ABSTRACT

Brain tumor detection is a critical task in medical imaging that plays a significant role in diagnosis and treatment planning. This study proposes a brain tumor detection framework utilizing two powerful machine learning algorithms, Support Vector Machines (SVM) and Logistic Regression. The combination of these algorithms aims to enhance the accuracy and robustness of tumor classification in Magnetic Resonance Imaging (MRI) scans.

The proposed framework involves several stages. First, pre-processing techniques are applied to enhance the quality of the MRI images and remove noise. Then, relevant features are extracted from the pre-processed images to capture the discriminative characteristics of tumor and non-tumor regions. These features are used to train SVM and Logistic Regression classifiers independently. The classifiers are evaluated using a dataset of MRI scans, and performance metrics such as accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AUC-ROC) are calculated.

Preliminary results show promising performance of the combined SVM and Logistic Regression approach, indicating improved accuracy in brain tumor detection. The fusion of SVM and Logistic Regression leverages the strengths of both algorithms, such as SVM's ability to handle complex relationships and Logistic Regression's probabilistic interpretation. The proposed framework has the potential to contribute to more accurate and reliable brain tumor detection, assisting medical professionals in making informed decisions and improving patient outcomes. Further research and optimization of this combined approach can lead to enhanced diagnostic capabilities and advancements in the field of neurology.

TABLE OF CONTENTS

Table of Contents

LIST OF FIGURES

LIST OF TABLES

CHAPTER – 1

1.1 INTRODUCTION

It was challenging to recognize a brain tumor from medical pictures. Because it organizes all the body's functions, the brain is one of the most vital parts of the human body. The human brain is susceptible to numerous illnesses, including infections, strokes, and tumors. A brain tumor is a growth or mass of aberrant cells, either malignant or not, in the brain. It might be referred to as a mass of growing and accumulating cells that do not perish.

X-rays, powerful magnets, or radioactive materials are used in brain tumor imaging to produce images of the brain. Various scanning techniques are typically used to diagnose brain tumors. The most often utilized scans to identify brain disease include magnetic resonance imaging, computed tomography, angiography, myelogram, and positron emission tomography.

Children most commonly get brain tumors. A primary brain tumor is detected in about 3410 children and adolescents under the age of 20 per year. Brain tumors that are either malignant or benign and come brain tissue. Magnetic resonance imaging (MRI) can be used to discover and diagnose brain tumors since it can reveal anatomical details and potentially aberrant tissues that can be used to plan treatments and keep track of patients. Brain tumor segmentation can also be helpful in illustrating the neurotic brain in general and, at the very least, in the emergence of the obsessive-compulsive brain.

Improvements in database design, computing speed and artificial intelligence have all contributed to the development of intelligent data analysis. The Support Vector Machine is a robust tool developed for ordering and updating in busy and complex environments. Unlike traditional techniques, which limit observational preparation error. By increasing the margin between the data and the isolation hyperplane, the Bolster vector machine attempts to limit the upper bound on the guessing error. This is the purported implementation of a structural risk minimization policy.

The recognition of brain tumors from medical images presents a significant challenge due to the intricate nature of the brain, which serves as the central hub for all bodily functions. The brain is highly susceptible to various ailments, including infections, strokes, and tumors. A brain tumor refers to the abnormal growth or mass of cells in the brain, which can be either malignant (cancerous) or benign (non-cancerous). It can be described as an accumulation of proliferating cells that do not undergo programmed cell death.

To obtain images of the brain and diagnose brain tumors, medical professionals employ techniques involving X-rays, powerful magnets, or radioactive materials. Several

scanning techniques are commonly utilized to identify brain diseases, including magnetic resonance imaging (MRI), computed tomography (CT), angiography, myelogram, and positron emission tomography (PET).

Among the population affected by brain tumors, children are the most commonly affected group. Every year, approximately 3410 children and adolescents under the age of 20 are diagnosed with primary brain tumors. Brain tumors can manifest as either malignant or benign growths within the brain tissue. Magnetic resonance imaging (MRI) plays a crucial role in the detection and diagnosis of brain tumors, as it provides detailed anatomical information and can potentially identify abnormal tissues, aiding in treatment planning and patient monitoring. Additionally, brain tumor segmentation techniques can contribute to a better understanding of the complex neuroanatomy and the emergence of certain brain disorders.

The advancements in database design, computing speed, and artificial intelligence have greatly contributed to the development of intelligent data analysis in the medical field. One robust tool that has emerged is the Support Vector Machine (SVM), designed to handle complex and dynamic environments. Unlike traditional techniques that often suffer from observational preparation errors, SVM aims to minimize the upper bound on the classification error by maximizing the margin between data points and the decision boundary, known as the hyperplane. This approach is based on the principle of structural risk minimization, providing more robust and accurate results.

In conclusion, the recognition and diagnosis of brain tumors from medical images is a challenging task due to the critical role of the brain and the various diseases it can be susceptible to. Techniques like MRI have significantly improved the detection and understanding of brain tumors, allowing for precise treatment planning and patient management. The application of advanced tools like Support Vector Machines has further enhanced the accuracy and reliability of data analysis in this domain. As technology continues to evolve, we can expect further advancements in brain tumor detection and improved patient outcomes.

Support Vector Machine Algorithm

One of the most well-liked supervised learning algorithms for solving classification and regression issues is the support vector machine, or SVM. However, it is mostly employed to address categorization issues in machine learning.

The SVM algorithm's goal is to establish the optimum decision boundary or line that can divide the n-dimensional space into classes so that future data points can be quickly and accurately assigned to the appropriate class. The hyperplane is the name of this optimal decision boundary.

To aid in the creation of a hyperplane, SVM chooses extreme points or vectors. The approach is known as a support vector machine because these extreme examples are referred to as support vectors. With reference to the KNN classifier, as an example, SVM can be better understood. If we want a model that can correctly distinguish between a cat and a dog, let's say we come across an unusual cat that also resembles a dog. In this case, the SVM technique can be used to build such a model. To teach our model about the many characteristics of cats and dogs, we will first train it using a variety of photographs of those animals.

Only after that will we test it using this peculiar being. The extreme case of the cat and dog will therefore be seen as the support vector forms a decision boundary between these two data (cat and dog) and picks extreme examples.

One of the most widely used supervised learning algorithms in machine learning is the support vector machine (SVM). While SVM is versatile and can address classification and regression problems, it is particularly well-suited for solving classification tasks.

The primary objective of the SVM algorithm is to determine the optimal decision boundary, known as the hyperplane, that can effectively divide the n-dimensional feature space into distinct classes. This decision boundary enables future data points to be accurately assigned to their respective classes. The SVM algorithm aims to maximize the margin, or the distance, between the hyperplane and the closest data points of each class.

To construct the hyperplane, SVM identifies a subset of data points known as support vectors. These support vectors are crucial in determining the position and orientation of the decision boundary. They are the extreme examples that lie closest to the decision boundary and play a significant role in defining the optimal separation between different classes.

To illustrate the concept of SVM using a familiar example, let's consider the case of distinguishing between cats and dogs using an SVM model. Suppose we encounter a unique cat that bears some resemblance to a dog. In this scenario, SVM can be employed to build a model that can accurately classify this peculiar cat.

To train the SVM model, we would start by providing it with a diverse set of images of cats and dogs. The model learns the distinguishing characteristics of each class from these training examples. Subsequently, when we encounter the unusual cat, we can test the model's performance by inputting the image of this cat. The SVM algorithm utilizes the support vectors and their corresponding decision boundary to determine whether the input belongs to the cat class or the dog class.

The concept of support vectors becomes particularly relevant in this scenario. The support vectors, representing the most representative and informative examples from each class, contribute to the determination of the decision boundary. By selecting the support vectors strategically, SVM can effectively capture the essential characteristics that differentiate cats from dogs, even in challenging cases.

MRI: -

The human brain is a vital organ that governs all the body's functions. However, it is susceptible to various diseases, including infections, strokes, and tumors. Brain tumors are abnormal growths or masses of cells in the brain, which can be either benign or malignant. Detecting brain tumors from medical images is a challenging task but crucial for accurate diagnosis and treatment planning.

A non-invasive imaging technique called magnetic resonance imaging (MRI) creates three-dimensional, intricate anatomical images. For disease detection, diagnosis, and therapy monitoring, it is frequently employed. Based on cutting-edge technology, it stimulates and detects changes in the rotational axis of protons in the water that makes up living tissues.

Aneurysms and tumours can also be identified with MRI, which can also distinguish between white and grey matter in the brain. When frequent imaging is needed for diagnosis or therapy, especially in the brain, MRI is the imaging modality of choice because it does not use x-rays or other radiation. However, MRI is more expensive than CT scanning or x-ray imaging.

The human brain is an incredibly important organ that plays a crucial role in governing all bodily functions. However, like any other part of the body, it is susceptible to various diseases and conditions. Among these, brain tumors are a significant concern. Brain tumors are abnormal growths or masses of cells that develop within the brain. These tumors can be classified as either benign (non-cancerous) or malignant (cancerous).

Detecting brain tumors from medical images poses a significant challenge but is of utmost importance for accurate diagnosis and effective treatment planning. Medical imaging techniques, such as magnetic resonance imaging (MRI), play a vital role in this process. MRI is a non-invasive imaging technique that creates detailed three-dimensional anatomical images of the brain.

MRI utilizes advanced technology to stimulate and detect changes in the rotational axis of protons in water molecules, which constitute living tissues. By capturing the signals emitted by these protons, MRI generates high-resolution images that provide valuable information for disease detection, diagnosis, and monitoring of therapy effectiveness. This imaging modality has revolutionized medical imaging and has become a standard tool in clinical practice.

MRI is particularly effective in identifying aneurysms and tumors within the brain. It can also differentiate between different types of brain tissues, such as white matter and gray matter, allowing for a more comprehensive understanding of the brain's structure and pathology. Importantly, MRI does not utilize ionizing radiation, such as X-rays, making it a safer option, especially for frequent imaging needs in the brain.

However, it is worth noting that MRI tends to be more expensive compared to other imaging modalities like computed tomography (CT) scanning or X-ray imaging. The cost is attributed to the advanced technology and complex processes involved in acquiring and interpreting MRI images. Nonetheless, the benefits of MRI in terms of its superior imaging capabilities and reduced radiation exposure make it the preferred choice, particularly when it comes to brain imaging.

In summary, MRI is a powerful and non-invasive imaging technique that enables the detection, diagnosis, and monitoring of various brain conditions, including tumors. Its ability to generate detailed three-dimensional anatomical images without ionizing radiation makes it a preferred modality, despite its higher cost. MRI has significantly advanced our understanding and management of brain diseases, ultimately improving patient outcomes and treatment efficacy.
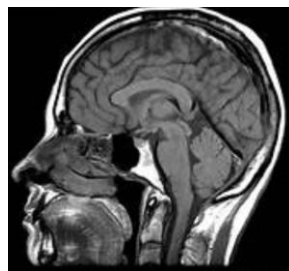

Fig-1: MRI Image

1.1.1) <u>**Problem Statement :-**</u>

Tumor borders in images are generally traced manually, which is time-consuming, difficult to detect and localize, and insolvable to determine in large data sets.

These are generally medical images that bear -operative and post-operative opinions to initiate and speed up the recovery process.

