**BRAIN TUMOR DETECTION USING CNN**

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Project Report

**Project Abstract**

Did you know an estimation of 700,000 people in United States are living with a Primary Brain Tumor.? Yes, according to the statistics provided by CBTRUS Statistical Report, about 700,000 people in the United States is affected from primary Brain Tumor in 2022 with only 35.7% survival rate. Brain tumors can be fatal and have a severe influence on quality of life, and completely change everything for a patient's and their loved ones' lives. Early detection of a tumor when it is smaller can reduce the impact of surgery and treatment, improving the survival rate for many patients. Several machine learning and deep learning techniques are being used in the medical field these days for early prediction of a disease. Our study aims to build a CNN model for prediction of brain tumor.

Previously collected MRI and CT scans of patients acts as the main source to analyse and predict the disease. There are several machine learning techniques and we specifically use Convolutional Neural Networks to analyze and classify brain scans into tumor or non-tumor categories. The model should be trained on a varied dataset and assessed using several assessment criteria that take into account the relevance of the medical profession and its direct relationship to human life.

This study is to demonstrate that machine learning and deep learning model can be effectively used for predicting the Brain tumor disease and can be a valuable tool for healthcare providers in making informed decisions for prevention and treatment of the disease.

**Visual Demonstration – Brain Tumor Detection**

A picture containing text, diagram, screenshot, plan

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**INTRODUCTION**

The problem addressed by this project is the detection of brain tumors using medical imaging data, such as MRI or CT scans. Brain tumors are abnormal growths that can lead to serious health problems and may call for prompt treatment. For directing medical therapies and improving patient outcomes, early and precise brain tumor identification is essential. Brain tumors can have serious consequences, and timely diagnosis plays a vital role in effective treatment planning.

Manual interpretation of medical images can be time-consuming and prone to human error. Automating the process using AI-based systems can enhance the accuracy and efficiency of tumor detection, potentially saving valuable time and improving patient care.The possibility of improving healthcare outcomes is what drives the investigation of this issue.

The objective is to give medical practitioners a trustworthy and effective tool to aid in the early identification and diagnosis of brain cancers by creating an AI-based brain tumor detection system. This can assist prompt treatment decisions, shorten the diagnostic process, and ultimately enhance patient outcomes.

The project utilizes deep learning methods, particularly convolutional neural networks (CNNs), for brain tumor detection. Deep learning frameworks such as TensorFlow, PyTorch, and Keras are used to develop and train the CNN models. Techniques such as image preprocessing, data augmentation, and model optimization are applied to enhance the performance of the system. Additionally, tools for data visualization, evaluation metrics, and user interface development are utilized to create a comprehensive and effective solution.

**Medical History Dataset:**

The Medical History Dataset is collection of MRI scans comprising both normal and tumor cases. Each scan produces comprehensive pictures of the brain, allowing possible tumor to be detected and analyzed.

**Data Pre-Processing:**

Preparing the MRI dataset for training is part of the preprocessing procedure. This task duties including resizing images, adjusting pixel intensities, removing noise, and maybe using image enhancing techniques to improve scan quality. We have four different types of brain tumor dataset for training and testing as glioma,meningioma ,notumorn and pituitary. The dataset is obtained from Kaggle. The features used in the project are typically derived from the medical imaging data itself. These features can include various characteristics, such as tumor size, shape, intensity, texture, or location within the brain scans.

**Training:**

The preprocessed MRI dataset is utilized to build a Convolutional Neural Network (CNN) model during the training stage. The CNN learns to extract key characteristics and patterns from MRI scans in order to distinguish between normal brain images and those with tumor indications.

**Testing:**

The testing stage analyzes the trained model's performance using a distinct set of MRI images that were not utilized during training. This enables an unbiased evaluation of the model's capacity to correctly categorize brain images as normal or tumor cases.

**New/Unseen Data:**

The system should be able to accept fresh or previously unknown MRI images of patients who were not included in the initial dataset. This enables the model to generate predictions based on real-world data and assist in brain tumor diagnosis.

**A collage of images of a brain

Description automatically generated with low confidence**

**METHODS**

Used a variety of AI techniques and tools to create a brain tumor detection system for this project. Convolutional neural networks (CNNs), a potent deep learning tool for interpreting visual data such as photographs, were the main methodology employed. In order to construct the CNN architecture, I used the TensorFlow and Keras libraries, especially importing layers such as Conv2D, MaxPooling2D, Flatten, Dense, Activation, Dropout, and BatchNormalization.

CNNs operate by applying filters or kernels to the input pictures and then using convolutional procedures to extract significant information. This process, which involves applying filters to the input picture to produce feature maps, is represented by the Conv2D layer. By choosing the largest value inside particular locations, MaxPooling2D layers downsample the feature maps, lowering the spatial dimensions while keeping the important data.

The ImageDataGenerator module from TensorFlow and Keras to train the model, which enabled data augmentation methods like resizing, rescaling, and transformations. This expanded the training set and improved the generalizability of the model.

Utilized the TensorFlow's Adam and Adamax optimizers for training, which adaptively changed the learning rate to enhance convergence. For multi-class classification problems like brain tumor identification, the loss function used the categorical\_crossentropy metric from TensorFlow.

Metrics from the sklearn.metrics package, such as confusion\_matrix and classification\_report, to assess the model's performance. These provide information on the model's performance and correctness, allowing for a thorough review.

**RESULTS**

**A screenshot of a computer

Description automatically generated**

Here, we have halted the training at epoch 5 to predict the model accuracy at early stage.

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The model performs well on both the training and validation datasets, achieving high accuracy and relatively low loss values.

**A screenshot of a computer program

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**A graph of a graph of a loss

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**A screenshot of a computer

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The classification report shows the precision, recall, and F1-score for each class, as well as the overall accuracy.

The true positive, true negative, false positive, and false negative predictions for each class are detailed in the confusion matrix. Following is a breakdown of the confusion matrix:

* There are 296 true positive predictions, 3 false positive predictions, 0 false negative predictions, and 1 true negative prediction for the "glioma" class.
* There are 302 true positive predictions, 2 false positive predictions, 1 true negative prediction, and 1 false negative prediction for the "meningioma" class.
* There are 405 true positive predictions for the "notumor" class, 0 false positive predictions, 0 false negative predictions, and 0 true negative predictions.
* There are 296 genuine positive predictions, 3 false positive predictions, 0 false negative predictions, and 1 true negative prediction for the "pituitary" class.

For each class, the classification report offers metrics for accuracy, recall, and F1 scores. The metrics are analyzed below:

1. Precision: The precision score assesses the reliability of optimistic forecasts. A low rate of false positives is indicated by high precision numbers. The accuracy scores are high for all classes, ranging from 0.98 to 1.00, showing that the model produces few false positives.
2. Recall: The recall score gauges how well a person can recognize good examples. A low rate of false negatives is indicated by high recall values. Recall ratings for all classes range from 0.99 to 1.00, which is a high number and shows that the model has a low percentage of false negatives.
3. F1-score: The F1-score, which is a balanced indicator of a model's performance, is the harmonic mean of accuracy and recall. High F1-scores for all classes, which range from 0.98 to 1.00, show strong overall performance.

The model's overall accuracy is 0.99, meaning that it consistently predicts the kinds of brain tumors in 99% of the instances.

These evaluation results show how well the model for detecting brain tumors performs. High accuracy, recall, and F1-scores for each class of the model demonstrate how well it can categorize various kinds of brain tumors. The model's great overall accuracy raises the possibility that it is trustworthy and useful for diagnosing brain tumors.

**Conclusion**

In this project, we developed a brain tumor detection system using deep learning techniques. The implemented model achieved high performance, accurately classifying different types of brain tumors. The key points of our findings are as follows:

Algorithm Performance: The convolutional neural network-based deep learning model showed great performance in identifying brain cancers. The Conv2D, MaxPooling2D, Dense, Dropout, and BatchNormalization layers were some of the particular techniques employed, which helped to explain the model's excellent accuracy.

Data Handling: The project made effective use of a variety of data handling technologies, including packages like OpenCV, NumPy, and Pandas. The preparation and structuring of the dataset were made easier by these technologies.

A deeper comprehension of the data and model performance was made possible through the use of visualization packages like Seaborn and Matplotlib to produce instructive plots and charts.

**Future Work:**

There are a number of opportunities for improvement given the room for growth:

Algorithm Optimization: Improving the model's architecture and hyperparameters, investigating other CNN architectures, or using ensemble approaches may improve the brain tumor detection system's overall performance and resilience.

Data Augmentation: By using cutting-edge data augmentation techniques, the training dataset may be made more diverse and large, which may help the model generalize to previously undiscovered brain tumor pictures.

Transfer Learning: By utilizing previously trained models on sizable datasets like ImageNet and modifying them for brain tumor detection, the model's performance may be enhanced by utilizing the learnt features.

Interpretability and Explainability: By including approaches for model interpretability and explainability, such as displaying the learnt characteristics or employing attention processes, it will be possible to get insights into the model's decision-making process, so fostering greater confidence and comprehension.

Collaboration: With more team members, research and development projects may go forward more quickly, enabling more thorough experiments, evaluations, and model validations.

Hardware and computational resources: The use of more potent computational resources, like as cloud computing platforms or high-performance GPUs, can facilitate larger-scale experiments, quicker training times, and the investigation of more complicated models.

Future research might improve the brain tumor detection system, increase its precision, and perhaps boost medical imaging and diagnosis by following these pathways.

**References**

**Datasets:**

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