



# Research Project Dissertation

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MSc Computing (Data Analytics)

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# Declaration

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## **Lists of abbreviations.**

ML: machine Learning

DALC: Data Analytics Life Cycle

CNN: Convolutional Neural Networks

NGH: National Guard Hospital.

KAAUH: King Abdullah bin Abdul-Aziz University Hospital

TL: Transfer Learning

## List of figures

Figure 4 - 1 A Histogram of No Tumor Label Aspect Ratio.....	20
Figure 4 - 2 The Images Frequency in each label .....	21
Figure 4 - 3 Dataset Samples .....	22
Figure 4 - 4 The FlowChart of the Transfer Learning Models .....	24
Figure 4 - 5 A FlowChart of the VGG16 Model.....	25
Figure 4 - 6 A FlowChart of the ResNet50 Model .....	26
Figure 4 - 7 A FlowChart of the InceptionV3 Model.....	26
Figure 4 - 8 A FlowChart of the Xception Model.....	28
Figure 5 - 1 VGG16 Training and Validation Curve.....	31
Figure 5 - 2 ResNet50 Training and Validation Curve.....	31
Figure 5 - 3 InceptionV3 Training and Validation Curve.....	32
Figure 5 - 4 Xception Training and Validation Curve.....	32
Figure 5 - 5 VGG16 Confusion Matrix.....	33
Figure 5 - 6 ResNet50 Confusion Matrix .....	34
Figure 5 - 7 InceptionV3 Confusion Matrix.....	35
Figure 5 - 8 Xception Confusion Matrix.....	36

## **List of tables**

Table 3 - 1 Summary of Previous Related Studies.....	17
Table 4 - 2 The Archeticture of the InceptionV3 Model .....	27
Table 4 - 3 The Special Features in Pre-Trained Models .....	28
Table 5 - 1 The Accuracy And Validation Curves of Each Model .....	31
Table 5 - 2 The Evaluation of The Prediction of The models .....	37

# Abstract

Brain tumor classification is paramount in accurate diagnosis and treatment planning, with significant implications for patient outcomes. This research project focuses on the classification of brain tumors using deep learning techniques, specifically transfer learning in Convolutional Neural Networks (CNNs). The dataset used in this study is obtained from National Guard Hospital.

The motivation for this study arise from the challenges associated with accurate brain tumor classification and the potential advantages offered by modern deep learning models. Transfer learning is employed to leverage the knowledge and pre-trained weights of existing CNN models trained on large-scale datasets. This approach enables efficient and accurate classification of brain tumor images.

The performance of different pre-trained CNN models, fine-tuned specifically for brain tumor classification, is compared through experimentation and evaluation. The effectiveness and reliability of these models are assessed using key performance metrics such as accuracy, precision, and recall.

The objective of this research is to identify the most accurate and robust model for brain tumor classification. The selected models for evaluation are VGG16, ResNet50, InceptionV3, and Xception. The accuracy results of these models are reported as 91.47%, 86.80%, 82.67%, and 82.13%, respectively.

# Contents

Declaration .....	1
Abstract .....	5
1 Introduction.....	7
1.1 Context of study .....	7
1.2 Problem Statement & Motivation.....	7
1.3 Objectives .....	8
1.4 Proposed solution and results.....	8
1.5 Structure of the Report .....	9
2 Background material .....	10
2.1 Brain Tumour .....	10
2.2 Deep Learning.....	10
3 Related work.....	12
3.1 Related Work .....	12
4 Methodology & Proposed solution .....	19
4.2 Methodology .....	24
5 Data Analysis and Results .....	30
5.1 Data preparation .....	30
5.2 Training the Models.....	30
5.3 Testing the Models .....	33
6 Conclusion .....	39
6.1 Summary of Findings .....	39
6.2 Key Contributions .....	39
6.3 Limitation .....	40
6.4 Future Work.....	40
6.5 Conclusion.....	40
7 Bibliography .....	41
Appendix A. Figures and diagrams.....	45
Appendix B. Other stuff .....	49

# 1 Introduction

## 1.1 Context of study

In recent years, there has been a growing interest in the development of advanced techniques for the accurate classification of brain tumors [1] [2]. Brain tumors are a significant health challenge, with the potential to cause severe neurological impairments and even death. Early detection and classification of brain tumors are crucial for effective treatment planning and improved patient outcomes [3]. Traditional methods of brain tumor classification rely heavily on the manual interpretation of medical images, which can be time-consuming [4]. Therefore, the use of deep learning algorithms, such as convolutional neural networks (CNNs), has shown promising results in various image recognition tasks, including medical image analysis. CNNs have the ability to learn complex patterns and features directly from raw input data, making them well-suited for the classification of brain tumors from magnetic resonance imaging (MRI) scans [5].

## 1.2 Problem Statement & Motivation

Brain tumors are a complex and challenging medical condition, that faces significant health risks to individuals. The accurate and timely classification of the brain tumor plays a crucial role in diagnosis, treatment planning, and patient outcomes. The traditional diagnostic methods often rely on manual interpretation of medical images, which can be time-consuming, subjective, and prone to human error. These limitations highlight the need for automated and reliable brain tumor classification programs. That can assist healthcare professionals in making precise and efficient diagnoses.

The motivation for this project arise from the need to address the challenges associated with brain tumor classification and utilize a modern Deep Learning model. Particularly, the dataset obtained from NGH presents an opportunity to employ advanced techniques for accurate classification and achieve significant performance

improvements. By leveraging Deep Learning techniques, the aim is to select a brain tumor classification model that can provide precise and reliable results. Through the utilization of Deep Learning techniques, the objective is to identify the optimal brain tumor classification model that can deliver precise and dependable results. The chosen models for evaluation consist of fine-tuned Transfer Learning models, including VGG16, ResNet50, InceptionV3, and Xception.

### **1.3 Objectives**

The main objective of this study is to develop and evaluate a deep learning model for the accurate classification of brain tumor types using MRI images. The objective of this research can be summarized in the SMART objectives:

Specific: Find and modified a Transfer Learning model in Convolutional Neural Networks for accurate classification of brain tumor types using MRI images.

Measurable: Achieve a classification accuracy of at least 90% on a test dataset.

Achievable: Train the model on a dataset with more than 1,000 MRI images with labeled tumor types.

Relevant: Address the need for accurate and efficient brain tumor classification, which can help in early detection and treatment planning.

Time-bound: Complete the model development and evaluation within 12 weeks.

### **1.4 Proposed solution and results**

In this brain tumor classification project, the utilization of a deep-learning model, particularly transfer learning in Convolutional Neural Networks (CNNs), is the focus. The objective is to identify the most accurate and optimal model for classifying a dataset of MRI brain tumor images gathered from the National Guard Hospital.

By employing transfer learning, the knowledge and pre-trained weights of existing CNN models, which have been trained on large-scale datasets, can be leveraged. This approach allows the benefits of their learned features to be utilized and adapted to the specific task of brain tumor classification.

Through rigorous experimentation and evaluation, various pre-trained CNN models will be explored, fine-tuned, and their performance on the dataset will be evaluated.

Metrics such as accuracy, precision, and recall, will be employed to assess the effectiveness of different models.

The ultimate goal is to identify the model that achieves the highest accuracy and demonstrates robust performance in classifying brain tumor images. By doing so, a reliable and efficient system that can assist healthcare professionals in accurate and timely diagnosis of brain tumors will be developed. This will contribute to improved patient care, treatment planning, and overall outcomes in the field of neurology. The project outcomes will be presented and discussed in subsequent sections.

## 1.5 Structure of the Report

In this research, the chapters are organized as follows:

1. Chapter 1: Briefly introduces the context of the study, the problem statement and motivation, objectives, proposed solution, and results.
2. Chapter 2: Presents a contextual understanding of the topics of this study. As the background of brain tumors, deep learning, convolutional neural networks, and transfer learning.
3. Chapter 3: Covers the related review of previous studies that searched in the same field of this research project.
4. Chapter 4: Extended the explanation of the methodology used to complete this project.
5. Chapter 5: Will disuses the data analysis and results of the models used in this project.
6. Chapter 6: Conclude the findings and outcomes of this research project.

## 2 Background material

In this chapter, a contextual understanding of the topics of this study will be presented Brain tumors, Deep Learning, Convolutional Neural Networks, and Transfer Learning.

### 2.1 Brain Tumour

Brain tumor disease is the 10<sup>th</sup> leading cause of death in men and women [6]. They are a heterogeneous group of common intracranial tumors that lead to substantial rates of death and illness. There some type of brain tumors considers being cancerous. The leading tumor in this category is the Glioma tumor. Which is the most common type and difficult to detect. And have the lowest survival rate. Glioma tumor is ranked in four grades (I, II, III, and IV). Other types of brain tumors are noncancerous. And they called Benign. This category includes multiple brain tumors. Such as Meningioma and Pituitary, With a high survival rate. These mutations cause the cells to grow and multiply uncontrollably, resulting in the formation of a mass or tumor. On the other hand, the secondary brain tumor or brain metastasis. when tumors from other parts of the body spread to the brain field [7].

### 2.2 Deep Learning

Deep learning approaches are one of the prime computational intelligence techniques used for medical imaging applications. It is inspired by the neural network of the human brain. It is a part of the pattern recognition applications [8]. Deep learning has been very successful in addressing many challenges by incorporating feature extraction and selection steps into the training process. Deep learning models usually consist of several layers and each layer is formed by combining elements from the previous layer. The first layer contains the data, and the last layer provides the output. The use of multiple layers enables the reproduction of complex mapping functions, which helps deep learning models to solve challenging problems with less human intervention compared to traditional

machine learning methods. Deep learning is currently the leading approach in machine learning and has been widely used in medical image analysis for various tasks in recent years [9].

### **2.2.1 Convolutional Neural Network**

Convolutional neural networks (CNNs), have become a powerful technique in the medical field, surpassing traditional methods that require manual feature extraction. By automatically learning abstract image features during training, deep CNNs have achieved impressive performance in various medical applications, including cancer detection and classification. In the context of glioma tumour, deep learning has shown promise in predicting molecular markers using MRI images. However, the limited availability of training data poses a significant challenge in the medical image domain. Moreover, deep learning methods have been proposed for classifying brain tumours from computed tomography (CT) images, utilizing either multiple CNNs or a single CNN with discrimination methods. In this process, CNNs extract features from input brain images through convolution and pooling operations field [10] [11].

### **2.2.2 Transfer Learning**

Transfer learning has proven to be an effective method in various studies, where deep convolutional activation features learned from ImageNet have been successfully applied to classify and segment histopathology images with limited training data. Additionally, pre-trained CNNs from ImageNet have shown a significant performance in detecting X-ray and CT images. By reducing the data distribution mismatch between training and testing data, transfer learning addresses the low accuracy issue of traditional machine learning methods. Therefore, combining deep learning with transfer learning holds the potential for achieving high accuracy in distinguishing WHO grades in gliomas. The use of pre-trained network weights or fixed feature extractors accelerates the training process and helps overcome the challenges posed by limited data and computational costs [10].

### 3 Related work

This chapter will introduce the criteria that the study followed to conduct the related previous work. And a summary of the research studies and their findings.

#### 3.1 Related Work

The study by [12] involved using five pre-trained models, namely AlexNet, VGG16, ResNet18, GoogleNet, and ResNet50, on three different magnetic resonance imaging (MRI) datasets, specifically T1W-MRI, T2W-MRI, and FLAIR-MRI. The predictions of these models were then combined using an ensemble algorithm called MajVot. This algorithm calculates the probability of each model's prediction for each test sample and employs a majority voting mechanism to determine the final class label. The algorithm ensures an odd number of voters (models) to avoid a tie between the classes. The accuracy of each model varied across the three datasets, with the MajVot algorithm demonstrating improved and consistent results on the T2W-MRI dataset. Out of all the other models, ResNet50 showed the highest range of accuracies in the results.

In [7] addressed the issue by attention-based mechanism is proposed to extract useful features from whole MRI and utilize them for segmentation. Additionally, transfer learning is used to reduce algorithmic and computational complexity while improving segmentation performance and accuracy. The proposed system includes an encoder and decoder parts, where the VGG19 encoder extracts features from MR images, and the decoder utilizes the output of the encoder with an attention mechanism to segment the image. The proposed method achieved multiclass segmentation of the tumorous region with four classes, including nontumorous, CT, WT, and ET. The encoder network performs convolution with a filter to produce feature maps, and the decoder network upsamples the feature maps to generate multichannel feature maps, which are fed to a SoftMax classifier to obtain a K- channel image of probabilities. After the decoder, the outcome showed overfitting. the paper used Markov Random Field algorithm. After adding 20% noise to the image This algorithm

is applied to denoising the resultant image. The accuracy result for the proposed model is 99%.

In [13] study, a new model named CGSSNet Model a semantic segmentation network designed to automatically segment MRI images of gliomas. It is established Based on DenseNet Algorithm. Where it improved the down parts of the DenseNet algorithm. The preprocessing was greyscale regularization. For their images had grayscale shift due to the inhomogeneity of the magnetic field. The model structure with four Dense modules and a CGSSNet module. The CGSSNet module is added to extract multiple semantic information to improve the feature utilization and recognition ability of the entire image. For the Classification the researchers used Traditional methods such as: support vector machines and Bayesian classifiers. the accuracy has been measured with The DSC, sensitivity, and HD values were 0.937, 0.811, and 1.201, respectively.

In [14] Two stages of preprocessing were carried out, the background intensity inhomogeneity and the non-standardized MRI intensity values. To reduce two artifacts The first issue refers to the slowly varying background component of image inhomogeneity, which has been widely addressed in the literature. The second issue implies the lack of a tissue-specific absolute intensity numeric meaning of MRI pixels. For segmentation, the study has used a modified U-Net architecture. The modified U-Net architecture includes changes such as an equally weighted dice coefficient, residual weight, and deep supervision. The network used in this study consists of a context pathway (contracting) on the left side and a localization pathway (expanding) on the right side. The context pathway encodes increasingly abstract feature representations of the input image as we progress deeper into the network, while the localization pathway propagates the rich contextual features to high-resolution layers. For tumor detection classification. Mask R-CNN (regional convolutional neural network) has been applied. Mask R-CNN consists of four main components: a backbone module for feature extraction, an RPN for picking the top ROIs likely to contain objects, a ROI classifier and bounding box regressor for classification and localization, and a segmentation mask network for generating masks for objects in ROIs. To address the problem of overfitting due to a lack of training data, augmentation techniques such as image translation, rotation, shearing, flipping, and

cropping are commonly used. For 3D classification ResNet is also used as the 3DCNN backbone module. In the testing phase, all models trained in 5-fold cross validation. And the accuracy for the 2D mask R-CNN and the 3DCNN were 97%, 96% respectively.

In [15], Started with pre-processing steps, such as N4ITK bias correction and Nyul's lighting normalization. The paper has used DCNN Deep Convolution Neural Network as an image segmentation. The DCNN architecture comprises of five convolutional layers and one fully connected layer in the output. Each of these convolutional layers contains a convolutional operation, pooling operation, and Rectified Linear Unit (ReLU) function. The final fully connected layer uses a softmax classifier to classify the output. In the learning algorithms, Gradient-based methods are typically used to obtain optimal parameters. These methods involve moving the cost function in the parameter space to search for the most accurate values. To obtain the optimal values of model parameters, a combination of methods was employed, including Momentum, Nesterov, and Adam. The datasets that have been used in this study are BRATS (2013- 2016) with the highest Dice Similarity Coefficient metric is 0.90, 0.85, and 0.84 respectively.

In [5] study, The proposed approach utilized a two-part cascaded deep learning convolutional neural network. The first subnetwork, called the tumor localization network (TLN), employed a fully convolutional network (FCN) and transfer learning techniques to process MRI data and identify the tumor region within an MRI slice. The second subnetwork, the intratumor classification network (ITCN), used a convolutional neural network (CNN) with a deeper architecture and smaller kernel to label the tumor region into multiple subregions. For the preprocessing step. The paper applied N4ITK method to correct the distortion of the MRI data. then data normalization applied. The DSC performance values were (0.89, 0.77, and 0.80) respectively.

In [16] the proposed architecture has two approaches; The first approach focuses on feature-based classification and compares two approaches, AIFC (Actual Image Feature-Based Classifier) and SIFC (Segmentation image feature-based classifier), as well as a combined approach. AIFC uses preprocessed MRI brain original image

features as input and the corresponding target outputs are labeled as benign or malignant. SIFC, on the other hand, uses preprocessed MRI brain segmented image features as input. The study suggests that a combined approach of AIFC and SIFC classifiers may produce more accurate results due to their respective strengths and limitations. The second approach focuses on image-based classification and compares two approaches, AIC (Actual Image-Based Classifier) and segmented image-based classifier, as well as a combined approach. AIC uses preprocessed MRI brain original images as input, while the segmented image-based classifier uses preprocessed MRI brain segmented images. The study proposes a combination of AIC and SIC classifiers using an LSF combiner. The highest accuracy results was from the CFIC with 98.83%.

In the work proposed by [17] , the pre-processing steps that are taken before feeding images into a structure. The first step is to decrease the size of the image, to make the computations easier and faster. After that, the data is shuffled and divided into three sets with individual target labels (training, test, and validation). then, the images are augmented using geometric augmentation and grayscale distortion to increase the dataset size and prevent overfitting. the proposed CNN includes 16 layers starting with the input layer. Followed by a convolutional layer and an activation function for the feature extraction function. Then normalization and pooling layers to avoid overfitting. a dropout layer is used and followed by, a fully connected layer and a softmax layer to predict the output and finally a classification layer that outputs the predicted class. The proposed model was applied to two studies. The proposed model was applied to two studies; the first to classify tumor types with an accuracy of 97%, and the second to classify glioma grades with an accuracy of 100%.

The focus of this study by [8], is to reduce the computational complexity of the DCNN, by reducing the number of parameter adjustments, the weight adjustment in the fully connected layer was eliminated with the replacement of a simple assignment used to find the weights of the fully connected layer. In the CDCNN training algorithm, two parameter has been adjusted, the first is the weights in the fully connected layer, and the other one is the filter coefficients (weights) available in the convolutional layers. To calculate the weight in the study they used Stochastic gradient descent algorithm and caried out by two passes: Forward Pass and Reverse Pass. In the Modified DCNN

only the weight in convolutional layer is adjusted but only simple modification are made for the fully connected layers. The accuracy for their modified model was an average of 96.4%.

In [2] study, they developed a Holistically Nested Neural Network model to improve tumor segmentation. However, the model cannot classify the entire tumor type. They used the N4ITK preprocessing method, which was followed by a normalization technique developed by the researchers. The model was trained using 2D MRI images, and it started as edge detection using deep CNNs. The model has demonstrated effectiveness in image segmentation, as evidenced by a DSC score of 0.78. the data used BRATS 2013.

A new CNN architecture was developed by [18] using data from Nanfang Hospital and General Hospital, and Tianjin Medical University, which was initially published online in 2015. The pre-processing step involved normalizing and resizing the images to 256\*256 pixels, followed by transforming the images by either rotating them 90 degrees or flipping them vertically. The CNN architecture was implemented in Matlab and consisted of an input layer, two main blocks with a Convolutional layer, ReLU, Dropout layer, and max pooling layer, but differed in the Convolutional layer, where the second block retained the same output size as the input size of the layer. The classification layer consisted of three hidden neurons in the fully connected layer followed by applying softmax. The accuracy achieved was 95.4%.

In [10] proposed a novel method for feature extraction, using a regularized extreme learning machine (RELM) with a hybrid approach. The proposed method consisted of three main steps: preprocessing, feature extraction, and classification. In the preprocessing phase, they utilized min-max normalization to enhance the edges and regions of the tumor in image. For feature extraction, they employed PCA- NGIST as a normalization and feature descriptor. Finally, the RELM classifier was used for classification. RELM is a type of feedforward neural network with an input and output layer, as well as a single hidden layer. The weights and biases of the input layer were initialized randomly before computing the weights of the output layer. The proposed method achieved an accuracy of 94.23%.

Below is a summary for the previous papers for their chosen models, Datasets, and the accuracy results:

*Table 3 - 1 Summary of Previous Related Studies*

Name of Study	Model	Dataset	Accuracy
[10]	MajVot model: Combination of 5 models (AlexNet, VGG16, ResNet18, GoogleNet, and ResNet50,)	public data repository Cancer Imaging Archive (TCIA)	95.70% - 98.22%
[7]	VGG19	BRATS'20	99%
[11]	Segmentation: CGSSNet  Classification: (SVM) and (BC)	BraTS public dataset	93%
[12]	Mask R-CNN	BraTS 2018, TCGA	97%
[13]	Segmentation: DCNN  Classification: SoftMax	BRATS 2013-2016	90%
[5]	Cascaded Deep Learning  Convolutional Neural Network	BRATS 2015	89%
[3]	Carious deep neural network, and deep	Kaggle Brain Tumor Detection 2020	98%

	convolutional neural networks		
[14]	CNN	Nanfang Hospital and General Hospital, Tianjing Medical University	97%
[8]	Modified DCNN	Devaki Scan Centre	96.4%
[2]	holistically nested neural network	BRATS 2013	83%
[15]	A new Convolutional Neural Network architecture	Nanfang Hospital and General Hospital, and Tianjin Medical University	95.4%
[16]	RELM	Public dataset	94.23%

After reviewing the related papers on the topic of brain tumor classification, it has been observed that many researchers have utilized pre-trained models and fine-tuning approaches on either newly acquired or publicly available data. In this study, we plan to employ data obtained from National Guard Hospital through the research chair in artificial intelligence in health care. We will compare the performance of the four most used pre-trained models, namely VGG16, ResNet50, InceptionV3, and Xception. by subjecting them to comprehensive evaluation that includes image pre-processing, feature extraction, and appropriate performance measures. Each model will be evaluated to assess its performance, and the results will be compared to determine the most effective approach.

# 4 Methodology & Proposed solution

This Chapter will present the collecting, preparation, and preprocessing of the data. as well as the methodology used in this research.

## 4.1.1 Data Collection

The data was originated from National Guard Hospital. And collected by the research chair in artificial intelligence in health care. The data consists of 3264 MRI images in different orientations of the human brain. The images are divided into four categories: Glioma Tumor, Meningioma Tumor, Pituitary Tumor, and No Tumor. The Glioma Tumor presented with 928 images. Meningioma Tumor has 939 images. Pituitary Tumor 903 images. And 502 images from the No Tumor category. Each image has a different dimension. And that's developed an issue for the model building and had to be resized. Where it will be explained later in the evaluation section.

## 4.1.2 Data Quality

- Image Resolution: The images in the dataset exhibit variations in resolution, which are dependent on their respective labels. Appendix A provides visual representations of the resolution distribution for each label. The "No tumor" label demonstrates a diverse range of image resolutions, spanning from 200 to 900 pixels, with the highest frequency observed at the 200 resolutions. The majority of "Glioma" tumor images are concentrated around the 500 resolutions, although a small number of images exhibit resolutions ranging from 100 to 900. For the "Meningioma" label, most images have resolutions around 500, with a smaller proportion falling between 200 and 500. Conversely, the "Pituitary" label predominantly consists of images with a resolution of 500, while only a few images have a resolution of 200.
- Image Ratio: which is the width-to-height division, is captured and visualized in a histogram in Appendix A. Each label in the dataset exhibits a range of different ratios. While a majority of the images have a ratio of 1, there are a few outliers, particularly

in the "no tumor" label, where the ratios range from 0.6 to 1.8. an example of the histogram of No tumor label is shown below.

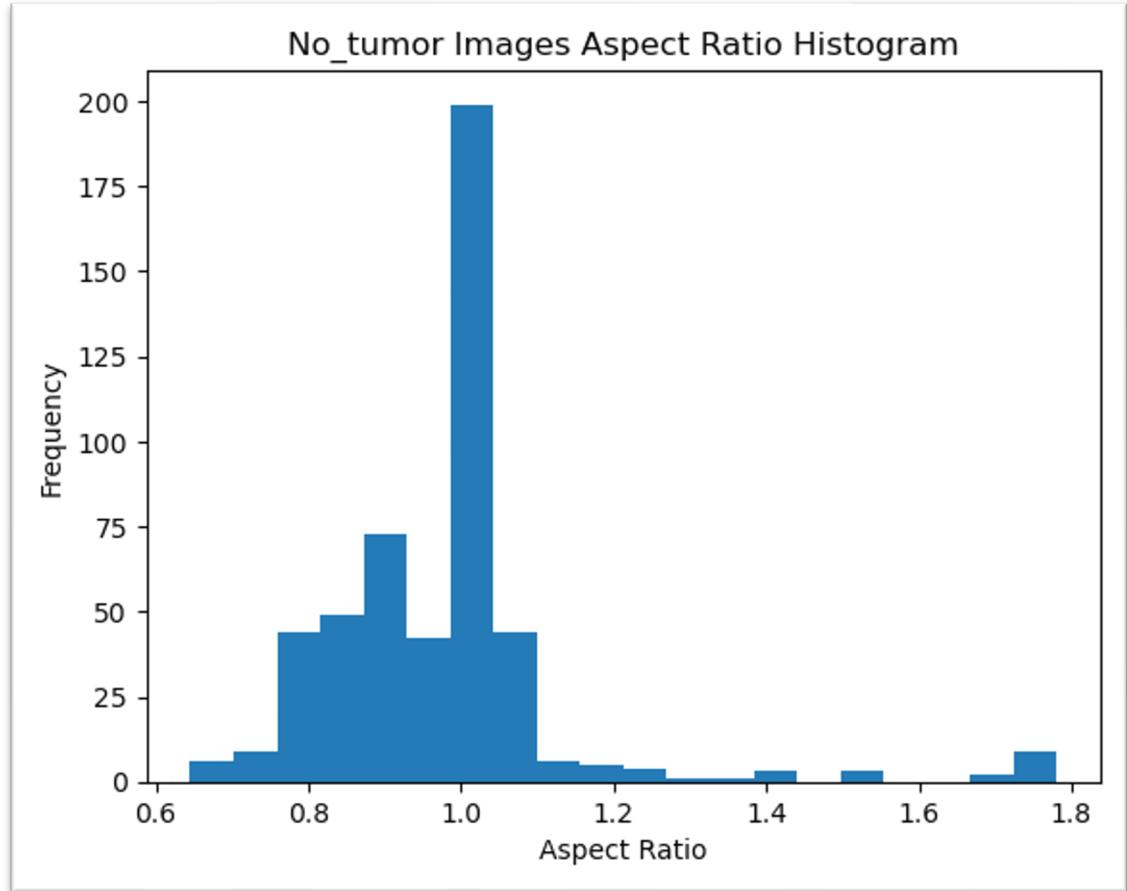
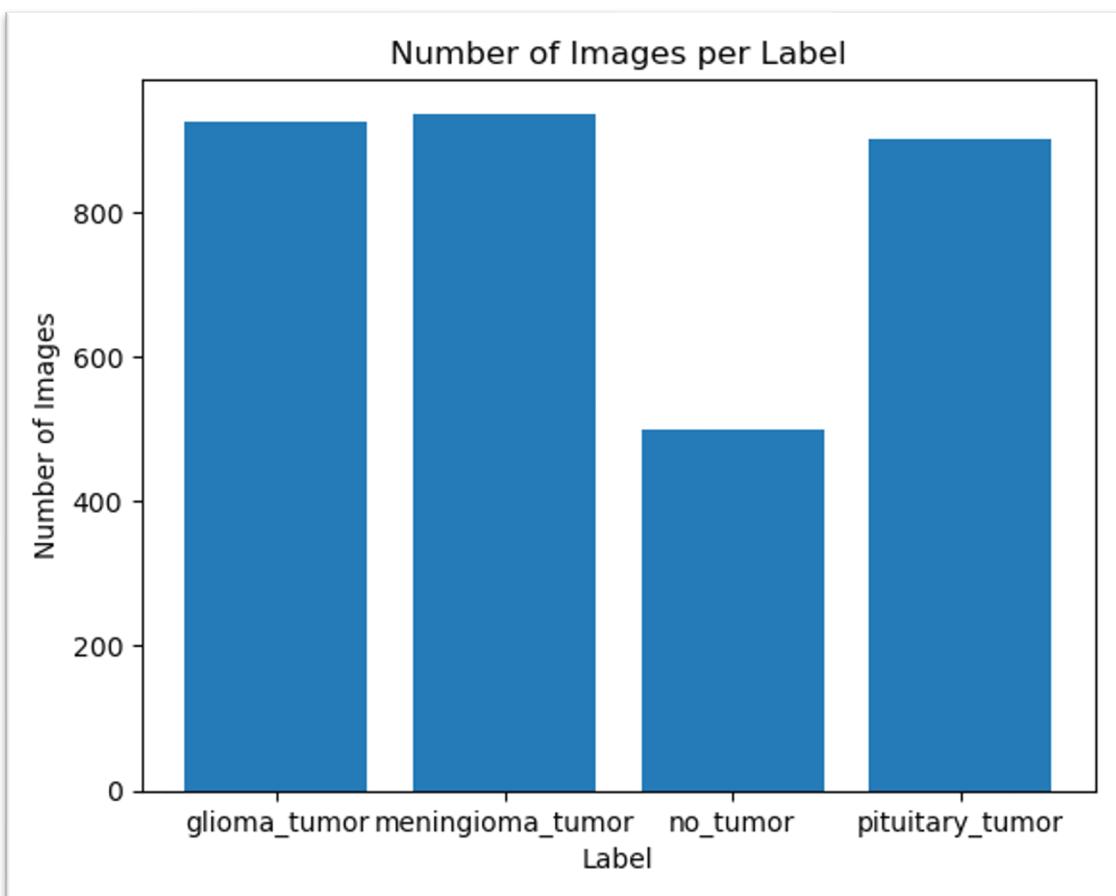


Figure 4 - 1 A Histogram of No Tumor Label Aspect Ratio

- **Image Labeling:** The histogram below showcases the distribution of images across different labels. It reveals that the three tumor categories have more than 800 images each, while the "no tumor" label only contains 502 images. This significant difference in the number of images among the labels can potentially lead to imbalanced results during model training.



*Figure 4 - 2 The Images Frequency in each label*

- **Image Variability** The images in the dataset are MRI images that exhibit various orientations of the brain. However, the different orientations did not have any impact on the performance of the models. As a result, the images were retained in their original form without any adjustments.
- **Data Preprocessing:** The data was resized to a one-dimensional format with dimensions of 224x224 to ensure compatibility with the models. Subsequently, an oversampling algorithm was utilized to balance the number of samples across the different labels in the dataset. Specifically, each label was adjusted to have 937 images.

In this figure below is an example of the images of each sample:

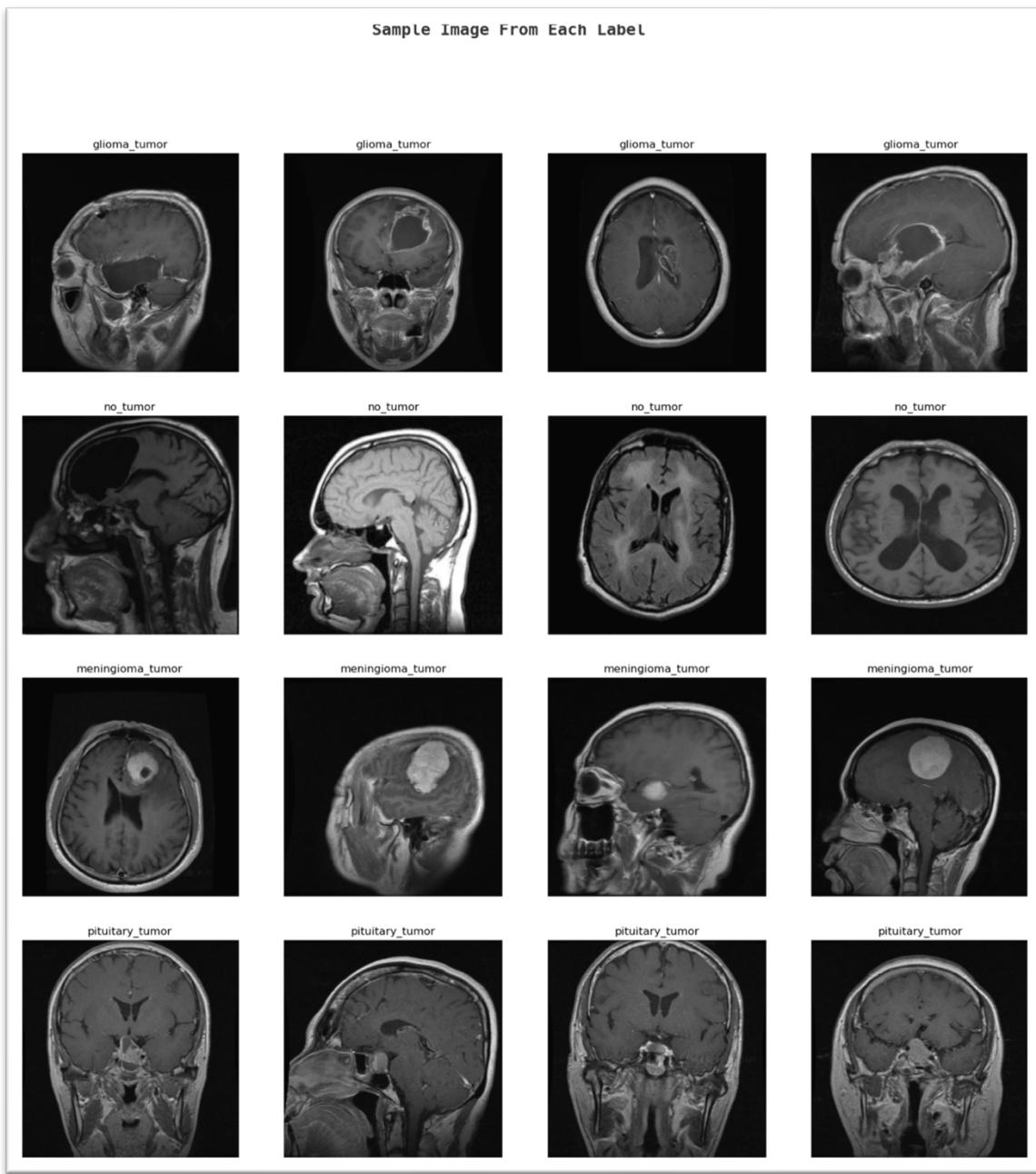


Figure 4 - 3 Dataset Samples

#### 4.1.2.1 Data Shuffle

Shuffling the data means randomly reordering the data instances in a dataset. It involves changing the order of the data samples. This process is applied before splitting the data into training, validation, and testing subsets. The purpose of the data shuffling is to prevent any inherent ordering or patterns that might occur in the data and leads to a biased decision in the learning process. Shuffling the data

encourage the model to learn more generalized and robust features. Therefore. In this study, the images dataset has been shuffled before splitting it into training and testing.

#### 4.1.2.2 One-Hot Encoder

A technique to represent categorical variables as binary vectors. This technique is commonly used in machine learning and data analysis tasks to convert categorical data into a numerical format that can be understood and processed by machine learning algorithms. In one-hot encoding, each category or level of a categorical variable is converted into a binary vector representation. The length of the binary vector is equal to the total number of unique categories in the variable. In the binary vector, only one element is set to 1 (hot) to indicate the presence of a specific category, while all other elements are set to 0 (cold). In this project, the one-hot encoder was applied to the labels of the Brain tumor. There are four categories: Glioma tumor, Meningioma tumor, No tumor, and Pituitary Tumor.

After applying the one-hot encoder the values would be as follows:

- Glioma [1, 0, 0, 0]
- Meningioma [0, 1, 0, 0]
- No tumor [0, 0, 1, 0]
- Pituitary [0, 0, 0, 1]

## 4.2 Methodology

### 4.2.1 Proposed Transfer Learning Models

Usually, building a CNN model from scratch can be difficult. This process demands a large number of training data as well as a team of experts in selecting the appropriate model architecture for appropriate convergence. To overcome this problem in this study, a transfer model has been used to eliminate the numerous parameters in the hidden layers and the immense validation processes of our study. This technique has been successfully used by many medical domains. When the dataset provided is limited [19] [11]. This study applied the transfer learning paradigm to four popular pre-trained CNN models. VGG16, ResNet50, Xception, InceptionV3. All these models were trained on the ImageNet dataset. Where it is a dataset containing more than 14 million images and categories in 1000 classified classes [20].

The flowchart of the Transfer Learning applied in this study is as follows:

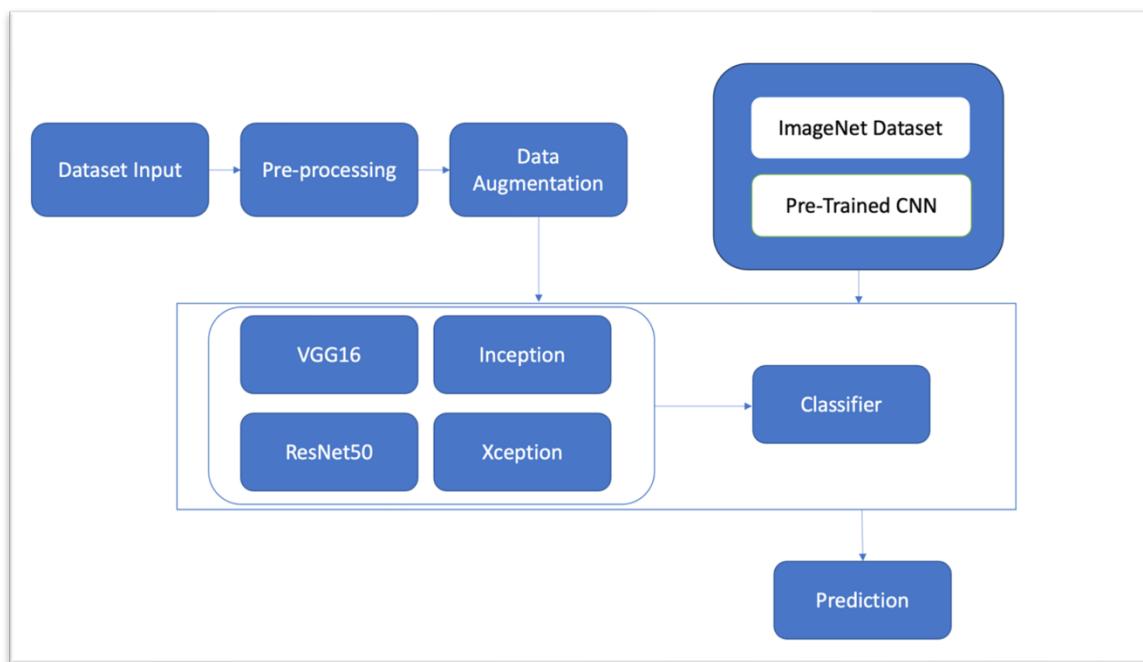


Figure 4 - 4 The FlowChart of the Transfer Learning Models

#### 4.2.2 VGG16

This model is one of the top-5 test accuracies of 92%. The model was initialized and developed in the Visual Geometry Group (VGG) Lab of Oxford University in 2014. It was designed by Karen Simonyan and Andrew Zisserman. And they won the first and second positions in the ILSVRC-2014 challenge field [12]. The model consists of 16 layers: 13 convolutional layers. And 3 fully connected layers. Partitioned in 5 blocks. With a very small convolutional filter (3\*3) [21]. a Flowchart of the Architecture of the Transfer Learning model VGG16 layers is shown below [22]:

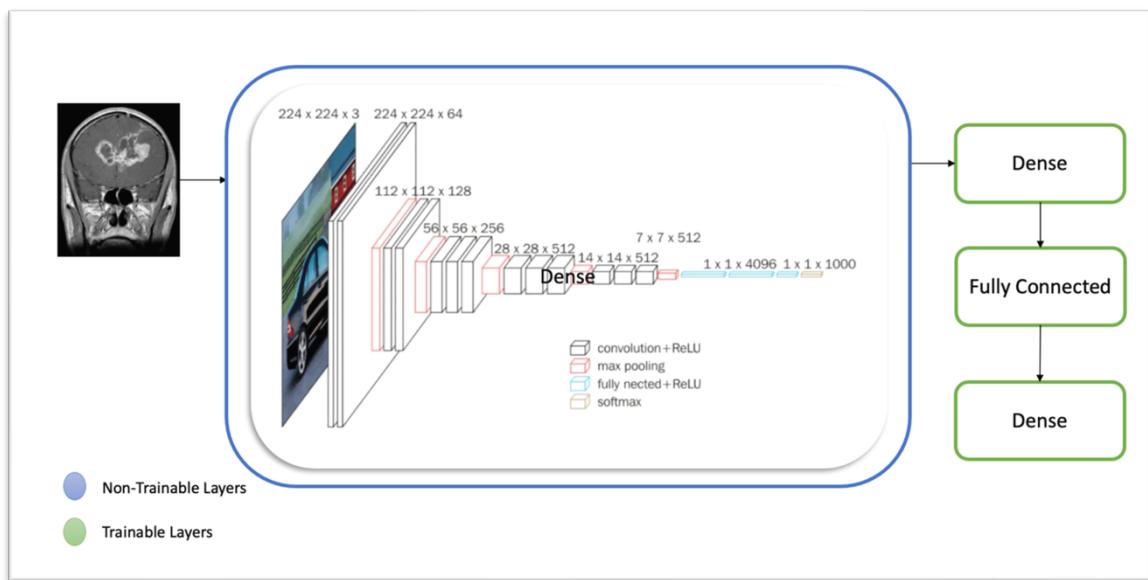


Figure 4 - 5 A FlowChart of the VGG16 Model

#### 4.2.3 ResNet50

The Residual Network (ResNet), which was originally introduced at ILSVRC 2015, was developed by Kaiming and his team at Microsoft Research [1]. This model stands out with the smallest error rate 3.75 percent in the ImageNet dataset. Reducing the computational time and increasing speed is a major benefit of this architecture. The ResNet models, ResNet18 with 18 layers and ResNet50 with 50 layers with Filter size 3\*3. For this study, only the ResNet50 was chosen to classify the data. below is the Architecture for the ResNet50 [23] [24].

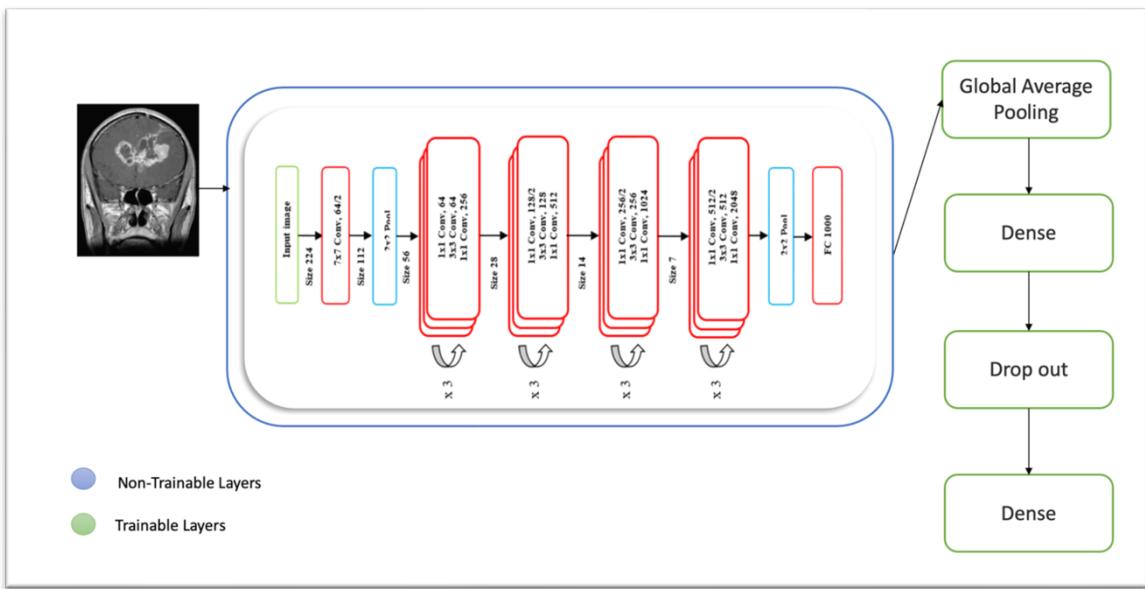


Figure 4 - 6 A FlowChart of the ResNet50 Model

#### 4.2.4 InceptionV3

This model was developed by Christian Szegedy, Sergey Ioffe, Vincent Vanhoucke, Alex Alemi, in University College of London [25]. The InceptionV3 Architecture is as follows [26]:

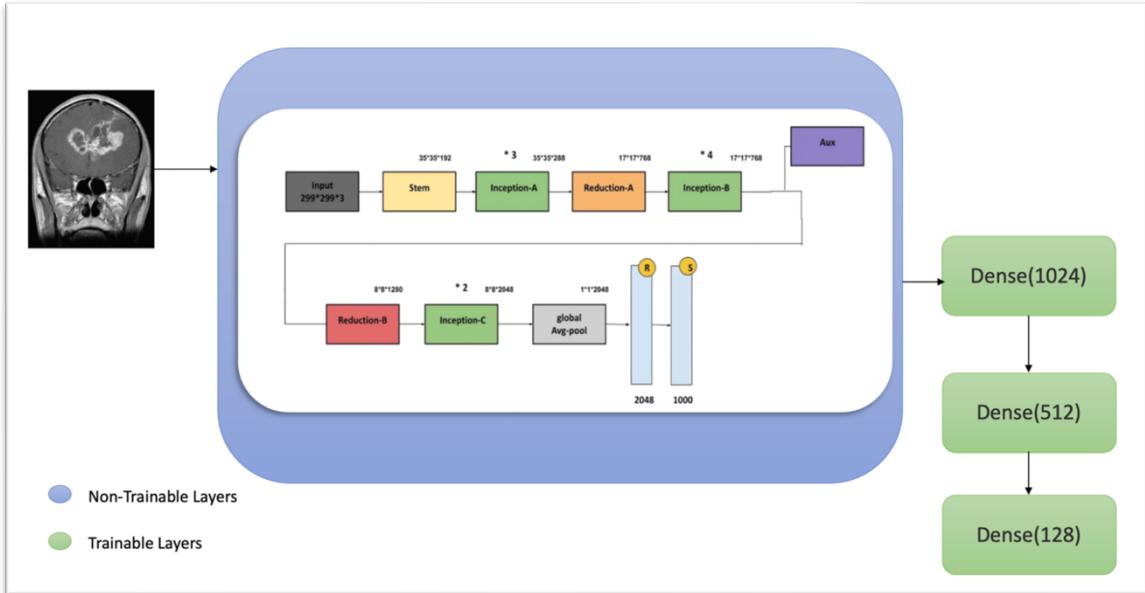


Figure 4 - 7 A FlowChart of the InceptionV3 Model

The architecture has Stem and multiple Inception and Reduction phases. And each stage is explained in the table shown below :

*Table 4 - 1 The Architecture of the InceptionV3 Model*

Layers	Number of Convolutional Layers	Number of Max-Pooling layer
Steam	4 Conv(3,3) and 1 Conv(1,1)	2 Max-Pooling (3,3)
Inception-A	3 Conv(3,3) and 4 Conv(1,1)	Max-Pooling (1,1)
Reduction-A	3 Conv(3,3) and 1 Conv(1,1)	Max-Pooling (3,3)
Inception-B	3 Conv(1,7), 3 Conv(7,1), and 4 Conv(1,1)	Max-Pooling (1,1)
Reduction-B	1 Conv(3,3), 1 Conv(7,1), 1 Conv(1,7), and 3 Conv(1,1)	Max-Pooling (3,3)
Inception-C	1 Conv(3,3), 2 Conv(1,3), 2Conv(3,1), and 4 Conv(1,1)	Max-Pooling (3,3)

#### 4.2.5 Xception

Xception is short for "Extreme Inception" and represents a more robust version of the hypothesis that underlies the Inception architecture. Was developed by Google Inc. [27]. The Xception architecture consists of a linear stack of depth-wise separable convolution layers that are connected by residual connections. This design allows for a straightforward definition and easy modification of the architecture field [27]. The workflow of the model starts from the entry flow. Then going through the

middle flow. That is repeated 8 times. Then passing through the exit flow. The figure below represents the model flowchart of the Xception architecture

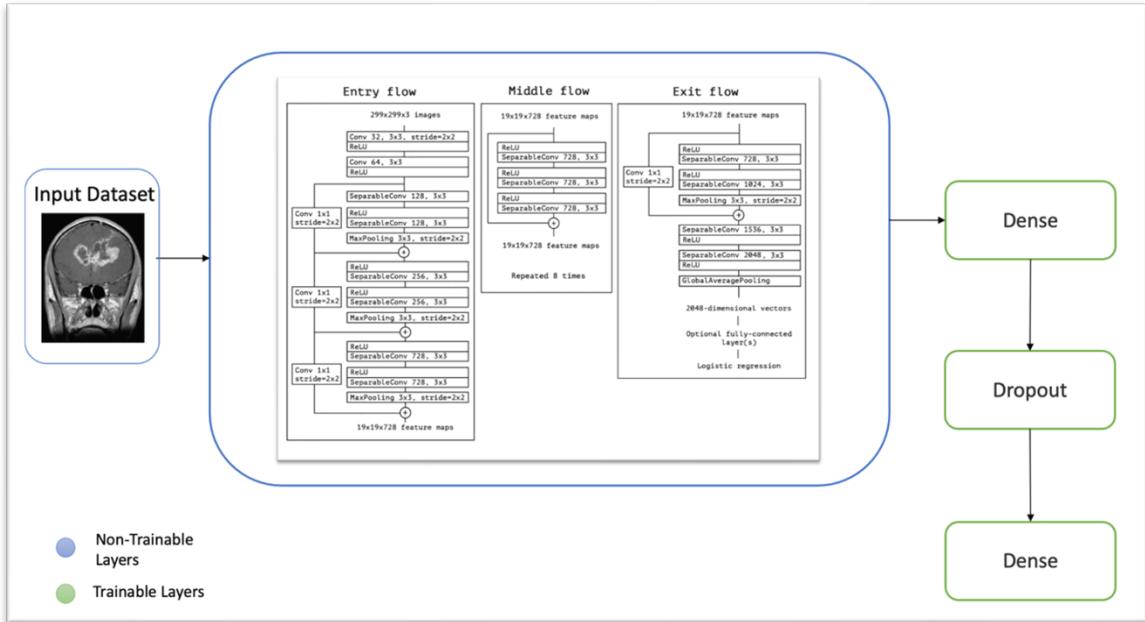


Figure 4 - 8 A FlowChart of the Xception Model

All the Transfer models have trained the ImageNet Dataset and received high accuracy and lower error rate. The table below presents the special features and the used pre-trained architecture of CNN models on the ImageNet dataset:

Table 4 - 2 The Special Features in Pre-Trained Models

Attributes	VGG16	ResNet50	InceptionV3	Xception
Layers count	16	50	48	71
Input size	224*224*3	224*224*3	224*224*3	224*224*3

<b>Model Description</b>	Conv: 13, FC: 3	Conv: 49, FC: 1		Conv: 36, FC: 1
<b>Special Features</b>	Object Localization and Image Classification	Skip Connections	Average max pooling	Average max pooling
<b>Top-5 Accuracy</b>	90.1%	95.3%	94%	94.5%
<b>Parameters (million)</b>	138	23.9	23.6	22.8

# 5 Data Analysis and Results

This Chapter will demonstrate the results of training the model and will present the accuracy and validation curves. And display the confusion Matrix and evaluate the performance measurements.

## 5.1 Data preparation

In the research project, the dataset consisted of images with varying dimensions, and each model required a specific image size for implementation. To address this, a process of resizing the images' shapes was applied prior to executing each model. Subsequently, the data was divided into training and testing sets, with 80% of the data used for training, 10% of the data for validation, and the remaining 20% reserved for testing purposes. Resulting in 937 samples, 750 training data, and 94 testing data.

The Institutional Research Board exempt Approval for training and using the data is shown in the Appendix B.

## 5.2 Training the Models

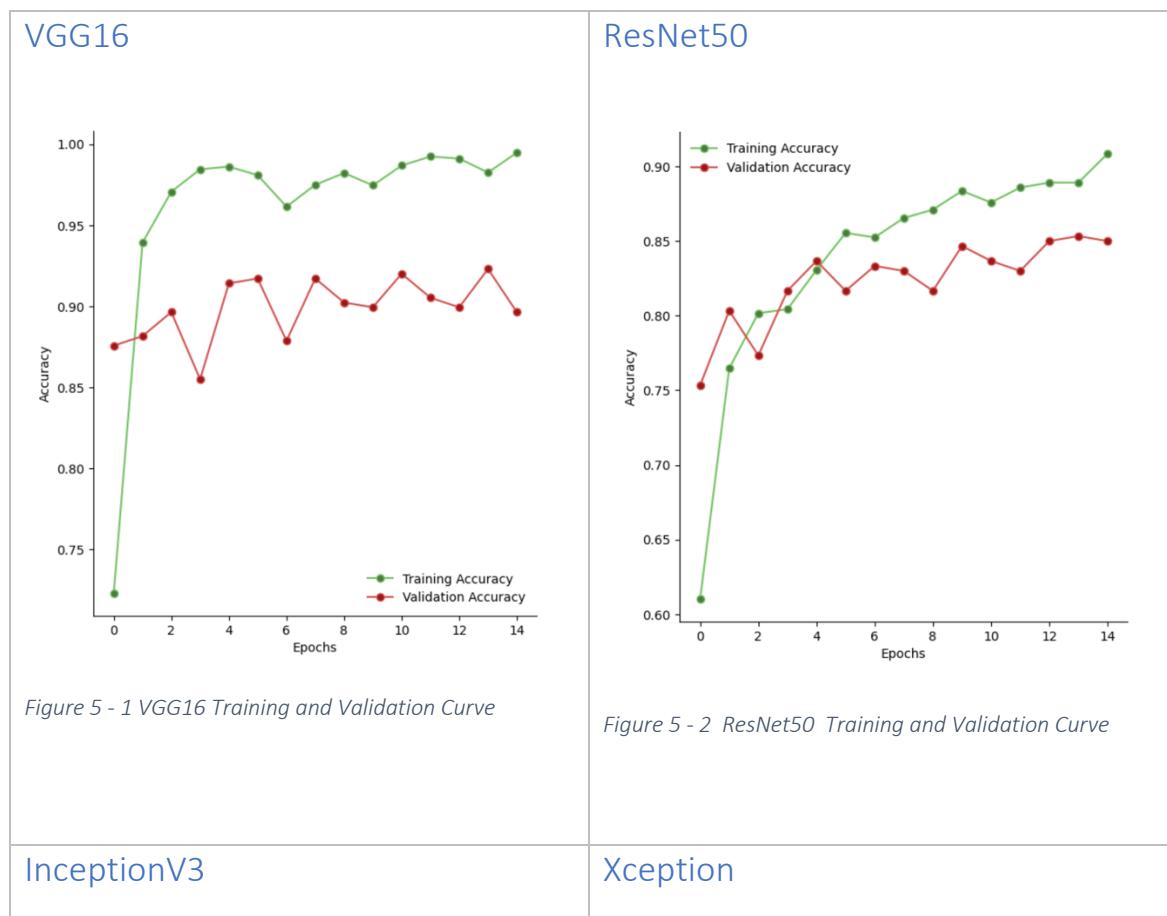
All the models in this paper were implemented using the Keras library, employing Python and TensorFlow platforms to construct the CNN architecture. The features were extracted from pre-trained models and fed into the classification layers. The models employed the Adam optimizer for optimization and utilized the ReLU activation function in the layers.

In order to assess the performance of each model in the research project, precision and loss metrics were computed for each Convolutional Neural Network (CNN) during both the training and validation phases. This enabled the evaluation and characterization of the effectiveness of the proposed model.

The accuracy curve shows how well the model is able to classify the training data correctly over epochs. It indicates the overall correctness of the predictions made by the model.

Below is the accuracy and validation curves of each model presented in this study by applying the Dataset.

*Table 5 - 1 The Accuracy And Validation Curves of Each Model*



*Figure 5 - 1 VGG16 Training and Validation Curve*

*Figure 5 - 2 ResNet50 Training and Validation Curve*

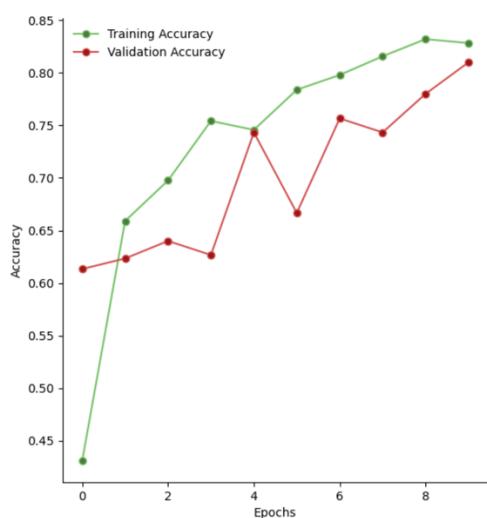


Figure 5 - 3 InceptionV3 Training and Validation Curve

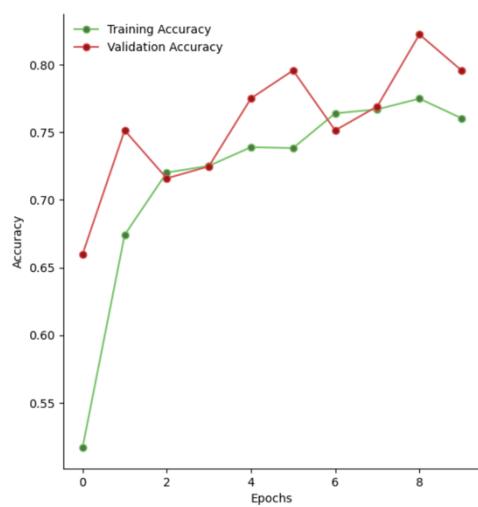


Figure 5 - 4 Xception Training and Validation Curve

Starting with VGG16, the accuracy curve demonstrates how well the model is performing on the training data over time. The accuracy starts at around 70% in the first epoch and steadily improves with each subsequent epoch, reaching approximately 98% by the fifth epoch. This indicates that the model is effectively learning and making accurate predictions on the training data. Similarly, the validation accuracy curve represents the model's performance on the validation data, which is data that the model has not seen during training. The validation accuracy starts at around 85% in the first epoch and shows some fluctuations, between the 85% and 95%. suggesting that there is some overfitting in the data.

In ResNet50, The training accuracy starts around 62% in the first epoch and gradually increases to 90% in the last epoch. This indicates that the model is learning and improving its ability to correctly classify the training data. while the validation accuracy starts at 75% in the first epoch, increases to 82% in the fifth epoch, and fluctuates around this value for the remaining epochs. The fluctuations suggest that the model's performance on the validation data may vary depending on the specific epoch. Meanwhile, In InceptionV3, the final accuracy is 83% after increasing steadily with each epoch. the validation showed some fluctuation after the 3rd epoch. This suggests that the model's performance on the validation data may vary depending on

the epoch. Finally, Xception progressively increased until it reached 78%, which is not optimal. But it showed some general accuracy improvements while the validation increased steadily but showed some overfitting to the model.

## 5.3 Testing the Models

The evaluation of the models in this research project involves the presentation of the confusion matrix for each model. And the assessment of the prediction, recall, and accuracy of each model.

### 5.3.1 VGG16 Model Confusion Matrix

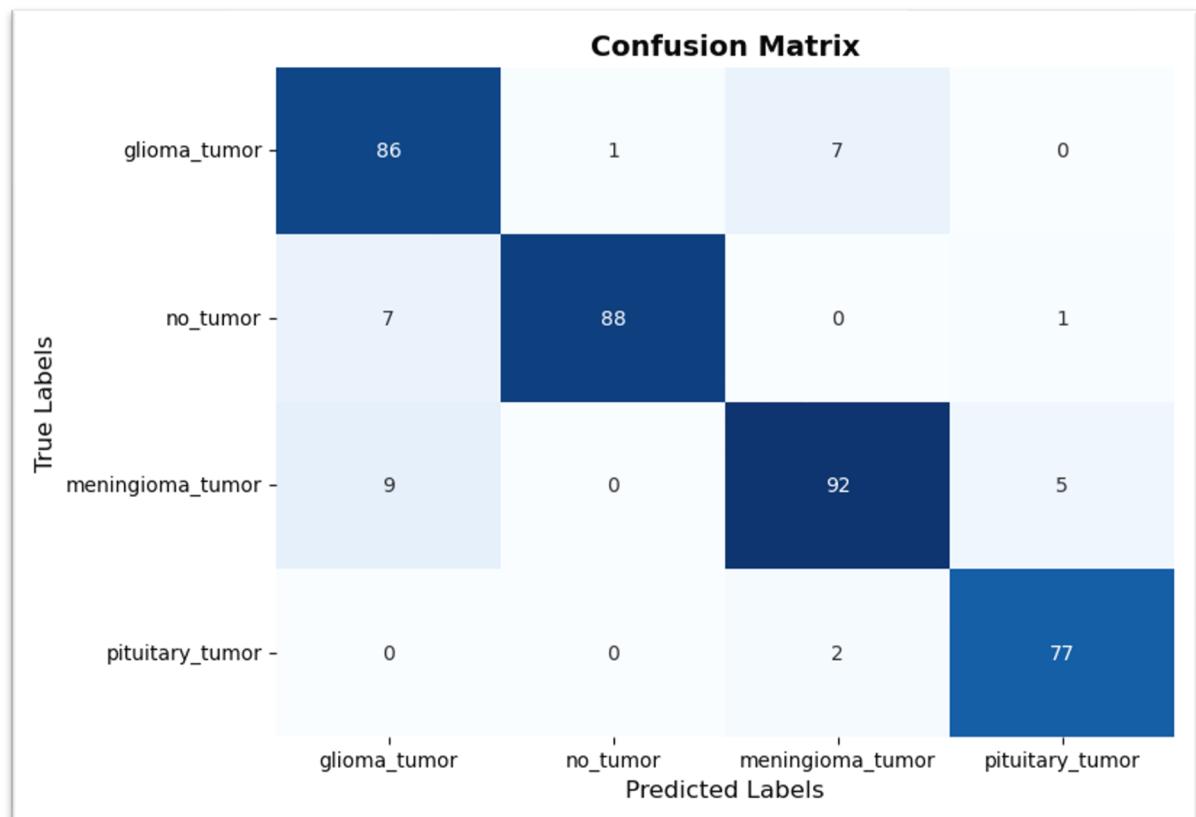


Figure 5 - 5 VGG16 Confusion Matrix

The confusion matrix of the VGG16 model demonstrates a prominent diagonal line, indicating accurate predictions for the majority of labels. However, there were instances of misclassification observed. Specifically, in the case of glioma, one image was misclassified as no tumor and 7 images were misclassified as meningioma.

Similarly, the no tumor label had 7 mispredictions, with 7 images misclassified as glioma and one image misclassified as pituitary. Meningioma experienced mispredictions with 9 images misclassified as glioma and 5 images misclassified as pituitary. Lastly, pituitary showed only 2 mispredictions, with both images being misclassified as meningioma.

### 5.3.2 ResNet50 Model Confusion Matrix

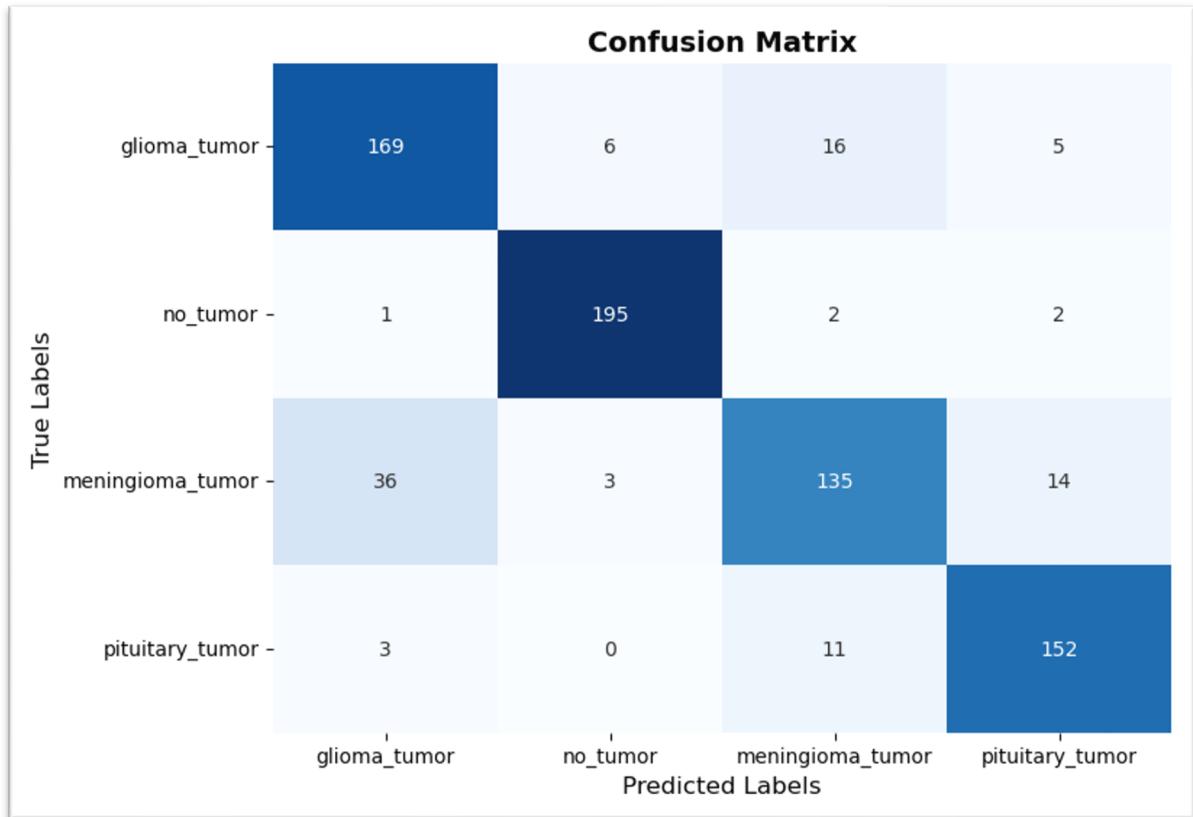


Figure 5 - 6 ResNet50 Confusion Matrix

The ResNet50 confusion matrix exhibits a clear diagonal line, indicating accurate predictions for most labels. However, there are instances of misclassification between Meningioma and Glioma labels. Specifically, 36 Meningioma samples were mistakenly classified as Glioma, and 16 Glioma samples were mispredicted as Meningioma. Additionally, 6 Glioma labels were incorrectly predicted as no tumor, and 1 no tumor labels were misclassified as Glioma. Furthermore, 2 no-tumor labels were predicted as Meningioma and 3 Meningioma labels were classified as no tumor. Among the Meningioma labels, 14 were mistakenly classified as Pituitary,

while 11 Pituitary labels were mispredicted as Meningioma. Notably, 5 Glioma samples were predicted as Pituitary and 3 Pituitary samples were misclassified as Glioma. Fortunately, there were no instances of misclassification between Pituitary and non-Glioma labels. Overall, the model accurately predicted 651 samples out of 750, resulting in a total accuracy of 86.8%.

### 5.3.3 InceptionV3 Confusion Matrix

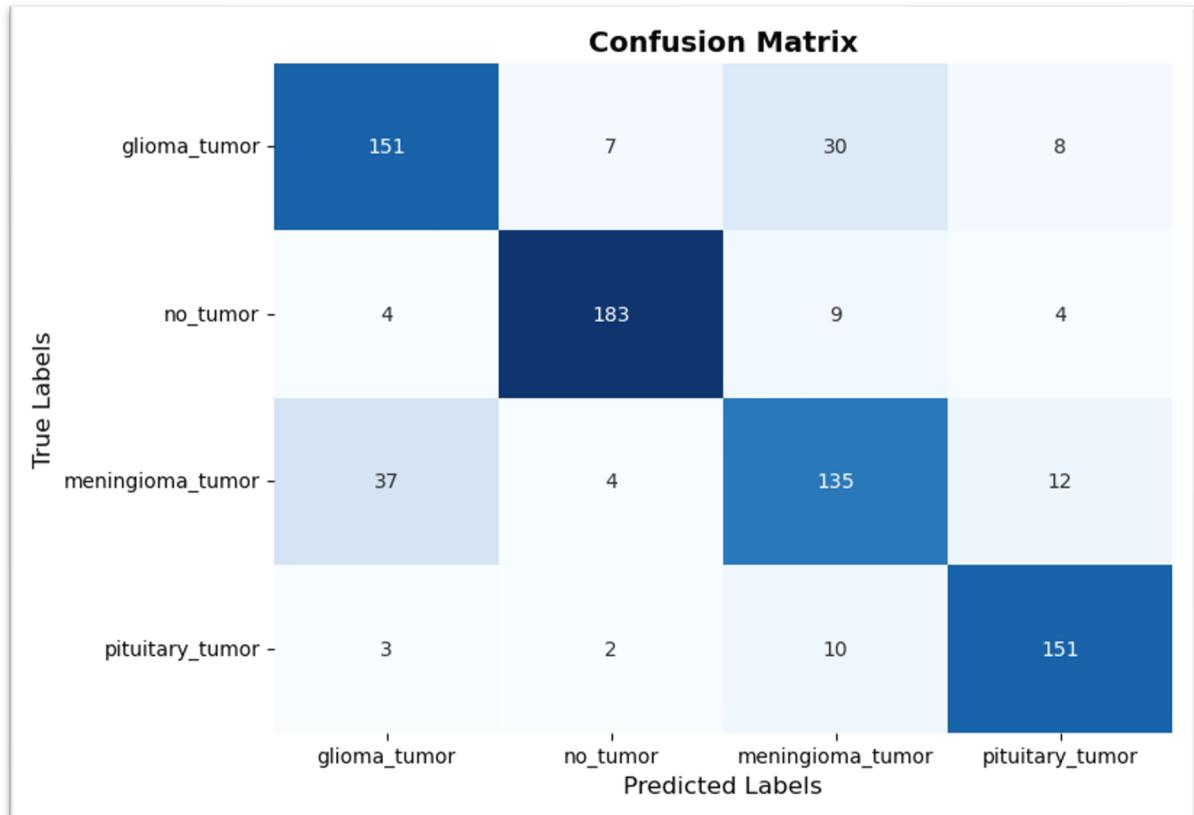


Figure 5 - 7 InceptionV3 Confusion Matrix

The InceptionV3 model exhibited similar misclassification patterns as the ResNet50 model, particularly in distinguishing between Meningioma and Glioma labels. Specifically, 37 Meningioma samples were incorrectly predicted as Glioma, while 30 Glioma samples were misclassified as Meningioma. Furthermore, Glioma labels

were mispredicted as no tumor in 7 samples, and as Pituitary in 8 samples. Similarly, no tumor labels were misclassified as Glioma in 4 samples and as Meningioma in 9 samples, and pituitary in 4 samples. Meningioma labels were also mispredicted as no tumor in 4 samples and as Pituitary in 12 samples. Lastly, Pituitary labels were mistakenly predicted as Glioma in 3 samples, as no tumor in 2 samples, and as Meningioma in 10 sample. Despite these misclassifications, the confusion matrix displays a clear diagonal line of correct predictions. Out of 750 samples, 620 were accurately predicted by the model, resulting in a total accuracy of 82.67%.

#### 5.3.4 Xception Confusion Matrix

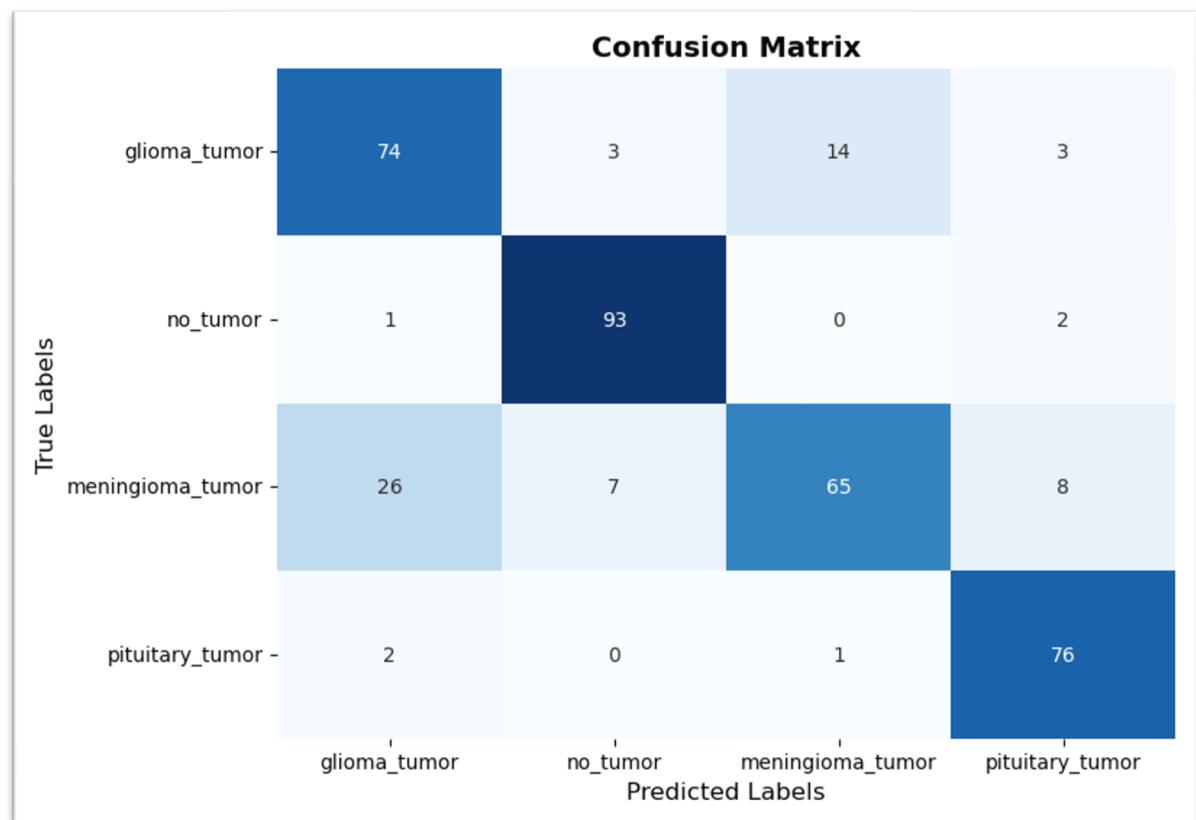


Figure 5 - 8 Xception Confusion Matrix

The Xception model displayed noticeable mispredictions, as its clearly shown by the heatmap colors. Specifically, the glioma label was incorrectly predicted as no tumor in 3 samples, Meningioma in 14 samples, and Pituitary in 3 samples. Likewise, the no tumor label was misclassified as glioma in 1 sample, and Pituitary in 2 samples.

Furthermore, Meningioma was mistakenly predicted as glioma in 26 samples, no tumor in 7 samples, and Pituitary in 8 samples. Additionally, the Pituitary was mispredicted as glioma in 2 samples and Meningioma in 1 sample. Despite these mispredictions, the diagonal line of the confusion matrix is clearly visible, indicating correct predictions. Out of 653 samples, a total of 510 were accurately predicted by the model, resulting in an accuracy of 78.11%.

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### 5.3.5 The Evaluation of Performance Metrics.

