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BRAIN TUMOUR IMAGE SEGMENTATION USING CONVOLUTIONAL NEURAL NETWORK

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ABSTRACT:

Brain tumors pose a significant threat to public health, with their prevalence and potentially devastating consequences. Timely and accurate detection of brain tumors is vital for effective treatment and improved patient outcomes. Traditional methods of brain tumor detection often rely on manual analysis by radiologists, which can be time-consuming, subjective, and prone to human error. Therefore, there is a pressing need for automated and reliable methods to assist healthcare professionals in the early detection and diagnosis of brain tumors. In this project, we propose a deep learning-based approach for brain tumor detection using Convolutional Neural Network (CNN) model architecture. The primary objective of this study is to develop a reliable and efficient system for automated brain tumor detection using MRI images. We leverage the power of deep learning, specifically CNNs, which have demonstrated exceptional performance in various computer vision tasks, including medical image analysis. For our experiments, we utilized a Brain MRI Images dataset obtained from Kaggle, a popular platform for machine learning datasets. This dataset contains a diverse collection of brain MRI images, including both tumor and non-tumor cases. The CNN model architecture employed in this project consists of multiple convolutional layers followed by pooling layers, leading to feature extraction and dimensionality reduction. The extracted features are then fed into fully connected layers for classification. We utilized appropriate activation functions, regularization techniques, and optimization algorithms to train the CNN model effectively. Our experimental results demonstrate the effectiveness of the proposed approach for brain tumor detection. The CNN model achieved an accuracy of 97% on the test dataset, indicating its robustness and

reliability. The high accuracy achieved by the proposed approach will contribute to reducing false-negative and false-positive rates, minimizing the risk of misdiagnosis and unnecessary invasive procedures.

LITERATURE SURVEY:

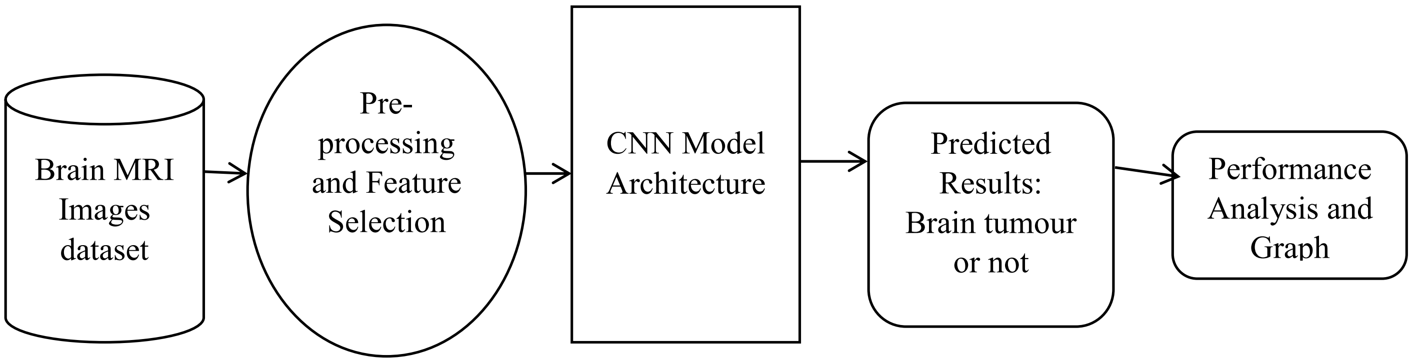
The 2016 World Health Organization Classification of Tumors of the Central Nervous System is both a conceptual and practical advance over its 2007 predecessor. For the first time, the WHO classification of CNS tumors uses molecular parameters in addition to histology to define many tumor entities, thus formulating a concept for how CNS tumor diagnoses should be structured in the molecular era. As such, the 2016 CNS WHO presents major restructuring of the diffuse gliomas, medulloblastomas and other embryonal tumors, and incorporates new entities that are defined by both histology and molecular features, including glioblastoma, IDH-wildtype and glioblastoma, IDH-mutant; diffuse midline glioma, H3 K27M-mutant; RELA fusion-positive ependymoma; medulloblastoma, WNT-activated and medulloblastoma, SHH-activated; and embryonal tumour with multilayered rosettes, C19MC-altered. The 2016 edition has added newly recognized neoplasms, and has deleted some entities, variants and patterns that no longer have diagnostic and/or biological relevance. Other notable changes include the addition of brain invasion as a criterion for atypical meningioma and the introduction of a soft tissue-type grading system for the now combined entity of solitary fibrous tumor / hemangiopericytoma-a departure from the manner by which other CNS tumors are graded. Overall, it is hoped that the 2016 CNS WHO will facilitate clinical, experimental and epidemiological studies that will lead to improvements in the lives of patients with brain tumors.

AUTHORS: David N. Louis, Arie Perry, et al.

