Comparing Methods for MRI Classification

David Pham [1] **Jaycee Sansom** [1] **Justin Smith** [1] **Bao-Nhi Vu** [1]

Abstract

Magnetic Resonance Imaging (MRI) is a form of imaging technology that results in detailed anatomical scans. In many cases, it is used to detect diseases and form diagnoses, such as diagnosing various types of brain tumors. However, traditional diagnoses require the attention of a medical professional that may be time consuming. A dilemma arises from this traditional method where a patient may be in need of immediate medical attention but must first wait for a diagnosis, which may take merely hours or even days. We describe an alternative approach to this dilemma based on comparing three machine learning models to accurately detect and classify brain tumors faster than a medical professional would take. With sufficient data and scale, this approach is competitive with traditional methods.

1. Introduction

Many patients with suspected brain tumors receive their results back 48 hours after their initial scan on average (Dana-Farber Cancer Institute, n.d.). Additionally, these scans require an assessment from a specialized medical professional. Although they are trained, there is always room for human error along with the difficulty of identifying what type of brain tumor it is. As such, our team believes that machine learning could be utilized to augment the process of identification to help medical professionals better identify and classify brain tumors.

To accomplish this task we utilized three separate machine learning models, each with their own advantages and disadvantages: neural networks, random forests, and k-nearest neighbors. Neural networks were used due to their high accuracy and relative ease of use. Random forests were used for a similar reason to neural networks, but random forests' use of voting may result in a higher accuracy. K-nearest neighbors were used due to their simplistic algorithm and their natural handling of multiclass classification problems.

Our dataset (Bhuvaji, S., et al. 2020) is composed of MRI scans of brains with glioma, meningioma, and pituitary tumors along with MRI scans of brains without any tumors to provide a basis for the prediction. However, the test set with the glioma tumors was heavily flawed, containing images of wildly different qualities and sizes that were vastly different from the data that was given to train upon. Due to these flaws, the images containing glioma tumors were often misclassified when testing the data and were removed, improving the accuracy of the models by roughly 20 percent.

2. Preliminaries

The following are the different types of data explored and what each type of data is.

2.1. Terms and Definitions

Glioma Tumor: A glioma tumor is a common type of brain tumor that affects all ages. Originating from a mutation in the brain matter and normal brain tissue, glioma tumors account for 33 percent of all brain tumors (John Hopkins Medicine, n.d.). There are 6 classifications of a glioma tumor: Astrocytomas, brain stem gliomas, ependymomas, mixed gliomas, oligodendrogliomas, and optic pathway gliomas.

Meningioma Tumor: Meningioma tumors are the most common brain tumor among adults. They develop within the membrane, called meninges, that surround the brain and spinal cord (Brigham and Women's Hospital, n.d.). They are slow growing and can develop in various locations throughout the central nervous system.

Pituitary Tumor: A pituitary tumor is a growth in the pituitary gland of the brain (John Hopkins Medicine, n.d.). The pituitary gland is a small gland located behind the nose. Tumors in this area can cause complications with hormone regulation and issues with your optic nerves.

Normal MRI: A normal MRI is a control scan of a healthy human brain. Generally, a normal MRI is free of pathophysiology, including brain tumors.

*Equal contribution [1]Department of Computer Science, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina. Correspondence to: Jorge Silva <jsilva@cs.unc.edu>.

2.2. Github Repository

To visit the Github repository demonstrating these models against the data set, see the url: https://github.com/jcsansom-cyber/brain_tumor_classification/tree/main

3. Methods

3.1. Convolutional Neural Networks

Convolutional neural networks (CNN) are a type of neural network designed to handle 2D input arrays. As such, CNNs are very good at handling image classification compared to other machine learning methods. CNNs make use of filters to identify patterns from subarrays of the input making them an exceptionally powerful tool to accomplish multiclass image classification.

