Brain Tumor Detection Using YOLO v8 Algorithm

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**Abstract.** Brain tumor disease is one of the most dangerous diseases in the medical world. One of the most common ways to detect tumors is by performing an MRI on the patient's brain. From the results of this MRI, the doctor will later conclude what type of tumor is in the patient's brain. This study aims to help the doctors in providing informed diagnosis, by automating the detection of type and location of tumor in the given MRI image. The author uses You Only Look Once (YOLO) v8 as a model in this study to detect tumor types. Four different classes (normal/no tumor, Glioma, Meningioma, and Pituitary) are to be classified, and segmented if the image is classified as having one of the tumors. The dataset consists 1012 images in total for the training, 536 images in validation, and 258 images in testing phase, each divided into four different classes. The system is shown to work very well. For the classification, the post-training F1 score is obtained to be 97%, while the F1 score for during testing phase against previously-unseen data reaches 95%. The comparison against earlier releases of YOLO, CNN, and ResNet50 also show a promising result

# INTRODUCTION

Brain tumor is a very dangerous disease. A systemic study in 2014 found that the global incidence rate for all primary brain tumors (a tumor which grows from within the brain itself) to be around 10.82 per 100 person-years [1]. According to Global Cancer Observatory (GLOBOCAN), in 2022 alone there were estimated 322,000 cases brain and Central Nervous System (CNS) tumors worldwide from which the age-standardized incidents rate per 100,000 people were highest in Western Europe (5.56), Northern America (5.46), and Eastern Asia (3.95) [2]. In America, an estimated of 1 million Americans are living with primary brain tumor, with five-year relative survival rate of about 76% [3].

Human brain is a crucial for controlling actions and decision-making, acting as the central hub of the nervous system [4]. Protecting it from harm is essential and among potential threats, tumors are a significant concern. Specific types of brain tumors, such as meningioma, glioma, and pituitary tumors, result from abnormal cell growth, typically originated from the brain itself which is why these were categorized as primary brain tumor [5].

One way to detect this brain tumors early is to carry out a radiological examination. The common radiological examination that needs to be carried out is in the form of Magnetic Resonance Imaging (MRI). One of the advantages of using MRI is that it can observe differentiation in soft tissue such as white matter and grey matter which can be clearly differentiated by MRI images [6]. From the acquired image, the doctor can then diagnose whether a tumor is present in the brain and if it does, classify the tumor. Indeed, the classification of brain tumors is very important for patients to determine their next course of action. Errors in reading MRI results or diagnoses will certainly have fatal consequences for the patient. That is why an accurate detection of tumors is a necessity.

There are three primary brain tumors which are the main focus of this research, namely glioma, meningioma, and pituitary. Glioma is a type of tumor that generally grows in the cerebrum, specifically in the front (frontal lobe) and side (temporal lobe) [7]. Meningioma is a common and most common brain tumor. A meningioma is a tumor that grows from the membranes that surround the brain and spinal cord. Even though meningioma is not actually a brain tumor, it may press on the nearby brain, nerves and vessels [8]. Pituitary tumors are abnormal developments created within the pituitary organ [9]. It's found behind the nose at the base of the brain.

# RELATED WORKS

With increasingly advanced technological developments, manual image reading classification by humans has begun to be replaced by deep learning [10], [11], [12], [13]. This advancement is also driven by the increase of the projected number of brain tumor patients in the future, which demands an automated process in detecting the tumors en masse. In recent years, many people have conducted research on brain tumors detection with various available algorithms.

Patel et al. for example, developed a Convolutional Neural Network (CNN) to detect tumor from MRI images [14]. Talukder implemented a deeper network of CNN via transfer learning with its implementation using ResNet50 and DensNet201 [15]. CNN seems to be the favorite framework for brain tumor detection in the literature, which is understandable since CNN performs really good in the object detection application, as shown in [16], [17], [18], [19], [20], [21]. Therefore, several specific models of CNN have been developed over the years, such as the aforementioned ResNet50 and You Only Look Once (YOLO).

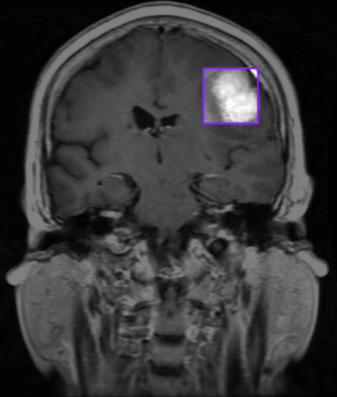
Unlike the more generalized CNN, YOLO is geared towards real-time processing, simplifying its internal CNN architecture for speed and efficiency [22]. Due to its focus on speed and efficiency, it is a very popular architecture to be used to solve real-time object detection problems such as in [23], [24], [25], [26]. With this popularity, the application of YOLO in medical imaging has also been increasing [27]. One of such attempts is in brain tumor identification using YOLO V5 and YOLO V7 by Almufareh et al. [5].

In this research, YOLO V8 algorithm is used to classify tumors that occur in the brain along with its location on the given MRI image. The success of YOLO in object detection ([28], [29], [30]) is the reason why it was chosen for this research.

# Methodology

## Dataset Collection

The dataset used in this study is obtained from [23]. It consists of four different classes, namely Glioma, Meningioma, Pituitary, and No tumor. The total number of images in the source was 1360 images. From the first three classes, each image is annotated manually, by drawing the bounding box around the area of the brain which is considered as the tumor region. An example of this annotation process can be seen in Figure 1.



**Figure 1.** Example of manual annotation. The manually-drawn bounding box is coloured purple in the figure*.*

It should be noted that none of the authors in the study have qualifications as doctors to accurately annotate every MRI images. Therefore, we were very careful in selecting a few images from the original dataset which clearly showed the tumor region in the image, while discarding those with ambiguous area or was suspected to have multiple regions of tumor. In the end, only 340 images were chosen to go through the next process. The dataset for each class is then split randomly into training set, validation set, and testing set.

## Data Augmentation

The 340 images obtained in the last phase was deemed to be insufficient to provide meaningful training process for the model. Therefore, we decided to use augmentation on these images. The augmentations used in this study were random rotation, random flip, and blurring. After the augmentation, the number of images per class is as shown in Table 1.

**TABLE 1.** Datasets splitting

| **Class** | **Pre Augmentation** | | | **Post Augmentation** | | |
| --- | --- | --- | --- | --- | --- | --- |
| **Train** | **Validation** | **Test** | **Train** | **Validation** | **Test** |
| Glioma | 57 | 43 | 24 | 250 | 120 | 66 |
| Meningioma | 40 | 34 | 14 | 270 | 132 | 66 |
| Pituitary | 20 | 15 | 15 | 252 | 164 | 66 |
| No tumor | 40 | 20 | 18 | 240 | 120 | 60 |

## Data Preprocessing

Before the images are put into training phase, several preprocessing is implemented to make sure the features are easily learnable by the model. The preprocessing implemented in this study were static cropping (10%-90% horizontal and 12-96% vertical), image resizing to 299x299, and applying Histogram Equalization to enhance the image.

## Evaluation Parameters

In this study, the model is evaluated in terms of Precision, Recall, and F1 Score. Each one of these parameters are explained in the following sections.

### Confusion Matrix

This matrix is used to measure the inaccuracies and precision of the model in detecting the given classes. Each element denotes the number of datapoints which are labelled as class while predicted as . A good model will have high numbers along the diagonal of this confusion matrix.

