((self.batch_size, self.img_h, self.img_w, 3))
    y = np.empty((self.batch_size, self.img_h, self.img_w, 1))

    #iterate through the dataframe rows, whose size is equal to the batch_size
    for i in range(len(list_ids)):
        #path of the image
        img_path = str(list_ids[i])

        #mask path
        mask_path = str(list_mask[i])

```

```

#reading the original image and the corresponding mask image
img = io.imread(img_path)
mask = io.imread(mask_path)

#resizing and coverting them to array of type float64
img = cv2.resize(img, (self.img_h, self.img_w))
img = np.array(img, dtype = np.float64)

mask = cv2.resize(mask, (self.img_h, self.img_w))
mask = np.array(mask, dtype = np.float64)

#standardising
img -= img.mean()
img /= img.std()

mask -= mask.mean()
mask /= mask.std()

#Adding image to the empty array
X[i,] = img

#expanding the dimnesion of the image from (256,256) to (256,256,1)
y[i,] = np.expand_dims(mask, axis = 2)

```

```

y = (y > 0).astype(int)
X = (X > 0).astype(int)

```

```

return X, y

```

```

train_data = DataGenerator(train_ids, train_mask)
val_data = DataGenerator(val_ids, val_mask)

```

## MODULE 3 - Model

### Dice Coefficient Metric

```
In [20]: #Defining dice coefficient metric
def dice_coef(y_true, y_pred):
    """
    Parameters
    -----
    y_true : numpy array of actual masks
    y_pred : numpy array of predicted masks
    """
    y_true_f = K.flatten(y_true)
    y_pred_f = K.flatten(y_pred)
    intersection = K.sum(y_true_f * y_pred_f)
    return (2. * intersection + K.epsilon()) / (K.sum(y_true_f) + K.sum(y_pred_f) + K.epsilon())
```

### Defining contraction path

```
In [21]: #U-NET MODEL
inputs = tf.keras.layers.Input((256,256,3))

#NORMALIZING THE INPUT
s = tf.keras.layers.Lambda(lambda x: x/255)(inputs)

#CONTRACTION PATH
#Convolution-1
c1 = tf.keras.layers.Conv2D(16, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(s)
c1 = tf.keras.layers.Dropout(0.1)(c1)
c1 = tf.keras.layers.Conv2D(16, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(c1)
#MaxPool-1
p1 = tf.keras.layers.MaxPool2D((2,2))(c1)
```

```
#Convolution-2
c2 = tf.keras.layers.Conv2D(32, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(p1)
c2 = tf.keras.layers.Dropout(0.1)(c2)
c2 = tf.keras.layers.Conv2D(32, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(c2)
#MaxPool-2
p2 = tf.keras.layers.MaxPool2D((2,2))(c2)
```

```
#Convolution-3
c3 = tf.keras.layers.Conv2D(64, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(p2)
c3 = tf.keras.layers.Dropout(0.2)(c3)
c3 = tf.keras.layers.Conv2D(64, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(c3)
#MaxPool-3
p3 = tf.keras.layers.MaxPool2D((2,2))(c3)
```

```
#Convolution-4
c4 = tf.keras.layers.Conv2D(128, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(p3)
c4 = tf.keras.layers.Dropout(0.2)(c4)
c4 = tf.keras.layers.Conv2D(128, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(c4)
#MaxPool-4
p4 = tf.keras.layers.MaxPool2D((2,2))(c4)
```

```
#Convolution-5
c5 = tf.keras.layers.Conv2D(256, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(p4)
c5 = tf.keras.layers.Dropout(0.3)(c5)
c5 = tf.keras.layers.Conv2D(256, (3,3), activation='relu', kernel_initializer='he_normal', padding='same')(c5)
```

## Defining expansion path

```
#EXPANSION PATH
#ConvolutionTranspose-1 (upsample)
u6 = tf.keras.layers.Conv2DTranspose(128, (2, 2), strides=(2, 2), padding='same')(c5)
u6 = tf.keras.layers.concatenate([u6, c4])
#Convolution-6
c6 = tf.keras.layers.Conv2D(128, (3, 3), activation='relu', kernel_initializer='he_normal',
padding='same')(u6)
c6 = tf.keras.layers.Dropout(0.2)(c6)
c6 = tf.keras.layers.Conv2D(128, (3, 3), activation='relu', kernel_initializer='he_normal',
padding='same')(c6)