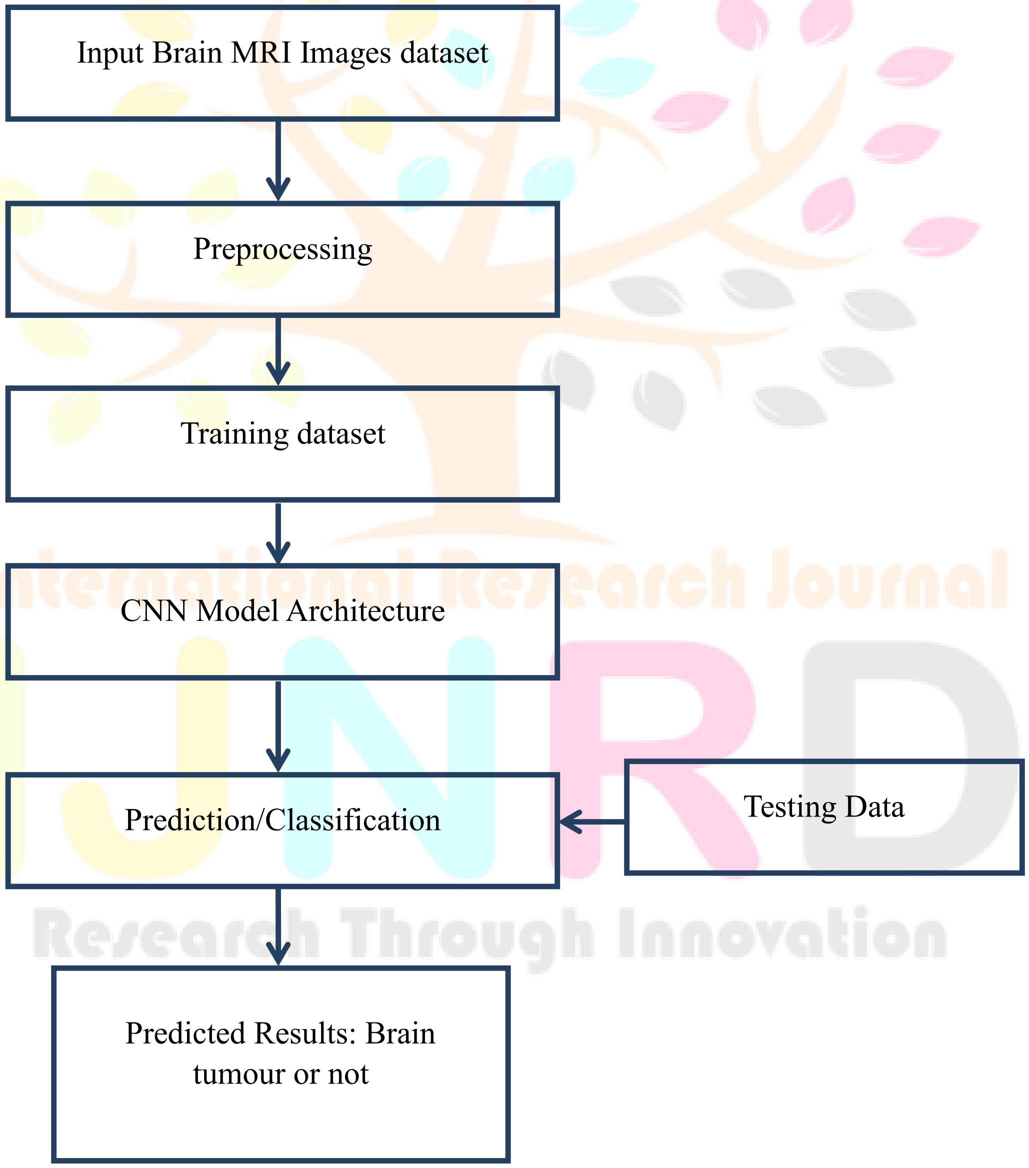
MODULES:

- ❖ Dataset
- ❖ Importing the necessary libraries
- ❖ Retrieving the images
- ❖ Splitting the dataset
- ❖ Building the model
- ❖ Apply the model and plot the graph
- ❖ Accuracy on test set
- ❖ Saving the Trained Model

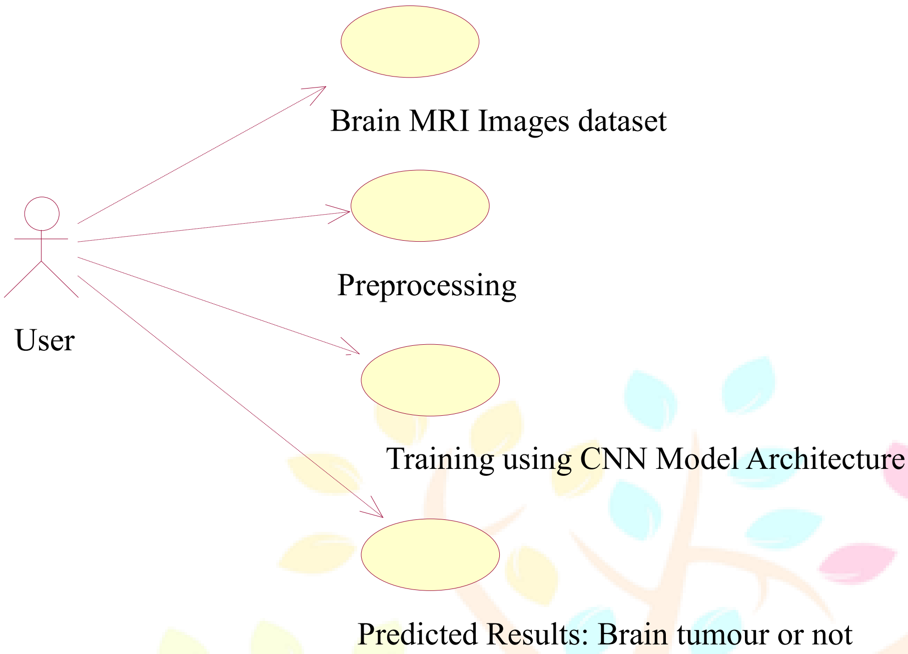
SYSTEM ARCHITECTURE:



UML DIAGRAMS



USE CASE DIAGRAM:



CLASS DIAGRAM: