

Brain Tumor Segmentation Using Support Vector Machine (SVM)

submitted by

Priti Mondal

Class Roll No: 002210503024

Exam Roll: MCA244023

Master of Computer Application

under the supervision of

Prof. (Dr.) Jamuna Kanta Sing

in the

Department of Computer Science and Engineering

Faculty of Engineering and Technology

Jadavpur University

2024

Faculty of Engineering and Technology
Jadavpur University

CERTIFICATE OF RECOMMENDATION

To Whom It May Concern

I hereby recommend that the project report entitled “Brain Tumor Segmentation Using Support Vector Machine (SVM)” has been carried out by Priti Mondal (Reg. No.: 163616 of 2022-23, Roll No.: 002210503024, Exam Roll: MCA244023), under my guidance and supervision and be accepted in partial fulfilment of the requirement for the degree of Master of COMPUTER APPLICATION in DEPARTMENT of COMPUTER SCIENCE and ENGINEERING, JADAVPUR UNIVERSITY during the academic year 2022-2024.

Prof. (Dr.) Jamuna Kanta Sing
Project Supervisor
Dept. of Computer Science and Engineering
Jadavpur University

Prof. (Dr.) Nandini Mukhopadhyay
Head of the Department
Dept. of Computer Science & Engineering
Jadavpur University

Prof. Dipak Laha
Dean, Faculty Council
of Engineering & Technology
Jadavpur University, Kolkata-032

Faculty of Engineering and Technology
Jadavpur University

CERTIFICATE OF APPROVAL

This is to certify that the project report entitled “Brain Tumor Segmentation Using Support Vector Machine (SVM)” is a bonafide record of work carried out by PRITI MONDAL, in fulfillment of the requirements for the award of the degree of Master of Computer Application in the Department of Computer Science and Engineering, Jadavpur University. It is understood that by this approval the undersigned do not necessarily endorse or approve any statement made, opinion expressed or conclusion drawn therein but approve the project report only for the purpose for which it has been submitted.

Signature of Examiner 1

Date :

Signature of Examiner 2

Date :

Faculty of Engineering and Technology
Jadavpur University

DECLARATION OF COMPLIANCE WITH ACADEMIC ETHICS

I hereby declare that this project report entitled “Brain Tumor Segmentation Using Support Vector Machine (SVM)” is an outcome of my genuine and independent work, as part of my Master of Computer Application program.

All information in this document has been obtained and presented in accordance with academic rules and ethical conduct.

I also declare that, as required by these rules and conduct, all materials and results that are not original to this work have been fully cited and referenced.

Priti Mondal

Registration No.: 163616 of 2022-23

Examination Roll No.: MCA244023

Thesis Title :- Brain Tumor Segmentation Using Support Vector Machine (SVM)

Signature with Date

ACKNOWLEDGEMENT

With my most sincere and gratitude, I would like to thank Prof. (Dr.) Jamuna Kanta Sing, Department of Computer Science & Engineering, my supervisor, for his overwhelming support throughout the duration of the project. His motivation always gave me the required inputs and momentum to continue with my work, without which the project work would not have taken its current shape. His valuable suggestions and numerous discussions have always inspired new ways of thinking. I feel deeply honored that I got this opportunity to work under him.

I would like to express my sincere thanks to all my teachers for providing sound knowledge base and cooperation.

I would like to thank all the faculty members of the Department of Computer Science & Engineering of Jadavpur University for their continuous support.

Last, but not the least, I would like to thank my batch mates for staying by my side when I needed them.

PRITI MONDAL

Class Roll No.:002210503024

Examination Roll No.: MCA244023

Department of Computer Science & Engineering
Jadavpur University

Table of Contents

Abstract.....	06
CHAPTER 1 Introduction.....	07
1.1) Brain Tumor.....	08
1.2) MRI Image.....	08
1.3) Treatments.....	08
1.4) Different Technique For Brain Tumor Segmentation.....	08
1.5) Literature Survey.....	10
CHAPTER2 Proposed Method.....	11
2.1) Support Vector Machines (SVM)	11
2.1.1) Types of SVM.....	12
2.1.2) Common kernel functions	14
2.2) Flow Diagram of Proposed Model.....	15
2.3) Algorithm of The Proposed Method	16
CHAPTER3 Experimental Results &Performance Analysis.....	18
3.1) Overview of dataset.....	18
3.1) Performance Evaluation Metrics.....	18
3.2) Experimental Results.....	20
3.3)Segmented Results.....	26
CHAPTER4 Conclusion.....	31
4.1) Conclusion of The Present Work.....	31
4.2)References.....	32

Abstract

Brain tumor segmentation is one of the most difficult procedures in the medical field, it involves extracting tumor patches from images. One non-invasive method that has emerged as a leading non-ionizing radiation brain tumor diagnosis tool is magnetic resonance imaging (MRI).

Gliomas are the most frequent and aggressive type of brain tumor, with a very short survival time in their maximum degree. Manual segmentation takes a lot of time in clinical practice, and the operator's expertise has a big impact on how well they execute.

This project proposes fully automatic segmentation of brain tumor using Support Vector Machine(SVM). Further, it uses brain image from BRATS 2020 database .BRATS 2020 focuses on the segmentation of fundamentally heterogeneous (in appearance, form, and histology) brain tumors, specifically gliomas, using multi-institutional pre-operative MRI data.

Hence, this project segments brain tumor into two classes like tumor region and non-tumor region. Brain tumor segmentation needs to separate healthy tissues from tumor region to distinguish between normal and abnormal pixels. This is an essential step in diagnosis and treatment planning, both of which need to take place quickly in case of a malignancy in order to maximize the likelihood of successful treatment.

CHAPTER 1 | Introduction

Brain tumor is the abnormal growth of cells within the brain .A brain tumor is a cancerous or non-cancerous mass or growth of abnormal cells in the brain. It can be termed as the cells which don't die but grows in size and accumulates as a mass. Generally, tumor is classified into primary and secondary tumor. primary tumor starts within the brain and secondary tumor will spread to the other parts of the body.

Image testing of a brain tumor is done using X-rays, strong magnets, or radioactive substances to create pictures of the brain . The brain tumors are generally diagnosed using different types of scans. [7]Magnetic Resonance Imaging(MRI), Computer Tomography(CT), Angiogram, Myelogram and Positron Emission Tomography are among the types of scans which are used most often to detect brain diseases.

These pictures are so efficient that they can provide with primary information about the presence and location of a tumor. There are already several *computer-aided diagnosis (CAD)* systems which are used in disease monitoring, operation guiding tasks, etc. In fact, CAD seeks to assist doctors by providing computer outputs, which are considered as a second opinion during abnormalities detection, disease progress survey, etc.

Magnetic Resonance Imaging (MRI) provides detailed images of brain studies. MRI data are used in brain pathology studies, where regions of interest (ROI's) are explored in detail .This project uses MRI brain images, because of its high resolution and good quality of image. After capturing MRI brain image, it is necessary to separate the tumor region from the MRI brain image.

The manual segmentation of brain tumors is labor-intensive, and the segmentation results obtained depend on the operator's experience and subjective decision-making. In order to accomplish this, we will suggest a supervised technique for segmenting brain images that is based on the Support Vector Machines (SVM).

1.1 Brain Tumor

Brain tumors are conditions where abnormal cells grow in the brain's tissues or where a tumor begins in another area of the body and subsequently spreads to the brain. Human brains are vital because they regulate numerous processes in the body. As a result, severe symptoms that could have an impact on the patient's body and life would appear when a brain tumor forms. According to Longo, D.L. (2012), the symptoms include headaches, seizures, visual issues, vomiting, and mental abnormalities.

Malignant and benign brain tumors can be broadly classified into two categories. Malignant tumors can be classified as primary tumors, which originate inside the brain, or secondary tumors, which have spread outside the brain and are referred to as brain metastases. The incidence of brain tumors is about 1.9 to 5.4 person (100,000 person per year), accounting for 1% to 3% of various tumors in the body. Since most people lack understanding of brain tumors, many patients have not received early diagnosis and treatment in time and have lost their lives.

1.2 MRI Image

MRI (Magnetic Resonance Imaging) scans can be a useful diagnostic tool for brain malignancies. The MRI image's working premise is that radio frequency pulses in a high magnetic field disrupt a particular area of human tissue to emit varying degrees of electrical signal intensity. After computer recombination and conversion, it can form an imaging technology that can display the influence of human internal tissues. MRI images display the anatomical structures of the human body with high resolution and no bone artifacts. They can diagnose brain tumors based on electrical signal strength, brain edema, ventricle compression, tumor tissue displacement, and secondary changes. Localization and qualitative diagnosis can be made for most brain tumors, making MRI technology a crucial tool for neurological disease diagnosis.

1.3 Treatments

Surgery is the initial treatment for brain tumors, providing a pathological diagnosis, removing tumor cells, and alleviating symptoms. Minimally invasive approaches are increasingly used due to their safety and completeness. High-grade tumors often require further radiosurgery, including local and stereotactic radiosurgery. Chemotherapy has also gained importance in treating brain tumors, but only about 20% of patients can receive it due to drug toxicity and uncertain results.

1.4 Different Technique For Brain Tumor Segmentation

- **Manual Segmentation**

Manual segmentation involves radiologists using specialized software tools to manually outline tumor boundaries on brain scans. This technique relies heavily on the expertise and experience of the radiologists, ensuring high accuracy. However, it is extremely time-consuming, subject to variability between different observers, and impractical for large-scale studies or routine clinical use due to its labor-intensive nature.

- **Thresholding Techniques**

Based on pixel intensity values, thresholding algorithms divide an image into segments. Adaptive thresholding actively modifies the threshold in response to local intensity variations, whereas simple thresholding uses a single cutoff intensity value to distinguish tumor from nontumor tissue. These techniques are computationally efficient and simple to apply, but they have trouble processing images with complicated tumor shapes and different intensity distributions.

- **Region-based Techniques**

Pixels are grouped into regions by region-based approaches according to predetermined criteria. By iteratively increasing the region, region expansion begins at a seed point and incorporates nearby pixels with comparable intensities. The image is divided into smaller parts via region splitting and merging, and the homogeneity criteria are used to combine the regions. Although these techniques can be sensitive to noise and the selection of beginning seed points, which could result in over- or under-segmentation, they are helpful for segmenting continuous and homogenous regions.

- **Edge-based Techniques**

Edge-based techniques focus on detecting the boundaries of tumors using edge detection algorithms. While active contours (snakes) iteratively modify a contour to fit the tumor borders by minimizing an energy function, the Canny edge detection approach finds edges by identifying locations with rapid intensity changes. These methods work well for tumors with distinct edges, but they struggle with weak or fuzzy edges and may need precise parameter adjustment.

- **Clustering Techniques**

Pixels are grouped into clusters according to their brightness using clustering techniques, which segment the image. By reducing the variance within each cluster, K-means clustering divides pixels into groups. Pixels can be a part of several clusters with different levels of membership thanks to fuzzy C-means, which offer resilience to changes in intensity. These techniques can manage some intensity inhomogeneity, but in order to improve the segmentation results, preprocessing and post-processing steps are frequently needed.

- **Deep Learning-Based Techniques**

Brain tumor segmentation has been transformed by deep learning-based methods, especially convolutional neural networks (CNNs). From the data, CNNs automatically extract hierarchical characteristics and carry out end-to-end segmentation. It is common practice to employ advanced architectures such as SegNet, U-Net, and Fully Convolutional Networks (FCNs). By utilizing a discriminator to discern between created and genuine segmentations and a generator to produce segmentations, Generative Adversarial Networks (GANs) improve segmentation even further. Large annotated datasets and substantial computer resources are needed for these approaches, which achieve excellent accuracy and can handle complicated and variable tumor formations.

1.5 Literature Survey

[1] This paper proposes a hybrid technique using support vector machine (SVM) and fuzzy c-means for brain tumor classification. The algorithm denoises the image, uses morphological operations for skull stripping, and uses fuzzy c-means clustering for segmentation. The feature extraction is then performed, resulting in more accurate and effective classification of brain MRI images.

Barjaktarovic et al. [2] proposed a novel CNN architecture for brain tumour classification based on modifying a pre-trained network's performance on T1-weighted contrast-enhanced MRI images. The model comprises two 10-fold cross-validation strategies that use augmented images. It is 96.56% accurate.

[3] A sophisticated method for identifying and categorizing these tumors is necessary to support the use of MRI (magnetic resonance imaging) images for the non-invasive diagnosis of brain tumors. Using MRI scans, a novel hybrid deep learning CNN-based structure can differentiate between three different forms of human brain tumors. In the first method, a pre-trained CNN (SqueezeNet) is used for feature extraction while an SVM for pattern classification is used for unsupervised classification. In the second method, a precisely calibrated SqueezeNet is used with the supervised soft-max classifier. The trial findings showed that the SqueezeNet model, which has been fine-tuned, achieved an accuracy of 96.5%. Nevertheless, recognition accuracy rose to 98.7% when SqueezeNet was employed as a feature extractor and an SVM classifier was deployed.

[4] Medical image processing plays a key role in medical practices that detect brain tumor. This paper suggests utilizing magnetic resonance imaging (MR) data to precisely detect tumor stages using the support vector machine (SVM) technique. Any brain tumor detection method's precision depends on its capacity to distinguish between different tissue types in an efficient and discrete manner. The most crucial step in characterizing, defining, and visualizing regions of interest in magnetic resonance imaging is the employment of segmentation-based detection techniques. This work assesses the capacity of lifting-based wavelet transformation (LWT) to extract distinct tissue classes from magnetic resonance images and support vector machine (SVM) to detect the type of tumor. The suggested method, known as SWFCM and based on segmentation using SVM, LWT, and fuzzy clustering method

[5] Wang et al. as mentioned in this paper presented an automatic approach for Glioblastoma brain tumor segmentation based on deep Residual Learning Network (ResNet) to get over the gradient problem of deep Convolutional Neural Networks (CNNs). This study presents an automatic approach for Glioblastoma brain tumor segmentation using deep Residual Learning Network (ResNet) to overcome the gradient problem of deep Convolutional Neural Networks. The ResNet algorithm improves accuracy and performance, allowing for a rapid training process. The proposed fusion method (ResNet-SVM) has increased classification results of accuracy (AC=89.36%), specificity (SP=92.52%), and precision (PR=90.12%) using 260 MRI data for training and 112 data for testing and validation of Glioblastoma tumor cases.

CHAPTER 2 | Proposed Method

2.1 Support Vector Machines (SVM)

A supervised machine learning approach called Support Vector Machine (SVM) is used for regression as well as classification. Classification problems are the most appropriate use for regression problems. The SVM algorithm's primary goal is to locate the best hyperplane in an N-dimensional space that may be used to divide data points into various feature space classes. The hyperplane attempts to maintain the largest possible buffer between the nearest points of various classes. The number of features determines the hyperplane's dimension. The hyperplane is essentially a line if there are just two input features. The hyperplane transforms into a 2-D plane if there are three input features. It gets harder to imagine when the number of features exceeds three.

Let's consider two independent variables x_1 , x_2 , and one dependent variable which is either a blue circle or a yellow circle. The hyperplane that depicts the greatest distance or margin between the two classes is an appropriate choice for the best one. For each side, we select the hyperplane whose distance to the closest data point is maximum. It's referred to as the maximum-margin hyperplane or Hard margin.

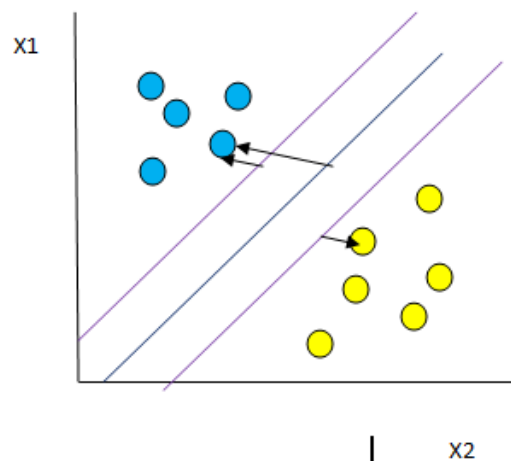


Fig:2.1 Multiple hyperplanes separate the data from two classes

2.1.1 Types of SVM

- **Linear SVM** : A linear decision boundary is used by linear SVMs to divide the data points into various classes. Linear SVMs are ideal when the data can be precisely divided along a linear path. This indicates that the data points may be completely divided into their corresponding classes by a single straight line in two dimensions or a hyperplane in three dimensions. The decision boundary is a hyperplane that optimizes the margin between the classes.

Under the assumption that a set of training datasets is acquired, its structure can be described as

$$(\vec{x}_1, \vec{y}_1), (\vec{x}_2, \vec{y}_2), \dots (\vec{x}_n, \vec{y}_n) \quad (2.1)$$

where x_i is the points in plane and y_i is the labels of point. And y_i equals -1 or 1, which represents negative class and positive class. If there is a hyperplane as the decision boundary in the feature space where the input data is located, the learning target is separated into positive and negative classes, and the point-to-plane distance of any sample is greater than or equal to 1.

$$\vec{\omega} \cdot x - b = 0 \quad (2.2)$$

Where the normal vector and hyperplane intercept are represented by the parameters ω , b , respectively, the classification problem is referred to as linear separability. The two data set classes can then be divided by choosing two parallel hyperplanes that are as far apart as feasible. The margin is the region enclosed by these two hyperplanes. The definition of these two hyperplanes is

$$\vec{\omega} \cdot x - b = 1 \quad (2.3)$$

$$\vec{\omega} \cdot x - b = -1 \quad (2.4)$$

For x_i in dataset, it would satisfy

$$\vec{\omega} \cdot x - b \geq 1, \text{ if } y_i = 1, \quad (2.5)$$

Or

$$\vec{\omega} \cdot x - b \leq -1, \text{ if } y_i = -1 \quad (2.6)$$

This type of margin can be called hard margin.

If SVM is applied to the case where the dataset is not linearly separable, the hinge loss function needs to be used.

$$\max(0, 1 - y_i(\vec{\omega} \cdot x - b)) \quad (2.7)$$

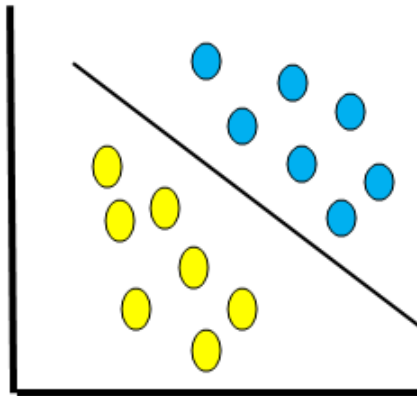


Fig:2.2 - Linear SVM

- **Non-Linear SVM:** In order to convert non-linear separable problems, from the original feature space to a higher-dimensional space and make them linearly separable, Bernhard Boser suggested using a technique known as the kernel trick. . At this time, the hyperplane as the decision boundary is expressed as follows

$$\omega^T \Phi(X) + b = 0 \quad (2.8)$$

where ϕ is the mapping function. Since the mapping function has a complicated form and it is difficult to calculate its inner product, the inner product of the mapping function can be defined as a kernel function.

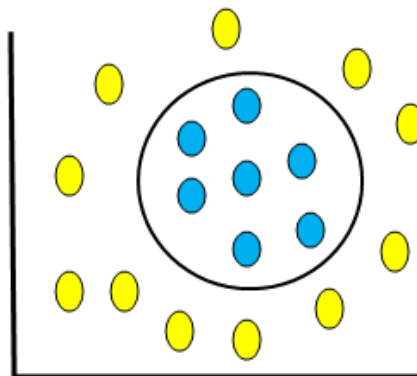


Fig:2.3 - Non-Linear SVM

2.1.2 Common kernel functions

The SVM kernel is a function that changes non-separable problems into separable problems by taking a low-dimensional input space and transforming it into a higher-dimensional space. It is most helpful in cases with non-linear separation. To put it simply, the kernel performs a number of incredibly intricate data transformations before determining how to divide the data according to the specified labels or outputs.

- Polynomial kernel :

$$k(\vec{x}_i, \vec{x}_j) = (\vec{x}_i \cdot \vec{x}_j)^d \quad (2.9)$$

- RBF kernel:

$$k(\vec{x}_i, \vec{x}_j) = \exp\left(-\frac{\|\vec{x}_i - \vec{x}_j\|^2}{2\sigma^2}\right) \quad (2.10)$$

- Sigmoid kernel :

$$k(\vec{x}_i, \vec{x}_j) = \tanh(\vec{x}_i^T \vec{x}_j + b)^d \quad (2.11)$$

- Linear kernel:

$$k(x, y) = x \cdot y \quad (2.12)$$

2.2 FLOW DIAGRAM OF PROPOSED MODEL

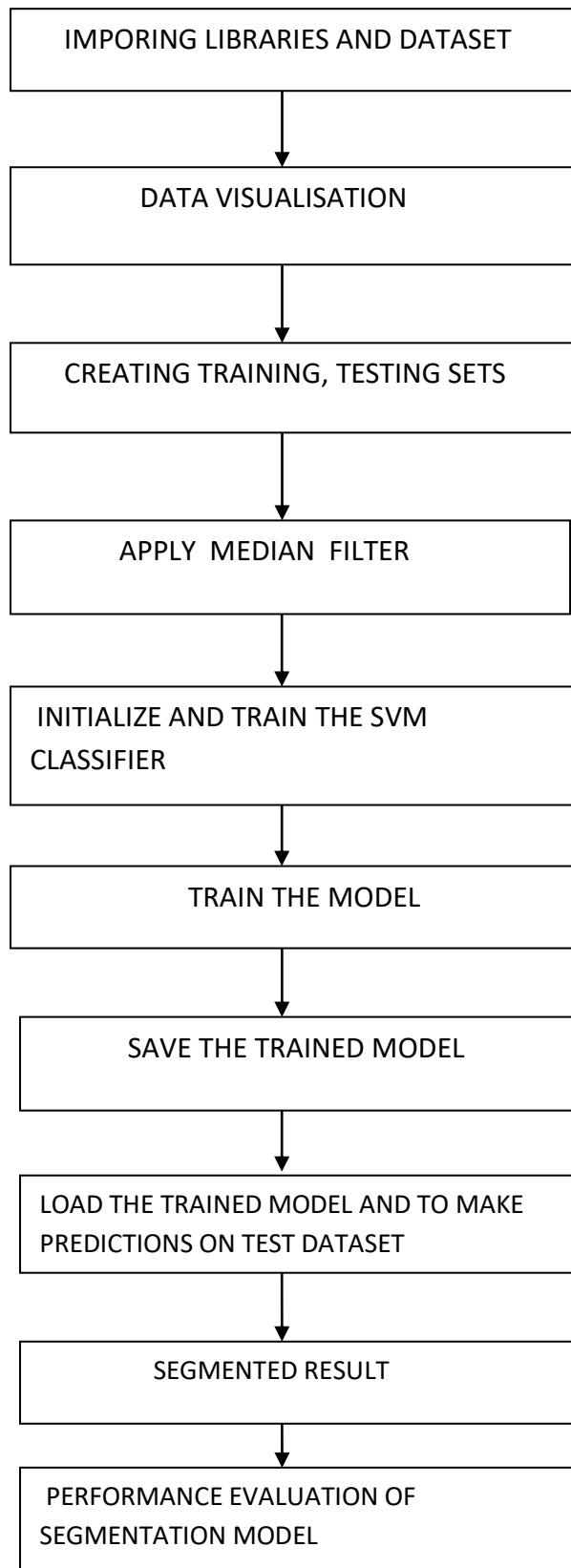


Fig:2.4- Flow Diagram of Proposed Work

2.3 Algorithm of The Proposed Method

STEP1: Data Preparation

- From BRATS2020 dataset there are four types of modalities of brain image, we only taking flair and its corresponding mask images which available in seg.nii format.
- Masks which highlighting tumor regions having the pixel value 1 or 2 or 3, and non-tumor regions having pixel value 0.
- Then split the dataset into training and testing sets.

STEP2: Pre-Processing

- Load the flair image and its corresponding mask image and take image data from both.
- Convert the segmentation data into binary labels (tumor/non-tumor): In mask image data we consider if pixel value is greater than zero then its label will be +1 otherwise its label will be -1 and store in one dimensional array.

```
if pixel_value > 0
    then label= 1
else
    label=-1
```

- Get flair image and traverse every pixel and make pixel wise two dimensional array and apply Median filter on them to reduce noise from it. The median filter with a 3×3 kernel is used to filter the impulse noise. Hence, noise reduction helps to improve the data processing and provides the better segmentation.

STEP3: Initialize And Train The SVM Classifier

- SVM is a supervised learning algorithm used for classification tasks. Taking an object of SVM classifier and apply linear kernel meaning the algorithm will try to find the linear decision boundary between classes and set regularization parameter $C=1.0$ which controls the trade-off between maximizing the margin and minimizing the classification errors.
- Then the fit() method used to train the SVM model with the provided training data and corresponding labels, means each pixel of training image has its corresponding label either +1 or -1.

STEP4: Save The Trained SVM Model

- The trained SVM model will be saved to a file which can be loaded later to make predictions on new data without needing to retrain the model.

STEP5: Testing SVM Model For Tumor Prediction

- Load the test sets and the trained model ,feed the test images into the trained model and obtain predicted probabilities for tumor class(+1) or non-tumor class(-1).

STEP6: Segmented Result

- Take the predicted probabilities and plot them to show the segmented tumor region .

STEP7: Performance Evaluation Of Segmentation Model

- Compare the predicted segmentation masks with ground truth masks to compute metrics such as accuracy, precision ,recall and F1-score to assess the model's performance.

CHAPTER 3 | Experimental Result & Performance Analysis

3.1 Overview of Dataset

This recommended method is tested and implemented on the BRATS 2020 Dataset, which had 369 training dataset and 125 validation dataset. MRI scans of patient's brains in following modalities:

1. native (T1) scan,
2. post-contrast T1-weighted (T1Gd),
3. T2-weighted (T2),
4. T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes

Pixel value of tumor area indicates (1 or 2 or 3), pixel is not on a tumor region (0). All BraTS multimodal scans are available as NIfTI files (.nii.gz) -> commonly used medical imaging format to store brain imagin data obtained using MRI and describe different MRI settings.

- T1: T1-weighted, native image, sagittal or axial 2D acquisitions, with 1–6 mm slice thickness.
- T1ce: T1-weighted, contrast-enhanced (Gadolinium) image, with 3D acquisition and 1 mm isotropic voxel size for most patients.
- T2: T2-weighted image, axial 2D acquisition, with 2–6 mm slice thickness.
- FLAIR: T2-weighted FLAIR image, axial, coronal, or sagittal 2D acquisitions, 2–6 mm slice thickness.

The provided data are already pre-processed, i.e., co-registered to the same anatomical template, interpolated to the same resolution (1 mm³) and skull-stripped. This project uses flair image from BRATS2020 dataset where dimension for each image 240 X 240 size.

3.2 Performance Evaluation Metrics

Performance analysis helps determine how well a model or system performs its intended task. By analyzing performance metrics, one can identify the strengths and weaknesses of the model. This process helps optimize the model for better results. Analyzing performance metrics can provide insights into the characteristics of the data. Accuracy, Precision, Recall, and F1-Score are evaluation metrics used to assess the performance of segmentation tasks. The performance of a model depends on true positive (TP), true negative (TN), false positive (FP), and false negative (FN) predictions.

- **True Positive (TP):** These are the cases where the model correctly predicted the positive class.
- **True Negative (TN):** These are the cases where the model correctly predicted the negative class.

- **False Positive (FP):** Also known as Type I error, these are the cases where the model incorrectly predicted the positive class when it was actually negative.
- **False Negative (FN):** Also known as Type II error, these are the cases where the model incorrectly predicted the negative class when it was actually positive.

1. **Accuracy:** Accuracy measures the proportion of correct predictions out of the total predictions made. It is calculated as the ratio of true positives (TP) and true negatives (TN) to the total number of samples. It's calculated using the formula:

$$\text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}} \quad (3.1)$$

2. **Precision:** Precision measures the proportion of true positive predictions out of all positive predictions made. It is calculated as the ratio of TP to the sum of TP and false positives (FP). It's calculated using the formula:

$$\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} \quad (3.2)$$

3. **Recall (Sensitivity):** Recall measures the proportion of true positive predictions out of all actual positives. It is calculated as the ratio of TP to the sum of TP and false negatives (FN). It's calculated using the formula:

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}} \quad (3.3)$$

4. **F1-score:** F1-score is the harmonic mean of precision and recall. It provides a balance between precision and recall. It's calculated using the formula:

$$\text{F1_Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (3.4)$$

3.2 Experimental Results

- After comparing the predicted segmentation masks with ground truth masks, the performance metrics for various brain's slices(91-110) of Patient No.-1 are displayed in these tables. Each row represents a specific slice of the brain and includes values for accuracy, precision, recall, and F1-score and finally calculate Average accuracy, Average precision, Average recall, and Average F1-score.

Slice_No.	Accuracy	Precision	Recall	F1-score
91	0.962	1	0.423	0.594
92	0.967	1	0.461	0.631
93	0.973	1	0.529	0.692
94	0.976	1	0.556	0.714
95	0.979	0.998	0.589	0.741
96	0.98	1	0.58	0.735
97	0.983	0.999	0.585	0.738
98	0.991	0.995	0.708	0.827
99	0.993	0.995	0.769	0.868
100	0.994	0.997	0.78	0.875
101	0.995	0.995	0.808	0.892
102	0.995	0.994	0.797	0.884
103	0.995	0.99	0.766	0.864
104	0.997	0.975	0.851	0.909
105	0.998	0.967	0.905	0.935
106	0.998	0.954	0.919	0.937
107	0.999	0.955	0.958	0.956
108	0.999	0.929	0.972	0.95
109	0.999	0.869	0.955	0.91
110	0.998	0.54	1	0.701
AVERAGE	0.98855	0.9576	0.74555	0.81765

Table 3.1: Average accuracy, Average precision, Average recall, and Average F1-score of Patient No.-1

- After comparing the predicted segmentation masks with ground truth masks, the performance metrics for various brain's slices (91-110) of Patient No.-5 are displayed in these tables. Each row represents a specific slice of the brain and includes values for accuracy, precision, recall, and F1-score and finally calculate Average accuracy, Average precision, Average recall, and Average F1-score.

Slice_No.	Accuracy	Precision	Recall	F1-score
91	0.992	0.836	0.422	0.561
92	0.993	0.911	0.463	0.614
93	0.993	0.91	0.495	0.641
94	0.993	0.903	0.505	0.648
95	0.992	0.907	0.484	0.632
96	0.992	0.926	0.479	0.631
97	0.994	0.95	0.523	0.675
98	0.995	0.972	0.565	0.714
99	0.997	0.981	0.663	0.791
100	0.996	0.995	0.63	0.771
101	0.995	0.982	0.545	0.701
102	0.995	0.935	0.535	0.68
103	0.995	0.945	0.522	0.672
104	0.995	0.955	0.512	0.667
105	0.994	0.952	0.397	0.56
106	0.992	0.881	0.332	0.482
107	0.993	0.813	0.327	0.467
108	0.993	0.876	0.295	0.441
109	0.992	0.862	0.25	0.388
110	0.993	0.886	0.254	0.394
AVERAGE	0.9937	0.9189	0.4599	0.6065

Table 3.2: Average accuracy, Average precision, Average recall, and Average F1-score of Patient No.-05

- After comparing the predicted segmentation masks with ground truth masks, the performance metrics for various brain's slices(91-110) of Patient No.-22 are displayed in these tables. Each row represents a specific slice of the brain and includes values for accuracy, precision, recall, and F1-score and finally calculate Average accuracy, Average precision, Average recall, and Average F1-score.

Slice_No.	Accuracy	Precision	Recall	F1-score
91	0.982	0.997	0.363	0.533
92	0.982	1	0.346	0.514
93	0.981	1	0.34	0.508
94	0.98	1	0.339	0.506
95	0.98	1	0.35	0.519
96	0.98	1	0.354	0.523
97	0.98	1	0.365	0.535
98	0.981	1	0.386	0.557
99	0.981	1	0.41	0.581
100	0.982	1	0.452	0.623
101	0.983	1	0.485	0.654
102	0.984	1	0.516	0.68
103	0.985	1	0.531	0.694
104	0.986	1	0.562	0.72
105	0.987	1	0.596	0.747
106	0.988	1	0.62	0.765
107	0.989	1	0.653	0.79
108	0.991	1	0.701	0.824
109	0.992	1	0.728	0.843
110	0.993	1	0.772	0.871
AVERAGE	0.98435	0.99985	0.49345	0.64935

Type equation here. Table 3.3: Average accuracy, Average precision, Average recall, and Average F1-score of Patient No.-22

- After comparing the predicted segmentation masks with ground truth masks, the performance metrics for various brain's slices(91-110) of Patient No.-24 are displayed in these tables. Each row represents a specific slice of the brain and includes values for accuracy, precision, recall, and F1-score and finally calculate Average accuracy, Average precision, Average recall, and Average F1-score.

Slice_No.	Accuracy	Precision	Recall	F1-score
91	0.984	0.995	0.455	0.624
92	0.984	0.992	0.456	0.625
93	0.983	0.994	0.439	0.609
94	0.981	0.994	0.421	0.591
95	0.981	0.992	0.418	0.588
96	0.981	0.995	0.439	0.609
97	0.982	1	0.44	0.611
98	0.98	1	0.413	0.584
99	0.98	1	0.398	0.569
100	0.98	1	0.402	0.573
101	0.981	1	0.417	0.589
102	0.983	1	0.449	0.62
103	0.984	1	0.488	0.656
104	0.986	1	0.54	0.701
105	0.988	1	0.574	0.73
106	0.988	1	0.557	0.715
107	0.99	0.999	0.604	0.753
108	0.991	0.999	0.616	0.762
109	0.991	0.999	0.59	0.742
110	0.992	0.999	0.606	0.754
AVERAGE	0.9845	0.9979	0.4861	0.65025

Table 3.4: Average accuracy, Average precision, Average recall, and Average F1-score of Patient No.-24

- After comparing the predicted segmentation masks with ground truth masks, the performance metrics for various brain's slices(91-110) of Patient No.-45 are displayed in these tables. Each row represents a specific slice of the brain and includes values for accuracy, precision, recall, and F1-score and finally calculate Average accuracy, Average precision, Average recall, and Average F1-score.

Slice_No.	Accuracy	Precision	Recall	F1-score
91	0.988	0.949	0.708	0.811
92	0.99	0.957	0.749	0.84
93	0.99	0.961	0.756	0.846
94	0.99	0.955	0.752	0.842
95	0.991	0.963	0.764	0.852
96	0.991	0.977	0.767	0.86
97	0.992	0.99	0.783	0.874
98	0.993	0.991	0.81	0.891
99	0.994	0.992	0.822	0.899
100	0.995	0.988	0.839	0.908
101	0.994	0.989	0.832	0.904
102	0.995	0.987	0.848	0.912
103	0.995	0.979	0.851	0.911
104	0.995	0.975	0.84	0.902
105	0.994	0.966	0.818	0.886
106	0.995	0.968	0.814	0.885
107	0.996	0.973	0.85	0.907
108	0.996	0.968	0.863	0.912
109	0.997	0.964	0.867	0.913
110	0.997	0.96	0.887	0.922
AVERAGE	0.9934	0.9726	0.811	0.88385

Table 3.5: Average accuracy, Average precision, Average recall, and Average F1-score of Patient No.-45

- After comparing the predicted segmentation masks with ground truth masks, the performance metrics for various brain's slices(91-110) of Patient No.-49 are displayed in these tables. Each row represents a specific slice of the brain and includes values for accuracy, precision, recall, and F1-score and finally calculate Average accuracy, Average precision, Average recall, and Average F1-score.

Slice_No.	Accuracy	Precision	Recall	F1-score
91	0.99	0.989	0.674	0.801
92	0.99	0.99	0.675	0.802
93	0.99	0.995	0.69	0.815
94	0.991	0.991	0.718	0.833
95	0.992	1	0.728	0.843
96	0.993	0.994	0.769	0.867
97	0.994	0.997	0.794	0.884
98	0.994	0.994	0.774	0.871
99	0.993	0.997	0.761	0.863
100	0.994	0.996	0.781	0.875
101	0.994	0.987	0.787	0.876
102	0.995	0.989	0.786	0.876
103	0.995	0.988	0.791	0.879
104	0.995	0.994	0.793	0.882
105	0.995	0.987	0.789	0.877
106	0.994	0.962	0.785	0.865
107	0.994	0.947	0.796	0.865
108	0.996	0.953	0.832	0.889
109	0.995	0.936	0.821	0.875
110	0.996	0.944	0.846	0.892
AVERAGE	0.9935	0.9815	0.7695	0.8615

Table 3.6: Average accuracy, Average precision, Average recall, and Average F1-score of Patient No.-49

3.3 Segmented Results

- Segmented Result for Patient No. -01 of brain slice number 95 of all the bellow images :-