For our problem, we designed two CNNS based on the AlexNet model, which we have deemed AlexNetLite (structure shown in Figure 1). The primary difference between AlexNet and AlexNetLite is the smaller filter sizes and fewer neurons to reduce training time, complexity, and space, but they share a similar structure. The two CNNs are designed to handle two separate datasets, one containing glioma tumors, and one not containing glioma tumors. The first CNN's model is summarized in Figure 1, the second is the same model, but with an output layer containing three neurons instead of four to account for the differing number of classes.

3.2. Random Forest

Random Forest classifiers are an ensembled form of the standard Decision Tree classifier. The Random Forest classifier is a collection of Decision Trees, independent from one another, each upon a randomized subset of the training data along with a randomized subset of the features of the data being trained upon. These Decision Trees are then ensembled together with a voting system on any particular prediction, with the majority opinion being outputted from the model.

Ensembling is useful in two main respects. The randomization reduces the effect of outliers in the training set upon the data itself, and since it is spread among the trees in the Random Forest, the voting further reduces the effect of any particular outlier tree upon the output of the algorithm. Ensembling also allows for parallelism, since every tree is being trained independently from the other trees, it is possible to train each tree on its own before ensembling them together to make the full Random Forest classifier.

```
Layer (type)                 Output Shape              Param #
=================================================================
conv2d (Conv2D)              (None, 150, 150, 32)      832

max_pooling2d (MaxPooling2D  (None, 75, 75, 32)        0
)

batch_normalization (BatchN  (None, 75, 75, 32)        128
ormalization)

conv2d_1 (Conv2D)            (None, 75, 75, 64)        18496

dropout (Dropout)            (None, 75, 75, 64)        0

max_pooling2d_1 (MaxPooling  (None, 37, 37, 64)        0
2D)

batch_normalization_1 (Batc  (None, 37, 37, 64)        256
hNormalization)

conv2d_2 (Conv2D)            (None, 37, 37, 32)        18464

conv2d_3 (Conv2D)            (None, 37, 37, 32)        9248

flatten (Flatten)            (None, 43808)             0

dense (Dense)                (None, 128)               5607552

dense_1 (Dense)              (None, 64)                8256

dense_2 (Dense)              (None, 4)                 260

=================================================================
Total params: 5,663,492
Trainable params: 5,663,300
Non-trainable params: 192
```

Figure 1. Model summary of the CNN with glioma tumors.

3.3. K-Nearest Neighbors

K-Nearest Neighbors (KNN) is a supervised learning classifier that uses proximity to make classifications and predictions about an individual data point. This model uses the assumption that similar data points are found near each other. KNN can be used in both regression and classification models but is used more in the latter. We will be using KNN to classify different brain tumors using hundreds of brain tumor images.

To evaluate our data using KNN, we have to establish the number of neighbors (K) that a data point will look at in order to be classified. These neighbors will be the closest to the data point. Figure 2 below shows a simple example of how KNN finds the nearest neighbors for a data point. After trial and error, our KNN model sets K to be 3 since this number yielded us the best accuracy results when it came to classifying the various brain tumors. Using this K, we then train and predict the model to obtain our results.

4. Results

4.1. Convolutional Neural Networks

The test accuracy of the first CNN (containing glioma tumors) was 72.3 percent, while the test accuracy for the CNN without glioma tumors was 97.6 percent. The first result was primarily due to the consistent misclassification of the
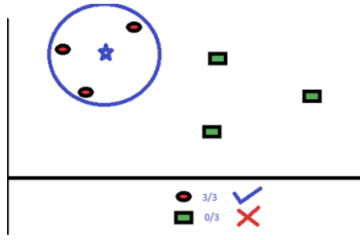
Figure 2. Finding the nearest neighbors for the star symbol using K as 3.