#ConvolutionTranspose-2 (upsample)
u7 = tf.keras.layers.Conv2DTranspose(64, (2, 2), strides=(2, 2), padding='same')(c6)
u7 = tf.keras.layers.concatenate([u7, c3])
#Convolution-7
c7 = tf.keras.layers.Conv2D(64, (3, 3), activation='relu', kernel_initializer='he_normal', padding='same')(u7)
c7 = tf.keras.layers.Dropout(0.2)(c7)
c7 = tf.keras.layers.Conv2D(64, (3, 3), activation='relu', kernel_initializer='he_normal', padding='same')(c7)

#ConvolutionTranspose-3 (upsample)
u8 = tf.keras.layers.Conv2DTranspose(32, (2, 2), strides=(2, 2), padding='same')(c7)
u8 = tf.keras.layers.concatenate([u8, c2])
#Convolution-8
c8 = tf.keras.layers.Conv2D(32, (3, 3), activation='relu', kernel_initializer='he_normal', padding='same')(u8)
c8 = tf.keras.layers.Dropout(0.1)(c8)
c8 = tf.keras.layers.Conv2D(32, (3, 3), activation='relu', kernel_initializer='he_normal', padding='same')(c8)

#ConvolutionTranspose-4 (upsample)
u9 = tf.keras.layers.Conv2DTranspose(16, (2, 2), strides=(2, 2), padding='same')(c8)
u9 = tf.keras.layers.concatenate([u9, c1], axis=3)
#Convolution-9
c9 = tf.keras.layers.Conv2D(16, (3, 3), activation='relu', kernel_initializer='he_normal', padding='same')(u9)
c9 = tf.keras.layers.Dropout(0.1)(c9)
c9 = tf.keras.layers.Conv2D(16, (3, 3), activation='relu', kernel_initializer='he_normal', padding='same')(c9)
```



## Adding Optimizer and loss metrics

```
outputs = tf.keras.layers.Conv2D(1, (1, 1), activation='sigmoid')(c9)

adam = tf.keras.optimizers.Adam(lr = 0.05, epsilon = 0.1)
model = tf.keras.Model(inputs=[inputs], outputs=[outputs])
model.compile(optimizer='adam', loss='binary_crossentropy', metrics=[dice_coef, 'accuracy'])
model.summary()
```

Model: "model"

Layer (type)	Output Shape	Param #	Connected to
input_1 (InputLayer)	[(None, 256, 256, 3)]	0	
lambda (Lambda)	(None, 256, 256, 3)	0	input_1[0][0]
conv2d (Conv2D)	(None, 256, 256, 16)	448	lambda[0][0]
dropout (Dropout)	(None, 256, 256, 16)	0	conv2d[0][0]
conv2d_1 (Conv2D)	(None, 256, 256, 16)	2320	dropout[0][0]
max_pooling2d (MaxPooling2D)	(None, 128, 128, 16)	0	conv2d_1[0][0]

```

-----
conv2d_2 (Conv2D)          (None, 128, 128, 32) 4640      max_pooling2d[0][0]
-----
-----
dropout_1 (Dropout)        (None, 128, 128, 32) 0       conv2d_2[0][0]
-----
-----
conv2d_3 (Conv2D)          (None, 128, 128, 32) 9248      dropout_1[0][0]
-----
-----
max_pooling2d_1 (MaxPooling2D) (None, 64, 64, 32) 0       conv2d_3[0][0]
-----
-----
conv2d_4 (Conv2D)          (None, 64, 64, 64) 18496      max_pooling2d_1[0][0]
-----
-----
dropout_2 (Dropout)        (None, 64, 64, 64) 0       conv2d_4[0][0]
-----
-----
conv2d_5 (Conv2D)          (None, 64, 64, 64) 36928      dropout_2[0][0]
-----
-----
max_pooling2d_2 (MaxPooling2D) (None, 32, 32, 64) 0       conv2d_5[0][0]
-----

```

