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Overall Survival Prediction in Glioblastoma with Radoimic Features using Machine Learning

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ABSTRACT: Detecting brain tumors using Convolutional Neural Networks (CNNs) is an advanced approach that involves several key steps. Firstly, a dataset of brain MRI scans needs to be collected, containing both positive cases with tumors and negative cases without tumors. These scans should be labeled accordingly for training purposes. The dataset is then preprocessed to enhance features and normalize intensities. Common preprocessing techniques include skull stripping to remove non-brain regions, intensity normalization to ensure consistency, and resampling to a standardizedresolution.To improve the generalization capability of the model and reduce overfitting, data augmentation techniques are applied. This involves applying transformations such as rotations, translations, and flips to create additional variations of the training samples. With the dataset ready, a CNN architecture is designed. Typical architectures used for brain tumor detection include variants of VGG, ResNet, or InceptionNet. These architectures consist of multiple convolutional layers that extract relevant features from the MRI scans, followed by pooling layers to reduce spatial dimensions. Fully connected layers are then added for classification.

KEYWORDS: CNN, Image processing, Machine Learning ,Brain Tumor.

I. INTRODUCTION

Glioblastoma, also known as a brain tumor, is a highly malignant and aggressive form of cancer that affects the brain. It originates in the glial cells, which are the supportive cells that surround and protect the neurons in the brain. Glioblastoma tumors are characterized by their rapid growth and invasive nature, often spreading into nearby brain tissue. They can occur in any part of the brain and are commonly found in the cerebral hemispheres. Glioblastoma tumors can cause a range of symptoms, depending on their size and location. Common symptoms include persistent headaches, seizures, cognitive impairment, changes in personality or behavior, difficulty with speech or motor functions, and vision or hearing problems.

The severity of symptoms can vary from person to person.Unfortunately, glioblastoma is a highly aggressive and challenging cancer to treat. The treatment typically involves a combination of surgery, radiation therapy, and chemotherapy. However, due to the invasive nature of the tumor and the difficulty in completely removing it, complete eradication is often not possible. Glioblastoma tumors have a high recurrence rate, and the prognosis for patients is generally poor, with a relatively short average survival time, even with treatment.

A brain tumor is defined as abnormal growth of cells within the brain or central spinal canal. Some tumors can be cancerous thus they need to be detected and cured in time. The exact cause of brain tumor is not clear and neither is exact set of symptoms defined, thus, people may be suffered fron it without realizing the danger. Brain tumor can be either malignant (contain cancer cells) or benign (do not contain cancer cells). CT scans, X-Ray, and MRI scans are the common imaging methods among magnetic resonance imaging(MRI) that are the most reliable and secure. Brain tumor occurred when the cells were divind and growing abnormally. It is appearing to be a solid mass when it diagnostic medical imaging techniques.

II. RELATED WORK

Glioblastoma (GBM), also referred to as a grade IV astrocytoma, is a fast-growing and aggressive brain tumor. It invades the nearby brain tissue, but generally does not spread to distant organs. GBMs can arise in the brain de novo or evolve from lower-grade astrocytoma. Here is a general outline of how a CNN can be used for glioblastoma detection:

1. Data Collection: Gather a dataset of brain MRI scans, including both glioblastoma-positive and glioblastoma-negative cases.These scans should be labeled accordingly.

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2. Data Preprocessing: Preprocess the MRI scans to enhance features and normalize intensities. Common preprocessing techniques include skull stripping, intensity normalization, and resampling to a consistent resolution.

3. Data Augmentation: Augment the dataset by applying transformations such as rotations, translations, and flips to increase the diversity of the training samples. This helps in generalizing the model and reducing overfitting.

4. Model Architecture: Design the CNN architecture for glioblastoma detection. A typical CNN architecture consists of multiple convolutional layers for feature extraction, followed by pooling layers to reduce spatial dimensions. Additional fully connected layers can be added for classification.

5. Training: Split the dataset into training and validation sets. Feed the training data into the CNN and optimize the model parameters using gradient descent algorithms such as Adam or RMSprop. During training, monitor the performance on the validation set to prevent overfitting.

6. Evaluation: Evaluate the trained CNN on an independent test set to assess its performance. Common evaluation metrics include accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AUC-ROC).

7. Interpretation and Visualization: Analyze the learned features and visualize the activation maps to gain insights into the decision-making process of the CNN. This can help in understanding which regions of the brain are more indicative of glioblastoma.

