

Data Mining in Brain Tumor Detection (Analysis and Results, Conclusion, Discussion)

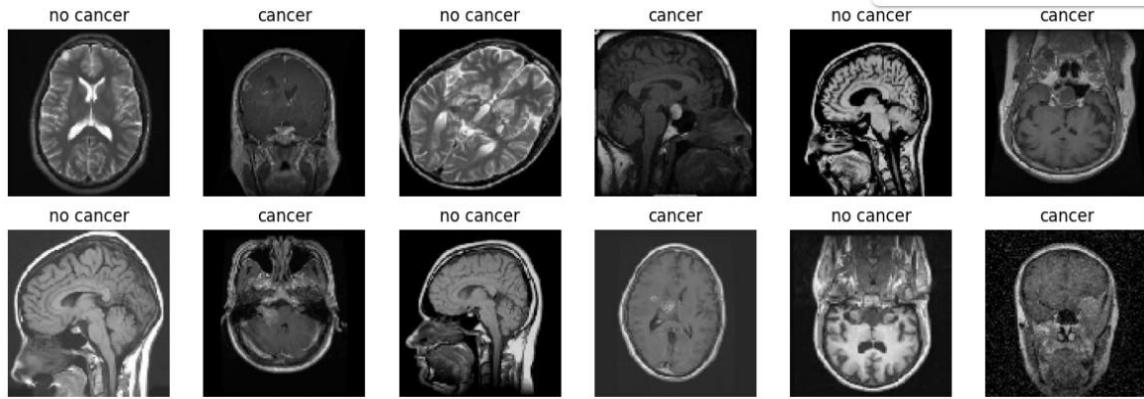
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Analysis and Results

The CNN architecture was structured as a sequential model that extracts hierarchical features from the input MRI images and makes a binary classification. The first convolutional block consisted of a Conv2D layer, which applied 32 convolutional filters to the input image to detect basic features such as edges/textures and a MaxPooling2D layer, to down-sample the feature maps, reduce spatial resolution and reduce computational load. Followed by the second convolutional block consisting of another Conv2D layer with 64 filters to capture more complex features and another MaxPooling 2D layer. Finally a third convolutional layer was applied with 128 filters on the Conv2D later and reduced spatial dimensions to a manageable size with a MaxPooling2D layer. Finally we had a flatten, dense, dropout and final dense layer. The flatten layer prepared out data for the dense layer, which then captured the most significant patterns for classification. The dropout layer was applied in order to reduce overfitting by preventing the network from relying too much on any one feature. The final dense layer used a sigmoid activation function to output a probability, and finally classify the images as cancerous or non-cancerous. The model had a total of 1,731,905 trainable parameters, a layered structure, and a layer to control overfitting, which demonstrates a good architecture for binary classification of MRI images.

Firstly, you visually want to acknowledge how you can tell clearly whether a MRI image displays a Normal or a Tumor Brain. As you can see below, the images are columned to distinguish a multi-viewed perspective between a normal brain and a Tumor brain. This is extremely important for doctors and even analytics to enforce these techniques in order for medical personnel to distinguish if a patient has any form of brain cancer or not visually. This is what's important about displaying MRI images for research. You are referring technology in order to display imaging to which help define your analysis on how you can determine if some form of tumor is embedded within a patient's brain.

Figure 1. Distinguishing Normal and Brain Tumor Images



With a total of 21,672 images, 18,606 tumor images and 3,066 normal images, the CNN model showed promising performance in detecting cancer vs non-cancer brain MRI images despite the significant class imbalance in the dataset. The CNN was trained over 10 epochs, and its performance improved consistently over time. Early epochs started with training accuracy around 85.8% and validation accuracy around 82.8%. By epoch 5, validation accuracy reached about 90.8%, and continued to improve, peaking around 92.6% by the final epoch. The decrease in training loss and the increase in training accuracy indicate that the CNN is effectively learning from the data. Overall, the trend was strongly positive.