```

-----
conv2d_6 (Conv2D)          (None, 32, 32, 128) 73856      max_pooling2d_2[0][0]
-----
-----
dropout_3 (Dropout)        (None, 32, 32, 128) 0        conv2d_6[0][0]
-----
-----
conv2d_7 (Conv2D)          (None, 32, 32, 128) 147584     dropout_3[0][0]
-----
-----
max_pooling2d_3 (MaxPooling2D) (None, 16, 16, 128) 0        conv2d_7[0][0]
-----
-----
conv2d_8 (Conv2D)          (None, 16, 16, 256) 295168     max_pooling2d_3[0][0]
-----
-----
dropout_4 (Dropout)        (None, 16, 16, 256) 0        conv2d_8[0][0]
-----
-----
conv2d_9 (Conv2D)          (None, 16, 16, 256) 590080     dropout_4[0][0]
-----
-----
conv2d_transpose (Conv2DTranspo (None, 32, 32, 128) 131200     conv2d_9[0][0]
-----
-----
concatenate (Concatenate)   (None, 32, 32, 256) 0        conv2d_transpose[0][0]
conv2d_7[0][0]

```

```

-----
conv2d_10 (Conv2D)          (None, 32, 32, 128) 295040 concatenate[0][0]
-----
dropout_5 (Dropout)         (None, 32, 32, 128) 0 conv2d_10[0][0]
-----
conv2d_11 (Conv2D)          (None, 32, 32, 128) 147584 dropout_5[0][0]
-----
conv2d_transpose_1 (Conv2DTrans (None, 64, 64, 64) 32832 conv2d_11[0][0]
-----
concatenate_1 (Concatenate) (None, 64, 64, 128) 0 conv2d_transpose_1[0]
[0]
conv2d_5[0][0]
-----
conv2d_12 (Conv2D)          (None, 64, 64, 64) 73792 concatenate_1[0][0]
-----
dropout_6 (Dropout)         (None, 64, 64, 64) 0 conv2d_12[0][0]
-----
conv2d_13 (Conv2D)          (None, 64, 64, 64) 36928 dropout_6[0][0]

```

```

-----
conv2d_transpose_2 (Conv2DTrans (None, 128, 128, 32) 8224      conv2d_13[0][0]
-----
-----
concatenate_2 (Concatenate)      (None, 128, 128, 64) 0      conv2d_transpose_2[0]
[0]
                                conv2d_3[0][0]
-----
-----
conv2d_14 (Conv2D)                (None, 128, 128, 32) 18464   concatenate_2[0][0]
-----
-----
dropout_7 (Dropout)              (None, 128, 128, 32) 0      conv2d_14[0][0]
-----
-----
conv2d_15 (Conv2D)                (None, 128, 128, 32) 9248   dropout_7[0][0]
-----
-----
conv2d_transpose_3 (Conv2DTrans (None, 256, 256, 16) 2064      conv2d_15[0][0]
-----
-----
concatenate_3 (Concatenate)      (None, 256, 256, 32) 0      conv2d_transpose_3[0]
[0]
                                conv2d_1[0][0]
-----

-----
conv2d_16 (Conv2D)                (None, 256, 256, 16) 4624   concatenate_3[0][0]
-----
-----
dropout_8 (Dropout)              (None, 256, 256, 16) 0      conv2d_16[0][0]
-----
-----
conv2d_17 (Conv2D)                (None, 256, 256, 16) 2320   dropout_8[0][0]
-----
-----
conv2d_18 (Conv2D)                (None, 256, 256, 1) 17      conv2d_17[0][0]
=====
=====
Total params: 1,941,105
Trainable params: 1,941,105
Non-trainable params: 0

```

## MODULE 4 - Training

### Defining callbacks and checkpoints

```
In [22]: #Defining callbacks for the model
callbacks = [
    tf.keras.callbacks.EarlyStopping(monitor='val_loss', patience=10, verbose=1, mode="min"),
    tf.keras.callbacks.TensorBoard(log_dir='logs'),
    tf.keras.callbacks.ReduceLROnPlateau(monitor='val_loss',
                                         mode='min',
                                         verbose=1,
                                         patience=5,
                                         min_delta=0.0001,
                                         factor=0.2
                                         ),
    tf.keras.callbacks.ModelCheckpoint('BrainTumorSegModel.h5', monitor='val_loss', verbose=1, save_best_only=True)
]
```

### Fitting model on data

```
In [23]: #Fitting model on data
h = model.fit(train_data,
              epochs = 60,
              validation_data = val_data,
              callbacks=callbacks
              )
```