The below table will show the evaluation of each model:

*Table 5 - 2 The Evaluation of The Prediction of The models*

Model	Precision	Recall	Accuracy
Vgg16	91.74%	91.47%	91.47%
ResNet50	86.70%	86.80%	86.80%
InceptionV3	82.62%	82.67%	82.67%
Xception	82.08%	82.13%	82.13%

VGG16: The precision is 91.74%, indicating that 91.74% of the positive predictions made by the VGG16 model were correct. The recall is 91.47%, meaning that 91.47% of the actual positive samples were correctly identified. The accuracy is also 91.47%, indicating that the VGG16 model achieved an overall accuracy of 91.47%.

ResNet50: The precision is 86.70%, suggesting that 86.70% of the positive predictions made by the ResNet50 model were correct. The recall is 86.80%, meaning that 86.80% of the actual positive samples were correctly identified. The accuracy is 86.80%, indicating that the ResNet50 model achieved an overall accuracy of 86.80%.

InceptionV3: The precision is 82.62%, indicating that 82.62% of the positive predictions made by the InceptionV3 model were correct. The recall is 82.67%, meaning that 82.67% of the actual positive samples were correctly identified. The accuracy is also 82.67%, indicating that the InceptionV3 model achieved an overall accuracy of 82.67%.

Xception: The precision is 82.08%, suggesting that 82.08% of the positive predictions made by the Xception model were correct. The recall is 82.13%, meaning that 82.13% of the actual positive samples were correctly identified. The accuracy is also 82.13%, indicating that the Xception model achieved an overall accuracy of 82.13%.

In summary, the VGG16 model performed the highest precision, recall, and accuracy, followed by ResNet50, InceptionV3, and Xception. The VGG16 model showed the highest level of correctness and identification of positive samples, resulting in the highest overall accuracy among the models.

# 6 Conclusion

This chapter will introduce the concluding, remarks, and summary of the research on the Classification of brain tumor classification project. And will discuss the key contributions, Limitations, and future work.

## 6.1 Summary of Findings

This research project aimed to develop an accurate and efficient Brain tumor classification model using Deep Learning algorithms. Through the analysis of various pre-trained CNN models. Including VGG16, ResNet50, InceptionV3, and Xception. The performance was evaluated by using raw data that is collected from the KAAUH. The data included different tumor types, such as Glioma, Meningioma, Pituitary, and No-tumor.

Overall, the CNN model experiments showed promising results in accurately classifying the brain tumor MRI images. The models achieved high accuracies ranging from 76.42% to 92.5% on the test dataset. That has been observed that the VGG16 model performed the most accurately, consistently demonstrating superior performance in terms of accuracy and minimizing misclassifications.

## 6.2 Key Contributions

1. Dataset Creation: the dataset consisted of images of the different tumor types. And was collected and gathered from the National Guard Hospital. The dataset was in jpg format.
2. Model Selection and Evaluation: this study explores the different pre-trained CNN models, including VGG16, ResNet50, InceptionV3, and Xception, to identify the most effective model for brain tumor classification.

3. Performance Evaluation: The effectiveness of the models was assessed by employing performance metrics such as accuracy, precision, recall, and the confusion matrix.

### 6.3 Limitation

Despite the positive outcomes, the study also encountered some limitations. Firstly, the availability of a larger and more diverse dataset could enhance the model's generalization capabilities. Secondly, the imbalance in class distribution, especially for the "no tumor" class, posed challenges in accurately classifying this category. Finally, computational resource limitations constrained the exploration of more complex architectures and extensive hyperparameter tuning.

### 6.4 Future Work

This research provides a solid foundation for future investigations in brain tumor classification. Several areas warrant further exploration and improvement:

1. Dataset Expansion: Obtaining a larger and more diverse dataset can enhance the model's ability to handle various tumor variations and improve generalization.
2. Ensemble Models: Investigating ensemble approaches, such as combining the predictions of multiple models, could potentially boost the overall performance and robustness of the brain tumor classification system.

### 6.5 Conclusion

In conclusion, this brain tumor classification project successfully applied deep learning techniques to accurately classify brain tumor images. The findings highlight the potential of pre-trained CNN models, with the VGG16 model showing the highest accurate performance in this study. Although there are limitations and areas for further improvement, our research contributes to the ongoing efforts in leveraging deep learning for brain tumor classification.

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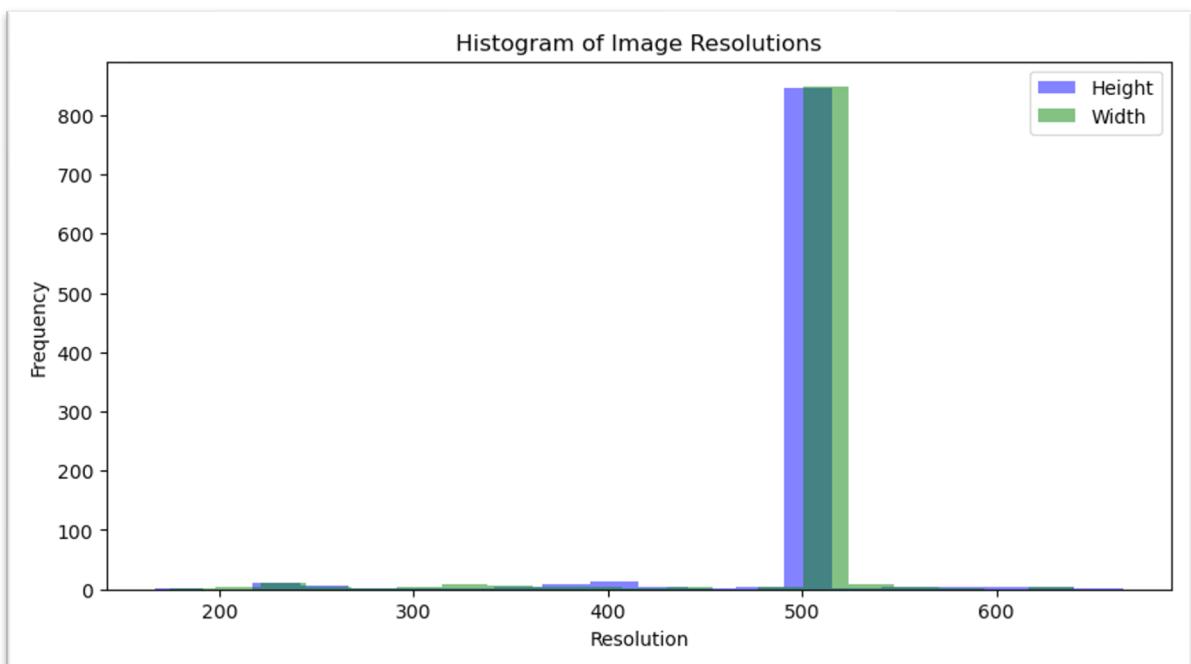
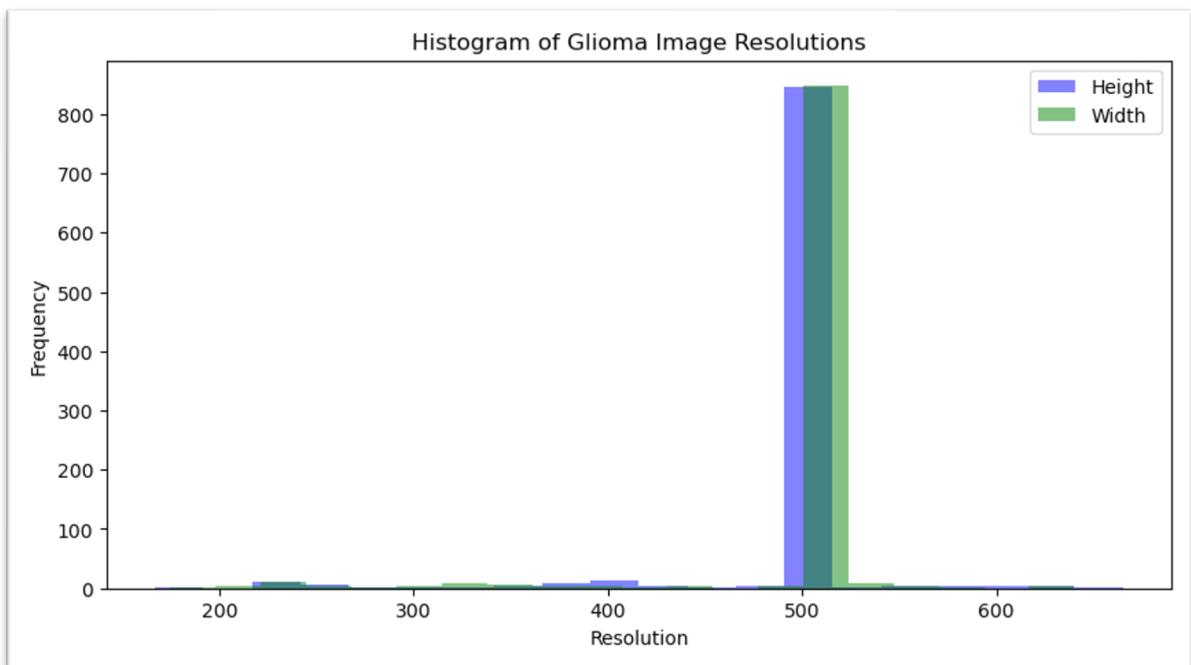
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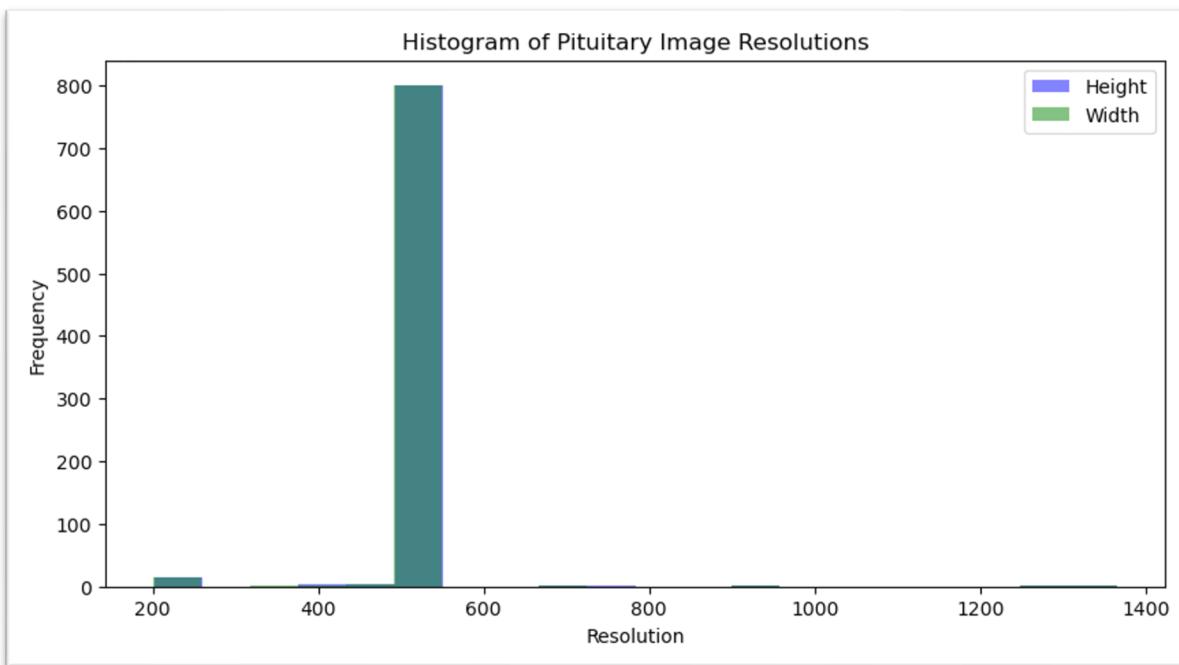
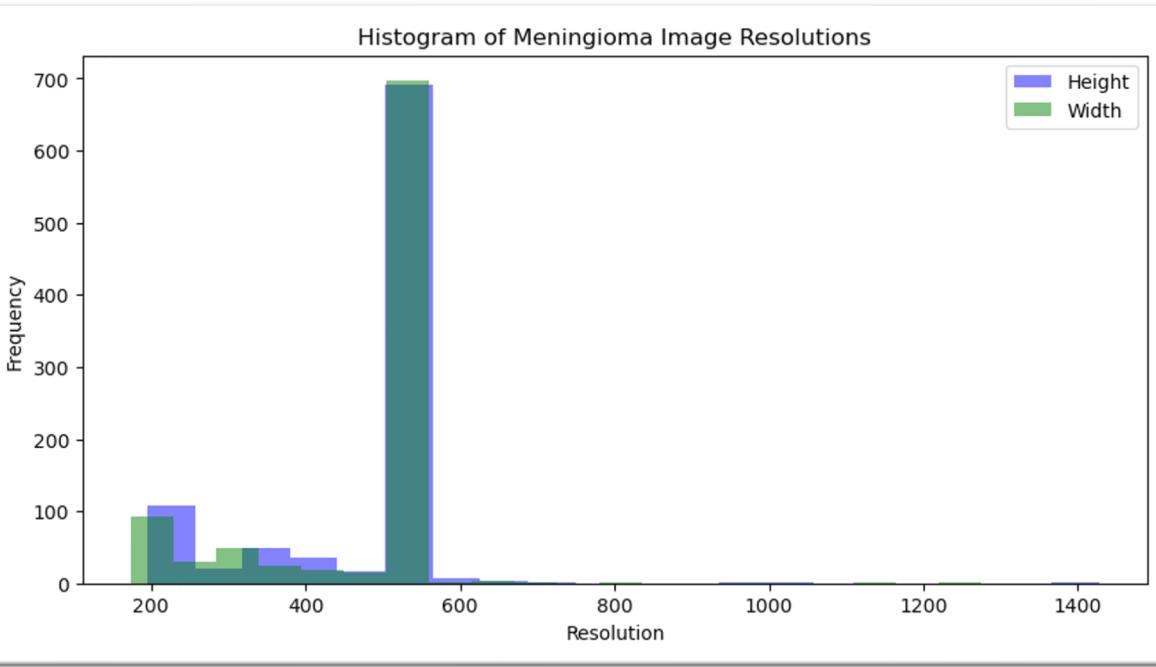
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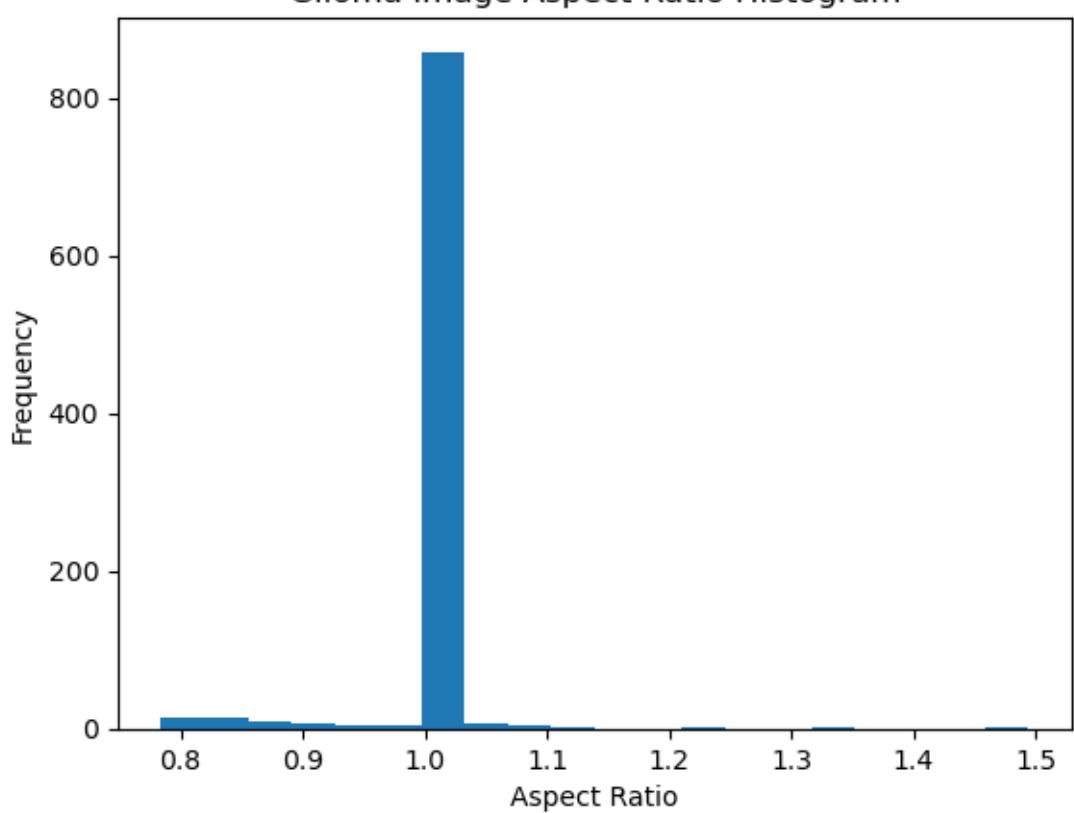
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## Appendix A. Figures and diagrams

