In this research, saliency based deep features are extracted from MRI. Then Support Vector Machine is used for classifying deep features. Design is the only solution which identifies the tumor very accurately with less time. Recently, many CA technologies are developed which helps many health care system. MRI image segmentation problems of identifying abnormal brain tissues and normal tissues addressed using feature extraction and Support Vector Machine (SVM) [1,2]. The proposed method is tested on BRATS 2015 dataset and it is compared with state-of-the-methods and recent methods. The proposed method achieves 0.94, 0.93 and 0.9 as dice score, precision and sensitivity respectively which is greater than other methods.

ABSTRACT: Tumor segmentation is the primary and tedious task for the clinical experts. Computer Aided Design is the only solution which identifies the tumor very accurately with less time. Deep learning models such as the convolutional neural network have been widely used in 3D biomedical segmentation and have achieved state-of-the-art performance. In this research, saliency based deep features are extracted from MRI. Then Support Vector Machine is used for classifying deep features. The proposed method is tested on BRATS 2015 dataset and it is compared with state-of-methods and recent methods. The proposed method achieves 0.94, 0.93 and 0.9 as dice score, precision and sensitivity respectively which is greater than other methods.

KEYWORDS: Saliency, Deep Features, Support Vector Machine

1. INTRODUCTION

Tumors can be identified by segmentation and detection. Identifying tumor from Magnetic Resonance (MR) images is a very time-consuming task for medical professionals and their accuracy is difficult to find. In order to overcome those limitations, the use of Computer Aided (CA) technology becomes very necessary.

According to the World Health Organization and the American Brain Tumor Association[3], tumors are ranked from grade I to grade IV scale to classify the types of benign and malignant tumors. Benign tumors fall below grade I and grade II glioma on that scale and malignant tumors fall under grade III and grade IV glioma. The former glioma, also known as low-grade tumor, has slow growth, whereas the latter glioma, also known as high-grade tumor, has rapid tumor growth. If the low-grade brain tumor are not treated at right type, it will be developed to high-grade brain tumor which is a malignant brain tumor. Hence patients with grade II gliomas require continuous monitoring. MRI or Computed Tomography (CT) observations scan half yearly. Brain tumor may likely affect any individual at any age, and the symptoms may not be the same for every individual.

The benign tumors can be cured under complete surgical treatment, while malignant tumors may be treated with radiotherapy, chemotherapy or a combination. The term malignant tumors are also referred to as anaplastic astrocytomas. An anaplastic astrocytoma is a mid-grade tumor that exhibits abnormal or unusual growth relative to other low-grade tumors and an elevated growth index. Additionally, the glioblastoma is the most malignant type of astrocytoma and is also the highest grade glioma.

Glioblastoma is differentiated from all other tumor class by the irregular rapid development of blood vessels and the presence of necrosis (dead cells) around the tumor. Grade IV tumor class that is glioblastoma is always fast-growing and highly malignant in tumor form compared to other tumor grades. Segmentation is employed to detect infected tumor tissue from medical imaging modalities. Brain tumor segmentation involves separating tumor tissues such as edema and dead cells from normal brain tissues and solid tumors [4] using MR images or other imaging methods[5–8].

Magnetic Resonance Imaging (MRI) is used for diagnosis in this study, including T1-weighted MRI, T2-weighted MRI, FLuid-Attenuated Inversion Recovery- weighted MRI (FLAIR) and proton density weighted MRI. Early detection of a brain tumor is the possible way of providing better treatment. Once a brain tumor is
suspected, it will require radiological evaluation to determine its location, size and impact on surrounding areas. The best treatment can be given based on this knowledge. It is obvious that a tumor-infected patient’s chances of survival may be significantly increased if the tumor is accurately detected at its early stage[9]. Hence the study of brain tumors using CA technology is very import for radiologists.

In this research, the 3D MRI data is segmented using saliency object detection. From the segmented area, the features are extracted using 24 layer 2D convolution neural network architecture. The proposed architecture is the outcome of various analyses of the limitations of many neural networks developed for similar applications. SVM is used to classify different levels of tumor.

The rest of the paper is organized as follows: Section 2 addresses the related works. Section 3 illustrates the proposed technique with its algorithm and architecture. Section 4 analyses the results and finally Section 6 discusses the conclusion.

II. RELATED WORKS

This section briefly discusses some recent researches in brain tumor segmentation that are done in BRATS 2015 dataset. The results of these methods are compared with the results of the proposed method in Section 4.

For the task of segmentation of medical image, an end-to-end Adversarial Neural Network called SegAN is introduced[10]. A Fully Convolutional Neural Network (FCNN) is used as the segmenter to generate segmentation label maps, and an adversarial critical network is developed with a multi-scale L1 loss function to force critics and segmenters to learn global and local features that capture long- and short-range spatial relationships between pixels.