### Loss Function

The loss function is a function which one wants to minimize during the training process. A model successfully learns the dataset properly when the loss function decreases at every step of the training phase. YOLO implements multi-component loss function consisting of bounding box regression which relates to how close the predicted bounding box is to the prior, classification loss which asses the accuracy of classification, and confidence loss which measures the error in predicting whether a bounding box contains an object and how accurate the predicted box is. The loss function is simply defined as the sum of these three components, as shown in Equation (1) [5], [22].

|  |  |
| --- | --- |
|  | (1) |

The bounding box regression is computed as in Equation (2).

|  |  |
| --- | --- |
|  | (2) |

Where represents the weight given to positional loss. represents actual central coordinate of the target and represents target height and width, respectively. If the anchor box located at contains targets, the value of is set to . Otherwise, . The classification loss is computed as Equation (3).

|  |  |
| --- | --- |
|  | (3) |

Here, represents the weight given to category/classification loss. denotes the probability of the target belonging to a specific class, while represents the actual class. Finally, the confidence loss is given by Equation (4).

|  |  |
| --- | --- |
|  | (4) |

### Precision and Recall

Precision is used to measure how correct the predicted bounding box is by calculation the ratio between True Positive (TP) and the sum of True Positive and False Positive (FP). The equation for this metric is shown in Equation (5). Meanwhile, recall is a metric which is used to measure the ability of a model to accurately predict True instances. This metric is calculated by taking the ratio of TP and the total of TP and False Negative (FN), as shown in Equation (6).

|  |  |
| --- | --- |
|  | (5) |
|  | (6) |

### Mean Average Precision (MAP)

This metric is used to measure the Intersection over Union (IoU) between the predicted bounding box and the prior. It is calculated using Equation (7).

|  |  |
| --- | --- |
|  | (7) |

Where refers to the average precision of class .

# Results and Discussion

In this section, the results from training and testing of the model are presented. We investigate the effect of epochs on the training results. The epoch values being tested are 25, 50, 100 and 200. From all these results, the epoch number which yields the best result is chosen.

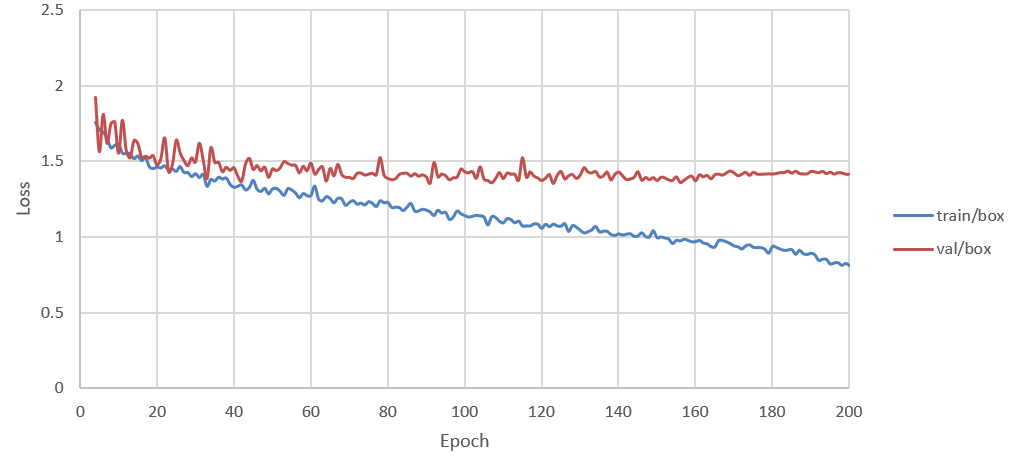
## Training Results

The results of this training phase are shown in Table 2. This training uses the Adam W optimizer with a learning rate of 0.01 every epoch.

From the results in Table 2, epoch 100 shows the most promising model. Thus, this model which was trained in 100 epochs are brought to the testing phase. As shown in Figure 2, the model starts to overfit around 100 epoch, which supports the decision to use 100 as the optimum number of epochs.

**TABLE 2.** Training results

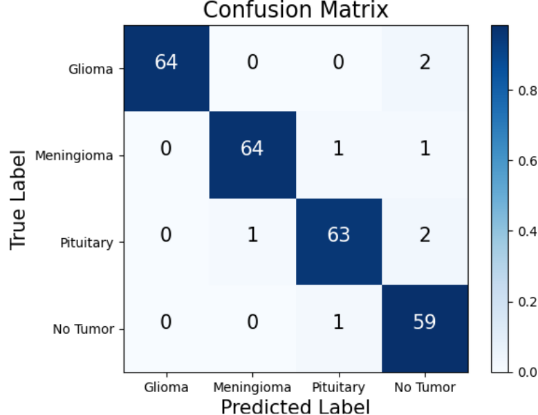
| **Model Training Results** | | | | | |
| --- | --- | --- | --- | --- | --- |
| **Epochs** | **Class** | **Precision** | **Recall** | **MAP** | **F1 Score** |
| 25 | Glioma | 0.94 | 0.704 | 0.862 | 0.80506 |
| Meningioma | 0.952 | 0.925 | 0.977 | 0.93831 |
| Pituitary | 0.93 | 0.966 | 0.96 | 0.94766 |
| No tumor | 0.89 | 0.891 | 0.975 | 0.8905 |
| 50 | Glioma | 0.983 | 0.866 | 0.931 | 0.9208 |
| Meningioma | 0.971 | 0.953 | 0.99 | 0.96192 |
| Pituitary | 0.91 | 0.932 | 0.976 | 0.92087 |
| No tumor | 0.983 | 0.982 | 0.987 | 0.9825 |
| 100 | Glioma | 0.954 | 0.931 | 0.953 | 0.94236 |
| Meningioma | 0.984 | 0.99 | 0.993 | 0.99194 |
| Pituitary | 0.968 | 0.959 | 0.981 | 0.96348 |
| No tumor | 0.972 | 0.99 | 0.99 | 0.9858 |
| 200 | Glioma | 0.977 | 0.8881 | 0.959 | 0.93043 |
| Meningioma | 0.995 | 1 | 0.995 | 0.99749 |
| Pituitary | 0.933 | 0.936 | 0.976 | 0.9345 |
| No tumor | 0.973 | 1 | 0.995 | 0.98632 |



**Figure 2.** Normalized loss per epoch. The model starts to show overfitting after 100 epochs

## Testing Results

The confusion matrix from the testing dataset is shown in Figure 3, which looks promising since the highest values are all in the main diagonal. The smaller numbers along the non-diagonal locations in the matrix indicate that there are low number of false positive (member from other classes being recognized as member of class X) and false negatives (member of class X not being recognized as member of X).



**Figure 3.** Confusion matrix

## Testing Result Against Other Models

We also tested the YOLO V8 model we have developed against other models, namely the YOLO V5 and YOLO V7 from [5]CNN from [14], and ResNet50 from [15]. The per-class-average result is as shown in Table 3.

**TABLE 3.** Training results

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Parameters** | **This Research** | **Previous Research** | | | |
| **Yolo v5** | **Yolo v7** | **CNN** | **ResNet 50** |
| Precision | 0.971 | 0.94 | 0.936 | 0.873 | 0.970 |
| Recall | 0.943 | 0.905 | 0.904 | 0.867 | 0.966 |
| F1 Score | 0.951 | 0.932 | 0.925 | 0.891 | 0.965 |
| Accuracy | 0.971 | 0.93 | 0.926 | 0.892 | 0.958 |

As can be seen from Table 3, YOLO V8 model developed in this study performs better than almost all of the other tested models, except against ResNet50 in some metrics. However, the difference between the proposed model and ResNet50 are not too significant.

# Conclusion

This study aims to create a machine learning model that can detect 4 types and locations of brain tumors. The algorithm used in this study is Yolo V8 with AdamW optimizer and a learning rate of 0.01. The author also uses various epochs, to be able to see the difference in performances of the model. After training, machine learning shows the best results, when it uses 100 epochs. YOLO v8 algorithm successfully detected 4 classes of brain tumors with F1 score results reaching 97%. The results also show that the model outperforms earlier YOLO releases and CNN. It is still beaten by ResNet50 in some metrics but not with big margin.

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