```
Epoch 1/60
72/72 [=====] - 41s 447ms/step - loss: 0.3330 - dice_coef: 0.05
87 - accuracy: 0.9395 - val_loss: 0.0794 - val_dice_coef: 0.2234 - val_accuracy: 0.9707

Epoch 00001: val_loss improved from inf to 0.07943, saving model to BrainTumorSegModel.h5
Epoch 2/60
72/72 [=====] - 31s 427ms/step - loss: 0.0731 - dice_coef: 0.25
45 - accuracy: 0.9706 - val_loss: 0.0631 - val_dice_coef: 0.3201 - val_accuracy: 0.9713

Epoch 00002: val_loss improved from 0.07943 to 0.06308, saving model to BrainTumorSegModel.h5
Epoch 3/60
72/72 [=====] - 31s 427ms/step - loss: 0.0648 - dice_coef: 0.34
82 - accuracy: 0.9727 - val_loss: 0.0479 - val_dice_coef: 0.4728 - val_accuracy: 0.9843

Epoch 00003: val_loss improved from 0.06308 to 0.04794, saving model to BrainTumorSegModel.h5
Epoch 4/60
72/72 [=====] - 31s 427ms/step - loss: 0.0530 - dice_coef: 0.48
95 - accuracy: 0.9822 - val_loss: 0.0462 - val_dice_coef: 0.5509 - val_accuracy: 0.9839

Epoch 00004: val_loss improved from 0.04794 to 0.04619, saving model to BrainTumorSegModel.h5
Epoch 5/60
72/72 [=====] - 31s 428ms/step - loss: 0.0417 - dice_coef: 0.60
30 - accuracy: 0.9849 - val_loss: 0.0354 - val_dice_coef: 0.6559 - val_accuracy: 0.9876
```

```
Epoch 00047: val_loss did not improve from 0.01482
Epoch 48/60
72/72 [=====] - 31s 428ms/step - loss: 0.0096 - dice_coef: 0.89
90 - accuracy: 0.9960 - val_loss: 0.0156 - val_dice_coef: 0.8707 - val_accuracy: 0.9941

Epoch 00048: val_loss did not improve from 0.01482
Epoch 49/60
72/72 [=====] - 31s 428ms/step - loss: 0.0095 - dice_coef: 0.89
95 - accuracy: 0.9960 - val_loss: 0.0165 - val_dice_coef: 0.8641 - val_accuracy: 0.9938

Epoch 00049: val_loss did not improve from 0.01482
Epoch 50/60
72/72 [=====] - 31s 427ms/step - loss: 0.0092 - dice_coef: 0.89
98 - accuracy: 0.9962 - val_loss: 0.0163 - val_dice_coef: 0.8683 - val_accuracy: 0.9938

Epoch 00050: ReduceLRonPlateau reducing learning rate to 1.6000001778593287e-06.

Epoch 00050: val_loss did not improve from 0.01482
Epoch 00050: early stopping
```

In [24]:

```
h.history.keys()
```

Out[24]:

```
dict_keys(['loss', 'dice_coef', 'accuracy', 'val_loss', 'val_dice_coef', 'val_accuracy',
'lr'])
```

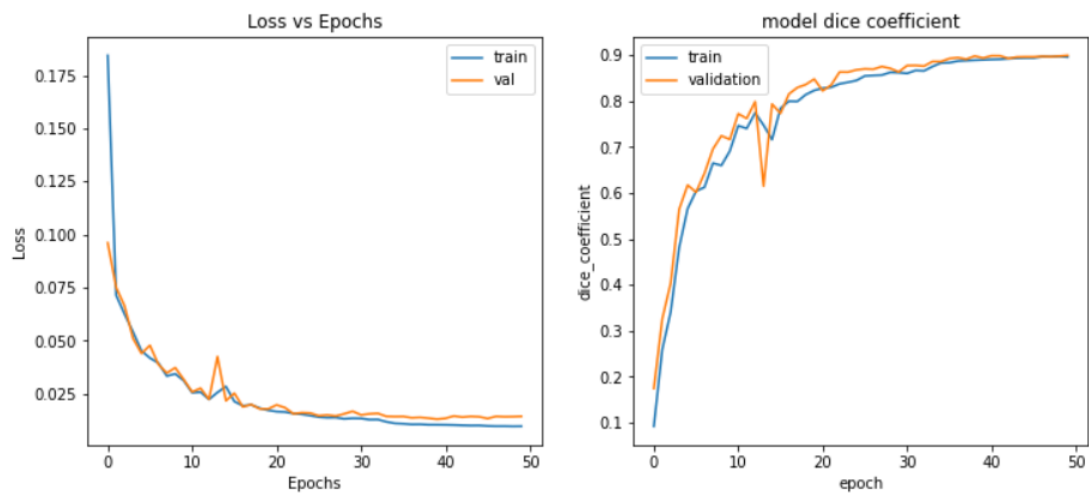


## Plotting metrics

In [25]:

```
#Plotting metrics
plt.figure(figsize=(12,5))
plt.subplot(1,2,1)
plt.plot(h.history['loss']);
plt.plot(h.history['val_loss']);
plt.title("Loss vs Epochs");
plt.ylabel("Loss");
plt.xlabel("Epochs");
plt.legend(['train', 'val']);

plt.subplot(1,2,2)
plt.plot(h.history['dice_coef'])
plt.plot(h.history['val_dice_coef'])
plt.title('model dice coefficient')
plt.ylabel('dice_coefficient')
plt.xlabel('epoch')
plt.legend(['train', 'validation'], loc='upper left')
plt.show()
```



## MODULE 5 - Testing

```
In [26]: #Displaying accuracy obtained
test_ids = list(X_test.image_path)
test_mask = list(X_test.mask_path)
test_data = DataGenerator(test_ids, test_mask)
_, accuracy, dice_coefficient = model.evaluate(test_data)
print("Segmentation accuracy is {:.2f}%".format(accuracy*100))
print("Segmentation dice_coefficient is {:.2f}%".format(dice_coefficient*100))
```

```
6/6 [=====] - 1s 165ms/step - loss: 0.0159 - dice_coef: 0.8738 - accuracy: 0.9940
Segmentation accuracy is 87.38%
Segmentation dice_coefficient is 99.40%
```

## Perform predictions

```
In [27]: def prediction(test, model_seg):
    """
    Prediction function which takes dataframe containing ImageID as Input prediction on the image
    """
    # empty list to store results
    mask, image_id, has_mask = [], [], []

    # iterating through each image in test data
    for i in test.image_path:
        #Creating a empty array of shape 1,256,256,1
        X = np.empty((1,256,256,3))
        # read the image
        img = io.imread(i)
        #resizing the image and converting them to array of type float64
        img = cv2.resize(img, (256,256))
        img = np.array(img, dtype=np.float64)

        # standardising the image
        img -= img.mean()
        img /= img.std()
        #converting the shape of image from 256,256,3 to 1,256,256,3
        X[0,] = img
```

```

#make prediction of mask
predict = model_seg.predict(X)

# if sum of predicted mask is 0 then there is no tumour
if predict.round().astype(int).sum()==0:
    image_id.append(i)
    has_mask.append(0)
    mask.append('No mask')
else:
    #if the sum of pixel values are more than 0, then there is tumour
    image_id.append(i)
    has_mask.append(1)
    mask.append(predict)

return pd.DataFrame({'image_path': image_id, 'predicted_mask': mask, 'has_mask': has_mask})

```

```

In [28]: # making prediction
df_pred = prediction(X_test, model)
df_pred

```

Out[28]:

	image_path	predicted_mask	has_mask
0	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	No mask	0
1	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00204809], [0.00014338], [8.759976e-05],...	1
2	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00169989], [0.00010918], [6.5773755e-05],...	1
3	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00194896], [0.00013319], [8.11708e-05], ...	1
4	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00171365], [0.00011058], [6.671945e-05],...	1
...	...	...	...
98	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00233464], [0.00017266], [0.00010627], [...	1
99	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.0008736], [4.1779218e-05], [2.383704e-05...	1
100	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.0016905], [0.00010822], [6.495547e-05], ...	1
101	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00116705], [6.3322e-05], [3.6960755e-05],...	1
102	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	[[[0.00196377], [0.00013468], [8.2080245e-05],...	1

103 rows × 3 columns