For training the deep network, a patch-based approach along with an inception module is used by extracting two co-centered patches of different sizes from the input images[11]. Recent developments in deep neural networks such as drop-out, batch normalization, non-linear activation and start-up module are used to build a new architecture of ILinear nexuses. This method solves the over-fitting problem using drop-out regularizer arising from data scarcity. Initially, images are normalized and then the features are extracted from the patch using Deep CNN (DCNN), which assigns the central pixel of each patch to an output label. Morphological operators are used in post-processing.

For the challenging task of brain lesion segmentation a dual pathway is developed, 11-layer deep, 3D CNN. To reduce the computation time, a dense training scheme is developed that combines the processing of adjacent patches through the network while adapting to the inherent class imbalance present in the data[12].

To integrate different MRI data, a deep encoder-decoder structure is built with cross-modality convolution layers[13]. In addition, Convolutional LSTM (CLSTM) is used to model a sequence of 2D slices and to jointly learn end-to-end multi-modalities and CLSTM. To avoid convergence with certain labels, a re-weighting and a two-phase training scheme are adopted to deal with the label imbalance.

A fully automatic method for the segmentation of brain tumors is developed using DCNN[14]. Most of them, however, are patch-wise learning models that ignore the contextual information within the whole region of the picture. In addition, the label imbalance issue often leads the CNN models to converge to the labels in question. This is overcome by leveraging global CNN methods (e.g., FCN or SegNet) and incorporating multi-data MRI modalities. To alleviate the problem of label imbalance, a re-weighing scheme is adopted on the CNN loss layer.

Loic Le Folgoec has improved decision forests classifier, and named as Cascade of Lifted Decision Forests (CLDF) [15]. It exploits mark semantics to decompose the segmentation function into a subtask sequence. It couples simple generic intensity-based features along with a novel node-splitting criterion that effectively introduces cross-validation at node level in DFs.

A technique named Variability Characterization of Tumor Boundaries (VCTB)[16] has been presented using multimodal MR images. The algorithm considers the variable nature of brain images and the tumor boundary is derived from the intrinsic tumor heterogeneity and segmentation error.

Bi Song has used Anatomy Guided (AG) technique[17] to find the Region Of Interest (ROI) and random forests for segmentation. The size is standardized and the entire tumor segmented by using details about the anatomy structure. By dilating the initial segmented tumor as the ROI, random forest classifier is used for multi-class tumor segmentation on the voxels that lie in the ROI. Followed by a new pathology-led refinement, it is possible to correct some mislabels of random forests.

3D Convolutional Networks (3DNet_2) were used to segment brain tumors to tackle the BRATS problem[18]. Experiments with three fully convolutionary 3D architectures were conducted. Future steps which include optimizing the hyperparameter, comparing the performance of the models and implementing a post-processing stage to remove false positive predictions are analyzed.

Zhao et al. developed a method for segmenting brain tumors by integrating FCNN and Conditional Random Fields (CRF)[19].
Bakas et al. who won the latest challenge at BRATS 2015 included the semi-automatic system [20]. Pereira et al.’s approach is based on grade-specific 2D CNNs and demands that the patient visually examines the tumor and classifies the grade before segmentation [21].

U-Net[22] consists of a multiple downsampling convolutions and an expansive path with multiple deconvolution layers to upsample the features and concatenate the cropped feature maps from the contracting path. Those 2D-based approaches, however, ignore depth information.

III. SYSTEM ARCHITECTURE

The conventional classification system consists of feature extraction and classification. An efficient classification system may include segmentation before feature extraction and optimization after feature extraction. This inclusion reduces the computation time and reduces the load given to feature extraction. The proposed method uses segmentation to efficiently extract the feature. In this research, the MRI images are segmented using saliency map and only the MRI portion is sent for features extraction. The overall system architecture of the proposed system is shown in Fig. 1.

The proposed method consists of three important phases: Segmentation, Feature Extraction and Classification. In the segmentation phase, the saliency map is generated from the MRI dataset from which the brain is segmented using detection window. A 24 layer 2D CNN is designed to extract deep features from the segmented image in the next phase. Finally, classification is done using SVM.

3.1 Salient Object Detection

By observing MRI in the BRATS 2015 dataset, it is clear that all the images in it contain salient object in very less area. Hence, the salient object is segmented using the algorithm described in [23]. Saliency map is generated from the MRI from which salient objects are segmented using detection window. The regions of the corresponding object should be segmented based on a detection window. In this step, the size of the plane may or may not be reduced which depends on the salient object presence.

