Design and Implementation of Deep Learning Methodologies for Brain Tumor Segmentation using MRI Images

Dr. Archana H. Sable, Associate professor, School of Computational Sciences, Swami Ramanand Teerth Marathwada University Nanded Maharashtra.

Mr. Vilas P. Salve, Research Scholar, School of Computational Sciences, Swami Ramanand Teerth Marathwada University Nanded Maharashtra.

Abstract:

In medical image processing, extracting and analyzing brain tumors are difficult challenges. Separating the various tumor tissues (solid or active tumor, edema, and necrosis) from the normal brain tissues—gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF)—is known as brain tumor segmentation. In the majority of brain tumor investigations, the presence of aberrant tissues may be readily apparent. However, it is not easy to segment and characterize anomalies in a way that is both precise and repeatable. As the population ages, cancer has emerged as a major global public health concern. MRI is an important diagnostic imaging tool that is used to identify pathological changes in tissues and organs early on. It is also a non-invasive imaging procedure. Medical image segmentation is a tough and demanding process since the pictures are intrinsic in nature. Because the intensity distributions of the tumor, surrounding edema, and healthy tissues overlap, several techniques put forth in the literature have only had sporadic success. Moreover, as the number of cancer patients being diagnosed is sharply rising year, the diagnosis necessitates extensive data access and, consequently, enormous volumes of storage. Numerous tumor forms that have not yet been described have been detected. For diagnosis, treatment, and research, patient medical information and MR images must be sent from a remote location to the other end

Keyword: ANN, MRI, RF, ML, WEKA, CNS

I Introduction:

1 Analysis of brain tumors encompasses a wide range of technological and medical research subjects. Each research endeavor described in this thesis is succinctly motivated in Section 1.1, along with its primary scientific achievements. The thesis's broad outline is covered in Section 1.2.

1.1 Motivation and Contributions:

The health care system and society are greatly impacted by primary malignant brain tumors. In contrast to other cancer forms in adults, they are linked to extremely low survival rates and make up around 2% of the adult cancer burden [13]. Both the medical and technical communities are paying close attention to the busy research area of brain tumor analysis nowadays. The three areas of brain tumor analysis covered in this thesis are brain tumor growth analysis, brain tumor categorization, and brain tumor segmentation and uncertainty assessment.

1.2 Brain tumor segmentation.

Segmenting brain tumors is very useful in therapeutic settings. First of all, it can help with the diagnosis and staging of brain tumors. Second, it can help with treatment planning, such as computer-assisted surgery and radiation planning. Last but not least, it can help with therapy evaluation and illness progression detection since it enables direct tumor volume monitoring. Automated brain tumor segmentation approaches are very intriguing when compared to manual brain tumor segmentation. They can be more objective, less expensive, and far less time-consuming. Within the medical image analysis community, (semi-)automated brain tumor segmentation has emerged as a key area of study in recent years. Since 2012, the international conference on Medical Image Computing and Computer Assisted Interventions (MICCAI) has been held annually in conjunction with the Multi-modal Brain Tumor Image Segmentation Benchmark (BRATS) challenge [2]. A large collection of precisely labeled and well-organized preprocessed training and test data are part of the BRATS challenge. Every year, this dataset, which is meticulously examined by several knowledgeable neuroradiologists, gets bigger and more precise. The success of the challenge is closely linked to the public availability and ease of access to the training data (including ground truth segmentations) and test data (without ground truth segmentations – these are kept to the organizers for internal validation), in addition to the size and quality of the training and test data.

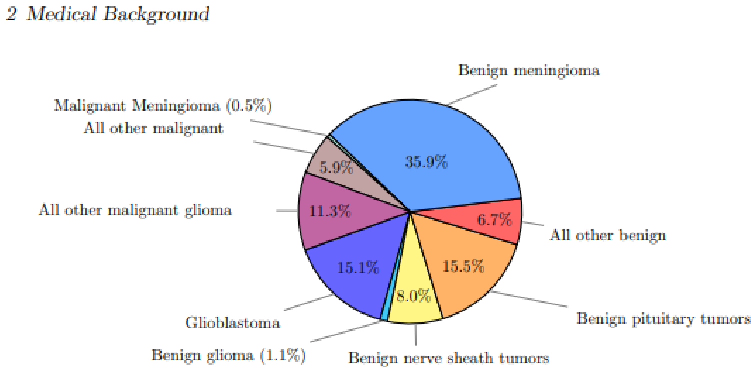


Fig : 1 Distribution of primary brain and CNS tumors by behavior (malignant or benign). N =356858, among which N = 239835 (67.2%) benign and N = 117023 (32.8%) malignant.

Malignant Brain Tumors: Glioma and Glioblastoma

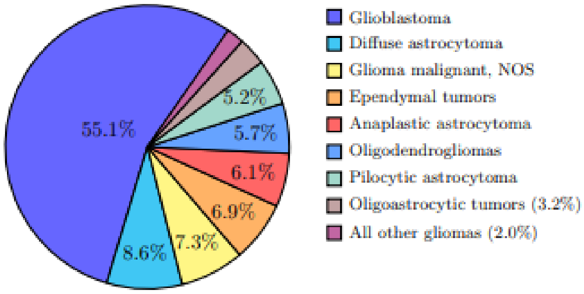
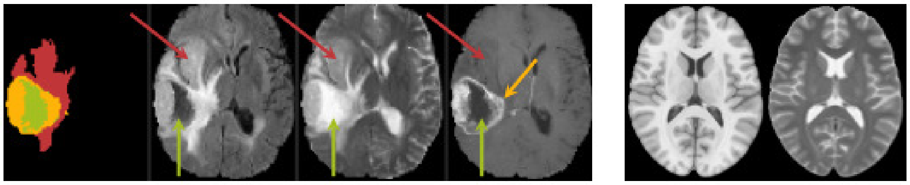


Fig. 2 Distribution of primary brain and CNS gliomas by history subtypes (N = 97910). Figure reconstructed from “ CBTRUS Statistical Report”



(a) Tumor structures in a glioblastoma patient (b) Healthy population atlas

Visualization of a brain tumor. (a) Tumor segmentation containing active tumor (●), edema (●) and necrotic tumor core (●) followed by three MR modalities: FLAIR, T2 and T1c (BRATS 2016 training case [2]). (b) T1 and T2 axial slices from the SRI24 [3] healthy population atlas.

In this thesis, a framework for reliable, quick, and precise (semi-)automated brain tumor segmentation is proposed, expanding upon the unsupervised segmentation technique introduced in [8]. In order to do this, it employs generative probabilistic models, which combine voxels with comparable statistics in an arbitrary high-dimensional feature space to produce brain tumor segmentations. In Chapter 4, a Conditional Random Field (CRF) is added to the probabilistic model and applied directly to the probabilistic segmentation maps that the probabilistic model produces. In order to create spatially coherent final segmentations, the CRF aims to integrate spatial neighborhood relationships. A combination of multivariate Gaussians is typically used to model the likelihood model in probabilistic models used for picture segmentation. In Chapter 7, Gaussian copulas and univariate Gumbel distributions are implemented in the likelihood model to particularly adapt the probabilistic model to non-Gaussian intensity distributions. Additionally, random forest supervoxel classifiers—which replace the CRF suggested in Chapter 4—are introduced as a novel method for both spatially regularizing the segmentations produced by the probabilistic model and producing trustworthy priors for the model.

Throughout the thesis, brain tumor segmentation will be crucial. Brain tumor segmentation frameworks are used in all other research initiatives examined in this thesis, including growth analysis, uncertainty evaluation, and brain tumor categorization.

1.3 Longitudinal datasets and growth analysis

The very first research project, reported in Chapter 4), was founded as a partnership with the neuroradiology department of the university hospital1 . In this research, a framework is proposed for longitudinal brain tumor segmentation, in which segmentations are generated for numerous time points at once. For this objective, the neuroradiology department offered a longitudinal imaging collection, encompassing 30 glioblastoma patients coupled with expert annotated ground truth for edema and active tumor [4].