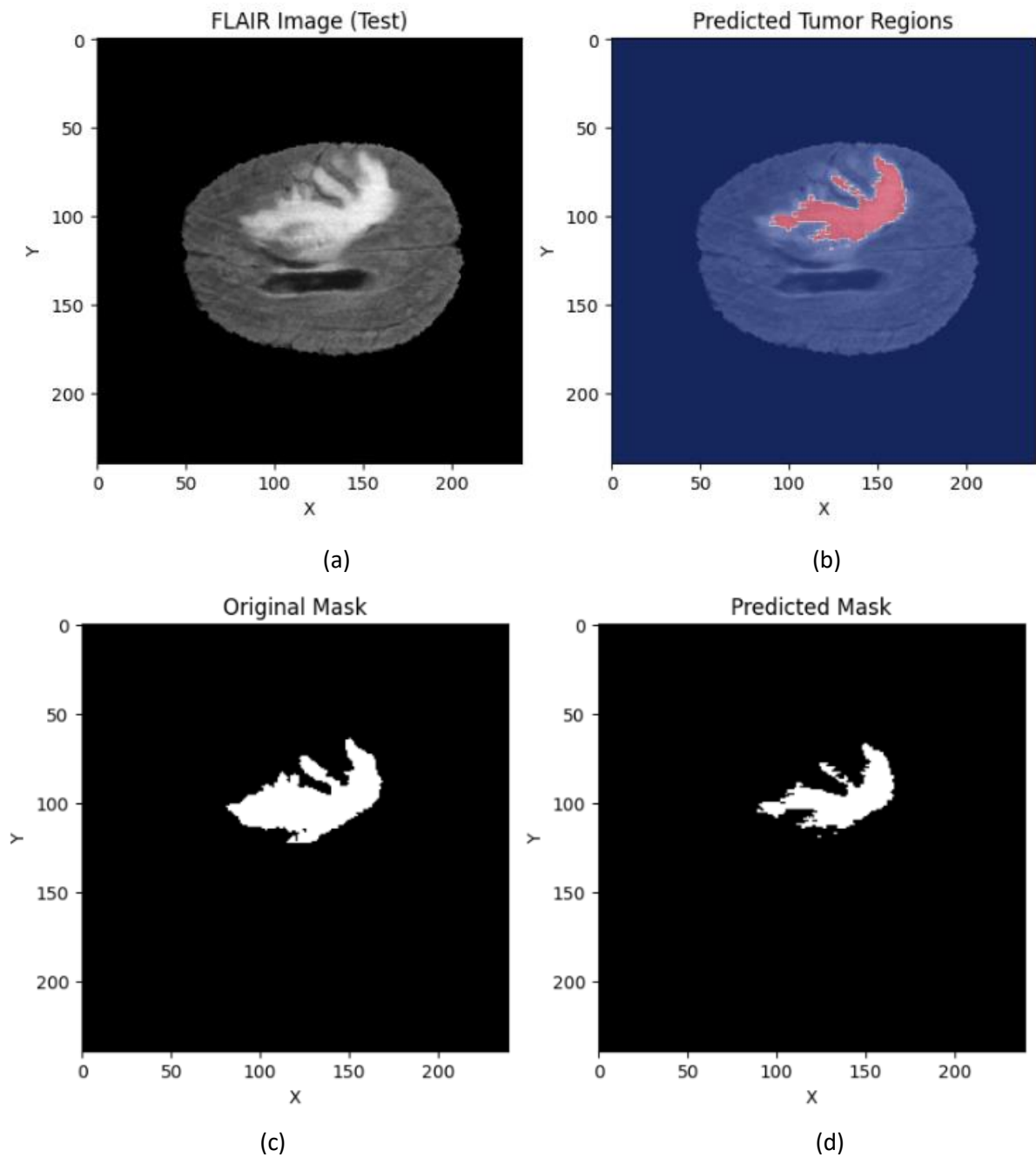


Fig.3.1: Segmented Results for Patient_Number-01 (a) Test flair image (b) Predicted tumor region on test flair image (c) Original Mask corresponding to the test flair image (d) Predicted Mask by our SVM model.

➤ Segmented Result for Patient No. -02 of brain slice number 95 of all the bellow images :-

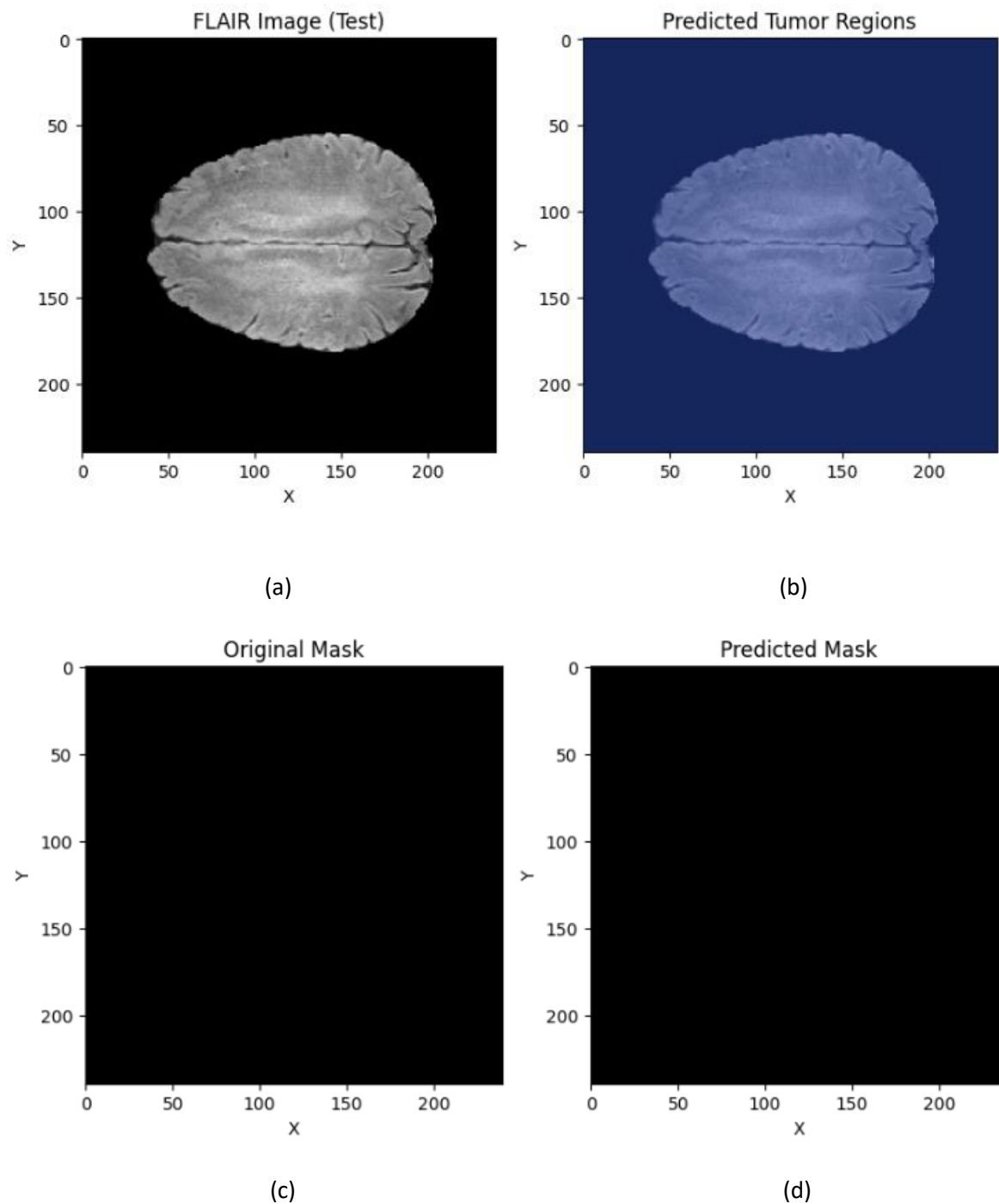


Fig.3.2:Segmented Results for Patient_Number-02 (a)Test flair image (b)Predicted tumor region on test flair image (c)Original Mask corresponding to the test flair image (d)Predicted Mask by our SVM model.