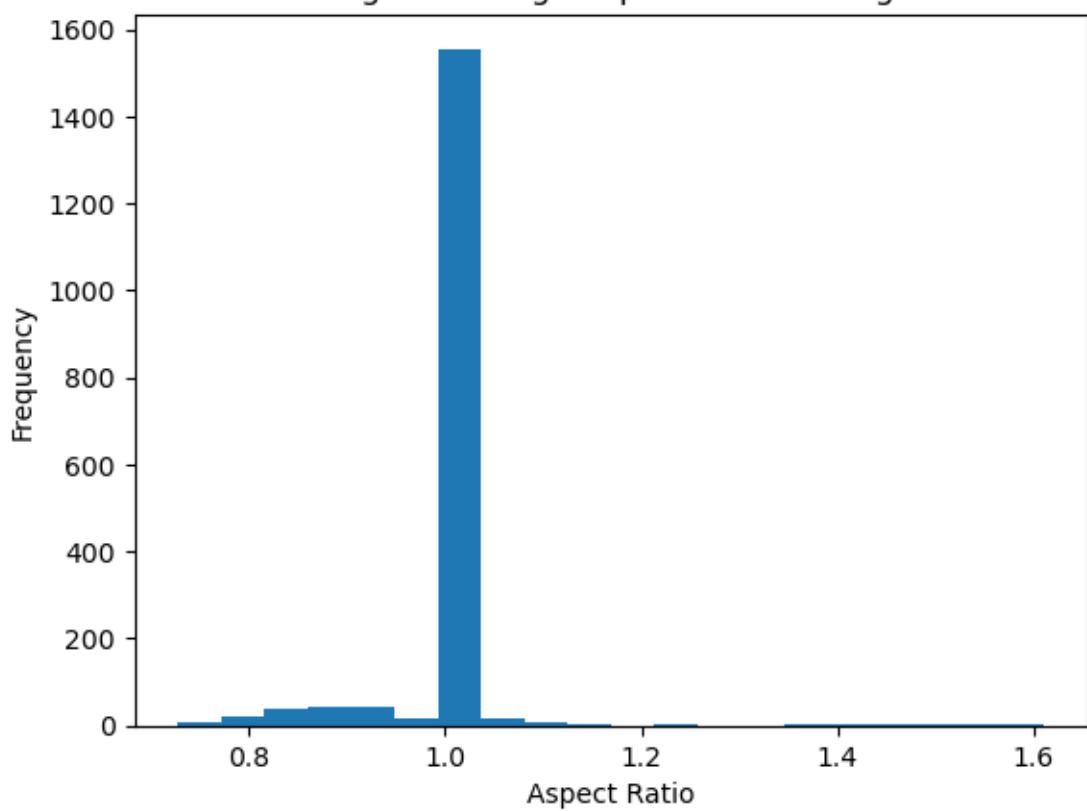


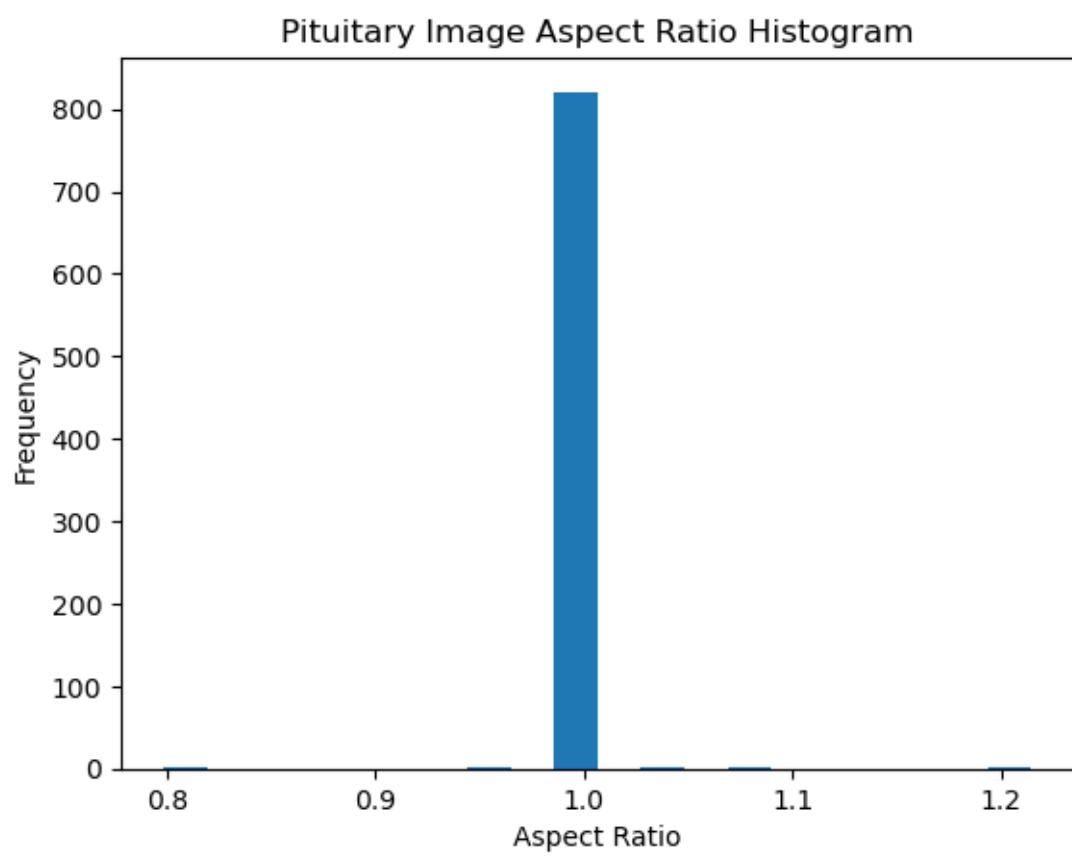


Glioma Image Aspect Ratio Histogram



Meningioma Image Aspect Ratio Histogram





## Appendix B. Other stuff

Kingdom of Saudi Arabia  
Ministry of Education  
Princess Nourah bint  
Abdulrahman University  
(048)

Graduate Studies and Scientific  
Research Vice- Rectorate



المملكة العربية السعودية  
وزارة التعليم  
جامعة الأميرة  
نورة بنت عبد الرحمن

وكالة الجامعة للدراسات العليا والبحث العلمي

(٤٨)

IRB Registration Number with KACST, KSA: HAP-01-R-059

Jun 04, 2023

**IRB Log Number:** 23-0500

**Project Title:** Brain Tumor Classification

**Category of Approval:** EXEMPT

Dear Noorah Ahmed Alsultan Alamri

Thank you for submitting your proposal to the PNU Institutional Review Board. Your proposal was evaluated considering the national regulations that govern the protection of human subjects. The IRB has determined that your proposed project poses no more than minimal risk to the participants. Therefore, your proposal has been deemed **EXEMPT** from IRB review. Please note that this approval is from the research ethics perspective only. You will still need to get permission from the head of the department in PNU or an external institution to commence data collection.

Please note that the research must be conducted according to the proposal submitted to the PNU IRB. If changes to the approved protocol occur, a revised protocol must be reviewed and approved by the IRB before implementation. For **any** proposed changes in your research protocol, please submit a Request for Modification form to the PNU IRB. Please be aware that changes to the research protocol may prevent the research from qualifying for exempt review and require submission of a new IRB application or other materials to the PNU IRB. In addition, if an unexpected situation or adverse event happens during your investigation, please notify the PNU IRB as soon as possible. If notified, we will ask for a complete explanation of the event and your response.

Please be advised that regulations require that you submit a progress report on your research every 6 months. Please refer to the protocol number denoted above in all communication or correspondence related to your application and this approval. You are also required to submit any manuscript resulting from this research for approval by IRB before submission to journals for publication.

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**IRB is not responsible** for accuracy of statements on religious and cultural affairs so researchers must consult competent authorities.

For statistical services you are advised to contact the Data Clinic at the Health Sciences Research Center ([hsr-DC@pnu.edu.sa](mailto:hsr-DC@pnu.edu.sa)) or the Scientific Research Center at the Deanship of Scientific Research ([dsr-rsc@pnu.edu.sa](mailto:dsr-rsc@pnu.edu.sa)) extension 30711.

We wish you well as you proceed with the study. Should you have additional questions or require clarification of the contents of this letter, please contact me.

You can apply for research funding at ([DSR-RS@pnu.edu.sa](mailto:DSR-RS@pnu.edu.sa)).

Sincerely Yours,

**Dr. Najla AlMasoud**



04 JUN 2023

Chairperson, Institutional Review Board (IRB)  
Associate Professor of Chemistry Science, Chemistry Department, College of Science  
Princess Nourah bin Abdulrahman University, Riyadh, KSA

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