```

In [29]: # merging original and prediction df
df_pred = X_test.merge(df_pred, on='image_path')
df_pred.head(10)

```

	patient_id	image_path	mask_path	mask	predicted_mask	has_mask
0	TCGA_HT_7605_19950916	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[6.559368e-05], [3.136308e-07], [3.7799356e...	1
1	TCGA_HT_A61B_19991127	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[0.0001239], [8.572905e-07], [1.0012718e-06...	1
2	TCGA_HT_7881_19981015	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[2.8541257e-05], [8.397716e-08], [1.0293023...	1
3	TCGA_DU_5871_19941206	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[6.996772e-05], [3.4844757e-07], [4.2036288...	1
4	TCGA_DU_7014_19860618	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[0.00012044], [8.261231e-07], [9.704437e-07...	1
5	TCGA_DU_A5TT_19980318	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[2.7969647e-05], [8.067815e-08], [9.778213e...	1
6	TCGA_DU_5852_19950709	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[4.659164e-05], [1.8259797e-07], [2.2359295...	1
7	TCGA_DU_6399_19830416	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[2.268693e-05], [5.83562e-08], [7.3514215e-...	1
8	TCGA_DU_5874_19950510	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[0.0001201], [8.185708e-07], [9.606875e-07]...	1
9	TCGA_DU_7309_19960831	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	/kaggle/input/lgg-mri-segmentation/kaggle_3m/T...	1	[[[[[4.4572935e-05], [1.7016156e-07], [2.088223...	1

In [30]:

```
#visualizing prediction
count = 0
fig, axs = plt.subplots(15,5, figsize=(30,70))

for i in range(len(df_pred)):
    if df_pred.has_mask[i]==1 and count<15:
        #read mri images
        img = io.imread(df_pred.image_path[i])
        img = cv2.cvtColor(img, cv2.COLOR_BGR2RGB)
        axs[count][0].imshow(img)
        axs[count][0].title.set_text('Brain MRI')

        #read original mask
        mask = io.imread(df_pred.mask_path[i])
        axs[count][1].imshow(mask)
        axs[count][1].title.set_text('Original Mask')

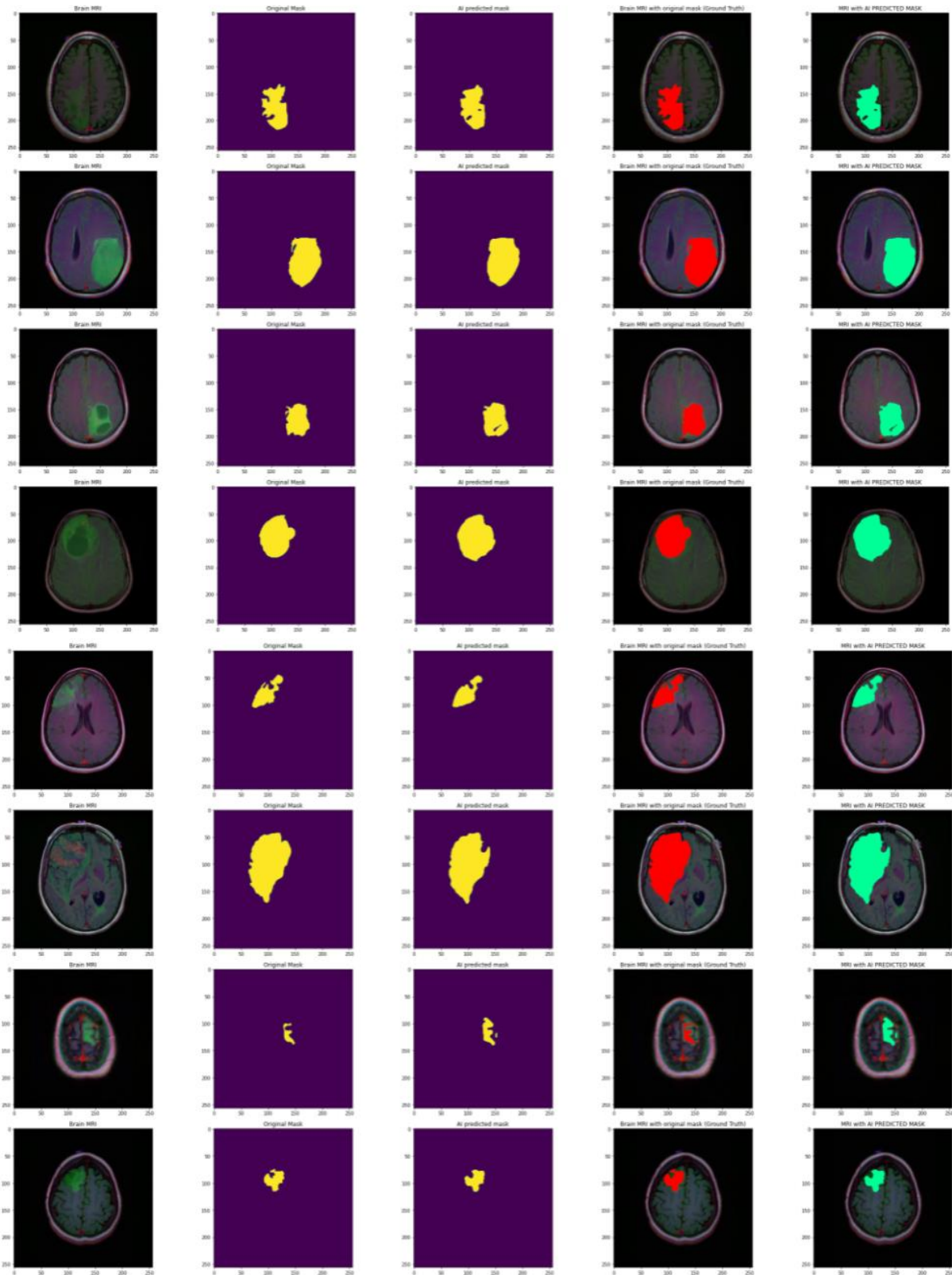
        #read predicted mask
        pred = np.array(df_pred.predicted_mask[i]).squeeze().round()
        axs[count][2].imshow(pred)
        axs[count][2].title.set_text('AI predicted mask')