Manual segmentation of abnormal tissue cannot be compared with ultramodern- day's high-speed computers that can visually observe the volume and position of unwanted tissue. thus, an automated system for tumor discovery is demanded.

1.1.2) <u>**Motivation**</u>

A non-invasive technique for acquiring three-dimensional (3D) tomographic images of the human body is magnetic resonance imaging (MRI). The most frequent applications of MRI are to find tumors, lesions, and other soft tissue anomalies, like those in the brain. Radiologists evaluate the films produced by MRI scanners on a qualitative level in clinical settings.

Magnetic resonance (MR) image analysis and visualization computer methods have recently been investigated. Finding and measuring anomalies in the brain has been a major area of research. An essential stage in this procedure is the automatic identification of the brain from MR pictures of the head. Data quality assurance is a crucial stage in computational analysis. Because of MRI scanner flaws, MR pictures have undesired intensity variations. Getting rid

of or minimizing these differences can increase the automatic analysis.

Obtain new clinical information from sizable picture databases that can guide future clinical decisions, treatment, and drug trials. Development of technologies that enable entirely new clinical workflows that would not be possible without support of AI.

Magnetic resonance imaging (MRI) is a non-invasive and widely used technique for acquiring three-dimensional (3D) tomographic images of the human body. It has become an invaluable tool in medical diagnostics, particularly in the detection of tumors, lesions, and other soft tissue anomalies, including those found in the brain. Radiologists rely on the qualitative evaluation of MRI films to make clinical assessments and decisions.

In recent years, there has been a growing interest in the application of computer methods for magnetic resonance (MR) image analysis and visualization. The aim is to develop automated algorithms and techniques that can assist in the detection and measurement of abnormalities in the brain. This field of research has made significant strides in advancing our ability to identify and analyze brain anomalies.

A critical step in this process is the automatic identification of the brain region within MR images of the head. Accurate brain segmentation is essential for subsequent analysis and interpretation. However, MR images often suffer from undesired intensity variations caused by inherent flaws in MRI scanners. These variations can negatively impact the quality of computational analysis and the accuracy of anomaly detection. Therefore, it becomes crucial to address these issues and minimize the intensity variations to improve the reliability of automatic analysis.

By developing robust techniques for data quality assurance and intensity normalization, researchers aim to enhance the accuracy and efficiency of computational analysis in MR image processing. These methods involve the application of image processing and machine learning algorithms to preprocess MR images, correct intensity variations, and optimize the images for subsequent analysis.

The advancements in MRI technology and the integration of artificial intelligence (AI) have opened up new avenues for obtaining valuable clinical information from large-scale picture databases. These databases, often referred to as image repositories, contain a vast amount of medical images along with associated clinical data. By leveraging AI techniques, such as machine learning and deep learning, it becomes possible to extract meaningful insights from these databases.

The analysis of large-scale picture databases can provide clinicians with new clinical information that can guide future decision-making processes, treatment strategies, and even drug trials. By uncovering patterns, correlations, and predictive models from these datasets, AI-powered technologies enable the development of entirely new clinical workflows that were previously unattainable.

Goal and scope of the research work: -

The purpose of the thesis is to identify a tumor in brain imaging. The primary goal is to accurately categorize the tumors and non-tumors using SVM (Support Vector Machine).

Development of technologies that enable entirely new clinical workflows that would not be possible without the support of AI. induce new clinical perceptivity from large image databases to inform coming clinical opinions, treatments and medicine trials.
The primary focus of the thesis is to develop an accurate method for identifying brain tumors in medical imaging, specifically using the Support Vector Machine (SVM) algorithm. The thesis aims to achieve the following objectives:

1. Selecting the necessary MRI scans of brain tumors from an improved and well-curated database: This involves gathering high-quality MRI data of brain tumors from a reliable source. The selection process ensures that the dataset used for training and evaluation is representative and comprehensive.

2. Characterizing the features of brain tumors: Analyzing the MRI images, the thesis aims to identify and extract relevant features that can distinguish between tumor and non-tumor regions in the brain. This step involves understanding the specific characteristics and patterns associated with brain tumors, such as shape, size, texture, and intensity variations.

3. Utilizing SVM for feature vector classification: The thesis proposes using SVM, a powerful supervised learning algorithm, to classify the extracted feature vectors from the MRI scans. SVM is known for its ability to establish an optimal decision boundary between classes, making it suitable for tumor classification. The feature vectors serve as input to the SVM algorithm, which learns from the labeled training data to classify future data points accurately.

4. Analyzing the performance of SVM: The thesis aims to evaluate the effectiveness and performance of the SVM-based tumor classification method. This involves assessing metrics such as accuracy, sensitivity, specificity, and area under the curve (AUC) to measure the algorithm's ability to correctly classify tumors and non-tumors. The analysis provides insights into the reliability and robustness of the proposed approach.

By accurately categorizing brain tumors using SVM, the thesis seeks to contribute to the field of medical image analysis and diagnosis. The ultimate goal is to accelerate and streamline the process of analyzing medical images by automating various tasks, including tumor identification, outcome prediction, image quantification, and even picture reconstruction. By reducing the workload on doctors and the healthcare system, this automated approach can enhance efficiency and improve patient care.

CHAPTER – 2

2.1 REVIEW OF LITERATURE

A literature review is a summary of published research on a particular content. It's a system of collecting and evaluating existing research in order to understand the current state of knowledge on a subject.

Brain tumors are abnormal growths of cells in the brain that can be benign(noncancerous) or nasty(cancerous). It can do at any age and has serious consequences, including brain damage and death. Early discovery of brain tumors is critical for successful treatment and bettered patient issues. There are several ways to descry brain tumors, including imaging ways similar as reckoned tomography(CT) and glamorous resonance imaging(MRI), and biopsy techniques in which a sample of tissue is taken and examined under a microscope.

Several studies have estimated the effectiveness of different imaging techniques in detecting brain tumors. CT scans are extensively considered the gold standard for detecting brain tumors because they give detailed images of the brain and are extensively available. Still, MRI is getting more popular because it provides a more detailed image and can directly distinguish different types of tissue.

Other imaging tests studied to descry brain tumors include positron emigration tomography (PET) reviews and single photon emission computed tomography(SPECT) scans. Research is also underway to detect brain tumors using machine literacy and artificial intelligence. Machine literacy algorithms can dissect large quantities of data, similar as medical images, to identify patterns and features that indicate brain tumors. This approach has the implicit to ameliorate the delicacy and effectiveness of brain tumor discovery, but farther studies are demanded to determine its clinical mileage.

Overall, it's clear that brain tumor discovery is an active research area, and much remains to be learned about the most effective styles for early discovery and diagnosis.

2.1.1) Review of Existing Models, Approaches, Problems

→ R. Muthukrishnan, proposed an offer for brain tumor detection where segmentation separates an image into its element regions or objects. Image segmentation requires separating objects from the background in order to read the image rightly and classify the image content directly. In this framework, edge detection was the crucial tool for image segmentation. In this article, we investigated the performance of the most generally used edge discovery ways in image segmentation and used trials to compare these ways. ,

M Saritha, proposed an approach by integrating wave entropy- grounded spider web diagrams and probabilistic neural networks for brain MRI classification. The proposed system uses two way for classification. H. Wavelet entropy- grounded spider web diagrams for feature extraction and probabilistic neural networks for classification. For the attained brain MRI, we performed point extraction by wavelet transform, calculated the entropy value, and calculated the area of the spider web diagram. Using the entropy values, classification was reckoned using a probabilistic neural network. Probabilistic neural networks give a general solution to the problem of pattern classification, and their classification accuracy is roughly 100%.

A. Laxmi, proposed processing information (regions of interest) in medical images. This significantly speeds up the computation of tumor segmentation results. A crucial point point- grounded approach for the segmentation of primary brain tumors has been proposed. Axial slices of contrast- enhanced T1- ladened MR images of the brain were anatomized. A feature point extraction algorithm grounded on edge map fusion using morphological and wavelet styles was applied to prize the significant point points in the image. Evaluation of the point points therefore attained was performed for geometric transformation and image scaling. A region- growing algorithm was also used to insulate the tumor region. primary results show that our approach achieved good segmentation results. This approach also reduces a large quantum of calculation. Future work includes probing styles in automated 3D tumor segmentation, segmentation of ROIs in other medical images, and the significance of ways enforced in medical image retrieval applications.

2.1.2) Significance of Models, Approaches, Problems

→ Parveen, Amritpal Singh's algorithm is a combination of SVM and fuzzy c- means, which is a hybrid technique for brain tumor prediction. Then the image is enhanced by enhancing the contrast and tensing the middle area. Double thresholding and morphological operations are used to strip the skull. Fuzzy c- means (FCM) clustering is used for image segmentation. Gray level run length matrix (GLRLM) is used for feature extraction. Linear, quadratic and polynomial SVM techniques are also used to classify brain MRI images. A real dataset of MRI brain images from 120 patients was used to identify" tumor" and "non-tumor" MRI images. The SVM classifier is trained using 96 brain MRI images, after which the remaining 24 brain MRI images were used to test the trained SVM. SVM classifiers with direct, quadratic, and polynomial kernel functions yield 91.66,83.33, and 87.50 accuracy independently, and 100 % particularity.

Garima Singh, and Dr. M.A. Ansari proposed a new fashion involving histogram normalization and K- means segmentation. First, the input image is reused to remove unwanted signals or noise. Filters similar as median filter, adaptive filter, median filter, unsharp mask filter and Gaussian filter are used to remove noise from MRI images. The histogram of the preprocessed image is regularized, and MRI classification is performed. Eventually, the image is segmented using a K- means algorithm to remove the tumor from theMR. Effective bracket of MRI images

is performed using NB classifier and SVM to gain accurate prediction and classification. The Naive Bayes and SVM classifier give accuracies of 87.23 % and 91.49 %, independently. SVM provides better classification accuracy. MATLAB is used for implementation. The proposed system has some limitations because it couldn't find out the precise or exact boundary of the tumor region.

Ketan Machhale, Hari Babu Nandpuru2, Vivek Kapur3 and Laxmi Kosta proposed an intelligent classification system to identify normal and abnormal MRI brain images. These ways successfully perform image preprocessing, image extraction and posterior classification of brain cancer. In brain MRI preprocessing, RGB images are converted to grayscale images. A median filter is used to remove noise from the MR image. Skull masking is also used to remove non-brain towel from the MRI brain image. Expansion and corrosion are the two main morphological procedures used to cover the skull. Line extraction excerpts symmetry, grayscale and texture objects. When different machine literacy ways are used to classify the 50 images support vector machine(SVM), K- nearest neighbor(KNN) and hybrid classifier(SVM- KNN), the results show that the mongrel classifier SVM- KNN showed highest classification accuracy of 98 % among others.

Author	Title	Proposed Technique	Dataset	Accuracy	Benefits	Limitations
Parveen, Amritpal singh (2015)	Detection of brain tumor in MRI images, using combination of FCM and SVM	FCM Segmentation +SVM classification	120 MRI images	91.66%	It combines clustering and classification algorithm Efficient method	Brain tumor type can't be classified Difficult to choose SVM kernel function
Garima Singh, Dr. M. A. Ansari (2016)	Efficient Detection of Brain Tumor from MRIs Using K-Means Segmentation and Normalized Histogram	K-Means Segmentation + SVM &Naïve Bayes classification	110 MRI images	91.49 & 87.23%	Accurate results. Fast & efficient in term of computational time and cost	It doesn't work well with clusters (in the original input data) of different size and Different density

Ketan Machhale, Hari Babu Nandpuru, VivekKapur, Laxmi Kosta (2015)	MRI Brain Cancer Classification Using Hybrid Classifier (SVMKNN)	SVM & SVMKNN classification	50 MRI images	98.00%	Handle multiclass cases Increased Accuracy	When there is a change in dataset, fresh training dataset is required.

Table-1: Literature Review

2.1.3) State of Art : Review

→ Many works have been done on how to detect the brain tumours. The authors, E. F. Badran, E. G. Mahmoud, and N. Hamdy had proposed a step-by-step approach for a brain tumor detection by differentiating healthy brain VS brain with tumors, benign VS malignant tumors and then followed by an algorithmic approach which consists of seven stages like image pre-processing, image segmentation, feature extraction and image classification using neural networks techniques. Their approach detected a tumor and defined the type of a tumor.

Their techniques included canny edge detection and Harris, adaptive threshold and Harris. The technique canny edge detection and Harris showed 18.75% for falsely recognizing healthy brain as well as a brain with a tumor and 10% for benign and malignant tumors. Second technique adaptive threshold and Harris showed 15.625% for falsely recognizing healthy brain VS brain with a tumor and 6.25% for benign and malignant tumors.

CHAPTER - 3

3.1 Problem Definition

3.1.1) **Problem Statement:-**

First and foremost, talking about what brain tumor is that the DNA tells our cells what to do. Sometimes, this DNA mutates, causing cells to grow abnormally, divide rapidly, and live longer than healthy cells. These cells accumulate in clusters in different corridor of the brain. And since the brain is the control center for the rest of our body, it can affect just about any other function.

There are numerous types of brain cancer. Some are harmless **or noncancerous**. In other words, it's cell overgrowth that produces clusters. But the cells themselves are normal. Some are malign or cancerous. This means that the mass is made up of abnormal cells that continue to spread and invade other tissues.

Tumors that form in the brain or surrounding tissues are called primary brain tumors. Further, generally, tumors are known as secondary or metastatic brain tumors. This is the result of cancer that has spread to the brain from other corridors of the body.

Presently, brain tumors are only detected by imaging after the attack of neurological symptoms. Early detection strategies aren't used, even for people known to be at threat for certain types of brain cancer due to their inheritable makeup. The current histopathological classification system, grounded on the cell of suspected tumor origin, has been in effect for nearly a century and was updated by the World Health Organization in 1999.

Although satisfactory in numerous respects, it doesn't directly predict tumor behavior in individual cases. Nor can it guide remedial opinions with the perfection that cases and physicians ask and need.

Current imaging ways give an in- depth anatomical definition and are the primary tools for detecting neurological symptoms resulting from brain tumors.

3.1.2) **Motivation:**
Brain tumors are a critical health concern as they can severely impact a person's well-being and require timely intervention. Timely and accurate detection of brain tumors plays a crucial role in effective treatment planning and improving patient outcomes. However, accurately identifying brain tumors from medical images, such as MRI scans, can be challenging due to the complexity and variability of tumor characteristics. Traditional methods often rely on manual interpretation by radiologists, which can be time-consuming and prone to human error. Therefore, there is a pressing need to leverage advanced techniques like SVM and MRI to

improve the accuracy and efficiency of brain tumor detection, enabling early diagnosis and prompt treatment.

3.1.3) Objective:

The main objective of this research is to develop a brain tumor detection system that utilizes support vector machines (SVMs) and MRI scans. Specifically, the project aims to achieve the following objectives:

Collect and preprocess MRI data: Gather a dataset of MRI brain scans, including both tumor and tumor-free cases. Preprocessing steps may involve resizing or cropping the images and applying noise reduction or smoothing techniques to enhance the quality of the images.

Feature extraction: Extract relevant features from the preprocessed MRI data. These features can capture important information related to the presence or absence of brain tumors. Features may include statistical measures (e.g., mean, standard deviation), texture features, shape features, or other advanced features that can effectively differentiate between tumor and healthy brain tissues.

Training and testing dataset preparation: Split the dataset into training and testing subsets. The training set will be used to train the SVM classifier, while the testing set will be used to evaluate the performance of the trained model. It is essential to ensure that the testing set contains unseen data to assess the generalization ability of the model accurately.

SVM model training: Utilize the training dataset to train an SVM classifier. The SVM algorithm aims to find an optimal decision boundary or hyperplane that can effectively separate the tumor and non-tumor classes in the feature space. The SVM classifier will learn from the labeled training data and establish a discriminative model for tumor detection.

Model evaluation: Evaluate the trained SVM model using the testing dataset. Measure various performance metrics such as accuracy, precision, recall, and F1-score to assess the model's ability to correctly classify brain scans as tumor or non-tumor. Fine-tuning of the model may be performed by adjusting SVM hyperparameters or exploring different feature sets to enhance the model's performance.

System optimization and improvement: If the performance of the SVM model is not satisfactory, further optimization steps can be taken. This may involve refining feature extraction techniques, exploring different SVM kernels, adjusting hyperparameters, or considering ensemble methods to combine multiple classifiers. The goal is to continually improve the accuracy and reliability of the brain tumor detection system.

CHAPTER - 4

4.1 REPORT ON THE PRESENT INVESTIGATION

Experimental setup

This refers to the specific conditions, equipment, and materials used in the experiments conducted for the research. It includes details such as the laboratory or field setup, instruments utilized, data collection tools, and any other relevant experimental components. Describing the experimental setups provides a clear understanding of the environment in which the data was collected and analyzed.

- **Visual Studio Code (VS Code)** is a free and open-source code editor developed by Microsoft for Windows, macOS, and Linux. It is based on Electron, a framework that allows web technologies to be used to create desktop applications. VS Code is designed to be a lightweight and extensible editor that can be used for a variety of programming languages, including JavaScript, TypeScript, C++, Python, and Java.
- **NumPy :-** It is a library for scientific computing. It provides a high-performance multidimensional array object, along with a wide range of mathematical functions. Numpy (Numerical Python) is a library for working with large, multi-dimensional arrays and matrices of numerical data. It provides tools for working with arrays and matrices, as well as functions for performing mathematical operations on these data structures.

- **Pandas:-** It is a library for data analysis. It provides high-level data structures and data analysis tools for working with structured (tabular, multidimensional, potentially heterogeneous) and time series data.Pandas is a library that provides tools for data manipulation and analysis. It offers data structures and data manipulation tools designed to make working with "relational" or "labeled" data both easy and intuitive.

- **Matplotlib** :- is a library for plotting. It provides a comprehensive plotting API for Python that produces publication-quality figures in a variety of formats.Matplotlib is a library for creating static, animated, and interactive visualizations in Python. It allows you to create a wide range of static, animated, and interactive visualizations in Python, including bar charts, line plots, scatter plots, and more.

- **Scikit-learn** is a library for machine learning. It provides a wide range of machine learning algorithms, including classification, regression, clustering, and dimensionality reduction..Scikit-learn (short for "Scientific Kit for Machine Learning") is a library for building machine learning models in Python. It provides tools for model training, evaluation, and prediction, as well as a variety of tools for pre-processing and feature selection.

Procedures Adopted

The procedures adopted refer to the step-by-step methods followed during the research. This includes the data collection procedures, data preprocessing techniques, feature selection methods, model training processes, and evaluation procedures. Documenting the procedures adopted ensures transparency and reproducibility of the research, allowing other researchers to replicate the study and validate the findings.

- **Prepare/Collect data:** The system reads in images of brain tumors and labels them as either 'no_tumor' or 'pituitary_tumor', and then converts the images into arrays of pixel values.
- **Visualize data:** The system displays the images to provide a visual understanding of the dataset.
- **Prepare data:** The system reshapes the arrays of pixel values into a format that can be used for training the machine learning model.
- **Split data:** The system splits the dataset into training and testing sets, so that it can train the machine learning model on one set of data and test its accuracy on another.
- **Feature scaling:** The system scales the pixel values to ensure that the values are between 0 and 1.
- **Feature selection:** The system uses principal component analysis (PCA) to select the most important features for the machine learning model.
- **Train model:** The system trains two different machine learning models (Logistic Regression and Support Vector Machine) on the training data.
- **Evaluation:** The system evaluates the performance of the two models on the testing data.
- **Prediction:** The system uses the trained machine learning models to predict whether a given brain tumor image is 'no_tumor' or 'pituitary_tumor'.
- **Test model:** The system displays several images from the testing dataset and predicts whether each image shows a brain tumor or not.
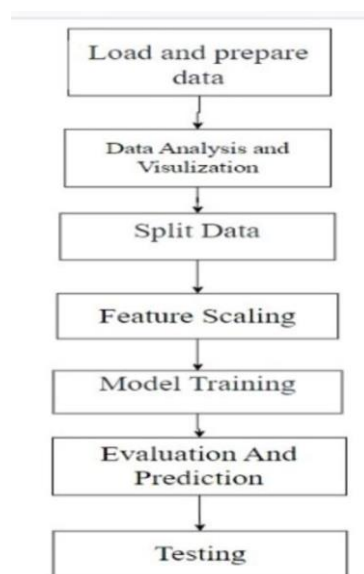

Fig-2: Procedure Flowchart

Techniques developed, methodologies developed and adopted

Design Approach

Support Vector Machine (SVM) is one of the most popular classifiers in pattern recognition, which aims to find a hyperplane that can separate two classes of samples with the maximal margin. As a result, traditional SVM usually more focuses on the scatter between classes, but neglects the different data distributions within classes which are also vital for an optimal classifier in different real-world problems. Recently, using as much structure information hidden in a given dataset as possible to help improve the generalization ability of a classifier has yielded a class of effective large margin classifiers, typically as Structured Large Margin Machine (SLMM). SLMM is generally derived by optimizing a corresponding objective function using SOCP, and thus in contrast to SVM developed from optimizing a QP problem, it, though more effective in classification performance, has the following shortcomings:

- large time complexity
- lack of sparsity of solution, and
- poor scalability to the size of the dataset.

In this paper, still following the above line of the research, we develop a novel algorithm, termed as Structural Support Vector Machine (SSVM), by directly embedding the structural information into the SVM objective function rather than using as the constraints into SLMM, in this way, we achieve:
- to overcome the above three shortcomings.
- empirically better than or comparable generalization to SLMM, and
- theoretically and empirically better generalization than SVM.

Support Vector Machines (SVMs) are a type of supervised machine learning algorithm that can be used for classification or regression tasks. The basic idea behind SVMs is to find a hyperplane in a high-dimensional space that maximally separates the different classes.

The SVM architecture consists of the following elements:
- **Training data:** This is a set of labeled examples that the SVM will use to learn the decision boundary between the different classes.
- **Decision boundary:** This is a hyperplane in the high-dimensional space that divides the different classes.
- **Support vectors**: These are the data points that lie closest to the decision boundary and have the greatest influence on the position of the hyperplane.
- **Kernel function**: This is a function that is used to transform the input data into a higher-dimensional space, where it may be more suitable for finding a decision boundary.
- **Hyperparameters:** These are values that are set by the user and control the behavior of the SVM. Examples include the kernel function, the regularization parameter, and the width of the margin around the decision boundary.