Deployment: Once the CNN model is trained and evaluated, it can be deployed to predict glioblastoma in new, unseen MRI scans. The model can be integrated into a medical imaging system to assist radiologists in the diagnosis process.

III. PROPOSED ALGORITHM/ PSEUDO CODE

1. Step 1: Upload Dataset. The MNIST dataset is available with scikit to learn at this URL. ...
2. Step 2: Input layer. ...
3. Step 3: Convolutional layer. ...
4. Step 4: Pooling layer. ...
5. Step 5: Second Convolutional Layer and Pooling Layer. ...
6. Step 6: Dense layer. ...
7. Step 7: Logit Layer.

IV. SIMULATION RESULTS

For the prediction of survival categories, the neural network demonstrated an accuracy of 70.2% in the training subset and 62.5 and 63.6% in the validation and testing subsets, respectively, which we divided from BraTS training dataset. The accuracy was 73% for the entire training dataset. The AUC was 0.799 (0.817 for Group 1, 0.709 for Group 2, and 0.784 for Group 3). A summary of the model performance is shown in Figure 6. The designed model performed better for patients in the mid-survivor groups, with the least accuracy for patients in the long-survivor group.

Survival prediction was divided into two tasks. One task aimed at classifying patients into three survival groups obtained by unsupervised two-step clustering. These groups roughly correspond to the known survival groups in GBM (PMID: 22517216). The survival groups were characterized as long survivors (e.g., >900 days), short survivors (e.g., 900 days' survival, n = 12). Pearson's correlation revealed a strong inverse relationship of age with this group, with younger patients having the greatest OS ($p = 0.000008$, $r = -0.368$), as shown in Figure 1.

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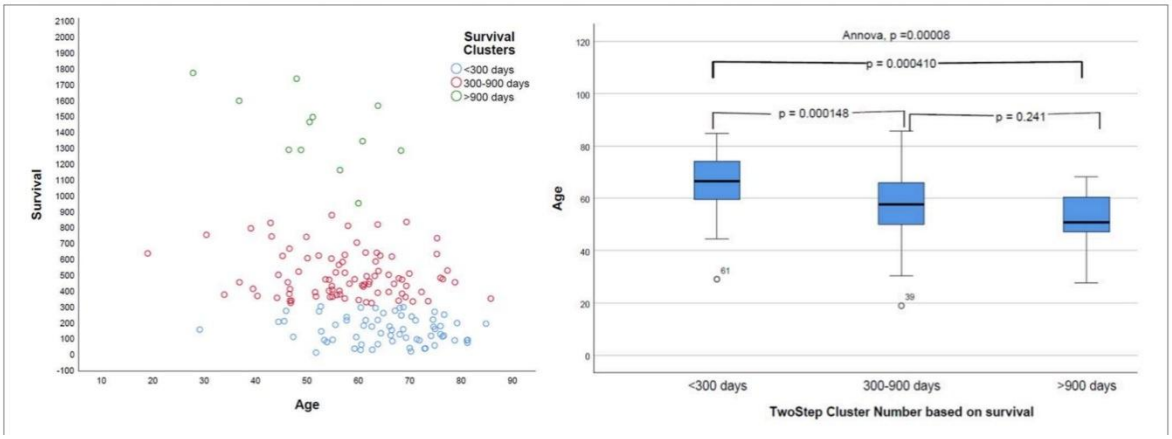

Fig 1

Assessment of Relationship With Survival and Radiomic Feature Vector Dimension Reduction.

In order to reduce the dimensionality of the feature vector, Spearman's correlation coefficient was calculated for each pair of radiomic features. The features having Spearman's correlation coefficient >0.95 with each other were discarded, retaining a single feature in each set (Supplementary Table 1). This reduced the feature vector size from 679 to 118. The feature set was further reduced to 54 by excluding all variables with statistically insignificant ($p > 0.05$) relationship with the survival groups (tested using ANOVA) identified above and with OS (tested using Pearson's correlation coefficient). It was observed that in terms of normalized importance age is the most important feature. Because whole tumor is visible in FLAIR modality with hyperintense pixels, their features followed age. The enhancement tumor and core tumor counts were of significant importance for survival prediction (Supplementary Table 1)