        #overlay original mask with MRI
        img[mask==255] = (255,0,0)
        axs[count][3].imshow(img)
        axs[count][3].title.set_text('Brain MRI with original mask (Ground Truth)')

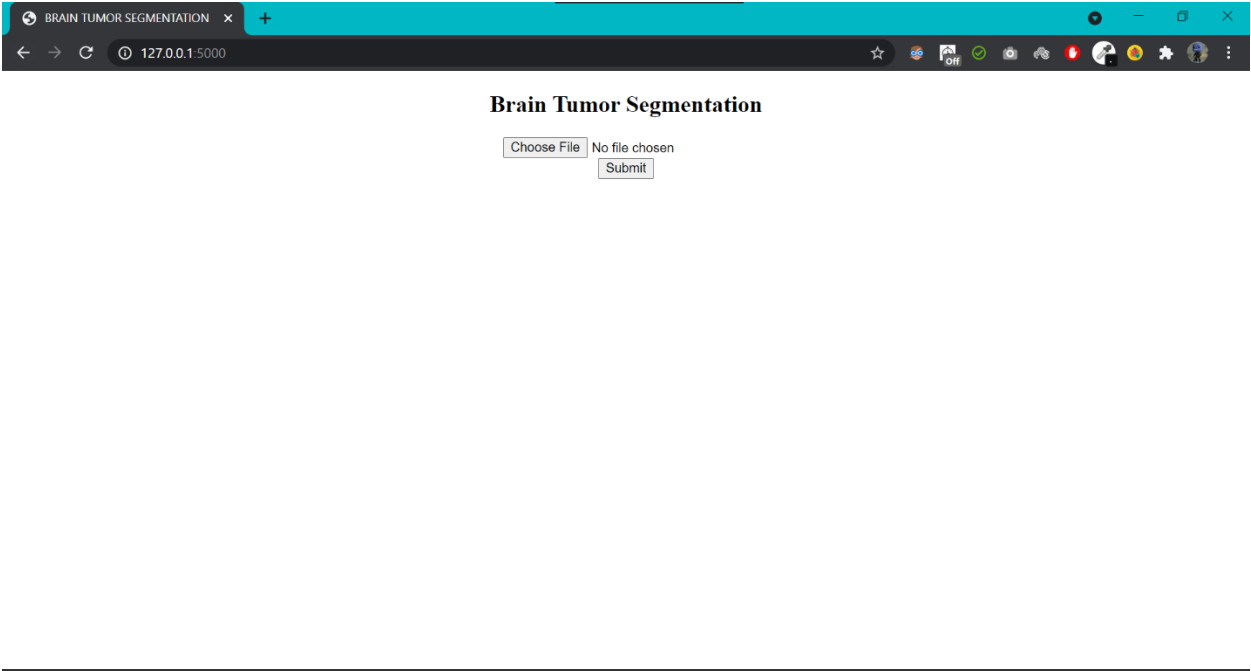
        #overlay predicted mask and MRI
        img_ = io.imread(df_pred.image_path[i])
        img_ = cv2.cvtColor(img_, cv2.COLOR_BGR2RGB)
        img_[pred==1] = (0,255,150)
        axs[count][4].imshow(img_)
        axs[count][4].title.set_text('MRI with AI PREDICTED MASK')