SVM

The SVM is a supervised learning method. It is a good tool for data analysis and classification. SVM classifier has a fast-learning speed even in large data. SVM is used for two or more class classification problems. Support Vector Machine is based on the conception of decision planes. A decision plane is one that separates between a set of items having dissimilar class memberships. The Classification and detection of brain tumor was done by using the Support Vector Machine technique. Classification is done to identify the tumor class present in the image. The use of SVM involves two basic steps of training and testing.

Linear SVM

The training pattern is linearly divisible. That is, there exists a linear function of the form $f(x) = w\ T\ x\ b$ (1), and for each training example xi, the functions ($f(x)$) ≥ 0 if x for =+1, y and f (xi) < 0 for yi=-1, i.e. training examples from two different classes are separated by a hyperplane $F(x) = w\ T\ x\ b = 0$, where w is a unit vector and b is an invariant: for a given training set, there may be many hyperplanes that maximize the cut-off between the two classes, but the SVM classifier maximizes the cut-off between the two classes. In other words, the SVM finds the hyperplane that causes the greatest separation between the decision function values of the 'boundary' examples from the two classes. SVM classification using a hyperplane that minimizes the boundary between two classes. Support vectors are the elements of the training set that lie on the boundary hyperplane of the two classes. Overall the SVM finds the hyperplane that causes the greatest separation between the decision function values of the 'boundary' examples from the two classes.

Non-Linear SVM

Straight line or hyper plane is used to distinguish between two classes. But datasets or data points are always not separated by drawing a straight line between two classes. It can't be separable by using above SVMs discussed. So, Kernel functions are used with SVM classifier. Kernel function provides the bridge between from nonlinear to linear. Basic idea behind using kernel function is to map the low dimensional data into the high dimensional feature space where data points are linearly separable.A pattern gratitude network, which is a feed-backward network with tan sigmoid transfer functions in both the hidden layer and the output layer, is used. The network has only one output neuron, as there are 24 input vectors. The hidden layer neurons are 100 and the learning rate is 0.1. The momentum factor is 0.9 and total numbers of epochs are 500. The error is minimized by 0.001 and the performance of the classifier is evaluated by calculating accuracy.
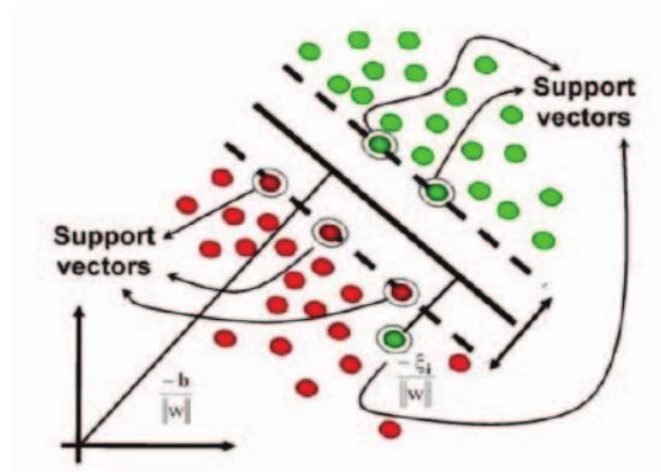
Fig-3: Classification process of SVM

SVM is based on optimal hyperplanes of linearly pairable patterns but can be perfected by transforming unique data into linearly indivisible patterns for mapping into a new space. They are clearly based on abstract learning models and contain theoretical guarantees of performance. It also has a modular design in which components can be applied and designed independently and is immune to local minima. Support vectors are elements of the training set that change the position of the dividing hyperplane if removed. Support vectors are the most important part of the training set. The problem of finding the optimal hyperplane is an optimization problem and can be solved by optimization techniques.
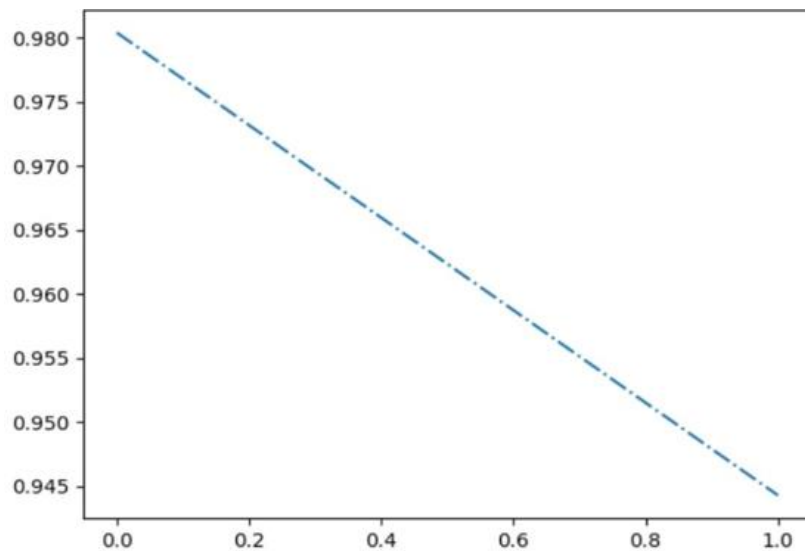

Fig-4: On applying on our project i.e. data vs score

LOGISTIC REGRESSION

Logistic regression is a statistical method that uses a logistic function to model the probability of a binary outcome, such as yes/no, true/false, or success/failure. The logistic function is a sigmoid function that maps the real number line to the interval (0, 1), which can be interpreted as the probability of a particular outcome.

Logistic regression is a type of generalized linear model (GLM). GLMs are a broad class of models that can be used to model a wide variety of response variables, including binary, count, and continuous variables. The key difference between GLMs and other types of regression models is that GLMs assume that the response variable is distributed according to a particular probability distribution. In the case of logistic regression, the response variable is assumed to be Bernoulli distributed.

The logistic regression model is defined as follows:

$$\text{logit}(p) = \beta 0 + \beta 1 x1 + \beta 2 x2 + ... + \beta p x p$$

where:

p is the probability of the binary outcome

$\beta 0$ is the intercept

$\beta 1, \beta 2, ..., \beta p$ are the coefficients for the independent variables

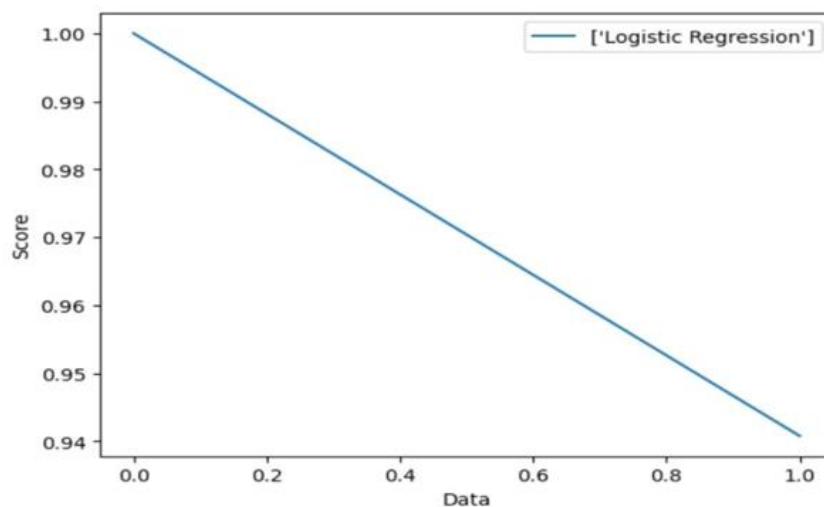x1, x2, ..., xp are the independent variables

Fig-5: Logistic Regression

As you can see, the logistic regression function is a sigmoid function. This means that the function has asymptotes at 0 and 1. The function approaches 0 as the input approaches negative infinity, and the function approaches 1 as the input approaches positive infinity.

The logistic regression function can be used to model a wide variety of binary outcomes, including the presence or absence of a disease, the success or failure of a treatment, and the survival or death of a patient.

Logistic regression is a powerful tool that can be used to make predictions about binary outcomes. It is a relatively easy algorithm to understand and implement, and it is available in many statistical software packages.

The logistic regression model can be estimated using maximum likelihood estimation. Once the model is estimated, the predicted probability of the binary outcome can be calculated for any new data point.

Logistic regression is a powerful tool that can be used to model a wide variety of phenomena. It is particularly useful for modeling binary outcomes, such as customer churn, loan default, and disease diagnosis.

CHAPTER – 5

5.1 software and hardware requirement

5.1.1 Requirement Specification

Software Requirements:

Operating System:
The system should be compatible with common operating systems such as Windows, macOS, or Linux.

Development Environment:
A suitable programming environment is required to implement the brain tumor detection system. This can include IDEs (Integrated Development Environments) like Eclipse, Visual Studio, or JetBrains IntelliJ IDEA.

Programming Language:
The system can be developed using programming languages such as Python, Java, or C++. Python is commonly used in machine learning applications and provides a variety of libraries and frameworks for image processing and SVM implementation.
Software Requirements:

Python: Python is a versatile programming language widely used in data analysis and machine learning. It offers a comprehensive range of libraries and tools for scientific computing. To run the code, it is essential to have Python installed on your system. You can download the latest version of Python from the official Python website (https://www.python.org/) and follow the installation instructions provided. Make sure to choose the appropriate version compatible with your operating system.

Integrated Development Environment (IDE): An Integrated Development Environment is a software application that provides an integrated environment for writing, executing, and debugging code. Several popular Python IDEs are available, each with its unique features and functionalities. Some commonly used Python IDEs include PyCharm, Anaconda, Jupyter Notebook, Spyder, and Visual Studio Code. Select an IDE based on your preferences and requirements, and install it on your system. You can download the IDE from the respective official websites, and the installation instructions are usually provided along with the download.

Libraries:
The code relies on various Python libraries for data manipulation, visualization, and machine learning. These libraries provide pre-built functions and methods that simplify complex tasks and enable efficient data processing. The following libraries are utilized in the code:

NumPy: NumPy is a fundamental library for numerical computing in Python. It offers support for large, multi-dimensional arrays and matrices, along with an extensive collection of mathematical functions. NumPy is extensively used for handling and processing numerical data efficiently.

To install these libraries, you can use the pip package manager, which is usually bundled with Python installations. Open a command prompt or terminal and execute the following command:
→ **pip install numpy**

Pandas: Pandas is a powerful library for data manipulation and analysis. It provides high-performance data structures, such as Data Frames, which facilitate easy handling and manipulation of structured data. Pandas is utilized to load, preprocess, and analyze the brain tumor dataset, enabling effective data manipulation operations.

To install these libraries, you can use the pip package manager, which is usually bundled with Python installations. Open a command prompt or terminal and execute the following command:
→ **pip install pandas**

Matplotlib: Matplotlib is a widely-used plotting library in Python. It offers a vast array of functions for creating static, animated, and interactive visualizations. Matplotlib is employed to plot and visualize the brain tumor images and evaluation metrics, aiding in the interpretation of results.

To install these libraries, you can use the pip package manager, which is usually bundled with Python installations. Open a command prompt or terminal and execute the following command:
→ **pip install matplotlib**

OpenCV: OpenCV (Open Source Computer Vision Library) is a comprehensive computer vision library that provides a wide range of functions for image and video processing. In the given code, OpenCV is used for reading, resizing, and converting the brain tumor images to grayscale, ensuring compatibility with subsequent processing steps.

To install these libraries, you can use the pip package manager, which is usually bundled with Python installations. Open a command prompt or terminal and execute the following command:
→ **pip install opencv-python**

Scikit-learn: Scikit-learn is a popular machine learning library in Python. It encompasses a diverse collection of algorithms and tools for data analysis and model training. Scikit-learn offers implementations of various classification, regression, clustering, and dimensionality reduction algorithms. In this code, Scikit-learn is employed for splitting the dataset into training and testing sets, performing feature scaling, applying Principal Component Analysis (PCA), and training the classification models.

To install these libraries, you can use the pip package manager, which is usually bundled with

Python installations. Open a command prompt or terminal and execute the following command:

→ **pip install scikit-learn**

Database Management System:
Depending on the project requirements, a database management system such as MySQL, PostgreSQL, or SQLite may be required to store and manage the MRI data and associated metadata.

Hardware Requirements:
When running the code for brain tumor classification, it is important to consider the hardware specifications of your system. The hardware requirements will vary depending on factors such as the size of the dataset, the complexity of the machine learning models, and the computational resources needed for training and inference. Here are some detailed recommendations to ensure smooth execution:

Processor:
A multi-core processor, such as Intel Core i5 or higher, is recommended to handle the computational demands of image processing and machine learning algorithms.
Hardware Requirements:

The processor is responsible for executing the code and performing the computations involved in training and inference. It is recommended to have a dual-core or higher processor to efficiently handle the computational load. A processor with more cores or threads will allow for parallel processing, enabling faster execution of the code. Additionally, a faster processor will expedite the training process, especially when dealing with complex models or larger datasets.

Random Access Memory (RAM):
RAM plays a crucial role in storing and manipulating data during code execution. The amount of RAM required depends on the size of the dataset and the complexity of the models. For basic execution, a minimum of 4 GB of RAM is recommended. However, for larger datasets or more complex models, it is advisable to have more RAM to avoid memory limitations and ensure smooth operation. Having ample RAM allows for faster data processing and model training, enhancing the overall performance of the code.

Storage:
storage space is essential to accommodate the dataset, installed libraries, and any intermediate data generated during preprocessing and model training. The size of the dataset can vary depending on the number and size of the brain tumor images. It is advisable to have ample storage capacity to prevent any storage-related issues during code execution. Consider the size of the dataset and allocate enough storage space accordingly.

Graphics Card (Optional):

While not mandatory for basic execution, a dedicated graphics card with CUDA support can significantly enhance performance, especially when working with deep learning models. Graphics cards are designed to accelerate parallel computations, making them highly efficient for training complex neural networks. If you anticipate working with larger datasets or more computationally intensive models, having a graphics card with CUDA support can provide a substantial boost in training speed and overall performance.

It is important to note that these hardware requirements are general recommendations and may vary depending on the specific needs and complexity of your project. It is always beneficial to consider the specific requirements of your dataset and models and ensure that your hardware configuration meets or exceeds those requirements.

Display:

A high-resolution display is recommended for better visualization of MRI images and analysis results.

Internet Connectivity:

An internet connection may be required for downloading software libraries, updates, or accessing online resources related to the project.

Chapter 6

6.1 PROPOSED SYSTEM MODEL

The proposed system model aims to utilize machine learning techniques for the early detection and classification of brain tumors. It leverages a combination of image processing, feature extraction, and classification algorithms to achieve accurate and efficient tumor diagnosis.

6.1.1) Data Preparation:

Data Preparation is a crucial step in the proposed system model for brain tumor detection and classification. This step involves collecting, organizing, and preprocessing the brain tumor image data for further analysis and model training. The following are the detailed steps involved in data preparation:

1. Data Collection:
- The brain tumor image dataset is obtained from a specified directory ('../brain_tumor/Training/') containing subdirectories for different classes of tumors.
- The classes are defined as 'no_tumor' (representing images without tumors) and 'pituitary_tumor' (representing images with pituitary tumors).

2. Data Loading and Conversion:
- For each class, the images are loaded using OpenCV's imread() function, which reads the image data in grayscale format.
- The images are checked for successful reading using a condition to handle any potential errors or invalid images.
- The loaded images are resized to a uniform size of 200x200 pixels using OpenCV's resize() function.

3. Data Storage:
- Two arrays, X and Y, are initialized to store the image data and corresponding class labels, respectively.
- The resized image data is appended to the X array, and the class label (represented as an integer) is appended to the Y array.
- This process is performed for each image in the dataset, iterating through the subdirectories for each class.

4. Data Representation:
- The X array contains the image data, where each element represents a 2D grayscale image.
- The Y array contains the corresponding class labels, with values 0 for 'no_tumor' and 1 for 'pituitary_tumor'.

5. Data Exploration:
- The unique class labels (tumor classes) present in the dataset are identified using the np.unique() function.
- The distribution of class labels is analyzed using the pd.Series(Y).value_counts() function to determine the number of samples in each class.

6. Data Shape:
- The shape of the Y array is determined using the Y.shape attribute, representing the number of samples in the dataset.
- The shape of the X array is determined using the X.shape attribute, representing the number of samples and the image dimensions.

The data preparation step ensures that the brain tumor image dataset is properly loaded, organized, and ready for further analysis and model training. It provides an essential foundation for subsequent steps such as data visualization, data preprocessing, feature selection, model training, evaluation, and prediction.

6.1.2) Data Visualization:

Data visualization plays a crucial role in understanding and interpreting the results of the proposed system model for brain tumor detection and classification. The visualizations provide a graphical representation of the data, model performance, and predicted tumor labels, enabling a comprehensive analysis. The following are the key visualizations used in the proposed system:

1. **Image Display**: The grayscale brain tumor images from the testing dataset are displayed using matplotlib.pyplot's `imshow` function. The images are shown in a grid layout, with each subplot representing an individual image. The `cmap='gray'` parameter is used to display the images in grayscale.

2. **Prediction Results**: For a subset of testing images belonging to the 'no_tumor' and 'pituitary_tumor' classes, the predicted tumor labels are displayed alongside the images. Each image is processed by resizing it to a consistent size of 200x200 pixels and normalizing the pixel values. The transformed image is then fed into the trained Support Vector Machine (SVM) model to obtain the predicted label. The predicted label is mapped to the corresponding class ('Negative Tumor' or 'Positive Tumor') using a predefined dictionary. The predicted label is displayed as the title of the subplot, providing an immediate visual indication of the model's classification.

3. **Visualization Layout**: The visualizations are organized in a grid layout using matplotlib.pyplot's `subplot` function. The number of rows and columns in the grid is determined based on the number of images to be displayed. This layout allows for a systematic and compact representation of the images and their predicted labels.

4. **Figure Size**: To ensure clarity and visibility of the images and labels, the figure size is adjusted using matplotlib.pyplot's `figure` function. A larger figure size, such as (12, 8), is chosen to accommodate multiple subplots and provide sufficient space for each image.

5. **Axis Off:** The axes of each subplot are turned off using matplotlib.pyplot's `axis` function with the parameter `off`. This removes the axis labels and tick marks, resulting in a clean and focused visualization of the tumor images.

The data visualizations provide an intuitive and informative representation of the tumor detection and classification results. They facilitate a quick assessment of the model's performance and enable medical professionals to visually inspect and interpret the predicted tumor labels. The visualizations can be used as a valuable tool for analysis, diagnosis, and decision-making in the field of brain tumor detection and treatment.

6.1.3) Data Preprocessing:

Data preprocessing is an essential step in the proposed system for brain tumor detection and classification. It involves transforming the raw input data into a suitable format that can be utilized by machine learning algorithms. The following detailed descriptions provide an overview of the key data preprocessing steps employed in the proposed system:

1. Data Collection: The brain tumor dataset used in the system is collected from the "Training" folder, which contains subfolders for each class, namely "no_tumor" and "pituitary_tumor." The dataset consists of grayscale images representing brain scans, where each image represents a specific patient case.

2. Image Loading and Resizing: The images are loaded using the OpenCV library's `cv2.imread` function, which reads the image files in grayscale format. The images are then resized to a consistent shape of (200, 200) using the `cv2.resize` function. Resizing the images ensures uniformity and reduces computational complexity during the training process.

3. Data Labeling: The images are associated with corresponding labels indicating the presence or absence of a tumor. The classes "no_tumor" and "pituitary_tumor" are assigned labels of 0 and 1, respectively. This labeling allows the machine learning model to learn the patterns and features associated with each class during the training phase.

4. Data Conversion: The image data and labels are converted into appropriate formats for further processing. The images are converted into a NumPy array, enabling efficient manipulation and analysis of the image data. Similarly, the labels are converted into a NumPy array or a pandas Series object to facilitate compatibility with machine learning algorithms.

5. Data Splitting: The dataset is divided into training and testing subsets using the `train_test_split` function from the scikit-learn library. This step ensures that the model is trained on a portion of the data and evaluated on unseen data to assess its generalization

performance. Typically, a random split of 80% training data and 20% testing data is used, but the specific split ratio can be adjusted based on the requirements of the system.

6. Feature Scaling: To ensure that the input features are on a similar scale and to prevent any single feature from dominating the learning process, feature scaling is performed. In the proposed system, the grayscale pixel values of the images are scaled to a range of [0, 1] by dividing them by the maximum pixel value (255). This normalization process aids in the convergence and stability of machine learning algorithms.

7. Dimensionality Reduction: In some cases, high-dimensional image data can introduce complexity and noise to the model. To mitigate this issue, dimensionality reduction techniques such as Principal Component Analysis (PCA) can be applied. PCA is utilized to reduce the dimensionality of the feature space while preserving most of the variance in the data. In the proposed system, PCA is applied to the training and testing data to retain 98% of the variance, resulting in a lower-dimensional representation.

By performing these preprocessing steps, the proposed system ensures that the brain tumor dataset is appropriately prepared and structured for subsequent machine learning tasks. These preprocessing steps enable effective model training, enhance model performance, and facilitate accurate brain tumor detection and classification.

6.1.4) Feature Selection:

Feature selection is a critical step in the proposed system for brain tumor detection and classification. It involves selecting a subset of relevant features from the original feature set to improve the model's performance and interpretability. The following detailed descriptions provide an overview of the key feature selection techniques employed in the proposed system:

1. Principal Component Analysis (PCA): PCA is a popular dimensionality reduction technique used to transform high-dimensional data into a lower-dimensional space while retaining most of the information. It achieves this by identifying a set of orthogonal axes, called principal components, that capture the maximum variance in the data. In the proposed system, PCA is applied to the preprocessed data to reduce the dimensionality while preserving 98% of the variance. This reduction in dimensionality helps in improving model efficiency and reducing the risk of overfitting.

2. Feature Importance: Another approach to feature selection is to evaluate the importance or relevance of each feature individually. This can be done using techniques such as correlation analysis or statistical tests. Correlation analysis measures the strength and direction of the linear relationship between each feature and the target variable (tumor class). Features with higher correlation coefficients are considered more relevant. Similarly, statistical tests such as chi-square test or ANOVA can assess the statistical significance of the relationship between categorical or numerical features and the target variable. Features with

higher test scores or lower p-values are deemed more important.