1. The salient maps are generated in each plane of the 4 MRI sequence.
2. If there is no salient object in a plane, that plane is skipped. If the plane has saliency map, then its salient object using detection window. In this step, the size of the plane may or may not be reduced which depends on the salient object presence.
3. The mean of all the cropped salient objects for each MRI sequence is obtained which is used for feature extraction.

The Salient Object Detection algorithm is shown in Algorithm 1 and the design is shown in Fig. 2. After salient object detection,

| Algorithm 1: Salient Object Detection |
|---------------------------------------|
| **Input:** 3D MRI data of a Patient |
| **Output:** Salient Object |
| **Steps:** |
| For each $\Gamma$ in $\{T_1, T_{1c}, T_2, Flair\}$ |
| For each image $I$ in $\Gamma$ |
| Calculate Saliency Map $S_k$ |
| If there is Saliency Map |
| 1.1.1.1 Crop Salient Object $S_k$ using detection window |
| 1.1.1.2 End |
| 1.1.2 End |
| 2. End |

Fig. 2 Segmenting Salient Objects

3.2 Cropping Salient Regions

Based on the detection window for salient objects, the salient regions are automatically cropped. By analyzing the salient regions, it is found that all the size of the salient objects is similar. In order to use CNN after cropping, the cropping size is set to 200 x 200. This size is used for CNN which influences the performance of the algorithm in identifying tumor.

3.3 CNN Architecture

As a branch of machine learning, deep learning has demonstrated impressive performance in image classification and object detection. In this work, CNN is designed for identifying tumor in the cropped images. Convolutional neural network extracts the image features of different layers from the shallower to the deeper by convolution operation. The weights of the convolution kernels are adjusted during the training process in order to produce characteristics which are the most suitable for classification. The main characteristics of CNN are that the weights of the kernels are shared and the connection is sparse. These characteristics make CNN easier to train and less prone to overfitting.

In this paper, we build a 24-layers deep, 2D CNN. The main architectures of CNN are in Table 1. Convolutional layers are separated by maximum pooling with stride 2. After all convolutional layers are the fully-connected layers, and each fully-connected layer is followed by one activation layer and one dropout layer.
### Table 1 The Main Architecture of CNN

| Layer Type | Filter Size | # Filters | FC Units | Input |
|------------|-------------|-----------|----------|-------|
| Conv.      | 3x3         | 32        | -        | 198x198x32 |
| Conv.      | 3x3         | 32        | -        | 196x196x32 |
| Relu.      | -           | -         | -        | 196x196x32 |
| Max-pool   | 2x2         | -         | -        | 98x98x32 |
| Conv.      | 3x3         | 64        | -        | 96x96x64 |
| Conv.      | 3x3         | 64        | -        | 94x94x64 |
| Relu.      | -           | -         | -        | 94x94x64 |
| Max-pool   | 2x2         | -         | -        | 47x47x64 |
| Conv.      | 3x3         | 64        | -        | 45x45x64 |
| Conv.      | 3x3         | 64        | -        | 43x43x64 |
| Relu.      | -           | -         | -        | 43x43x64 |
| Max-pool   | 2x2         | -         | -        | 21x21x64 |
| Conv.      | 3x3         | 128       | -        | 19x19x128 |
| Conv.      | 3x3         | 128       | -        | 17x17x128 |
| Relu.      | -           | -         | -        | 17x17x128 |
| Max-pool   | 2x2         | -         | -        | 8x8x128 |
| Conv.      | 3x3         | 256       | -        | 6x6x256 |
| Conv.      | 3x3         | 256       | -        | 4x4x256 |
| Relu.      | -           | -         | -        | 4x4x256 |
| Max-Pool   | 2x2         | -         | -        | 2x2x256 |
| FC         | -           | 256       | -        |       |
| FC         | -           | 256       | -        |       |
| FC         | -           | 5         | -        |       |

### IV. EXPERIMENTAL RESULTS

The proposed method is tested on BRATS 2015 dataset [24] which consists of 3 subsets: Training, Testing and Leaderboard dataset. Among these subsets, the training dataset is publicly available to all. The training dataset consists of 220HGG cases, out of which 146 are training and 74 are test cases. The size of the input 3D image is 240 x 240 x 155. The training dataset contains ground truth values within it. The annotated 5 labels are: 1 - necrosis, 2 - edema, 3 - non-enhancing tumor, 4 - enhancing tumor and 0 - everything else. The evaluation is performed for the enhancing tumor (only the enhancing tumor region considered positive, everything else considered negative), the core (necrosis, enhancing tumor and non-enhancing tumor taken together as the positive class), and the complete tumor (all tumor structures lumped together as the positive class). Brain tumor segmentation is considered as a multi-class classification problem in this research as it contains 5 classes.