➤ Segmented Result for Patient No. -05 of brain slice number 95 of all the bellow images :-

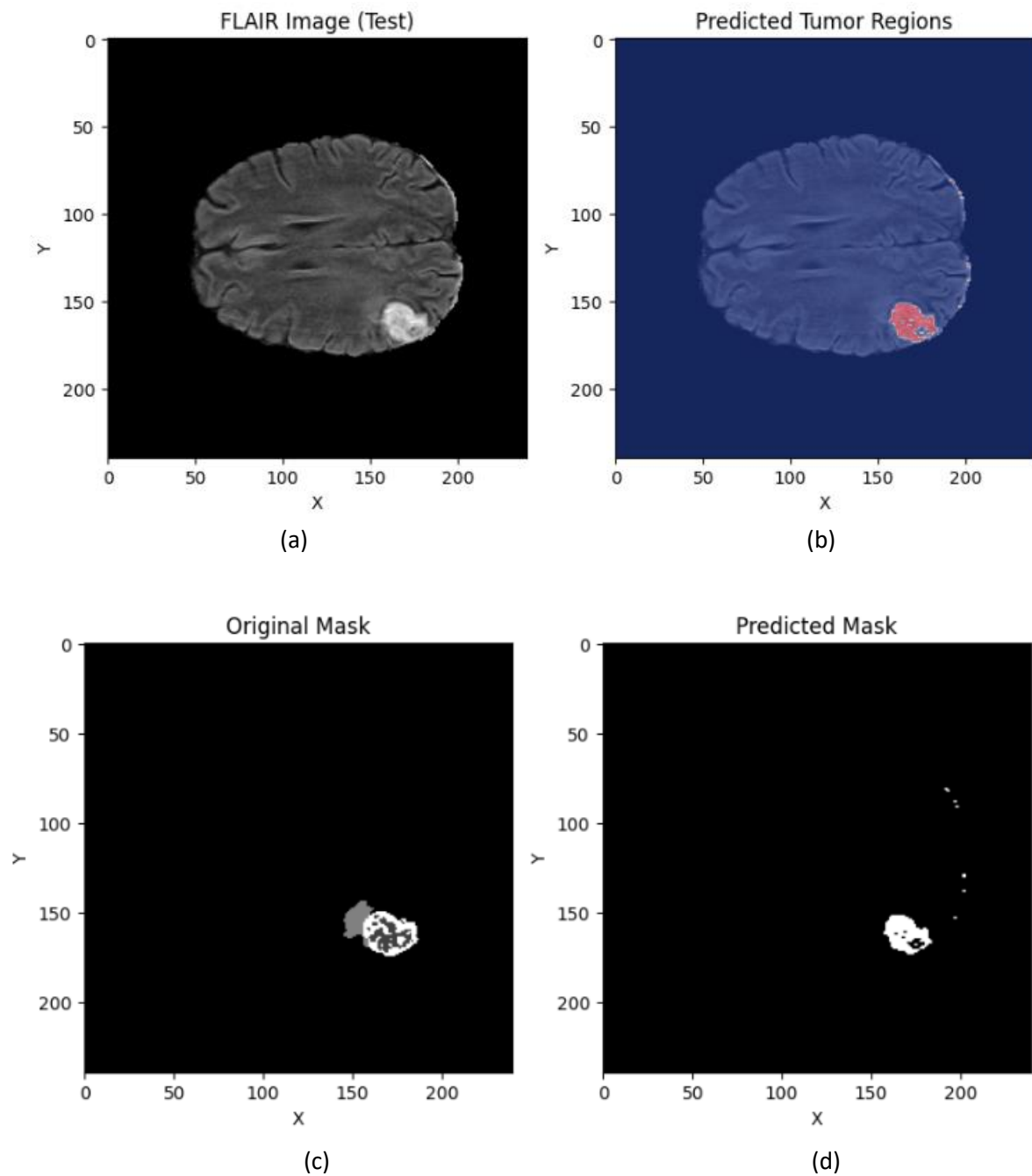


Fig.3.3: Segmented Results for Patient_Number-05 (a) Test flair image (b) Predicted tumor region on test flair image (c) Original Mask corresponding to the test flair image (d) Predicted Mask by our SVM model.

➤ Segmented Result for Patient No. -45 of brain slice number 95 of all the bellow images :-

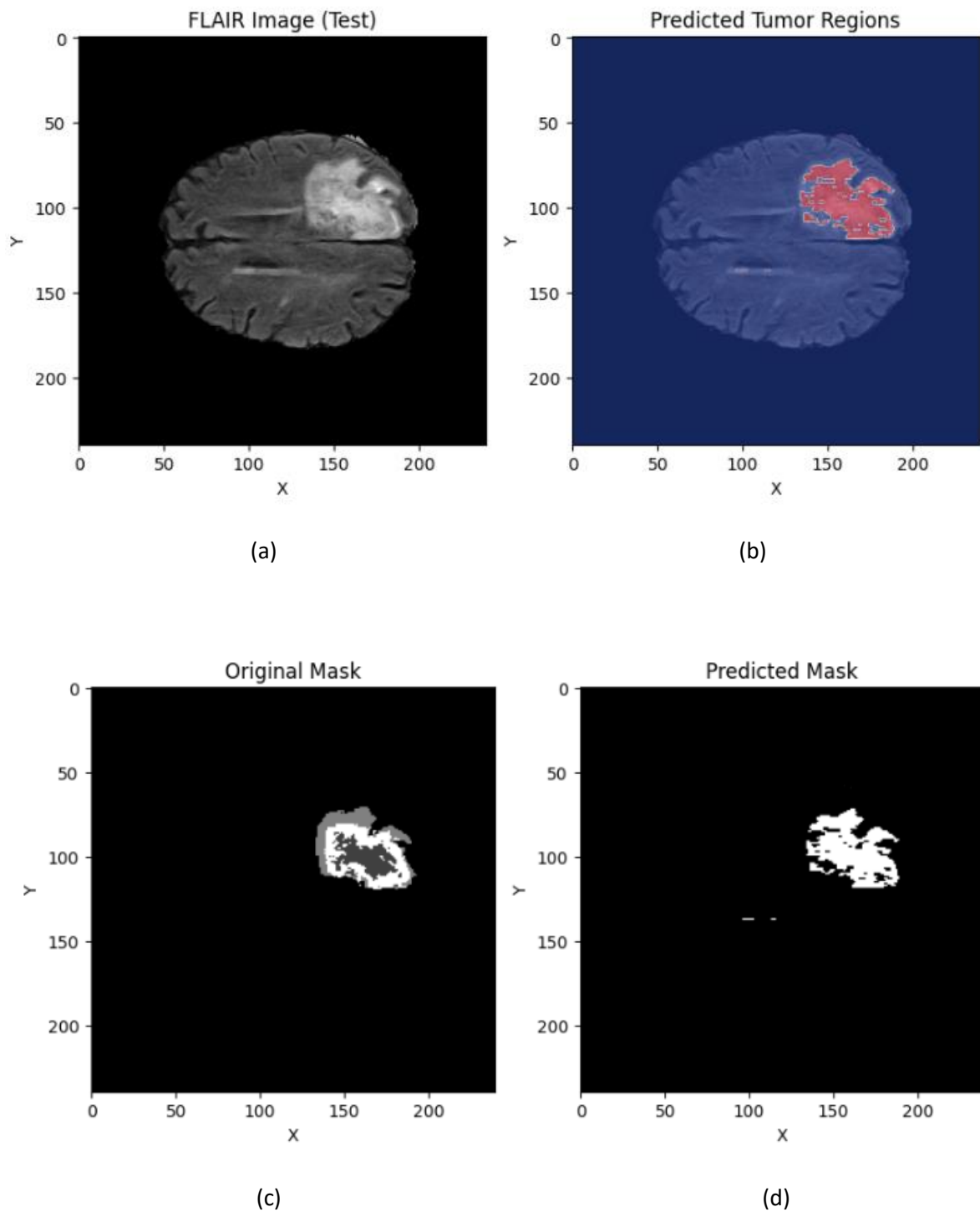


Fig.3.4: Segmented Results for Patient_Number-45 (a) Test flair image (b) Predicted tumor region on test flair image (c) Original Mask corresponding to the test flair image (d) Predicted Mask by our SVM model.

➤ Segmented Result for Patient No. -45 of brain slice number 95 of all the bellow images :-

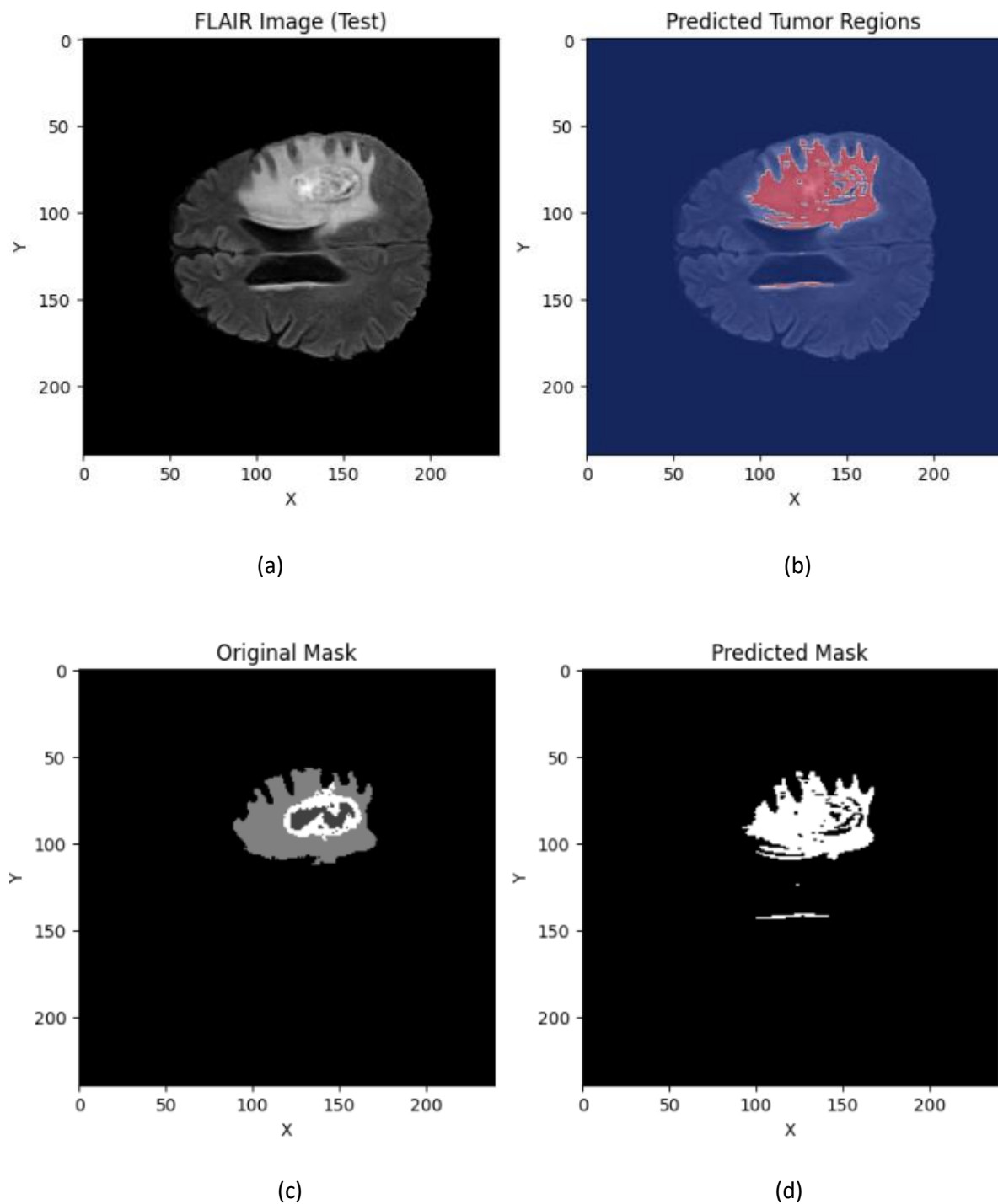


Fig.3.5: Segmented Results for Patient_Number-49 (a) Test flair image (b) Predicted tumor region on test flair image (c) Original Mask corresponding to the test flair image (d) Predicted Mask by our SVM model

CHAPTER 4 | Conclusion

4.1 Conclusion of The Present Work

In conclusion, we analyzed FLAIR images to identify and predict tumor regions using support vector machines (SVM) . The initial FLAIR images provided a clear visualization of brain tissues, facilitating the identification of potential abnormalities. The overlay of predicted tumor regions on the FLAIR images enabled a comprehensive view of how the algorithm detected and highlighted these regions, demonstrating the effectiveness of the prediction model. We assessed the precision and accuracy of our prediction model by contrasting the anticipated tumor regions with the initial segmentation masks.

Predicting tumor areas from FLAIR images with high accuracy has important implications for treatment planning and clinical diagnostics. With the use of this technology, radiologists and oncologists may be able to more accurately define tumor boundaries, which could result in improved decisions about the care of their patients.

In this project, Support Vector Machines (SVM) played a crucial role in segmenting brain tumor regions from FLAIR MRI images. SVM was used to find the optimal hyperplane that best separates tumor pixels from non-tumor pixels in the high-dimensional feature space. The application of a median filter and standardization before feeding the data into the SVM helped in minimizing noise and improving the robustness of the predictions .The trained SVM model was capable of generalizing well to unseen test slices, accurately predicting tumor regions across different sections of the brain, which is critical for consistent and reliable tumor segmentation.

4.2 References

- [1] Dipali B.Birnale¹, Prof .S. N et al. "A Hybrid Technique based on Fuzzy-C-Means and SVM for Detection of Brain Tumor in MRI Images." (2016).
- [2] Gholami, A.; Kwon, K.; Wu, B.; Tai, Z.; Yue, X.; Jin, P.; Zhao, S.; Keutzer, K. Squeezenext: Hardware-aware neural network design. In Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition Workshops, Salt Lake City, UT, USA, 18–22 June 2018; pp. 1638–1647.
- [3] Rasool, M.; Ismail, N.A.; Al-Dhaqm, A.; Yafooz, W.M.S.; Alsaeedi, A. A Novel Approach for Classifying Brain Tumours Combining a SqueezeNet Model with SVM and Fine-Tuning. *Electronics* **2023**, *12*, 149. <https://doi.org/10.3390/electronics12010149>.
- [4] Ray, A.K., Bahadure, N.B., & Routray, S. (2017). SVM-LWT ENABLED FUZZY CLUSTERING-BASED IMAGE ANALYSIS FOR BRAIN TUMOR DETECTION 1.
- [5] Sahli H, Ben Slama A, Zeraii A, Labidi S, Sayadi M. ResNet-SVM: Fusion based glioblastoma tumor segmentation and classification. *J Xray Sci Technol.* 2023;31(1):27-48. doi: 10.3233/XST-221240. PMID: 36278391.
- [6] L. Guo, L. Zhao, Y. Wu, Y. Li, G. Xu and Q. Yan, "Tumor Detection in MR Images Using One-Class Immune Feature Weighted SVMs," in *IEEE Transactions on Magnetics*, vol. 47, no. 10, pp. 3849-3852, Oct. 2011, doi: 10.1109/TMAG.2011.2158520. keywords: {Support vectormachines;Tumors;Sensitivity;Immunesystem;Feature_extraction;Training;Kernel;Feature weight;immune algorithm;support vector machine;tumor detection},
- [7] Kumar, A., Pandey, S.K., varshney, N. *et al.* Distinctive approach in brain tumor detection and feature extraction using biologically inspired DWT method and SVM. *Sci Rep* **13**, 22735 (2023). <https://doi.org/10.1038/s41598-023-50073-9>