        count +=1
    if (count==15):
        break

fig.tight_layout()
```

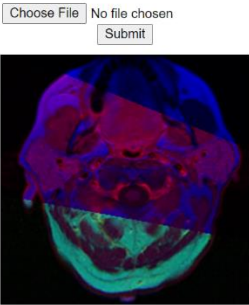


# Web Application



---

## Brain Tumor Segmentation

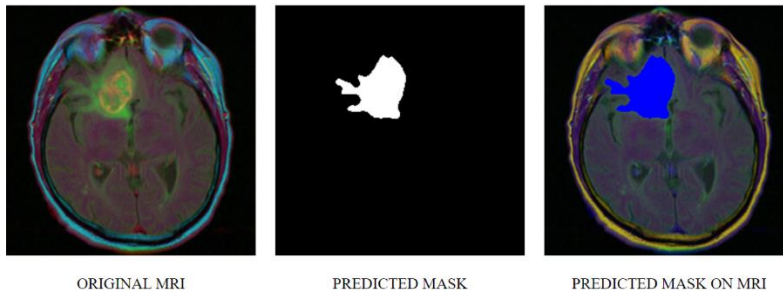


NO TUMOR

---

### Brain Tumor Segmentation

No file chosen



---

## Performance Measure and Evaluation

### Metrics

**Accuracy** - Accuracy is the most intuitive performance measure and it is simply a ratio of correctly predicted observation to the total observations. One may think that, if we have high accuracy then our model is best. However, in the case of brain MRI segmentation, accuracy alone is not a sufficient evaluation metric because of class imbalance.

**Dice-Coefficient** - A common metric measure of overlap between the predicted and the ground truth. The calculation is  $2 \times \text{the area of overlap}$  (between the predicted and the ground truth) divided by the total area (of both predict and ground truth combined). This metric will be used together with the Binary cross-entropy as the loss function for training the model.



## Loss

**Binary Cross Entropy** - A common metric and loss function for binary classification for measuring the probability of misclassification. Binary cross entropy compares each of the predicted probabilities to actual class output which can be either 0 or 1. It then calculates the score that penalizes the probabilities based on the distance from the expected value. That means how close or far from the actual value.

## Conclusion and Results

Dice Coefficient (on test data)	99.4%
Accuracy (on test data)	87.38%

In this project, we have implemented a U-Net type of architecture, which is based on convolutional neural networks for medical image segmentation. Our proposed network has two parts, 1) an encoder part 2) decoder part of the network. Encoder is the first half of the model in which convolution blocks are followed by maxpool and down sampling to encode the input image into feature representations, thus learning the context of the image. Decoder is the second half of the model where the features (lower resolution) learnt by the encoder are projected onto the pixel space (higher resolution), thus enabling localization of the tumor on the MRI image. We have also added skip connections which enables the use of low-level features for tumor localization.

## References

- 1) Ronneberger, O., Fischer, P., & Brox, T. (2015, October). U-net: Convolutional networks for biomedical image segmentation. In International Conference on Medical image computing and computerassisted intervention (pp. 234-241).
- 2) Springer, Cham. S. Pereira, A. Pinto, V. Alves and C. A. Silva, "Brain Tumor Segmentation Using Convolutional Neural Networks in MRI Images," in IEEE Transactions on Medical Imaging, vol. 35, no. 5, pp. 1240-1251, May 2016, doi: 10.1109/TMI.2016.2538465.