

A Mini Project Report on

# **Brain Tumor Classification**

Submitted in partial fulfilment of the requirements for the award of the  
degree of

**Bachelor of Engineering**

in

**Computer Engineering**

by

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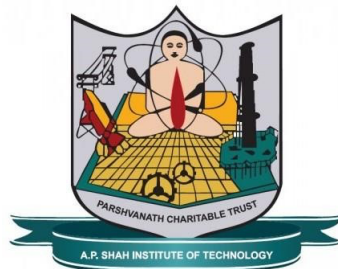
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## Approval Sheet

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## CERTIFICATE

This is to certify that the mini project entitled “*Brain Tumor Classification*” submitted by “*Hritika Kucheriya*” (18102026), “*Somesh Fengade*” (19102050), “*Atiq Kazi*”(19102066), “*Janvi Parakh*” (19102012) for the partial fulfilment of the requirement for award of a degree *Bachelor of Engineering* in *Branch Name*, to the University of Mumbai, is a bonafide work carried out during academic year 2020-2021.

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## DECLARATION

We declare that this written submission represents our ideas in our own words and where others' ideas or words have been included, We have adequately cited and referenced the original sources. We also declare that We have adhered to all principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea/data/fact/source in our submission. We understand that any violation of the above will be cause for disciplinary action by the Institute and can also evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed.

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## **Abstract**

The detection of brain tumour from MRI images is a tedious task with the application that we are building we aim to ease the judgement if brain tumour in a patient and make brain tumour classification more efficient. It is evident that brain tumour classification is a binary problem as in it exists in only two states that is yes or no but in our case tumour exists or it does not. Aiming at the problem of low accuracy of traditional brain tumor classification, in this project, a combination of multimodal information fusion and convolution neural network classification method of brain tumors, we call it a Multi-CNNs. First, the project uses the extension of the 2D-CNNs to multimodal 3D-CNNs and can obtain brain lesions under different modal characteristics of three-dimensional space. It can solve the 2D-CNNs raw input that requires a large neighborhood of faults, at the same time better to extract the model of the differences between information. Then the real normalization layer is added between the convolution layers and pooling layer to improve the convergence speeds of the network and alleviate the problem of overfitting. In the end, the loss function will be improved, and the weighted loss function will be used to enhance the feature learning of the lesion area. The experimental results will show that the brain tumor classification method proposed in this project could effectively differ tumor lesions, and better results could be obtained in correlation coefficient, sensitivity, and specificity. Compared with two-dimensional classification networks and single-mode brain tumor classification methods, the classification accuracy can be high-priority significantly improved.

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# Chapter 1

## Introduction

Glioblastoma (GBM), and diffuse astrocytic glioma with molecular features of GBM (WHO Grade 4 astrocytoma), is the most common and aggressive malignant primary tumor of the central nervous system (CNS) in adults, with extreme intrinsic heterogeneity in appearance, shape, and histology [1–7]. GBM patients have an average prognosis of 14 months, following standard of care treatment (comprising surgical resection followed by radiotherapy and chemotherapy), and 4 months left untreated [8]. Although various experimental treatment options have been proposed during the past 20 years, there have not been any substantial differences in patient prognosis.

### 1.1 Problem Definition

Mathematical models have been ubiquitously employed in various applications. One of these applications that arose in the past few decades is cerebral tumor modeling. Simultaneously, medical imaging techniques, such as magnetic resonance imaging, computed tomography, and positron emission tomography, have witnessed great developments and become the primary clinical procedure in tumor diagnosis and detection. Studying tumors via mathematical models from medical images is an important application that is believed to play a significant role in cancer treatment by predicting tumor evolution, quantifying the response to therapy, and the effective treatment planning of chemotherapy and/or radiotherapy. In this project, we focus on the classifying of brain tumors, mainly glioma, and highlight the current achievements in state-of-the-art methods. In addition, we discuss some challenges and perspectives on this research that can further promote the research of this field.

### 1.2 Objectives

- Our Main Objective of medical imaging of BRAIN TUMOR is to extract meaningful and accurate information from these images with least error possible and Finally conclude whether it's a tumor image or not.
- MGMT values shows the generation of carcinogenic cells



- Our model is based on the basis of prediction of MGMT values which generates in the body for eliminating carcinogenic cells
- The secretion of MGMT values shows the growth of tumor we are predicting brain tumor based on MGMT values

### **1.3 Scope**

The experimental results will show that the brain tumor classification method proposed in this project could effectively differ tumor lesions, and better results could be obtained in correlation coefficient, sensitivity, and specificity. Compared with two-dimensional classification networks and single mode brain tumor classification methods, the classification accuracy can be significantly improved.

### **1.4 Existing System**

Accurate identification of brain tumor sub-regions boundaries in MRI is of profound importance in many clinical applications, such as surgical treatment planning, image-guided interventions, monitoring tumor growth, and the generation of radiotherapy maps. However, manual detection and tracing of tumor sub-regions are high, time-consuming, and subjective. In a clinical setup, this manual process is carried out by radiologists in a qualitative visual manner and hence becomes impractical when dealing with numerous patients. This highlights the unmet need for automated deterministic segmentation solutions that could contribute to expediting this process. The release of the current revised World Health Organization (WHO) classification of CNS tumors [9] highlighted the appreciation of integrated diagnostics and transitioned the clinical tumor diagnosis from a purely morphological histopathologic classification to integrating molecular-cytogenetic characteristics. O<sup>6</sup>-methylguanine-DNA methyltransferase (MGMT) is a DNA repair enzyme that the methylation of its promoter in newly diagnosed GBM has been identified as a favorable prognostic factor and a predictor of chemotherapy response. Currently, genetic analysis of cancer requires surgery to extract a tissue sample. Then it can take several weeks to determine the genetic characterization of the tumor. Depending upon the results and type of initial therapy chosen, a subsequent surgery may be necessary.

# Chapter 2

## Technology Stack

Hardware Requirement-

GPU - Tesla T4

RAM -16 GB and more

OS - Windows 10 ++ / Linux 14.0.1 + / Mac

Software Requirement-

Cloud Space up to 150 GB

Pytorch

Python

PyTorch : Python library for deep learning

Streamlit : Deployment platform

opencv : Used for rendering images and modification of images

# Chapter 3

## Benefits and Applications

- If successful, we'll help brain cancer patients receive less invasive diagnoses and treatments.
- The introduction of new and customized treatment strategies before surgery has the potential to improve the management, survival, and prospects of patients with brain cancer.
-

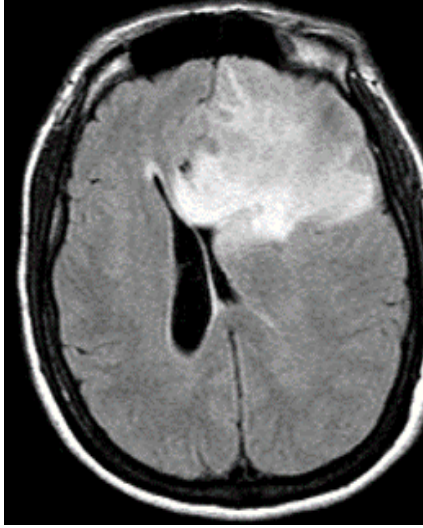
# Chapter 4

## Project Design

### 4.1 Proposed System

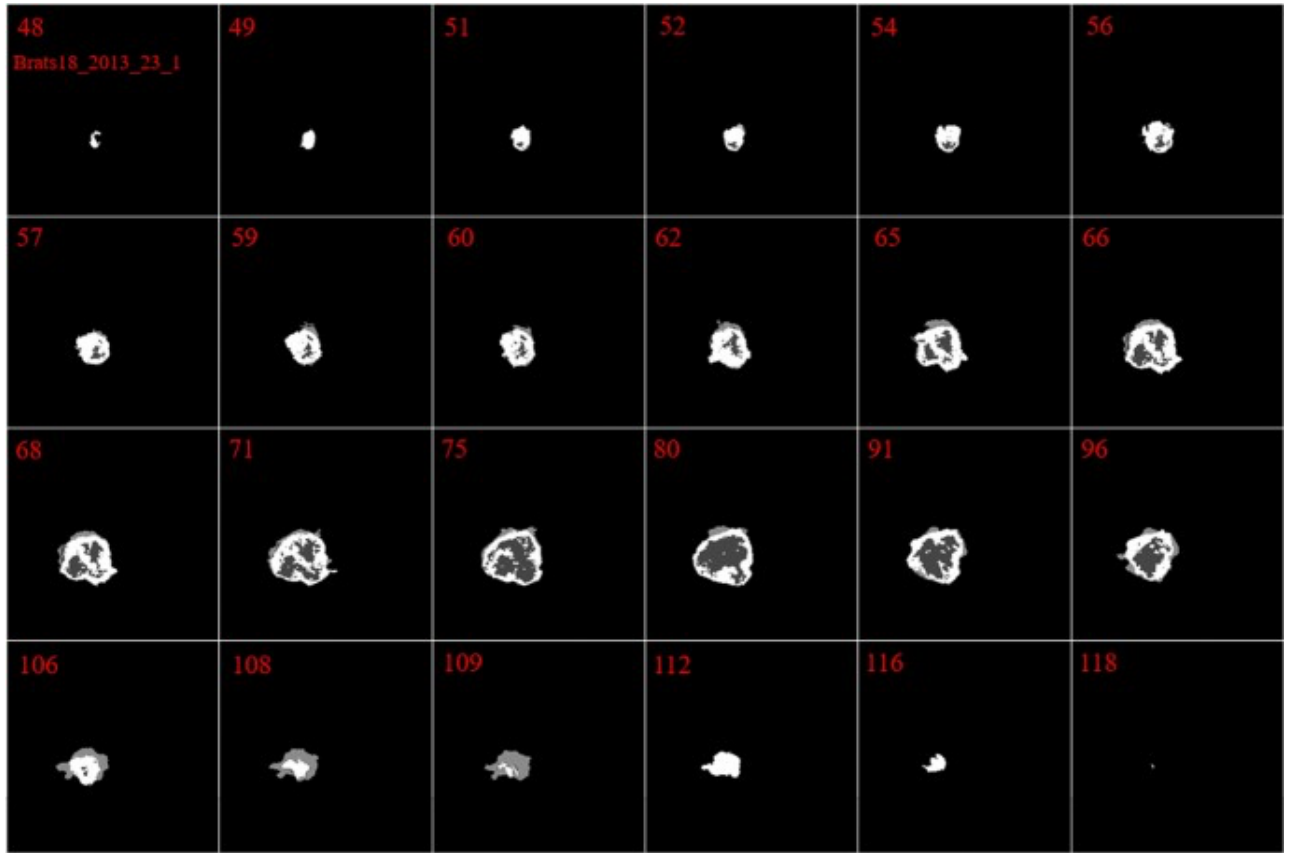
We aim to utilize multi-institutional multi-parametric Magnetic Resonance Imaging (mpMRI) scans, to address both the automated tumor sub-region segmentation and the prediction of one of the genetic characteristics of glioblastoma (MGMT promoter methylation status) from preoperative baseline MRI scans. Specifically, BraTS 2021 focuses on the evaluation of state-of-the-art methods for the accurate segmentation of intrinsically heterogeneous brain glioma sub-regions and the evaluation of classification methods distinguishing between MGMT methylated (MGMT+) and unmethylated (MGMT-) tumors. A malignant tumor in the brain is a life-threatening condition. Known as glioblastoma, it's both the most common form of brain cancer in adults and the one with the worst prognosis, with median survival being less than a year. The presence of a specific genetic sequence in the tumor known as MGMT promoter methylation is a favorable prognostic factor and a strong predictor of responsiveness to chemotherapy. If an accurate method to predict the genetics of cancer through imaging (i.e., radio genomics) alone could be developed, this would potentially minimize the number of surgeries and refine the type of therapy required.

The Radiological Society of North America (RSNA) has teamed up with the Medical Image Computing and Computer-Assisted Intervention Society (the MICCAI Society) to improve diagnosis and treatment planning for patients with glioblastoma. In this competition you will predict the genetic subtype of glioblastoma using MRI (magnetic resonance imaging) scans to train and test your model to detect the presence of MGMT promoter methylation. A cascade CNN model has been proposed that combines both local and global information from across different MRI modalities. Also, a distance-wise attention mechanism is proposed to consider the effect of the brain tumor location in four input modalities. This distance-wise attention mechanism successfully applies the key location feature of the image to the fully-connected layer to overcome overfitting problems using many parallel convolutional layers to differentiate between classes like the self-co-attention mechanism. Although many CNN-based networks have been employed for similar multi-modality tumor segmentation in prior studies, none of them uses a combination of an attention-based mechanism and an area-expected approach.



To improve the final segmentation accuracy, we use four brain modalities, namely T1, FLAIR, T1C, and T2. To enforce the MRI data more uniform and remove the effect of the anisotropic (especially for the FLAIR modality), we conduct the Z-Score normalization for the used modalities. By applying this approach to a medical brain image, the output image has zero mean and unit variance. We implemented this step by subtracting the mean and dividing by the standard deviation in only the brain region (not the background). This step was implemented independently for each brain volume of every patient. We found that the size and the shape of the tumor in sequential slices increase or decrease steadily. The tumor emerges in the first slices with a small size at any possible location of the image. Then, in the following slices, the tumor will remain in the same location inside the image, but it will have a bigger size. Next, after reaching maximum size, the tumor size will start to decrease until it vanishes entirely. The main reason for using the mentioned four brain modalities is their unique characteristics for detecting some parts of the tumor. Moreover, to find a tumor, we need to find all three parts in each of the four modalities, then combine them to make a solid object. So, our first goal is to find one part of the tumor in each modality. Another important fact is that to the best of our knowledge no sharp difference can be observed in the size of continuous slices and tumor size can be varied slightly. During the investigation phase, we noticed that finding the location of the emerging and vanishing tumor is a hard and challenging task. But this is not true when we are looking for the biggest tumor inside the image. To detect the tumor area in each slice we follow four main steps: (1) read all modalities except the T1 image and compute the Z-Score normalized image, (2) binarize the obtained image with the thresholds 0.7, 0.7, and 0.9 for FLAIR, T2, and T1ce, respectively, (3) apply a morphological operator to remove some irrelevant areas, (4) multiply both binary images of FLAIR and T2 to create a new image and 5) combine the obtained areas from each image together. After detecting all binary objects using morphological operators, we need to add them to each other to create a binary tumor image. But there is still another condition before adding the binarized T1ce to the obtained image from the binary dot product of the FLAIR and T2 images. We can only consider the effect of a binary object inside the T1ce images if it has an overlapping area bigger than 20 pixels with a binary object inside the image obtained from the binary dot product of FLAIR and T2. In the next step, we need to find the location of the big tumor inside the slices. To this end, we need to be sure that all detected objects are truly

tumor objects. To overcome this issue, we track each tumor object in sequential slices. It means if a tumor object is found in almost the same position with a small change in the size in the sequential slices, we can be sure that this object is a true tumor object. After finding the true tumor object in a slice, we search in the same area inside all other slices to find the biggest object. This procedure is explained in Fig. 6 in details. Finally, using morphological operators this object can be enlarged to cover all possible missing tumor areas (we call this area the biggest expected area). By finding this object and its location, we can search only in this area to find the tumor and segment it in all slices. So, we can create a binary mask for all slices in which the size of the expected areas differs slightly from the expected slice to slice difference.



## 6.1 Gantt Chart



# Bibliography

D. N. Louis, D. W. Ellison, D. J. Brat, K. Aldape, D. Capper, C. Hawkins, W. Paulus, A. Perry, G. Reifenberger, D. Figarella-Branger, et al., “impact-now: a practical summary of diagnostic points from round 1 updates,” *Brain Pathology*, vol. 29, no. 4, pp. 469–472, 2019.

D. N. Louis, P. Wesseling, W. Paulus, C. Giannini, T. T. Batchelor, J. G. Cairncross, D. Capper, D. Figarella-Branger, M. B. Lopes, W. Wick, et al., “cimpact-now update 1: not otherwise specified (nos) and not elsewhere classified (nec),” *Acta neuropathologica*, vol. 135, no. 3, pp. 481–484, 2018

D. N. Louis, C. Giannini, D. Capper, W. Paulus, D. Figarella-Branger, M. B. Lopes, T. T. Batchelor, J. G. Cairncross, M. van den Bent, W. Wick, et al., “cimpact-now update 2: diagnostic clarifications for diffuse midline glioma, h3 k27m-mutant and diffuse astrocytoma/anaplastic astrocytoma, idh-mutant,” *Acta neuropathologica*, vol. 135, no. 4, pp. 639–642, 2018

D. J. Brat, K. Aldape, H. Colman, E. C. Holland, D. N. Louis, R. B. Jenkins, B. Kleinschmidt-DeMasters, A. Perry, G. Reifenberger, R. Stupp, et al., “cimpactnow update 3: recommended diagnostic criteria for “diffuse astrocytic glioma, idh-wildtype, with molecular features of glioblastoma, who grade iv”,” *Acta neuropathologica*, vol. 136, no. 5, pp. 805–810, 2018.

D. W. Ellison, C. Hawkins, D. T. Jones, A. Onar-Thomas, S. M. Pfister, G. Reifenberger, and D. N. Louis, “cimpact-now update 4: diffuse gliomas characterized by myb, mybl1, or fgfr1 alterations or braf v600e mutation,” *Acta neuropathologica*, vol. 137, no. 4, pp. 683–687, 2019

. D. J. Brat, K. Aldape, H. Colman, D. Figarella-Branger, G. N. Fuller, C. Giannini, E. C. Holland, R. B. Jenkins, B. Kleinschmidt-DeMasters, T. Komori, et al., “cimpact-now update 5: recommended grading criteria and terminologies for idhmutant astrocytomas,” *Acta neuropathologica*, vol. 139, no. 3, pp. 603–608, 2020.

D. N. Louis, P. Wesseling, K. Aldape, D. J. Brat, D. Capper, I. A. Cree, C. Eberhart, D. Figarella-Branger, M. Fouladi, G. N. Fuller, et al., “cimpact-now update 6: new entity and diagnostic principle recommendations of the cimpact-utrecht meeting on future cns tumor classification and grading,” 2020.



S. Bakas, G. Shukla, H. Akbari, G. Erus, A. Sotiras, S. Rathore, C. Sako, S. Min Ha, M. Rozycki, R. T. Shinohara, M. Bilello, and C. Davatzikos, "Overall survival prediction in glioblastoma patients using structural magnetic resonance imaging (mri): advanced radiomic features may compensate for lack of advanced mri modalities," *Journal of medical imaging* (Bellingham, Wash.), vol. 7, p. 031505, May 2020.

D. N. Louis, A. Perry, G. Reifenberger, A. Von Deimling, D. Figarella-Branger, W. K. Cavenee, H. Ohgaki, O. D. Wiestler, P. Kleihues, and D. W. Ellison, "The 2016 world health organization classification of tumors of the central nervous system: a summary," *Acta neuropathologica*, vol. 131, no. 6, pp. 803–820, 2016.

L. Rivera, C. E. Pelloso, M. R. Gilbert, H. Colman, C. De La Cruz, E. P. Sulman, B. N. Bekele, and K. D. Aldape, "MGMT promoter methylation is predictive of response to radiotherapy and prognostic in the absence of adjuvant alkylating chemotherapy for glioblastoma," *Neuro-Oncology*, vol. 12, pp. 116–121, 12 2009.

H. Menze, A. Jakab, S. Bauer, J. Kalpathy-Cramer, K. Farahani, J. Kirby, Y. Burren, N. Porz, J. Slotboom, R. Wiest, et al., "The multimodal brain tumor image segmentation benchmark (brats)," *IEEE transactions on medical imaging*, vol. 34, no. 10, pp. 1993–2024, 2014

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