glioma tumor as a meningioma tumor or not recognizing a tumor. In fact, glioma tumors were only properly classified 20 percent of the time. This is most likely due to the inconsistent nature of the glioma tumor images in the test set compared to the training set. Unfortunately, this result gets even worse as glioma tumors are often misclassified as having no tumors (as shown in Figure 3). In a high-priority situation like this false negatives are more harmful than false positives, so this result is particularly distressing. The second CNN shows just how bad the test set of the glioma tumors is by being able to accurately classify all three classes. There are a few false negatives but at a much smaller rate than the original CNN. In the future, there will need to be some tweaking of the test set to more accurately represent the glioma tumors.
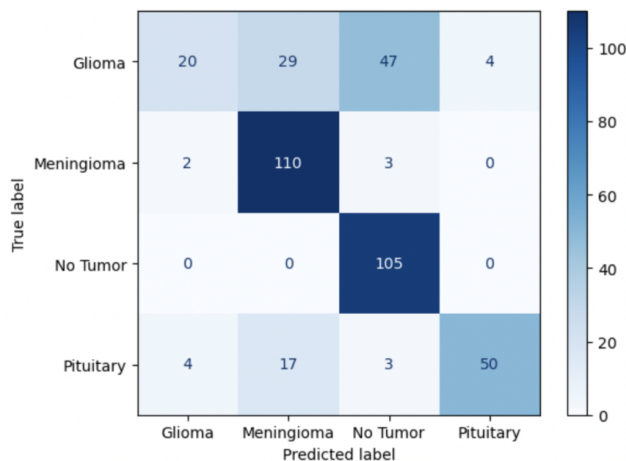

Figure 3. Confusion matrix of the CNN containing glioma tumors.

4.2. Random Forest

The accuracy of the Random Forest model including the glioma tumor was 74.873 percent, while the accuracy without the glioma tumors was 94.898 percent. The large in-
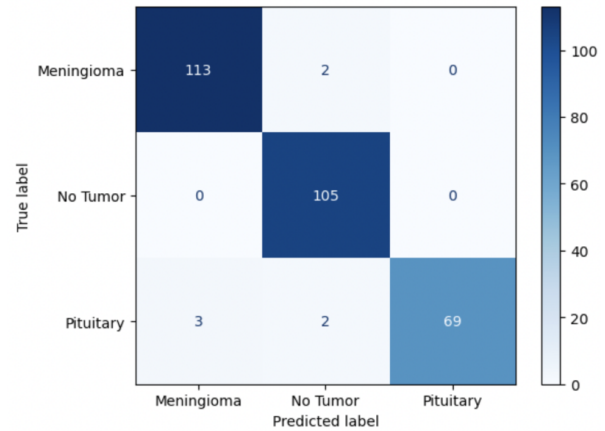

Figure 4. Confusion matrix of the CNN not containing glioma tumors.

crease in accuracy was due to issues as described in the introduction. The model that was used to produce the output with the glioma tumors reached its peak accuracy with a max depth of 15 and 100 decision trees, with a random seed of 912983. The model that was used to produce the output without the glioma tumors reached its peak accuracy with a max depth of 50 and 100 decision trees, with a random seed of 912983.

While the accuracy of the model without the glioma tumor test set is very high, the CNN model is higher, and in serious matters like tumor identification, precision is very important. As shown in Figure 5, the model actually has a higher false negative rate than a false positive rate, which is very dangerous. It would be unwise to use this model's predictions as a statement of fact, as it would be better to have a false positive rather than a false negative, since a tumor is not the only thing being checked for with an MRI scan. If doctors were not mainly looking for a brain tumor, they might be inclined to fully ignore a false classification of "no tumor" than a false classification of one of the types of tumors that the model was trained upon.

4.3. K-Nearest Neighbors

Using the KNN model, the test accuracy including glioma tumors is 59.6 percent, while the test accuracy without glioma tumors is 72.8 percent. Overall, this outcome is lower than both CNN and random forest classifiers. Similar to the other models, the jump in accuracy is due to taking out the glioma tumors from being classified. The glioma images were highly varied which made it hard for the KNN model
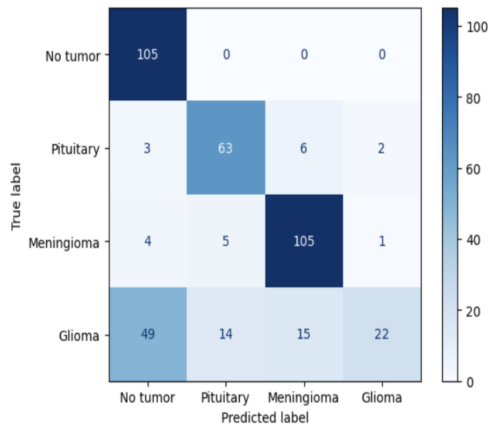
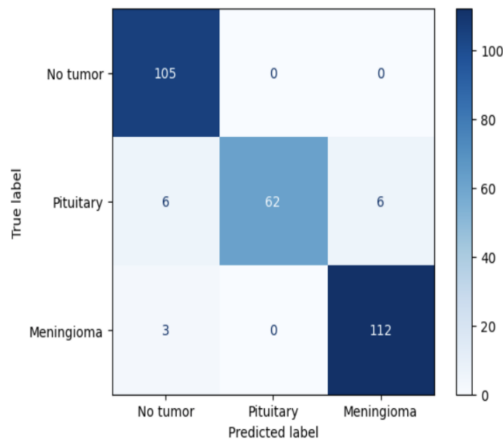*Figure 5.* Confusion matrix of the RF containing glioma tumors.

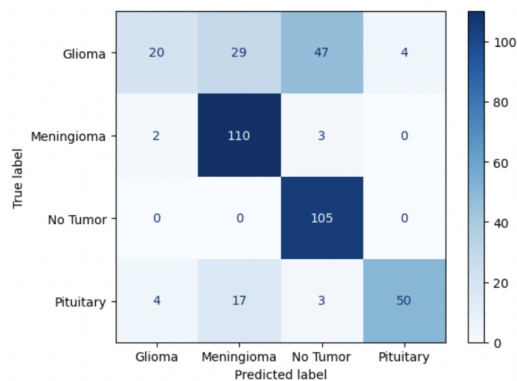*Figure 6.* Confusion matrix of the RF not containing glioma tumors.

Figure 7. KNN model's confusion matrix with Glioma Tumors.

to classify them. Compared to the other models, the KNN model was lower in accuracy when trying to classify the various brain tumors. Figures 7 and 8 are the confusion matrices for the KNN models that include glioma and do not include glioma.
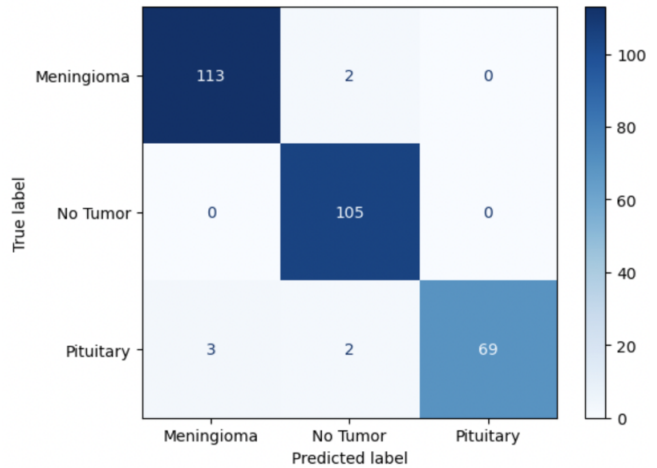

Figure 8. KNN model's confusion matrix without Glioma Tumors.

5. Conclusion

Over the course of this project, our group has learned just how important well-formatted image data is for accurate training and assessing machine learning models. Many of the pieces of data in the glioma training and test set were inconsistent with each other; taking these inconsistencies out greatly increased the Convolutional Neural Networks and Random Forest accuracy rate from 70 percent to over 90 percent, an increase of over 20 percent for these models. This is also mirrored in K-Nearest Neighbors.

We found that convolutional neural networks classified the MRI scans the best followed by random forest and then K-nearest neighbors. These results were expected, as this is the general consensus for multiclass classification of images. The only result we were surprised by was the consistent misclassification of glioma tumors as containing no tumor in the test set for our models. This result is particularly harmful as false negatives can be extremely damaging to patients. The usefulness of these models, however, is still invaluable as an aid to doctors as it is fast to get a first opinion from the model before having specialists look at it. With further development and more consistent development, we believe our solution can be used in the professional and medical world.

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