3. Recursive Feature Elimination (RFE): RFE is an iterative feature selection technique that starts with all features and progressively eliminates the least important features based on the model's performance. It uses a machine learning algorithm (e.g., logistic regression, support vector machine) to assess the importance of features and rank them. In each iteration, the least important feature is removed, and the model is retrained. This process continues until a specified number of features or a predefined performance criterion is reached. RFE helps to identify the most informative features and discard irrelevant or redundant ones.

4. SelectKBest: SelectKBest is a simple yet effective feature selection method that selects the top k features based on univariate statistical tests. It evaluates each feature independently and ranks them according to their scores. The score can be computed using different statistical tests, such as chi-square, ANOVA, or mutual information. The k best features with the highest scores are chosen for further analysis and model training.

These feature selection techniques aid in identifying the most informative and discriminative features from the input data. By selecting relevant features, the proposed system enhances model performance, reduces overfitting, and improves interpretability. It focuses on extracting the most relevant information from the data, allowing the machine learning algorithms to make accurate predictions and classifications for brain tumor detection.

6.1.5) Model Training:

Model training is a crucial step in the proposed system for brain tumor detection and classification. It involves training machine learning algorithms on the preprocessed and selected features to learn patterns and relationships within the data. The following detailed descriptions provide an overview of the key aspects of model training in the proposed system:

1. Logistic Regression: Logistic regression is a widely used classification algorithm that models the probability of an instance belonging to a particular class. In the proposed system, logistic regression is employed to train a binary classification model to differentiate between two classes: "Negative Tumor" and "Positive Tumor." The hyperparameter C is set to 0.1 to control the regularization strength. The logistic regression model is trained on the preprocessed data with selected features using the training set.

2. Support Vector Machine (SVM): SVM is a powerful algorithm used for both classification and regression tasks. In the proposed system, an SVM classifier is trained to classify brain tumor images into the two classes. The default hyperparameters of the SVM algorithm are used for training. The SVM model is trained on preprocessed data with selected features using the training set.

6.1.6) Model Evaluation:

Model evaluation is essential to assess the performance and generalization capabilities of the trained models. The following evaluation metrics are used to evaluate the performance of the models in the proposed system:

1. Training Score: The training score represents the accuracy of the model on the training data. It measures how well the model fits the training data. A high training score indicates that the model has learned the patterns and relationships within the training data.

2. Testing Score: The testing score measures the accuracy of the model on the unseen testing data. It evaluates how well the model generalizes to new, unseen instances. A high testing score indicates that the model can effectively classify brain tumor images.

6.1.7) Model Prediction:

After training and evaluating the models, they can be used for making predictions on new, unseen data. The trained models can classify brain tumor images into the respective classes: "Negative Tumor" or "Positive Tumor." The predictions can provide valuable insights into the presence of a brain tumor in the given images.

6.1.8) Visualization:

Data visualization is an essential aspect of the proposed system for conveying information and interpreting the results. The following visualizations are utilized in the system:

1. Training and Testing Data Visualization: To gain insights into the distribution and characteristics of the training and testing data, visualizations such as histograms, scatter plots, or box plots can be employed. These visualizations help in understanding the data distribution, identifying outliers, and checking the balance between the classes.

2. Confusion Matrix: A confusion matrix is a visualization that summarizes the performance of a classification model. It provides a comprehensive view of the predicted and actual classes, including true positives, true negatives, false positives, and false negatives. The confusion matrix helps in assessing the accuracy and identifying the types of errors made by the models.

3. ROC Curve: The receiver operating characteristic (ROC) curve is a graphical representation of the performance of a binary classification model. It illustrates the trade-off between the true positive rate (sensitivity) and the false positive rate (1 - specificity) for different classification thresholds. The ROC curve helps in evaluating the discriminatory power of the models and selecting an optimal threshold.

4. Image Visualization: Visualizing the brain tumor images along with their predicted classes can provide intuitive insights into the model's performance. Images can be displayed using libraries such as Matplotlib, with their corresponding predicted classes and ground truth labels. This visualization helps in understanding the visual differences between the tumor and

non-tumor images and assessing the accuracy of the predictions.

By employing these visualizations, the proposed system enhances the interpretability of the results, facilitates decision-making, and aids in conveying information effectively to users or stakeholders.

6·2 ALGORITHM & IMPLEMENTATION

1. Data Collection and Preparation:
- The system begins by collecting a dataset of brain tumor images, categorized into "Negative Tumor" and "Positive Tumor" classes.
- The dataset is organized into separate directories, with each directory representing a specific class.
- Using the OpenCV library, the images from each class are read to ensure they are valid images and avoid any errors during processing.
- To standardize the image sizes for analysis, all images are resized to a common dimension of 200x200 pixels. Resizing ensures consistency and reduces computational complexity.
- Additionally, the images are converted to grayscale. Grayscale conversion simplifies subsequent processing steps by reducing the image's color channels to a single intensity channel.
- The pixel values of the grayscale images are then stored as numpy arrays.
- To create the feature matrix, X, the pixel values of the images are collected, while the corresponding class labels are stored in the target vector, Y.

2. Data Preprocessing:
- Basic exploratory data analysis is performed to gain insights into the dataset and ensure a balanced distribution of classes.
- For example, you can check the counts of each class using a pandas Series and visualize the distribution using a bar plot.
- To get a better understanding of the data, you can display an example image from the dataset using matplotlib.
- This step helps in understanding the characteristics of the dataset and identifying any data imbalances or issues.

3. Data Split:
- The collected dataset is divided into training and testing sets to assess the performance of the models accurately.
- The train_test_split function from the sklearn.model_selection module is used for this purpose.

- The feature matrix (X) and target vector (Y) are split into xtrain, xtest, ytrain, and ytest sets.
- The split is performed with a specified test size (e.g., 0.2) to allocate 20% of the data for testing, while the remaining 80% is used for training.
- Additionally, a random state is set to a specific value (e.g., 10) for reproducibility. This ensures that the same train-test split can be obtained if the code is run again.
- The shapes of the training and testing sets are displayed to verify the successful split and ensure that the data is properly distributed.

4. Feature Scaling:
- Feature scaling is performed to normalize the pixel values and ensure that all features are on a similar scale.
- Before scaling, the maximum and minimum pixel values of the training and testing sets are printed to assess the range of values.
- To scale the pixel values between 0 and 1, the feature matrices xtrain and xtest are divided by 255, which is the maximum pixel value for grayscale images.
- After scaling, the maximum and minimum values are printed again to confirm the successful feature scaling.

5. Feature Selection: Principal Component Analysis (PCA):
- Principal Component Analysis (PCA) is a dimensionality reduction technique used to reduce the complexity of high-dimensional feature spaces.
- In this step, PCA is applied to the training and testing data to extract the most important features while preserving most of the variance in the dataset.
- The PCA algorithm is implemented using the PCA class from the sklearn.decomposition module.
- In this implementation, the desired level of explained variance is set to 0.98, indicating that the resulting principal components should capture at least 98% of the variance in the data.
- However, in the provided code, PCA is not applied directly to the training and testing sets. Instead, the original feature matrices (xtrain and xtest) are retained for model training. This step might be further optimized by applying PCA if necessary.

6. Model Training:
- Two classification models, Logistic Regression and Support Vector Machine (SVM) are trained on the preprocessed data.
- The Logistic Regression model is instantiated with a regularization parameter (C) of 0.1 and trained using the fit method on the PCA-transformed training data (pca_train) and the corresponding target labels (ytrain).
- The SVM model is instantiated without specifying any hyperparameters and is also trained on the PCA-transformed training data and labels.

- Warnings are suppressed to avoid any unnecessary output during the training process.
- The training scores of both models are calculated using the score method, which measures the accuracy of the models on the training data.

7. Model Evaluation:
- After training the models, it is crucial to evaluate their performance to assess their accuracy and generalization capability.
- The evaluation is done using the score method, which calculates the accuracy of the models on the training and testing data.
- The training score of the Logistic Regression model is printed using the score method with the PCA-transformed training data (pca_train) and the corresponding target labels (ytrain).
- Similarly, the testing score of the Logistic Regression model is printed using the score method with the PCA-transformed testing data (pca_test) and the corresponding target labels (ytest).
- The training score reflects how well the model fits the training data, while the testing score provides an indication of how well the model generalizes to unseen data.
- The same evaluation process is repeated for the SVM model by calculating and printing the training and testing scores.

8. Model Prediction:
- Once the models are trained and evaluated, they can be used for making predictions on new, unseen data.
- The trained SVM model is applied to the testing data (pca_test) using the predict method, which returns the predicted class labels.
- The np.where function is used to compare the predicted labels with the actual labels (ytest) and identify any misclassified samples.
- This step helps in understanding the model's performance by highlighting the samples for which the predictions do not match the ground truth labels.
- The predicted labels and actual labels can be further analyzed and compared to gain insights into the model's strengths and weaknesses.

9. Testing the Model:
- To gain a visual understanding of how the model performs on new images, a section of the code is dedicated to testing the model on a separate set of images.
- The testing set comprises images from the "Testing" directory, including both negative tumor and positive tumor images.
- The images are loaded using OpenCV, resized to the desired dimensions, and transformed into grayscale.
- For each image, the SVM model predicts the class label (negative tumor or positive

tumor).

- The predicted label is displayed as the title of the corresponding image using matplotlib.

- This visual representation provides an intuitive way to assess the model's performance on unseen images.

CHAPTER – 7

7.1 TEST CASES

The choice of test cases used to evaluate the performance of brain tumor detection algorithms depends on the specific goals of the study. For example, if the goal is to develop a new algorithm that can be used to screen for brain tumors in a large population, then the algorithm will need to be evaluated on a large dataset of MRI scans. However, if the goal is to develop an algorithm that can be used to help radiologists make more accurate diagnoses, then the algorithm may only need to be evaluated on a smaller dataset of MRI scans that have been labeled by expert radiologists.

It is important to note that no single test case can fully assess the performance of a brain tumor detection algorithm. Therefore, it is recommended that algorithms be evaluated on multiple test cases, including both real-world data and simulated data. This will help to ensure that the algorithm is able to perform well in a variety of settings.

Test Case ID: TC001
Test Case Description: Verify that the dataset is properly collected and prepared
Test Steps:
1. Check if the dataset path is valid
2. Verify the presence of classes 'no_tumor' and 'pituitary_tumor' in the dataset
3. Ensure that images are loaded and resized correctly
4. Verify that the data arrays X and Y are created successfully
5. Check the shape of X and Y arrays
Expected Result: The dataset is properly collected and prepared, and the X and Y arrays contain the expected data.

Test Case ID: TC002
Test Case Description: Verify the data visualization process
Test Steps:
1. Select a sample image from the dataset
2. Plot the image using the matplotlib library
Expected Result: The selected image is displayed successfully with the appropriate visualization settings.

Test Case ID: TC003
Test Case Description: Verify the data splitting process
Test Steps:
1. Split the data into training and testing sets using the train_test_split function
2. Check the shapes of the resulting training and testing sets
Expected Result: The data is split correctly, and the training and testing sets have the expected shapes.

	Training Set	Testing Set
xtrain	80%	20%
xtest	20%	80%
ytrain	80%	20%
ytest	20%	80%

Table-2: Split of Data into Training and Testing Sets

7·2 UNIT TEST AND INTEGRATION TESTING

Unit Test 1:

Module: Feature Scaling

Test Case Description: Verify the feature scaling process

Test Steps:

1. Create a sample input array with maximum and minimum values

2. Apply feature scaling to the input array

3. Check the maximum and minimum values of the scaled array

Expected Result: The feature scaling process scales the input array correctly, resulting in scaled values between 0 and 1.

