BRAIN TUMOR DETECTION USING MACHINE LEARNING TECHNIQUES

A PROJECT REPORT

Submitted by

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ABSTRACT

Our project aims to develop an efficient and accurate method for detecting brain tumors in medical images using machine learning (ML) approaches. Brain tumors pose a significant health risk, and early detection is crucial for effective treatment. The project involves multiple stages, including preprocessing of MRI images to enhance quality, extraction of relevant features, and utilization of these features to train and test different ML models. In the preprocessing phase, standardization, noise reduction, and feature extraction techniques, including wavelet transformation and texture analysis, were employed. A comprehensive dataset encompassing both benign and malignant brain tumors was utilized for training and validation. Classifiers, including K Nearest Neighbors (KNNs), Support Vector Machines (SVMs), Naïve Bayes, Decision Trees, and Logistic Regression were employed and carefully fine-tuned. The proposed approach leverages the power of ML to discern intricate patterns and relationships within the images, enabling accurate tumor classification. Our system demonstrated exceptional performance, achieving an accuracy of 98.78% in brain tumor detection. Comparative analyses confirmed its superiority over existing state-of-the-art methods. Successful implementation of this project stands to significantly impact the medical field by providing a reliable tool for timely and accurate brain tumor diagnosis. This would facilitate better patient care and treatment planning. The flexible framework of our system allows for seamless adaptation to emerging imaging modalities, ensuring its relevance in the evolving landscape of medical diagnostics. In conclusion, our study presents a robust machine learning-based approach for early detection of brain tumors using multi-modal imaging data. The proposed system offers high accuracy and sensitivity, holding significant potential for aiding healthcare professionals in timely and accurate diagnosis. Its integration into clinical workflows can lead to improved patient outcomes and more efficient healthcare delivery.

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LIST OF ABBREVIATIONS

BRATS/BRATS	BRAIN TUMOR SEGMENTATION
FP	FALSE POSITIVE
FN	FALSE NEGATIVE
HOG	HISTOGRAM OF ORIENTED GRADIENT
ID	IMAGE DATA
MRI	MAGNETIC RESONANCE IMAGE
NN	NEURAL NETWORKS
RF	RADIO FREQUENCY
ROC	RECEIVER OPERATING CHARACTERISTICS
SD	SYNTHETIC DATA
SVM	SUPPORT VECTOR MACHINE
TP	TRUE POSITIVE
TN	TRUE NEGATIVE

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CHAPTER 1

INTRODUCTION

Detecting brain tumors through medical imaging has always been a formidable task. The human brain, a vital control center for bodily functions, is vulnerable to a range of conditions, including infections, strokes, and neoplasms. A brain neoplasm refers to an abnormal growth or proliferation of cells within the cranial region, which can manifest as either malignant, containing cancerous cells, or benign, lacking malignancy.

Cerebral neoplasms are typically categorized as primary or secondary. Primary cerebral neoplasms originate within the brain and can be either malignant or benign. In contrast, secondary or metastatic cerebral neoplasms occur when malignant cells from distant anatomical sites spread to the brain and undergo proliferation. These neoplasms are commonly evaluated using image-based diagnostic methods, utilizing techniques such as X-rays, powerful magnetic resonance imaging, or radiopharmaceutical agents to generate detailed brain visualizations.

A variety of scans play a crucial role in diagnosing brain conditions. These imaging techniques produce highly detailed images that provide valuable information about the presence and precise location of cerebral neoplasms.

COMPUTED TOMOGRAPHY:

This scan is a diagnostic technique that utilizes X-ray technology to create a three-dimensional representation of the brain. Unlike traditional X-rays, which capture single snapshots, a CT scan involves the acquisition of numerous images. During the procedure, the CT scanner orbits around the patient while they lie on a table. These multiple images are then combined to generate cross-sectional images of the body. CT scans provide essential data about the tumor's dimensions and its potential effects on the integrity of the cranial bones.

CT ANGIOGRAM:

It is a diagnostic procedure that utilizes a series of X-ray images to visualize the complex network of arteries and blood vessels in the brain. During this process, contrast material is injected through an intravenous (IV) line while the patient is inside the CT scanner. This diagnostic technique is crucial for surgical planning as it provides detailed information about the vascular structure.

MYELOGRAM:

It is a diagnostic technique that uses a contrast agent to determine whether a tumor has spread to neighboring areas of the body, including the spinal cord. This method entails the precise injection of contrast dye into the Cerebrospinal Fluid (CSF).

POSITRON EMISSION TOMOGRAPHY:

In this procedure, a radioactive substance called FDG is introduced into the bloodstream. The quantity of FDG administered is minimal, and it naturally clears from the body within a day. Tumorous cells, characterized by their rapid growth, exhibit higher uptake of this sugar compared to most other cell types. Approximately an hour after FDG administration, the patient is positioned on a table inside the PET scanner. A specialized camera then generates an image that highlights areas of radioactivity within the patient's body.

While PET scans may not provide detailed specifics, they offer crucial insights into whether the abnormalities detected in previous tests suggest the presence of tumors. PET scans are often used in conjunction with CT scans to assess the success of tumor treatment or to detect any recurrence after treatment. Typically, the initial stage of treatment involves the use of a PET-CT scan.

MAGNETIC RESONANCE IMAGING:

It is a fundamental diagnostic imaging technique that distinguishes itself from other scanning methods by its use of radio waves and powerful magnetic fields instead of X-rays. During the procedure, the energy from radio waves is absorbed and subsequently re-emitted, with the pattern determined by the specific body tissue and any underlying conditions. This intricate pattern is then transformed into a highly detailed image of specific body regions through computer processing. To enhance clarity, an injectable contrast agent called gadolinium is intravenously administered prior to the scan, effectively boosting the level of detail.

WHAT MAKES MRI IMAGES PREFERABLE TO OTHER IMAGING METHODS?