This data is utilized to develop and evaluate a system that combines growth assessment with longitudinal brain tumor segmentation, drawing inspiration from the work reported in [14]. First, a generative probabilistic model is used to create segmentations for each time point independently. A conditional random field (CRF) covering the whole multi-modal, longitudinal sequences is then used to improve these segmentations for every time point simultaneously. Through the use of directed linkages with unlimited weight, the CRF is expanded with growth and shrinkage limitations throughout time. The energy values associated with the maximum-a-posteriori (MAP) tumor segmentation produced under various configurations of the growth and shrinkage constraints can be used to evaluate the likelihood of such a constraint.

1.4 Uncertainty assessment of brain tumor segmentation.

Because of the substantial diversity in tumor location, shape, and volume, motion artifacts in pictures, or the intrinsic uniformity of clinical data, segmentation algorithms frequently have to make conclusions in the face of high uncertainty. As a result, the clinical interpretation of the segmentation findings can greatly benefit from uncertainty evaluation.

The second project, which is described in Chapter 5, uses the architecture from [8] to segment brain tumors and extends it with a CRF for regularization. For the aim of assessing the uncertainty of CRF inference, brain tumor segmentation uncertainty is evaluated at both the voxel and supervoxel levels using random MAP perturbation models that were first suggested in [15, 16].

1.5 Genomic brain tumor classification.

A new kind of dataset is made accessible in a third project, which is described in Chapter 6. This dataset consists of both genomic and imaging data. After processing the dataset, medical colleagues from the University Hospital1's neuroradiology department chose around 120 patients who had multimodal MR images and a single genetic tumor class designation. A biopsy is used to identify the genetic tumor profile, which serves as the basis for these genetic tumor types. According to medical research investigations, the choice of therapy and the course of the disease are significantly influenced by certain characteristics in the genetic tumor profile [17], [18]. The question of whether the genetic tumor profile can be predicted from imaging data alone, without a biopsy, is examined in this difficult undertaking. From a medical standpoint, this third endeavor falls within a brand-new area of study called radiogenomics, which examines genetic factors in connection to imaging characteristics. Technically speaking, the computer vision task has changed from segmenting images to classifying them. Classifying medical images is a whole distinct discipline with unique difficulties. Specifically, the dimensionality of the feature space, which is made up of many 3D pictures, is quite high. These classification problems are commonly represented symbolically as p n, where the complexity of the feature space significantly surpasses the number of samples. Feature engineering, which includes feature extraction and feature selection, is more important in these issues. These high-dimensional picture classification challenges may be elegantly solved by deep-learning frameworks, which employ a single error function to optimize both feature creation and classification simultaneously.

A variety of picture feature types are retrieved in Chapter 6. These consist of low-dimensional image representations produced by deep convolutional denoising auto-encoders, 3D linear binary patterns (LBPs), and effective 3D local binary descriptors called BRIEFs. Additionally, a number of classifiers are tested on both the full set of features and subsets of the produced features, both with and without a PCA on the feature space beforehand. Random forests, logistic regression, k-nearest neighbors, support vector machines, and multi-layer perceptrons are among the classifiers that have been studied. It is demonstrated that the suggested framework achieves promising classification accuracies, outperforming a majority-voter, despite the fact that neuroradiology professionals can scarcely complete this classification assignment.

1.6 Semi-automated brain tumor segmentation. In a final project, a framework for segmenting brain tumors is presented with semi-automated modifications to give medical professionals or other users who want to quickly and transparently segment brain tumors a helpful tool. In order to abstract the fine voxel level, the system uses supervoxel classifiers in addition to the probabilistic network introduced in [8]. These supervoxel segmenters are used in the probabilistic model to first create label prior maps, as previously explained. A second supervoxel segmenter is used to spatially regularize the segmentations after the probabilistic model. The interactive framework's implementation on the supervoxel level rather of the fine voxel level is a significant addition. This makes user engagement incredibly quick and effective.

II Methodology:

2.1 Medical Image Acquisition

Brain cancers are often diagnosed via magnetic resonance (MR) imaging. Furthermore, computed tomography (CT) or nuclear medicine imaging (including SPECT or PET) may be obtained in certain institutions or for special circumstances. This section offers a comprehensive overview of all medical imaging modalities pertinent to brain tumor diagnosis. The most prevalent diagnostic medical imaging techniques are radiography, computed tomography (CT), single-photon emission computed tomography (SPECT), positron emission tomography (PET) and ultrasound (US) imaging. All these imaging techniques are based on the production or detection of electromagnetic waves, except from US imaging, which is based on the propagation of sound waves. Table 2.3 delineates several medical imaging modalities, together with the corresponding kind and wavelength of the electromagnetic waves generated during picture collection.

Both both radiography and CT, X-rays are generated by an X-ray tube, travel through human body tissues and are detected by an X-ray detector. SPECT and PET are methods of nuclear medical imaging, in which a tracer molecule, containing radionuclides, is delivered to the patient (typically intravenous). These radionuclides are unstable isotopes that produce γ-rays. For PET, a proton in the nucleus of the radionuclide is converted into a neutron and a positron. This positron subsequently annihilates shortly after with an electron, generating two γ-photons in opposing directions. That is, in nuclear medical imaging, γ-rays often originate within the human body and are detected by γ-ray detectors closely situated to the patient. Some studies demonstrate that PET scans, in particular (18)F-fluoro-ethyl-tyrosine (18F-FET) PET scans, can have a high diagnostic value for primary brain tumor patients [26]. In Figure 2.5, 18F-FET PET images are presented for two glioblastoma patients.

In radiography, CT, PET and SPECT, patients are exposed to X-rays or γ-rays. Due to their high frequency (or short wavelength), X-rays and γ-rays are ionizing. Ionizing EM waves are able to expel electrons from their atoms, which implies they can harm or kill cells in the body. Several investigations have demonstrated that, depending on the radiation dose absorbed by individual cells, radiation might possibly lead to genetic alterations or even malignant tumors [27]. For medical picture capture, the radiation dose is consequently kept as low as feasible, following the "As low as reasonably achievable (ALARA)" approach [10]. Ionizing radiation is measured in Gray (Gy), for the total absorbed dosage, or in Sievert (Sv), for the effective dose. Yearly, humans are normally exposed to 2-3 mSv owing to natural sources. In comparison, the effective dosage of a skull CT is 1-2 mSv [10]. Eventually, exams requiring ionizing radiation, notably CT and PET examinations, should be maintained to a minimum and every individual scan should be medically justified.

III Result and Discussion:

3.1 Data Cleansing: The preprocessing (background removal, resizing), the input MRI brain image is filtered using the Fast Averaging Peer group (FAPG) filtering technique. Furthermore, because the gray level distribution of the tumor and the skull is similar, the skull can significantly disrupt categorization. A new technique for removing the skull is suggested in order to guarantee the outstanding performance. The outliers at the picture limits are interpreted as skull components as the backdrop must be entirely eliminated from the image. After the skull is removed from the MRI, these pieces are automatically chosen as seeds to identify the region growth.

- The following stage involves segmenting the skull-removed picture using Multilevel Threshold based Social Ski-Driver (MTSSD) optimization. Additionally, filtered pictures are subjected to the extraction of hybrid features, such as intensity-based features, modified completed local binary pattern (MCLBP), pyramid histogram of the oriented gradient (PHOG), and gray-level co-occurrence matrix (GLCM). The best characteristics are then chosen from the retrieved hybrid features using the Adaptive Sun Flower Optimization (ASFO) method. Finally, the Hybrid Deep Neural Network with Deer Hunting (HDDH) algorithm is used to detect the tumors based only on the chosen attributes. Furthermore, convex criteria are used to detect the tumor's grade.
- Because it contributes to a higher fitness function value, the HDDH is also very important. It is possible for weight optimization to substantially converge to the best or nearly best solution. As a result, Deer Hunting (DH) has the potential to scap local minima and the quickest convergence rate. In order to reduce error, the Deep Neural Network (DNN) training procedure essentially consists of choosing the connection weights between the neurons. In order to find the global optimum and avoid becoming trapped in a local optimum, an adaptive sunflower optimization (ASFO) is suggested. For the purpose of precise segmentation and classification, ASFO is a population-based iterative heuristic global optimization approach that precisely extracts the best features from the filtered pictures.
- Suggested that a literature research and medical survey be used to demonstrate the necessity of tumor segmentation and identification. It is suggested that a literature research and medical survey be used to demonstrate the necessity of tumor segmentation and identification.
- Determine the necessary techniques for putting brain tumor segmentation and detection algorithms
- The suggested approach will be entirely automated; first, pre-processing methods will be used to enhance image quality and achieve the intended outcomes. Method is to be

used on the Python working, and the efficacy of our suggested system will be demonstrated by comparing its performance to that of the current method.

IV Conclusions

Several segmentation methods used in medical picture segmentation are included in the literature review. There includes discussion of strategies for categorization based on thresholds, regions, edges, and pixels. The segmentation techniques that are now available have several drawbacks. The researcher is using Segmentation and Detection methods

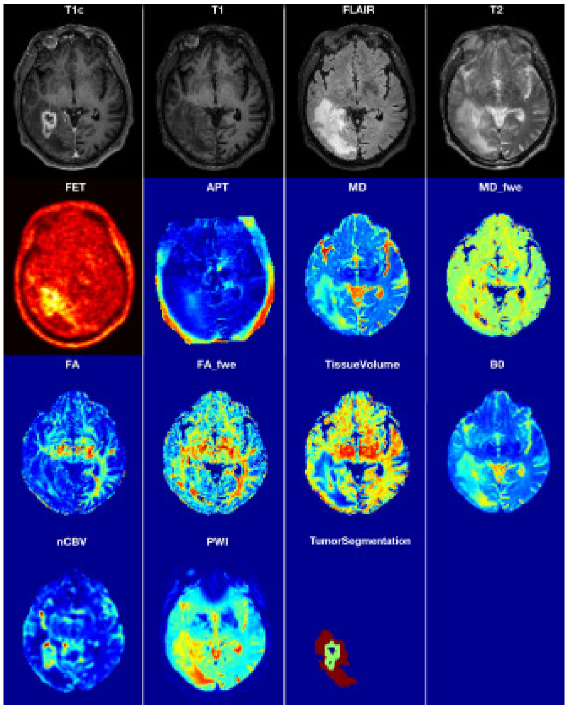


Fig: 3 A Set of image modalities acquired for a glioblastoma patient. The four standard modalities are shown at the top row. Other modalities include FET (PET Scan), APT MRI (amide proton transfer), diffusion-weighted MRI (MD: Mean diffusivity, FA: fractional anisotropy),

Tumor segmentation that is automated, precise, and quick has not yet been established, • K-means clustering may need several iterative cycles then the skull covers the brain and brain tumors don't show many distinct clinical signs, it might be challenging to discover them early. This work's main goal is to efficiently construct a segmentation model that predicts brain tumors in MRI images using the Hybrid Deep Neural Network with Deer Hunting (HDDH) algorithm. It also aims to demonstrate that the generated model can be used to forecast the data with a decent level of accuracy when applied to MRI brain medical datasets.The process of clustering involves arranging a collection of items so that they are more similar to one another than to those in other groupings. Here, we'll create an algorithm that separates an image into distinct classes in order to produce a useful description. The algorithm is feature-based and unsupervised. In order to demonstrate that the algorithm is effective, it must be compared to all other clustering algorithms, including the supervised techniques such as Bayes and Artificial Neural Networks (ANN) and CNN, as well as the unsupervised algorithms such as fuzzy C-Means (FCM), k-means, Markov Random Fields (MRF), brain tumor presence detection, unsupervised brain tumor extraction, segmentation, and detection. The contour refinement algorithm is utilized to enhance the initial tumor region's contour, decrease incorrect determination and missing spots close to the boundary, and ultimately provide the tumor identification results. Preprocessing's primary goal is to enhance the picture in ways that raise the likelihood that the subsequent procedures will be successful. Techniques for improving contrast, eliminating noise, and separating areas are usually covered in preprocessing. This will include combining techniques based on standardizing picture intensities and noise reduction.

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