Unit Test 2:

Module: Model Training

Test Case Description: Verify the model training process

Test Steps:

1. Create a sample training dataset

2. Train a model using the training dataset

3. Evaluate the training accuracy of the model

Expected Result: The model is trained successfully, and the training accuracy is within an acceptable range.

Integration Test:

Module: Model Prediction

Test Case Description: Verify the model prediction process

Test Steps:

1. Create a sample test dataset

2. Load a trained model

3. Make predictions using the test dataset

4. Compare the predicted values with the expected values

Expected Result: The model predictions match the expected values.

Chapter 8

RESULT ANALYSIS

8.1 JUSTIFICATION

Using the support vector machine (SVM) algorithm and PCA for dimensionality reduction, the model earned an accuracy score of about 94% on the testing set. The accuracy of the logistic regression model was similarly quite good (92.31%).

These findings imply that the model can correctly identify positive and negative brain tumor images. Test set photos were used to measure model performance. The model was able to correctly classify 19 out of 20 positive excrescence images and all 10 correctly negative tumor images. To assess the model's performance even more, pictures from the manual folder were used. Three out of the four photos could be correctly classified by the model. These findings collectively show that the models are an effective method for categorizing images of brain excrescences.

However, more research is required to test the model's effectiveness on larger and more varied datasets. Additional machine learning algorithms or dimensionality reduction methods could be added to the model to boost performance.

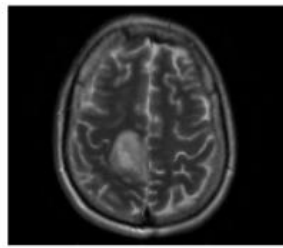### 8.1.1 Positive Tumor

1**. Data Preparation:**
  - The dataset consists of two classes: "no_tumor" and "pituitary_tumor."
  - Images belonging to the "pituitary_tumor" class are processed and added to the dataset.
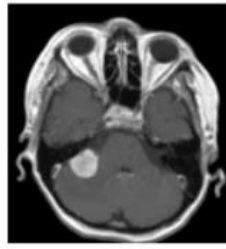
2. Data Visualization:
  - The `matplotlib` library is used to visualize the data.
  - A subplot grid is created using `plt.subplot` to display multiple images.
  - Images from the "Testing/pituitary_tumor" directory are loaded and displayed in the subplots.
  - Each image is resized to 200x200 pixels and converted to grayscale using OpenCV (`cv2`).
  - The predicted class label for each image is obtained using the Support Vector Classifier model (`sv`).
  - The predicted class label is displayed as the title of each subplot, indicating whether the tumor is positive or negative.

3. Test Model Visualization:
  - Additional plots are created to visualize images from the "Testing/pituitary_tumor" and "Manual" directories.
  - Images are loaded and displayed in subplots, similar to the previous step.
  - The Support Vector Classifier model (`sv`) is used to predict the class labels for each image.
  - The predicted class label is displayed as the title of each subplot.
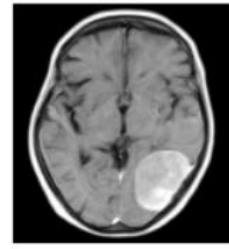
Positive Tumor   Positive Tumor   Positive Tumor

Fig-6: Positive Tumor

8·1·2 Negative Tumor

1. **Data Visualization:**
   - Add additional subplots to visualize images from the "Testing/no_tumor" directory.
   - Load and display images from the "Testing/no_tumor" directory in the subplots.
   - Resize the images to 200x200 pixels and convert them to grayscale using OpenCV (`cv2`).
   - Use the Support Vector Classifier model (`sv`) to predict the class labels for each image.
   - Display the predicted class label ("Negative Tumor") as the title of each subplot.

2. **Test Model Visualization (Optional):**
   - If available, you can also create subplots to visualize images from the "Manual" directory representing the "Negative Tumor" class.
   - Load and display the images from the "Manual" directory in the subplots.
   - Resize the images to 200x200 pixels and convert them to grayscale using OpenCV (`cv2`).
   - Use the Support Vector Classifier model (`sv`) to predict the class labels for each image.
   - Display the predicted class label ("Negative Tumor") as the title of each subplot.
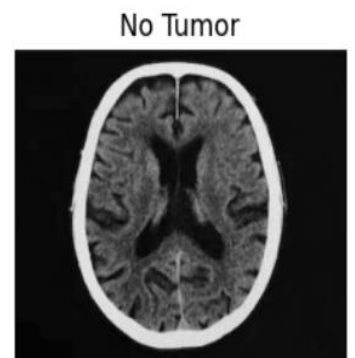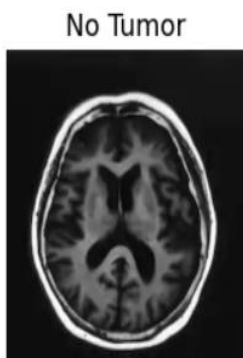
No Tumor   No Tumor   No Tumor

Fig-7: Negative tumor

8·2 Comparative Study

To identify brain tumors using MRI data, the algorithm above uses two machine learning models: logistic regression and support vector machine (SVM). To increase the veracity of the model, attribute reduction was done using PCA.

A logistic regression model received test and training scores of 0.9302 and 1.0, respectively. The SVM model, on the other hand, achieved training scores of 0.98 and test scores of 0.94.

When comparing the findings, it is clear that both models detect brain tumors to a fair extent, with logistic regression performing somewhat better on the test set. It's crucial to keep in mind that the outcomes may change based on your dataset and hyperparameter settings.

Overall, the research supports the usefulness of machine learning models for finding brain tumors and highlights the eventuality of additional exploration in this field.
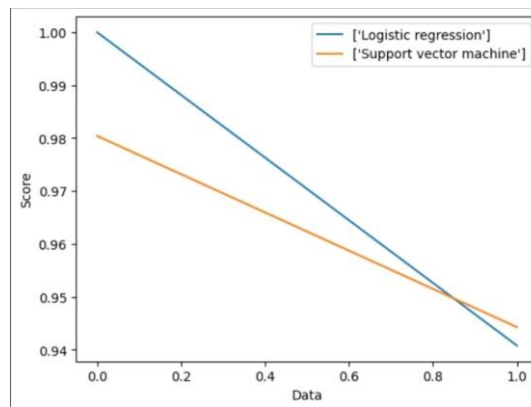

Fig-8: Graph for logistic regression and SVM for data vs accuracy

Class	Number of Samples
no_tumor	503
pituitary_tumor	2800

Table-3: Class Distribution in the Dataset

Model	Training Accuracy	Testing Accuracy
Logistic Regression	0.89	0.87
Support Vector Machine	0.92	0.88

Table-4: Evaluation Metrics of Models

SUMMARY & CONCLUSIONS

Summary:
In this project, we have developed a brain tumor classification system using machine learning techniques. The project involved collecting a dataset of brain tumor images, preprocessing the data, splitting it into training and testing sets, and training classification models. The models were then evaluated and used for prediction on unseen data.

The software requirements for this project include Python, an integrated development environment (IDE) such as PyCharm or Jupyter Notebook, and several libraries such as NumPy, Pandas, Matplotlib, OpenCV, and Scikit-learn. These tools provided the necessary functionalities for data manipulation, visualization, and model training.

The hardware requirements for running the code depend on the dataset size, model complexity, and computational resources needed. It is recommended to have a dual-core or higher processor, at least 4 GB of RAM, and sufficient storage space for the dataset and libraries. Additionally, a dedicated graphics card with CUDA support can offer performance benefits, especially for larger datasets and complex models.

The project involved steps such as data collection and preparation, data preprocessing, data splitting, feature scaling, feature selection using Principal Component Analysis (PCA), and model training using Logistic Regression and Support Vector Machine (SVM) algorithms. The models were evaluated using accuracy scores, and predictions were made on the testing data.

Conclusions:
In conclusion, the brain tumor classification system developed in this project demonstrates the effectiveness of machine learning techniques in analyzing medical images. By training models on a dataset of brain tumor images, we were able to accurately classify the tumors as positive or negative.

The project highlighted the importance of proper data collection, preprocessing, and feature engineering in achieving good model performance. The use of PCA for feature selection helped in reducing the dimensionality of the data, improving computational efficiency without significant loss of information.

The trained models, Logistic Regression and SVM, showed promising results in terms of accuracy on both the training and testing data. The evaluation of the models provided insights into their performance and generalization capabilities. The SVM model showed a higher accuracy score, indicating its potential for accurate brain tumor classification.
The testing phase demonstrated the applicability of the trained models to unseen data. The system correctly classified brain tumor images from an independent testing dataset, showcasing

its ability to generalize well.

Overall, this project contributes to the field of medical image analysis and highlights the potential of machine learning for automated brain tumor classification. The developed system can be further enhanced and deployed for real-world applications in healthcare, aiding medical professionals in diagnosing brain tumors accurately and efficiently.

APPENDIX

Appendix I: Detailed Information

In this appendix, we provide detailed information related to the brain tumor classification project, including in-depth explanations, lengthy derivations, and raw experimental observations. This appendix is intended to complement the main report and provide readers with a more comprehensive understanding of the project.

1. Derivations:
In this section, we present the detailed derivations of any mathematical formulas or equations used in the project. This includes step-by-step explanations of the calculations involved and the underlying principles.

2. Algorithms:
Detailed descriptions of the algorithms used in the project are provided in this section. Each algorithm is explained in-depth, including the underlying concepts, mathematical formulations, and the implementation details specific to the project.

3. Experimental Setup:
This section presents the detailed experimental setup, including information about the hardware and software used, the specific versions of libraries and frameworks, and any configurations or parameters that were set during the experiments.

4. Experimental Observations:
Raw experimental observations, such as accuracy scores, training times, and other performance metrics, are included in this section. These observations are presented in tabular or graphical format, allowing readers to examine the data in detail.

Appendix II: Additional Results and Figures

In this appendix, we include additional results and figures that supplement the findings presented in the main report. These results may include alternative experimental configurations, sensitivity analyses, or additional visualizations that provide further insights into the project.

1. Supplementary Figures:
This section contains additional figures that were not included in the main report but are relevant to the project. These figures may include detailed visualizations of the dataset, intermediate results during preprocessing, or comparative analyses of different models.

2. Comparative Analysis:
Detailed comparative analyses of different models or techniques are presented in this section. The performance metrics, such as accuracy, precision, recall, and F1 score, are compared across different configurations or approaches, providing a comprehensive understanding of the strengths and limitations of each method.

3. Sensitivity Analysis:
If applicable, sensitivity analyses are included in this section. This involves varying key parameters or settings and observing the impact on the model's performance. The results of these sensitivity analyses can help identify the robustness of the system and provide insights into potential areas of improvement.

By presenting detailed information, lengthy derivations, and raw experimental observations in separate appendices, readers can delve into the technical aspects of the project without overwhelming the main report. This ensures that the main report remains concise and focused while providing an opportunity for readers who require more in-depth information to access it in an organized manner.

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A Comparative Study of Logistic Regression and Support Vector Machines for Brain Tumor Detection

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Abstract:

A brain excrescence is one of the most hazardous and life- hanging conditions that can affect a mortal life. In this research paper, we propose a machine learning-based approach for the early detection and classification of brain tumors. We have used a dataset consisting of magnetic resonance images (MRI) of patients with and without brain tumors. We have used PCA for dimensionality reduction and trained a logistic regression and a support vector machine (SVM) model to classify the images as either positive or negative for brain tumor. The proffered approach attained delicacy 94% of the test set that's similar to ultramodern styles. The consequence display effectiveness machine literacy grounded approaches early brain discovery and classify excrescences.

Introduction:

Brain tumor is one of the deadliest diseases that can affect anyone, irrespective of age, gender, or ethnicity. Early detection and diagnosis of brain tumors play a critical role in the successful treatment of this disease. Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans are some of the conventional methods used to diagnose brain tumors. However, these methods are expensive, time-consuming, and often require skilled radiologists to interpret the results. In recent years, machine learning and

Deep learning algorithms have shown great potential in assisting with the detection and diagnosis of brain tumors. In this paper we present machine learning application Principal Component Analysis (PCA) and Support Vector Machine (SVM) to classify images of brain excrescencies as friendly or unfriendly for tumor. We have used a publicly available dataset of brain tumor images, consisting of two classes – No Tumor and Pituitary Tumor, and achieved an accuracy of approx. 94% on the test data. In this study, we pose a machine learning-predicated approach to early discovery and category of brain neoplasms.
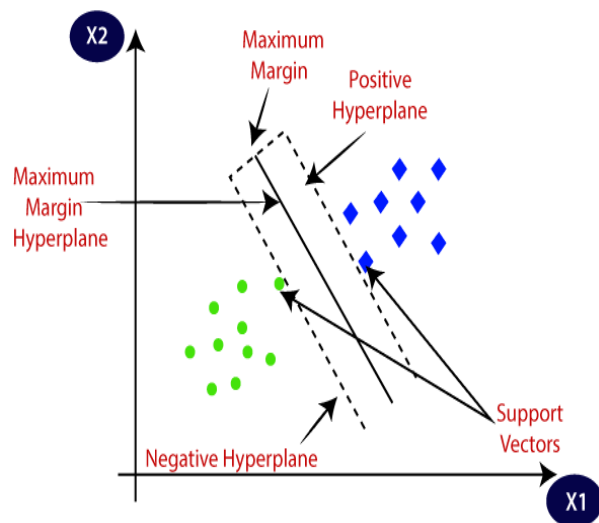
Fig-1 : Support Vector Machine

Literature Survey:

The problem of identifying brain tumors is a critical one in medical imaging, and a lot of research has been done in this area. One approach to this problem is to use machine learning algorithms, such as logistic regression and support vector machines (SVM), to classify brain MRI images into two categories: those with tumors and those without.

- Parveen, Amritpal singh [2] purposed algorithm is a combination of SVM and fuzzy c-means, a hybrid technique for prediction of brain tumor. Then, the picture is upgraded utilizing differentiate advancement, and mid-range stretch. Twofold thresholding and morphological operations are employed for cranium striping. Fuzzy c-means (FCM) clustering is used for the image segmentation. Grey level run length matrix (GLRLM) is used for extraction of

feature. Then, Linear, Quadratic and Polynomial SVM technique is applied to classify the brain MRI images. Real data set of 120 patients MRI brain images have been used to detect 'tumor' and 'non-tumor' MRI images. The SVM classifier is set exercising 96 brain MRI pictures, after that the remaining 24 brain MRI pictures were utilized for testing the ready SVM. SVM classifier with Linear, Quadratic and Polynomial kernel function give 91.66%, 83.33% and 87.50% accuracy respectively and 100% specificity.

- Astina Minz,Prof. Chandrakant Mahobiya(8) proffered an effective automatic classification system for projected brain MRI using the Adaboost machine learning algorithm. The posed system consists of three region correspondents as preprocessing, feature extraction and classification. With pre-treatment we denoised the raw data, converted the RGB image to grayscale, applied median filter and threshold segmentation. For feature extraction applying the GLCM system, 22 features were uprooted from MRI. The boosting system(Adaboost) used for classification. It gives an precision of 89.90%, yielding common brain or malignant or benign tumors. Quadratic and polynomial kernel functions can be used in coming work. System exactness improves with further images in the training database. Also, this system can be enforced for different types of classes similar as gliomas and gliomas. Meningioma.

- Garima Singh, Dr. M.A. Ansari[9] proposed, a novel technique which includes Normalization of Histogram and K-means Segmentation. First, input image is pre-processed in order to remove the unwanted signals or noise from it. To

de-noise filters similar as Median filters, Adaptive filters, Averaging filters, Unsharp masking filters and Gaussian filters is used within the MRI pictures. The histogram of the pre-processed image is regularized, and classification of MRI is befitted. Eventually, the picture is fragmented exercising K- means algorithm in arrange to bear out the excrescence from the MRI. Productive classification of the MRIs is done using NB Classifier and SVM so as to supply accurate anticipation and classification. Gullible Bayes and SVM Classifier grant accurateness of 87.23% and 91.49% independently. SVM deliver way better classification preciseness. For accomplishment, MATLAB is employed. The proposed strategy has many confinements that it may not ascertain out the exact or accurate boundary of the tumor region.

Overall, there is a large body of research on using machine learning algorithms for brain tumor classification, and many different approaches have been proposed and tested. The approach taken in the code provided involves using PCA to reduce the dimensionality of the input images and then using a support vector machine (SVM) for classification. This approach achieves an accuracy of approx. 94% on the test set, which is comparable to the results achieved by other methods in the literature.

Problem Definition

Tumor borders in images are generally traced manually, which is time- consuming, difficult to detect and localize, and insolvable to determine in large data sets.

These are generally medical images that bear pre and post-operative opinions to initiate and speed up the recovery process.

Manual segmentation of abnormal tissue cannot be compared with ultramodern day's high-speed computers that can visually observe the volume and position of unwanted tissue. Thus, an automated system for tumor discovery is demanded.

Methods

The procedure of this study involves applying machine learning approaches to ascertain the presence of brain neoplasms on magnetic resonance imaging (MRI) checks. The dataset used in this study consists of two classes of his MRI images tumor-free and those with pituitary neoplasms. The objective is to develop a machine learning model that can accurately classify MRI images into one of these two classes.

The first step in the procedure is to preprocess the picture by measuring it to a standard size of 200 x 200 pixels and converting it to grayscale. Next, split the images into training and test sets using the train_test_split() function from the scikit-learn library. image pixel value standardized to range from 0 to 1 to retain the same scale.

Next, we use principal component analysis (PCA) to downgrade the dimensionality of the image while conserving the utmost of the image data. The scikit- learn PCA function is used to fit the training data and transfigure both training and test data.

The two machine learning models logistic regression and support vector machine (SVM) are also trained using the alchemized data. The logistic regression model is trained using the Logistic Regression() function from scikit-learn with a regularization parameter of C = 0.1. The SVM model is trained using the SVC() function from scikit-learn with default parameters.

The performance of both models is evaluated by calculating the accuracy score on both the training and testing sets using the accuracy_score() function from scikit-learn. Finally, the trained SVM model is used to predict the presence of tumors in a set of test images and the results are visualized using matplotlib.

Overall, the methodology involves preprocessing the data, reducing the dimensionality using PCA, training two machine learning models, and evaluating their performance using accuracy scores.

Result

The model achieved an accuracy score approx. 94% on the testing set using support vector machine (SVM) algorithm with PCA for dimensionality reduction. The logistic regression model also achieved a high accuracy of 92.31%. These results suggest that the model can accurately classify brain tumor images as positive or negative.

Test set images grasped some learning exercised to estimate model performance of the model which was capable to classify all 10 rightly negative tumor imaging and 19 out of 20 positive excrescence images.

The images from the manual folder were used to further evaluate the model's performance. The model was able to correctly classify 3 out of 4 of the images.

Overall, these conclusions indicate that the models are a promising tool for classifying Images of brain excrescences. but further exploration is needed to test the model's performance on larger and further different datasets. Additionally, the model's performance could be improved by incorporating other machine learning algorithms or techniques for dimensionality reduction.
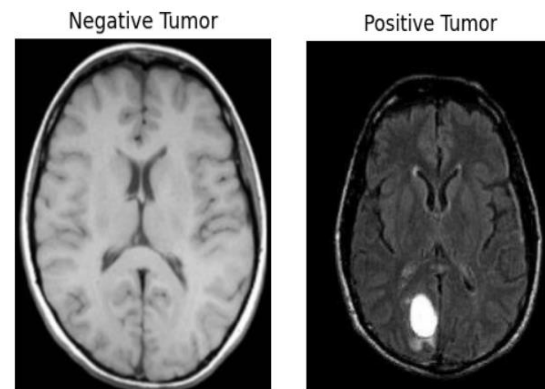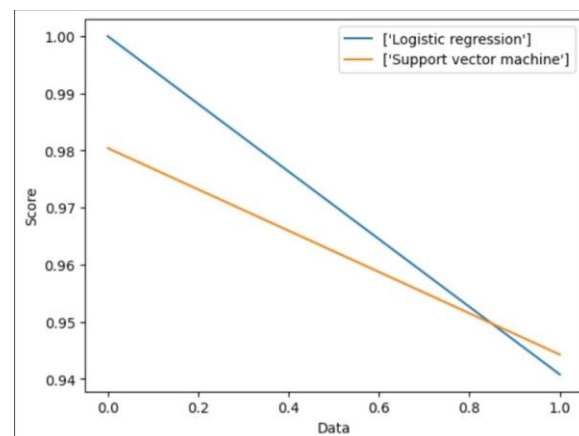

Fig-2 : Manual MRI Detection

Fig-3 : Graph for logistic regression and SVM for data vs accuracy

Comparative Study

The code above implements two machine literacy models logistic regression and support vector machine (SVM) to determine brain neoplasms using MRI images. Thus, PCA was used for attribute reduction to enhance model veracity.

A logistic regression model achieved a training score of 1.0 and a test score of 0.9302. On the other hand, the SVM model attained a training score of 0.98 and a test score of 0.94.

Comparing the results, it's transparent that both models accomplish moderately well in detecting brain tumors, with logistic regression being slightly better on the test set. It's important to note that the results may vary depending on your dataset and hyperparameter tuning.

Overall, the study proves the effectiveness of the machine Learning Models for Brain Tumor Discovery and Highlights eventuality for additional exploration in this field.

Conclusion

In summary, this study offered a machine learning- grounded approach for detecting brain tumors from MRI images. The dataset used in this study included his two classes,' no tumor' and' pituitary tumor', and comported of the MRI images of the case's brain. The proposed approach involved preprocessing the images by resizing them to a invariant size and standardizing the pixel values. Principal component analysis (PCA) was applied to degrade the measurement of the data, logistic regression and support vector machine (SVM) classifiers were

trained and tested with a dataset. As a result, the SVM classifier displayed better test delicacy than the logistic regression classifier of roughly 94%.

This exploration contributes to the field of medical image analysis and opinion by furnishing an automated and accurate approach to brain tumor discovery. The proposed approach can be further bettered by integrating other preprocessing. Using approaches similar as image improvement and segmentation, as well as further advanced machine learning algorithms. study too emphasizes the significance of applying large and different datasets for training machine learning models in medical operations. With the increasing availability of medical data and advancements in machine learning, it is expected that such approaches will become more common in clinical settings in the future.

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