![Fig. 3 Segmentation of the Proposed Method](image)

For analyzing the performance of the proposed system, Dice Score (DSC), Positive Predictive Value (PPV) and Sensitivity measures are used. These evaluation metrics were computed by the organizers of the challenge. Dice Score finds matches between the segmented region and ground-truth image. It finds how much similarity existed when the segmented region is overlapped with the ground-truth image. To find the percentage of the overlapped region of the ground-truth and segmented region, PPV is used. Sensitivity gives the percentage of overlapped region between the obtained segmented result and the ground truth with regard to the ground truth region.
The above discussed measures are formulated below.

\[ \text{DiceScore} = \frac{2 \times \text{TruePositive}}{\text{FalsePositive} + (2 \times \text{TruePositive}) + \text{FalseNegative}} \]  

(1)

\[ \text{PPV} = \frac{\text{TruePositive}}{\text{FalsePositive} + \text{TruePositive}} \]  

(2)

\[ \text{Sensitivity} = \frac{\text{TruePositive}}{\text{FalseNegative} + \text{TruePositive}} \]  

(3)

Table 2 Comparison of the Proposed Method with Recent Methods

| Method            | Dice   | Precision | Sensitivity |
|-------------------|--------|-----------|-------------|
|                   | Complete | Core | Enhanced | Complete | Core | Enhanced | Complete | Core | Enhanced |
| SegAn [10]        | 0.85    | 0.70   | 0.66    | 0.92     | 0.80  | 0.69    | 0.80     | 0.65  | 0.62     |
| ILinear [11]      | 0.86    | 0.87   | 0.90    | -        | -    | -      | -        | -    | -        |
| Ensemble+CRF [12] | 90.1    | 75.4   | 72.8    | 91.9     | 85.7  | 75.5    | 89.1     | 71.7  | 74.4     |
| DeepMedic+CRF [12]| 89.8    | 75.0   | 72.1    | 91.5     | 84.4  | 75.9    | 89.1     | 72.1  | 72.5     |
| CLSTM [13]        | 0.85    | 0.68   | 0.69    | 0.91     | 0.79  | 0.72    | 0.87     | 0.65  | 0.77     |
| DCNN [14]         | 0.92    | 0.85   | 0.72    | -        | -    | -      | -        | -    | -        |
| CLDF [15]         | 0.79    | 0.67   | 0.70    | -        | -    | -      | -        | -    | -        |
| VCTB [16]         | 0.74    | 0.54   | 0.54    | -        | -    | -      | -        | -    | -        |
| AG [17]           | 0.85    | 0.70   | 0.73    | -        | -    | -      | -        | -    | -        |
| 3DNet_2 [18]      | 0.89    | 0.76   | 0.37    | -        | -    | -      | -        | -    | -        |
| FCNN [19]         | 0.80    | 0.68   | 0.65    | -        | -    | -      | -        | -    | -        |
| Bakas et al. [20] | 0.88    | 0.77   | 0.68    | 0.90     | 0.84  | 0.68    | 0.89     | 0.76  | 0.75     |
| Peres et al. [21] | 0.87    | 0.73   | 0.68    | 0.89     | 0.74  | 0.72    | 0.86     | 0.77  | 0.70     |
| U-Net [22]        | 0.85    | 0.62   | 0.68    | 0.84     | 0.79  | 0.71    | 0.87     | 0.53  | 0.72     |
| Proposed Method   | 0.94    | 0.88   | 0.76    | 0.93     | 0.89  | 0.78    | 0.9      | 0.78  | 0.72     |
A deep convolutional neural network introduced by Tseng Kuan Lun has achieved the best results for complete tumor region [14]. A method using Ensemble and CRF has achieved the second best results on BRATS 2015 dataset. The proposed method achieves still more better result of 0.94 dice score. SegAn [10] achieves a high precision score of 0.92 among all other methods. But the proposed method achieves even higher than that.

VI. CONCLUSION

Tumors have significant impact on the health of the human. Brain tumors are hazardous which should be identified and treated early. In order to improve the performance of the tumor segmentation, this work proposes salient based feature extraction using convolutional neural network. The extracted features are classified using Support Vector Machine. The proposed method is tested on BRATS 2015 dataset and it is evaluated using Dice score, Sensitivity and Prediction Value. The performance of the proposed method is analyzed by comparing it with several recent methods. It is proved that the proposed method achieves 0.94, 0.93 and 0.9 as dice score, precision and sensitivity respectively which are better than other methods.

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