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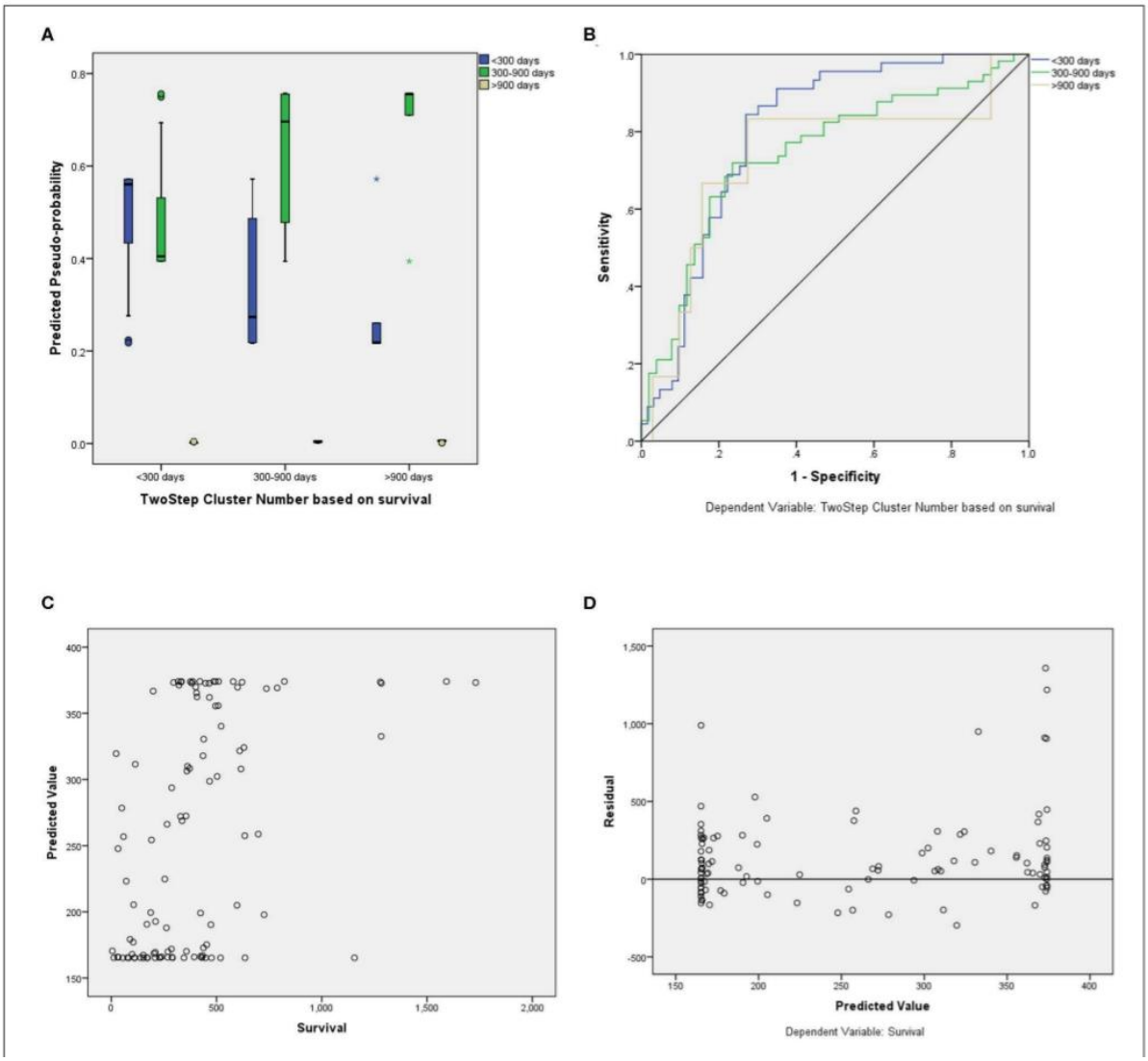

V. CONCLUSION AND FUTURE WORK

As we all know the brain tumor is one of the dangerous diseases. It can cause the human death. This disease is not possible to detect early using manual processing. So, in this paper we used some Deep Learning models to detect tumor as early as possible. In our system we have used CNN algorithm as well as SVM algorithm which is very important for image processing and classification. In CNN there are three main layers i.e., convolutional layer, activation layer and pooling layer. These all layers are interconnected so that CNN can process and perceive data in order to classify images. Based on classification prediction is done. Another module is used i.e., localization using specific object detection. Defected area of brain will be highlighted using localization. An automated system is developed for tumor extraction and classification from MRI. It is based on marker-based watershed segmentation and features selection. Five primary steps are involved in the proposed system including tumor contrast, tumor extraction, multimodel features extraction, features selection, and classification.

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