Figure 2: Evaluation of the CNN model

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Epoch 1/10
407/407 355s 863ms/step - accuracy: 0.8588 - loss: 0.3994 - val_accuracy: 0.8238 - val_loss: 0.4217
Epoch 2/10
407/407 357s 877ms/step - accuracy: 0.8713 - loss: 0.3125 - val_accuracy: 0.8055 - val_loss: 0.4586
Epoch 3/10
407/407 342s 840ms/step - accuracy: 0.8878 - loss: 0.2694 - val_accuracy: 0.8987 - val_loss: 0.2265
Epoch 4/10
407/407 342s 840ms/step - accuracy: 0.8965 - loss: 0.2368 - val_accuracy: 0.8265 - val_loss: 0.4093
Epoch 5/10
407/407 409s 908ms/step - accuracy: 0.9076 - loss: 0.2130 - val_accuracy: 0.8881 - val_loss: 0.3327
Epoch 6/10
407/407 342s 841ms/step - accuracy: 0.9161 - loss: 0.1929 - val_accuracy: 0.8955 - val_loss: 0.2843
Epoch 7/10
407/407 338s 830ms/step - accuracy: 0.9213 - loss: 0.1845 - val_accuracy: 0.9170 - val_loss: 0.2103
Epoch 8/10
407/407 336s 824ms/step - accuracy: 0.9207 - loss: 0.1794 - val_accuracy: 0.8851 - val_loss: 0.2989
Epoch 9/10
407/407 409s 1s/step - accuracy: 0.9255 - loss: 0.1712 - val_accuracy: 0.9123 - val_loss: 0.2200
Epoch 10/10
407/407 343s 843ms/step - accuracy: 0.9378 - loss: 0.1495 - val_accuracy: 0.9156 - val_loss: 0.2081
136/136 30s 222ms/step - accuracy: 0.9224 - loss: 0.1943
Test Accuracy: 0.9217993021011353

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In consideration to the dataset imbalance, it was important to consider metrics beyond accuracy (e.g., precision, recall, F1-score). With a final test accuracy of 93.75% and test loss of 0.1436, the CNN not only matches the linear SVM in terms of accuracy but also benefits from not needing any intermediate steps or feature engineering, which is particularly advantageous for image data.

Figure 3 and 4: CNN Sample Prediction Images and Confusion Matrices

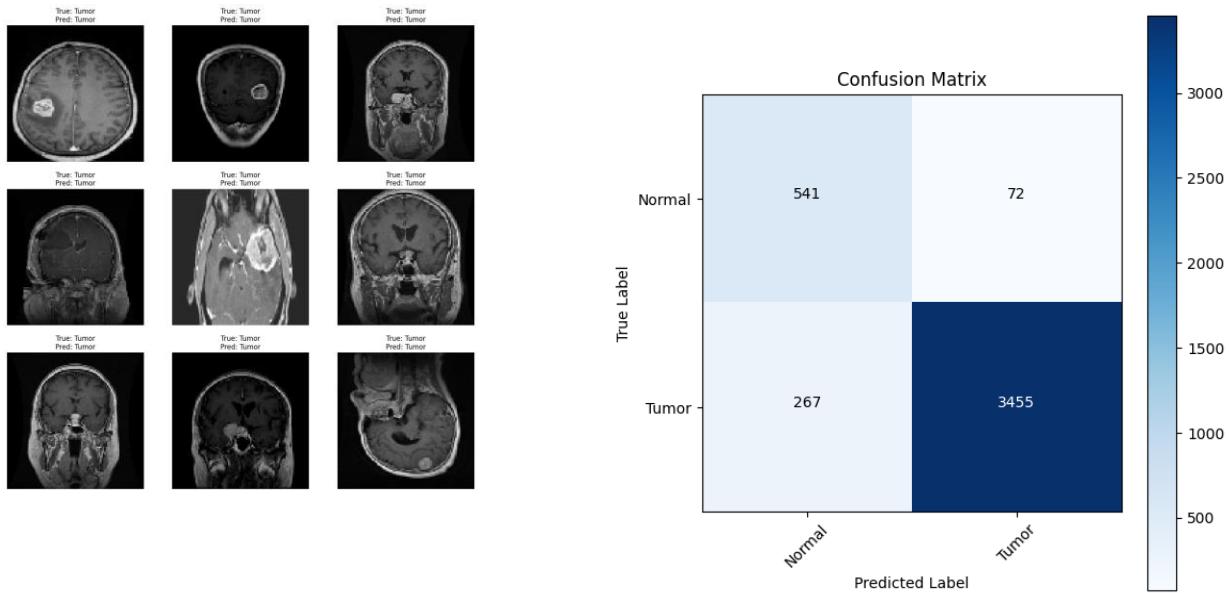


Figure 5: CNN Precision, Recall, F1-score and ROC AUC Score

	Precision	Recall	F1- Score	Support
Normal	0.67	0.88	0.76	613
Tumor	0.98	0.93	0.95	3722
Accuracy			0.92	4355
Macro. Avg	0.82	0.91	0.86	4355
Weighted Avg	0.94	0.92	0.93	4355

ROC AUC Score: 0.9674699967478761

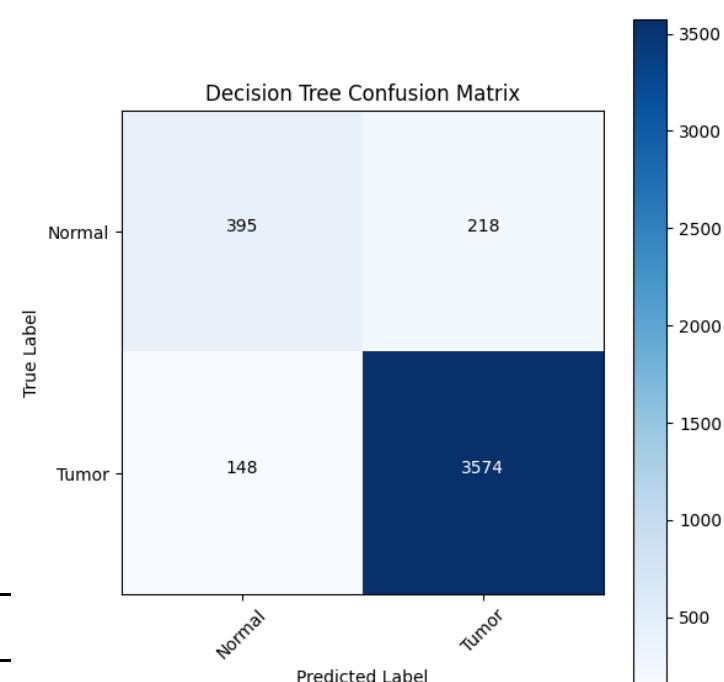
When predicting a normal image, the model is correct 67% of the time as shown in its precision value, and it successfully identifies 88% of the normal cases as shown in the recall value, indicating a high possibility of false negatives. When classifying the tumor images, the model is correct in identifying them 98% of the time and detects 93% of the tumor cases successfully. According to precision value, when the model predicts a tumor, it is correct 98% of the time and according to the recall value, the model detects 93% of tumor cases successfully. Having an F1-score of 0.76 for Normal images and 0.95 for Tumor images, the model performs much better on the Tumor class. The ROC AUC Score of 0.967 indicated that there is an excellent overall ability for the model to discriminate between the two classes. Overall, the model being able to detect tumors in the brain scans most likely has to do with the imbalance of data where the dataset consists of about 86% of tumor images, making it biased towards the tumor class.

Following the CNN, we decided to use a decision tree and an SVM to weigh out which option would make the best classifier in our case. Decision trees being a good option to visualize and understand how decisions are being made, and SVMs being useful in high-dimensional spaces extending to handle non-linear decision boundaries, both options were important to gauge the performance of the CNN and assess whether or not the additional complexity of a CNN leads to improvement.

Figure 6: Decision Tree, Precision, Recall, F1-score and ROC AUC Matrix and Calculation

Decision Tree Validation and Test Accuracies

- **Decision Tree ROC AUC Score:**
0.77472928891874336
- **Decision Tree Validation Accuracy:**
0.9121107266435986
- **Decision Tree Test Accuracy:**
0.9155709342560554
- **Decision Tree Precision:**
0.9425105485232067
- **Decision Tree Recall:**
0.9602364320257926
- **Decision Tree F1:** 0.9512909236092627



	Precision	Recall		
Normal	0.73	0.64		
Tumor	0.94	0.96	0.95	3722
Accuracy			0.92	4355
Macro. Avg	0.83	0.80	0.82	4355
Weighted Avg	0.91	0.92	0.91	4355

The Decision Tree classifier achieves 92% accuracy, demonstrating its ability to classify the majority of the samples accurately. The classifier's limitations are revealed when considering the classifier's overall discriminative power, as provided by its ROC AUC score of 0.7747, the lowest of the classifiers considered. This suggests that while the Decision Tree can be powerful in tumor class image classification, it is less powerful in its ability to consistently separate tumor and normal classes. Therefore is less suitable for more subtle medical image classification issues.

Figure 8 and 9: SVM Precision, Recall, F1-score and ROC/AUC Score Matrix and Calculations

SVM Validation and Test Accuracies

- **Linear SVM Validation Accuracy:**
0.8747404844290657
- **Linear SVM Test Accuracy:**
0.8777393310265282
- **Linear SVM Precision:**
0.8909848113669769
- **Linear SVM Recall:** 0.977162815690489
- **Linear SVM F1 Score:**
0.9320861096873398
- **Linear SVM ROC AUC Score:**
0.8443639643651389



	Precision	Recall	F1- Score	Support
Normal	0.66	0.27	0.39	613
Tumor	0.89	0.98	0.93	3722
Accuracy			0.88	4355
Macro. Avg	0.78	0.63	0.66	4355
Weighted Avg	0.86	0.88	0.86	4355

The SVM classifier recorded 88% overall accuracy, yet it does not sufficiently discriminate between tumor class images and normal class images, thus lacking detection performance reliability for both classes. Its ROC AUC measure, which is a measure of its discriminative power, is 0.844, indicating higher overall predictive power compared to the decision tree classifier. Though the SVM presents a worthy enhancement over the decision tree by way of classification quality, neither of the two models comes close to the high results obtained with the CNN.

Discussion

The development of these CNN models can help predict or detect tumors and they can provide the possibility of reducing mortality. Furthermore, the integration of genetic data with imaging could help in the identification of treatment plans that are most suitable to the patient, thus improving the outcomes of the patient. There is a great potential for this critical interface of medicine, technology, and data science to improve diagnostic precision and therapeutic strategies by enforcing these models and networks

When comparing the three classifiers, a convolutional neural network (CNN), a decision tree, and a linear support vector machine (SVM)—for brain tumor detection from MRI images. The CNN achieved an overall accuracy of 92% with a remarkable ROC AUC of 0.967, demonstrating excellent discriminative ability between normal and tumor classes. Although its performance on the normal class (precision: 0.67, recall: 0.88, f1-score: 0.76) was lower than on the tumor class (precision: 0.98, recall: 0.93, f1-score: 0.95), it demonstrated good performance overall. The Decision Tree classifier also reached an accuracy of 92%, performing strongly in identifying Tumor cases (precision: 0.94, recall: 0.96, f1-score: 0.95) but with lower ROC AUC of 0.775. Therefore, it is effective under a fixed threshold to discriminate across varying decision thresholds. The Linear SVM classifier, with an accuracy of 88%, showed high performance for the tumor class (precision: 0.89, recall: 0.98, f1-score: 0.93) but significantly underperformed on the normal class (f1-score: 0.39), showing its susceptibility to an unbalanced datasets.

Conclusion

Early diagnosis of brain tumors remains an essential role in improving outcomes and quality of life for survivors. New findings in deep learning and data mining have established promising paths to employing the diagnostic process for automation with fewer human errors and faster and more precise treatments. By using powerful predictive models, e.g., Decision Trees, Support Vector Machines (SVMs), Neural Networks, and Convolutional Neural Networks (CNNs), the detection of brain tumors from MRI images by medical practitioners becomes more precise. Image pre-processing, data augmentation, and feature selection help to improve such models to handle complex cases, e.g., localized and small-sized tumors.

The CNN model demonstrated superior performance, particularly in terms of its high ROC AUC, making it a possible candidate where accurate tumor detection is needed. The validation metrics, while slightly variable, generally mirror this trend, suggesting good generalization. With further refinement working out the CNNs limited ability to manage the dataset, it can be very reliable.

In summary, the application of data mining techniques in medical imaging is a breakthrough time for healthcare. With the development of models that are not only accurate but also efficient and cost-effective, we are able to unveil doors to early diagnosis and personalized treatment plans, ultimately leading to better patient outcomes for patients with brain tumors. Support from ongoing collaboration between medical experts and data experts will be at the forefront of unlocking the full potential of such technologies and assisting no patient have to endure brain cancer.

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