1. MRI represents a non-invasive imaging method.

2. Choosing an MRI is a cost-effective decision.

3. MRI offers exceptional distinction when it comes to identifying tumors within the cranial area.

4. The total duration for a thorough full-body MRI is shorter compared to PET and X-ray scans.

5. MRI provides unparalleled clarity in visualizing the skeletal structure and concealed organs, such as the lungs protected by ribs and the brain situated within the skull.

1.1 AIM AND OBJECTIVE

The primary objective of this thesis is the identification of brain tumors within medical images. The key aim involves the precise classification of these tumors and non-tumorous regions using the Support Vector Machine (SVM) technique. This classification process is facilitated by the utilization of the feature extraction algorithm known as HOG, which stands for Histogram of Oriented Gradients.

Our specific goals include the following phases:

a) Curating relevant MRI brain images with tumors from an existing database that requires refinement.
b) Utilizing the HOG feature extraction algorithm to capture distinctive features that define brain tumor characteristics.
c) Employing the extracted feature vectors as input for SVM to execute the classification process.
d) Assessing the SVM's performance by applying Receiver Operating Characteristics (ROC) to ensure robust tumor detection and classification.

1.2RESEARCH QUESTIONS

1: What strategies can be employed to achieve precise brain tumor classification?

2: Does the utilization of the HOG feature extraction method enable dependable brain tumor detection?
3: How effective is SVM in discriminating between tumor and non-tumor cases?

4: Is it feasible to attain a 100% classification accuracy in distinguishing tumor and non-tumor cases using the HOG algorithm?
5: Can SVM proficiently categorize tumors and non-tumors when image features are directly extracted without relying on the HOG technique?

1.3 ORGANIZATION OF REPORT

Chapter 1 serves as a comprehensive introduction to this thesis, providing an overview, outlining our primary objectives, and defining the research questions we aim to address. Moving into Chapter 2, we conduct an in-depth analysis of previous research efforts related to brain tumor detection. In Chapter 3, we embark on an extensive exploration of 2 crucial components: the Histogram of Oriented Gradients and the Support Vector Machine. Chapter 4 offers a detailed account of the integration of the feature vector with the SVM classifier. In the subsequent chapter, Chapter 5, we present the results derived from our analytical work. Finally, in Chapter 6, we conclude the report while also discussing future prospects for advancements in brain tumor detection methodologies.

CHAPTER 2

LITERATURE SURVEY

Numerous research endeavors have been undertaken in the domain of brain tumor detection. Haenssle et al. [2] introduced a comprehensive methodology for the identification of brain tumors. Their approach aimed to differentiate between healthy brains and those affected by tumors, as well as distinguish between benign and malignant tumors. The methodology comprised a seven-stage algorithmic process, which involved tasks such as pre-processing of images, feature extraction, and classification of images using ml techniques. Various methods were explored, including Canny edge detection, Harris corner detection, adaptive thresholding, and Harris corner detection once more. The combination of Canny edge detection and Harris corner detection yielded 19% false recognition rate for distinguishing healthy brains from those with tumors, and a 10% rate for distinguishing benign from malignant tumors. On the other hand, the integration of adaptive thresholding and Harris corner detection resulted in a 15.6% false recognition rate for discriminating healthy brains from those with tumors, and a 6% rate for differentiating malignant and benign tumors.

Codella et al. presented a novel algorithm for textural feature extraction, which focused on utilizing kurtosis and was named KWCEM (Kurtosis Wavelet Coefficient Energy Modeling). This algorithm was developed with the specific goal of extracting and detecting brain tumors. Their approach not only improved the quality of image segmentation but also reduced the size of the feature set. Additionally, they incorporated this algorithm into Canny edge detection, leading to a significant enhancement in the quality of the segmented images.
Han et al. introduced a methodology that involved the evaluation of different techniques for the detection of brain tumors. They utilized image mining methods, including Grey Level Co-Occurrence (GLCM). These techniques were applied to the BRATS database, resulting in notable levels of accuracy. GLCM achieved an accuracy rate of 95%, showcasing its impressive performance.

Ha et al. developed a graphical user interface (GUI) algorithm aimed at the detection, extraction, and identification of lesions. At the core of this algorithm's effectiveness is the utilization of the Otsu method, which transforms a 2D image into a 3D representation, enhancing the accuracy and efficiency of tumor detection. Furthermore, the algorithm underwent a comparative analysis in which it was evaluated alongside the Multimodal MRI segmentation of ischemic lesions. The results of this analysis demonstrated favorable outcomes in lesion evaluation.

Ribeiro et al. presented a novel method for the detection and classification of brain tumors using Gabor wavelets and Probabilistic Neural Network. Their approach involved feature extraction through wavelet transformation, followed by the use of PNN to categorize tumors into groups, including malignant, metastatic, or benign. This method exhibited a notably high degree of accuracy in the classification process.

Hussain et al. introduced a detailed four-step methodology for classifying brain tumors. This methodology involved four key stages: preprocessing, segmentation, feature extraction, and the crucial classification step. To achieve tumor categorization, the authors employed an innovative technique called TANN (Tumor Area Neural Network). TANN was applied to various datasets, including BRATS, OASTS, and NBTR, and it demonstrated impressive detection rates and rapid classification. Notably, it exhibited exceptional performance when applied to the BRATS dataset.

Oakden-Rayner et al. performed a comparative assessment of segmentation techniques, which encompassed mean shift, histogram-based thresholding (ThH), and Support Vector Machine (SVM). These techniques were applied to both PET and MRI images for tumor detection. The outcomes of this analysis indicated that, when dealing with MRI images, SVM and ThH proved to be effective in detecting tumors. In contrast, for PET images, SVM outperformed the other methods.

Barata et al. proposed a hybrid approach to the detection and classification of brain tumors. This method encompassed three fundamental stages: skull identification, feature extraction using the gray-level co-occurrence matrix (GLCM), and the application of the least square Support Vector Machine (SVM) for tumor categorization. It is noteworthy that the SVM demonstrated an outstanding accuracy rate of 5.6%, surpassing the performance of Radial Basis Function (RBF) and Backpropagation (BP) techniques, as evidenced in the comparative evaluation.

This comprehensive effort primarily focuses on improving the detection and classification of brain tumors by combining a wide range of techniques and algorithms to produce accurate and efficient results. The methodologies detailed in these research studies offer valuable insights into the ever-evolving field of medical image analysis and tumor diagnosis.

Our objectives after the literature survey are:

1. Develop a brain tumor detection system using Histogram of Oriented Gradients (HOG) and AI/ML techniques to enhance texture-based analysis.
2. Leverage HOG's gradient-based features to create a robust system that overcomes challenges of inter-patient variability and captures tumor heterogeneity.
3. Improve tumor localization accuracy and boundary delineation by utilizing HOG's capacity to capture fine-scale texture variations within heterogeneous regions.
4. Enhance algorithm flexibility by providing simplified yet informative HOG features, enabling the use of diverse AI/ML algorithms based on problem complexity.

CHAPTER 3

ARCHITECTURE AND ANALYSIS OF BRAIN TUMOR DETECTION

3.1UNDERSTANDING OF MRI

Magnetic Resonance Imaging (MRI) functions based on the principle of harnessing the inherent magnetization property of atomic nuclei. The process begins with the application of a strong and uniform external magnetic field to the targeted tissue, aligning the protons within the water nuclei. Initially, these protons are randomly oriented, but they undergo a phenomenon known as "magnetization" [15]. This state of magnetization is temporarily disrupted by Radio Frequency (RF) energy, triggering the relaxation processes of the nuclei, causing them to return to their original alignments while emitting RF energy. After a specific time, interval, the resulting signals are recorded. These signals contain frequency data, which is then transformed into corresponding levels of intensity through Fourier Transform, manifesting as varying shades of gray within a pixel grid. Different types of images are produced by manipulating the sequence of applied and recorded RF pulses.

Figure 3.1 SCANNING MRI

3.1.1 MRI RELATED DEFINITIONS

REPETITION TIME:

This term refers to the interval between the emission of an initial excitation pulse and the following pulse, signifying the time span between consecutive pulses [15].

TIME TO ECHO:

This denotes the timeframe starting from the commencement of the RF excitation pulse to the termination of the signal acquired in the coil, delineating the duration that encompasses the transmission of the RF pulse and the reception of signal [15].

LONGITUDINAL RELAXATION TIME:

It indicates the time parameter utilized to measure the speed at which stimulated protons revert to their original state. This represents the duration required for the rotating protons to realign themselves with the external field.

TRANSVERSE RELAXATION TIME:

This term represents the time parameter used to assess whether the stimulated protons reach equilibrium or experience a departure from phase coherence with one another. It signifies the duration it takes for the rotating protons to lose coherence while interacting with nuclei that are spinning perpendicular to the main magnetic field.

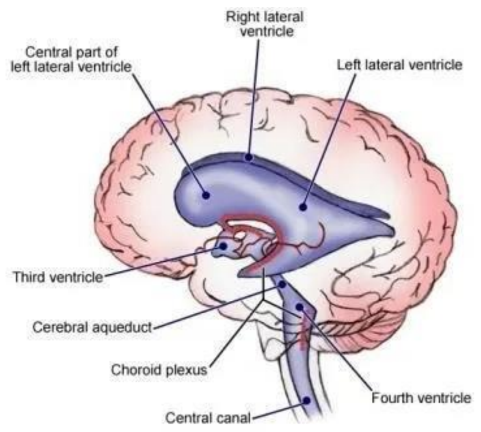


Figure 3.2 CSF

CEREBROSPINAL FLUID

It is a transparent and colorless fluid found within the brain.

GADOLINIUM:

It is a safe and non-toxic paramagnetic contrast agent. When introduced during an MRI examination, it plays a vital role in enhancing and improving the quality of the MRI image. Images enhanced with GAD are highly valuable for evaluating vascular structures and detecting any anomalies in the barriers.

3.1.2 SEQUENCE OF MRI IMAGING:

IMAGES T1-WEIGHTED:

These images are created by employing brief Echo Time (TE) and Repetition Time (TR) intervals. The tissue's T1 properties govern the visual contrast and brightness of the image [16].

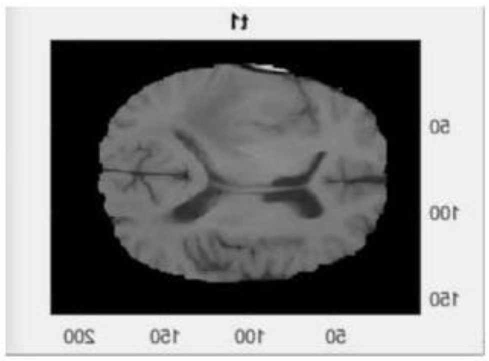


Figure 3.3 IMAGE T1 -WEIGHTED

IMAGES T2-WEIGHTED:

These images are generated by employing extended Echo Time (TE) and Repetition Time (TR) intervals, with the visual contrast and brightness of the image influenced by the T2 characteristics of the tissues. Notably, cerebrospinal fluid (CSF) serves as a distinguishing factor between T1-weighted and T2-weighted images, appearing bright on T2-weighted images and darker on T1-weighted images [16].

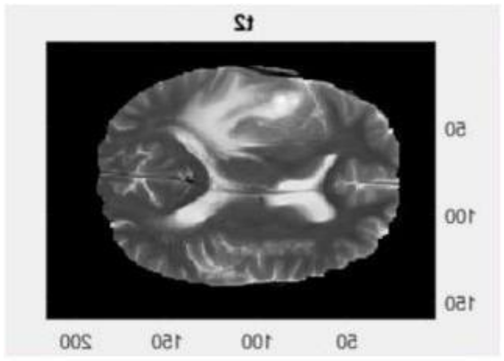


Figure 3.4 IMAGE T2 -WEIGHTED

FLUID ATTENUATED INVERSION RECOVERY:

It has similarities with T2-weighted images, although it incorporates significantly extended Echo Time (TE) and Repetition Time (TR) intervals. This unique approach results in anomalies retaining their brightness, while normal cerebrospinal fluid (CSF) is suppressed, appearing dark. FLAIR images excel in their ability to differentiate between anomalies and CSF, exhibiting heightened sensitivity to pathological changes.

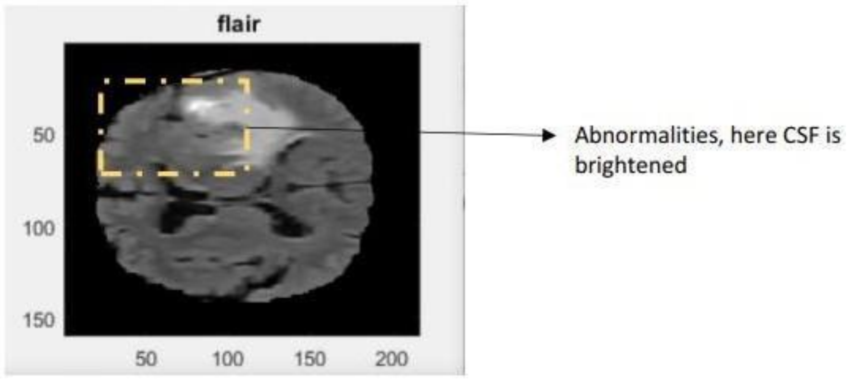


Figure 3.5: FLAIR

Table I TE AND TR VALES AND MODALITIES

MODALITIES	TR (msec)	TE (msec)
T1	500	14
T1- Weighted images	4000	90
FLAIR	9000	114

The introduction of Gadolinium into the process of capturing T1-weighted images contributes to its prominent brightness in these scans. Various RF pulse sequences are utilized to emphasize specific tissue characteristics. For instance, in a "T1-weighted" scan, fluids are depicted as dark, while in a "T2-weighted" scan, fluids appear bright. It is worth noting that fat exhibits brightness in both types of scans.

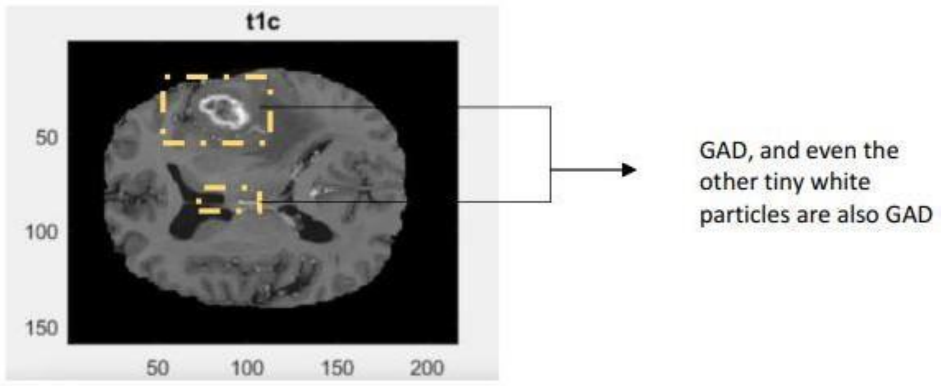


Figure 3.6: IMAGE T1C-WEIGHTED

Since many pathological conditions commonly result in reduced fat content and increased water content, performing a comparative evaluation of scans weighted T1 and T2, frequently referred to as an "irritation pattern," plays a crucial role in highlighting these changes.

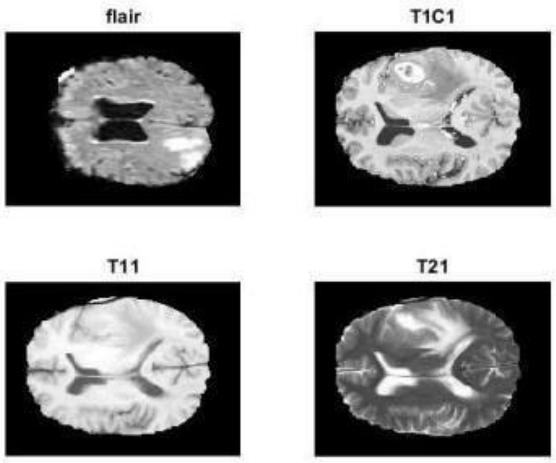


Figure 3.7: SAME SLICE DIFFERENT MODALITIES IMAGE

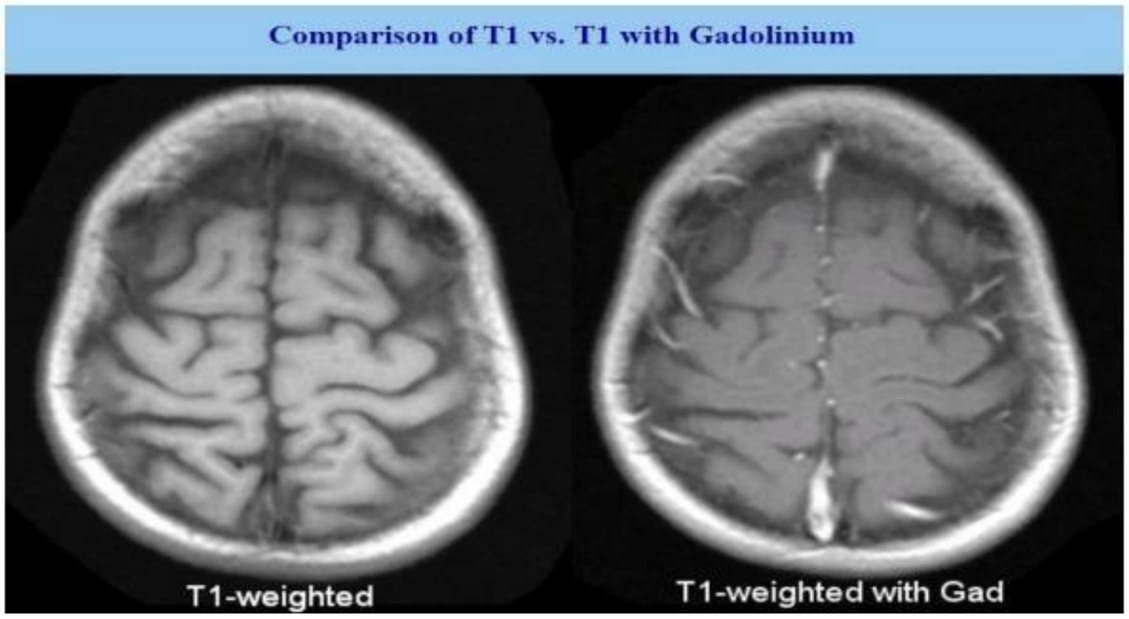


Figure 3.8: T1 VS T2 COMPARISON

3.2 UNDERSTANDING HISTOGRAM OF ORIENTED GRADIENTS

This technique, initially introduced by Dalal and Triggs, was originally developed for the purpose of detecting individuals in images. HOG functions as a distinctive feature descriptor widely employed in the field of image processing, with a particular focus on object detection. This feature descriptor's primary objective is to provide a generalized representation of an object within an image, ensuring that identical feature descriptors can be extracted from images containing the object under various conditions, including different angles, lighting, distances, and other variables.

1. The HOG method initially divides the images into cells, which can have rectangular or radial configurations.

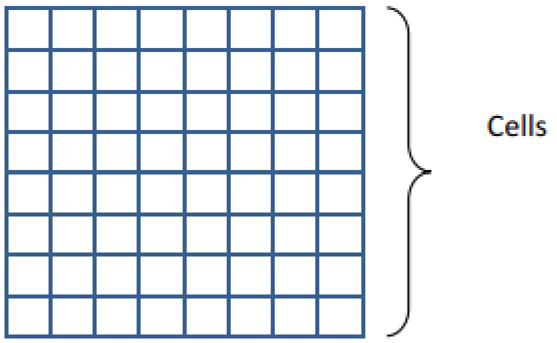
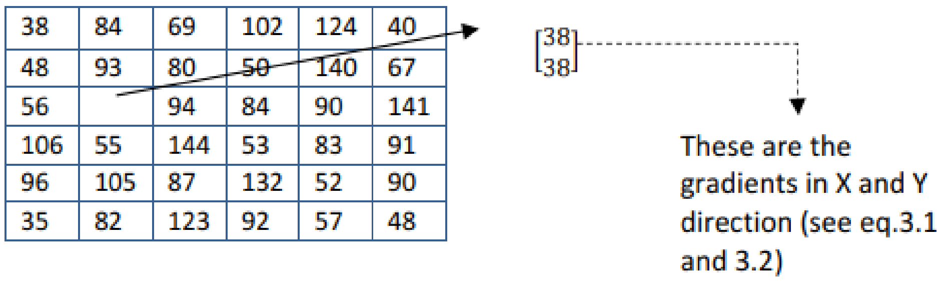


Figure 3.9: HOG CELLS

2. In each cell, a gradient vector is computed for every pixel [17].



38	84	69	102	124	40
48	93	80	50	140	67
56		94	84	90	141
106	55	144	53	83	91
96	105	87	132	52	90
35	82	123	92	57	48

$\begin{bmatrix} 38 \\ 38 \end{bmatrix}$

These are the gradients in X and Y direction (see eq.3.1 and 3.2)

Figure 3.10: GRADIENT VECTOR

3.2.1 IMAGE GRADIENT:

It is often referred to interchangeably as the gradient vector, plays a vital role in the domain of computer vision.

IMAGE GRADIENT APPLICATIONS:

1. Edge detection

2. Feature extraction

Calculating the gradient vector at a given pixel entails evaluating the difference between adjacent values along both the horizontal and vertical axes. These gradients can be computed by subtracting values either from left to right or right to left in the horizontal plane, as well as from top to bottom or bottom to top in the vertical plane.

X-axis: 94 - 56 =38 ….(3.1)

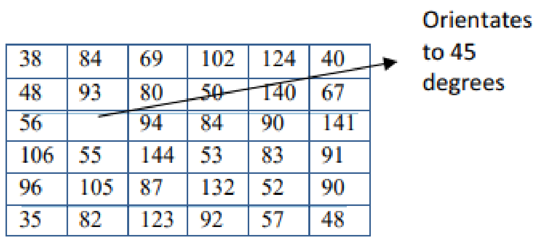
Y-axis: 93 - 55 = 38 …. (3.2)

After the calculation of gradient vectors for each pixel in the image, the next step involves determining their magnitudes.

$$\text{Magnitude}=\sqrt{X2+Y2} \quad \ldots (3.3)$$
$$=\sqrt{382+382} \quad \ldots (3.4)$$
$$=53.74 \quad \ldots (3.5)$$

In the realm of HOG (Histogram of Oriented Gradients), the concept of orientation plays a crucial role. Orientation refers to a change in direction, representing a shift in pixel intensity values. This shift can manifest in either the X-axis or the Y-axis. Calculating the orientation of a gradient vector involves the following process

$$\text{Orientation} = arctan\ (YX) \quad \ldots (3.6)$$
$$= arctan\ (38\ 38) \quad \ldots (3.7)$$
$$= 0.785\ radians \quad \ldots (3.8)$$
$$=45\ degrees \quad \ldots (3.9)$$



38	84	69	102	124	40
48	93	80	50	140	67
56		94	84	90	141
106	55	144	53	83	91
96	105	87	132	52	90
35	82	123	92	57	48

Figure 3.11: PIXEL ORIENTATION IN A CELL

The orientation of individual pixels depends on the values of their gradient vectors. These gradients are subsequently categorized into bins within the histogram, with each bin corresponding to a specific orientation.

10	30	50	70	90	110	130	150	170

Figure 3.12: HISTOGRAM BINS

In Figure 3.11, the gradient vector is inclined at a 45-degree angle. We distribute one-fourth of its magnitude to the bin at thirty degrees, and allocate three-fourths of its magnitude to the bin centered at 50 degrees. This distribution is made because the histogram does not have a designated bin for 45 degrees.

3.2.2 IMAGE NORMALISATION:

The magnitude of gradient vectors associated with each pixel can vary. To ensure uniformity and consistency in these values, a technique known as normalization is applied. In this context, normalization involves dividing the vector values by their respective magnitudes. It's important to note that this normalization process primarily affects the magnitude part of the gradient vectors, while the orientation component remains unchanged.

3.2.3 REPRESENTATION OF CELLS:

Each image is partitioned into cells with dimensions of $m \times n$, typically varying from 2×2, 4×4, 6×6, to 8×8 pixels. This partitioning is primarily done to create a more compact and effective representation of the image.

3.2.4 NORMALISATION OF BLOCKS:

The fundamental process that facilitates both histogram grouping and normalization is the combination of cells into blocks. A block histogram can be defined as the result of normalizing these groups of cells. One significant benefit of computing histograms using image blocks is their ability to strengthen the image's resistance to local lighting variations, thus increasing its reliability in diverse lighting.

3.3 SUPPORT VECTOR MACHINES OVER NEURAL NETWORKS

Support Vector Machines (SVMs) and shallow neural network structures exhibit certain similarities but differ significantly in their structural capabilities. Unlike neural networks, SVMs lack the ability to incorporate hidden layers. Furthermore, SVMs require more meticulous feature engineering efforts, while neural networks can to some extent autonomously learn features.

Contrastingly, neural networks feature a more complex architecture with multiple layers, potentially providing them with greater computational power. However, it comes with a trade-off – requiring large amounts of data for effective training

Due to a small dataset, SVMs present themselves as the more advantageous option. They offer a more direct solution, ensuring swift implementation and decreased costs, which align more effectively with the available resources.

3.3.1 SUPPORT VECTOR MACHINE ADVANTAGES

• **Effective in High-Dimensional Spaces:** SVMs excel in managing high-dimensional data, making them suitable for datasets with dimensions exceeding 10^6.

• **Efficient Operations through Subset Selection:** SVMs streamline their operations by focusing on a specific subset of training points, enabling quick decision-making.

• **Well-Suited for Compact, Well-Structured Datasets:** SVMs deliver excellent performance when dealing with smaller datasets that are meticulously organized and free from significant noise or outliers.

• **Optimal Memory Usage:** SVMs are memory-efficient as they retain only essential subsets of training points required for decision-making, resulting in minimal memory usage during predictions or classifying new data points.

3.3.2 SUPPORT VECTOR MACHINE DISADVANTAGES

• **Challenges with Extensive Datasets**: SVMs may encounter limitations when dealing with large datasets, leading to extended training times that could impact their practicality in such scenarios.

• **Diminished Effectiveness in High-Dimensional Data**: SVM performance tends to decline when the number of features per object exceeds the quantity of training data samples, making it challenging to achieve reliable generalization.

• **Limited Applicability in Noisy, Overlapping Datasets**: SVMs exhibit reduced effectiveness when applied to datasets characterized by substantial noise or significant overlap between class boundaries. This complexity can impede accurate class differentiation.

• **Absence of Direct Probabilistic Interpretation**: SVMs function as non-probabilistic classifiers, separating objects based on their position relative to the hyperplane without offering a direct probability estimation for class membership. Instead, the distance from the decision boundary can serve as an indicator of classification confidence.

3.3.3 SUPPORT VECTOR MACHINE USES

• **Text Classification Applications**: Encompassing tasks such as category assignment, spam detection, and sentiment analysis.

• **Image Recognition Challenges**: Involving various facets of image recognition.

• **Aspect-Oriented Recognition**: Concentrating on the identification of particular aspects

• **Color-Based Object Classification**: Entailing the categorization of objects based on their color features.
• **Handwritten Digit Recognition**: Specifically, the recognition of manually written digits.

The Support Vector Machine, commonly referred to as SVM, is a supervised machine learning method primarily employed for data classification tasks. The fundamental idea behind SVM revolves around finding an optimal hyperplane to effectively separate the dataset. This concept is visually explained in figure 3.13.

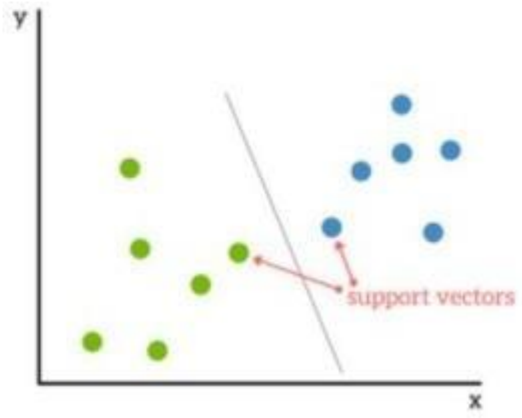


Figure 3.13 HYPERPLANE BASED CLASSIFICATION

The Support Vector Machine constructs a feature space of finite-dimension, essentially forming a vector space. In this space, every dimension corresponds to a unique object attribute. These feature vectors collectively constitute the vector space.

3.3.4 HYPERPARAMETER TUNING

Hyperparameters are predetermined settings or configurations of a machine learning algorithm that are not derived from the data but are manually defined by developers or researchers before the model training. These hyperparameters include parameters like learning rate, batch size, the number of hidden layers, neurons in each layer, regularization strength, and the chosen activation function.

Hyperparameter tuning is the process of carefully selecting the most suitable values for these parameters to improve the model's performance on the test data. This is necessary because different hyperparameter configurations can have a significant impact on the model's effectiveness. If hyperparameters are not appropriately chosen, the model may perform poorly on the test data. Here are several reasons highlighting the importance of hyperparameter tuning.:

i. Improving Model Accuracy: The primary aim of hyperparameter tuning is to increase the model's accuracy on the test data. Optimal hyperparameter selection enhances the model's ability to generalize effectively to new, unseen data.
ii. Avoiding Overfitting: Overfitting occurs when the model becomes overly complex and fits the training data too closely, resulting in poor performance on the test data. Hyperparameter tuning helps control the model's complexity, reducing the risk of overfitting.
iii. Accelerating Training Time: Fine-tuning hyperparameters can speed up the model's training process by identifying the most effective configurations that lead to faster convergence.
iv. Enhancing Model Interpretability: Some hyperparameters impact the ease of model interpretation. For example, the regularization parameter governs the model's complexity. Increasing its value results in a simpler and more understandable model.

Here is our approach for incorporating hyperparameter tuning into our project:

i. Data Preparation: The initial step involves data preparation, which includes cleaning, transformation, and splitting the data into training and testing sets. Algorithm Selection: We have a range of algorithms to choose from for tasks like dementia and mental health churn analysis, including logistic regression, decision trees, random forests, and neural networks. Each algorithm comes with its own set of hyperparameters that can be fine- tuned to enhance its performance.

ii. Hyperparameter Selection: The subsequent stage is selecting the specific hyperparameters to be tuned. For instance, in a neural network, these hyperparameters might include the number of hidden layers, the quantity of neurons in each layer, the learning rate, and the strength of regularization.
iii. Defining the Search Space: The search space denotes the allowable range of values for each hyperparameter. For example, the search space for the learning rate might span from 0.001 to 0.1, while the number of hidden layers might be explored within the range of 1 to 5.

iv. Hyperparameter Tuning: Various techniques can be employed to tune the hyperparameters, such as grid search, random search, and Bayesian optimization. Grid search involves testing all possible combinations of hyperparameters and selecting the best set based on performance on the validation set. Random search explores random combinations of hyperparameters to find the optimal set. Bayesian optimization uses a probabilistic model to predict the performance of different hyperparameter settings, facilitating the selection of the best set based on these predictions.

3.3.5 SUPPORT VECTORS

They are essential data points located in immediate neighborhood to the hyperplane. Their significance lies in their pivotal role in precisely positioning the separating hyperplane.

3.3.6 HYPERLANE

In a feature space with numerous dimensions, the linear hyperplane serves as a geometric construct residing one dimension lower than the entire space, and its primary purpose is to partition the feature space into two distinct regions. These hyperplanes act as planes that enable the linear separation of a given dataset. To illustrate simply, consider a scenario with only two features, as depicted in Figure 3.14.
When classifying objects based on their features', newly encountered objects are positioned either above or below the hyperplane. This specific arrangement is pivotal in their classification
It's important to note that a linear separating hyperplane is not required to pass through the origin of the feature space, meaning that zero vectors are not mandatory for this plane. These hyperplanes are technically known as "affine." In precise mathematical terms, SVM is designed to establish these linear separating hyperplanes within high-dimensional vector spaces.

Data points are represented as (x, y) where

$x = (x1 \dots . xp)$
xj is the feature value …. (3.10)[20]
$y = (+1\ or - 1)$ is the class of vector X classification

It becomes evident that data points are positioned at varying distances from the hyperplane, and the effectiveness of classification hinges on the extent of data separation. This evaluation is guided by an intuitive principle: our objective is to have data points maximize their distance from the hyperplane, while ensuring they remain on the correct side of it, as referenced in [20].

3.3.7 DATA AUGMENTED SEGRAGATION

The margin can be defined as the degree of demarcation between the hyperplane and the nearest data point in either dataset. In the pursuit of achieving superior classification, the aim is to secure a substantial margin, as a broader margin is indicative of enhanced performance.

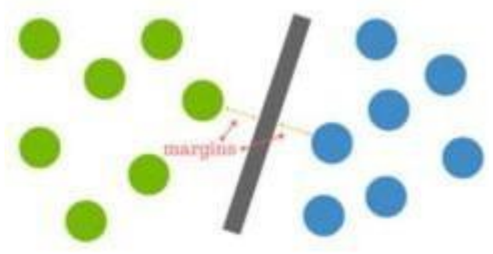


Figure 3.14 SEGREGATION MARGIN

Real-world data often introduces complexities that render it more intricate than the prior example implies. There are situations where datasets exhibit overlap, rendering them challenging to separate through linear methods. In such cases, a practical approach involves a transformation that can be likened to converting a 2D image into a 3D representation. To illustrate this concept, envision the previous example with the balls, but now picture them being lifted into the air and divided by an intervening plane. This imaginative elevation of the balls corresponds to a mathematical technique known as "kernelization," which effectively maps data into higher dimensions, facilitating improved separation.

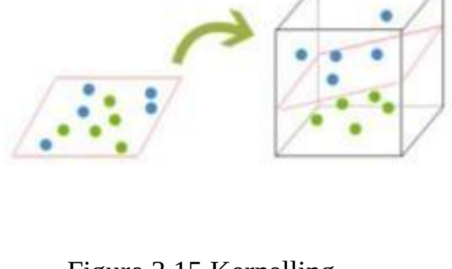


Figure 3.15 Kernelling

In the realm of three-dimensional images, the hyperplane undergoes a transformation into a surface, departing from its conventional linear representation. The core concept revolves around the continuous mapping of data into dimensions that are higher until an effective hyperplane can be established for optimal separation. In a feature space denoted as $\mathbb{R}p$, where p represents the number of dimensions, the hyperplane takes on the characteristics of an affine space with p-1 dimensions, intricately embedded within the broader p-dimensional feature space.

3.3.8 SUPPORT VECTOR MACHINE MAJOR GOALS

• Construct a model capable of categorizing novel objects into predefined classes.

• Identify a hyperplane that maximizes the margin from any point in the training set, enhancing the accuracy of classifying new data.

The training process entails establishing a linear partition in the feature space to separate it into two distinct categories using a hyperplane.

3.4 METHODS OF EVALUATION

LEAVE ONE OUT CROSS VALIDATION

Leave-one-out cross-validation has a dual purpose within the dataset, fulfilling roles as both the training and testing sets. This approach utilizes n-1 out of n data samples for training, while the remaining single sample is set aside for testing. Leave-one-out cross-validation proves especially valuable for assessing recognition systems, particularly in scenarios where data is limited. [25]

RECEIVER OPERATING CHARACTERISTICS

This curve is a graphical illustration that depicts how the true positive rate and false positive rate change under different threshold values employed in a diagnostic test.

The origins of Receiver Operating Characteristics analysis can be traced to the field of Signal Detection Theory, which emerged during World War II for the analysis of radar imagery. During this period, radar operators faced the crucial challenge of distinguishing between blips on their screens, discerning whether they represented friendly vessels, enemy targets, or mere background noise. Signal Detection Theory was devised to assess the radar operator's capacity to make these vital distinctions. The term "Receiver Operating Characteristics" (ROC) was coined to encapsulate this ability, giving the analysis its name.

Table II: RECEIVER OPERATING CHARACTERISTICS

	Condition A	Condition NOT A
Test says A	True positive (TP)	False positive (FP)
Test says NOT A	False negative (FN)	True negative (TN)

TRUE POSITIVE RATE:

The true positive rate, also known as sensitivity or recall, is a metric in binary classification that quantifies the proportion of actual positive instances correctly identified by a model or classifier out of the total number of true positive and false negative instances.

$$TPR = TP / (TP + FN) \qquad …... (3.12)$$

TRUE NEGATIVE RATE:

The true negative rate, also known as specificity, is a metric in binary classification that quantifies the proportion of actual negative instances correctly identified by a model or classifier out of the total number of true negative and false positive instances. It measures the model's ability to accurately distinguish and classify negative cases within a dataset.

TNR = TN / (FP + TN) …… (3.13)

FALSE POSITIVE RATE:

The false positive rate is a metric in binary classification that quantifies the proportion of actual negative instances incorrectly classified as positive by a model or classifier, out of the total number of true negative and false positive instances. It measures the model's tendency to generate false alarms by erroneously labeling negative cases as positive.

FP = 1 – Specificity …. (3.14)

FALSE NEGATIVE RATE (FNR):

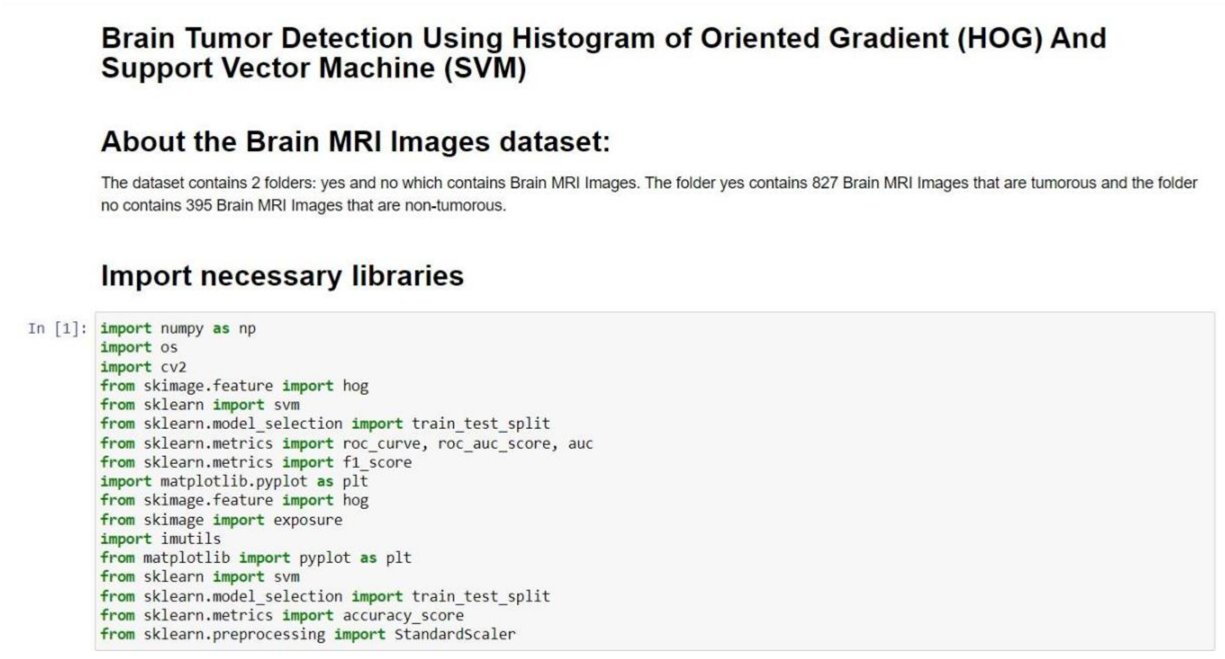
The false negative rate is a metric in binary classification that quantifies the proportion of actual positive instances incorrectly classified as negative by a model or classifier, out of the total number of true positive and false negative instances. It measures the model's failure to identify positive cases correctly, resulting in missed detections or Type II errors.

FNR = 1 – TPR …. (3.15)
ACCURACY = TN + TP/ (TP+FP+TN+FN) …. (3.16)

CHAPTER 4

IMPLEMENTATION

The process begins by choosing a database that contains brain images. From these images, features are extracted using the HOG technique. These extracted features are then labeled and fed into the SVM. The SVM's role is to differentiate between regions with tumors and those without. The final phase involves assessing the SVM's performance, considering ROC characteristics, which include accuracy, sensitivity, and specificity.



Brain Tumor Detection Using Histogram of Oriented Gradient (HOG) And Support Vector Machine (SVM)

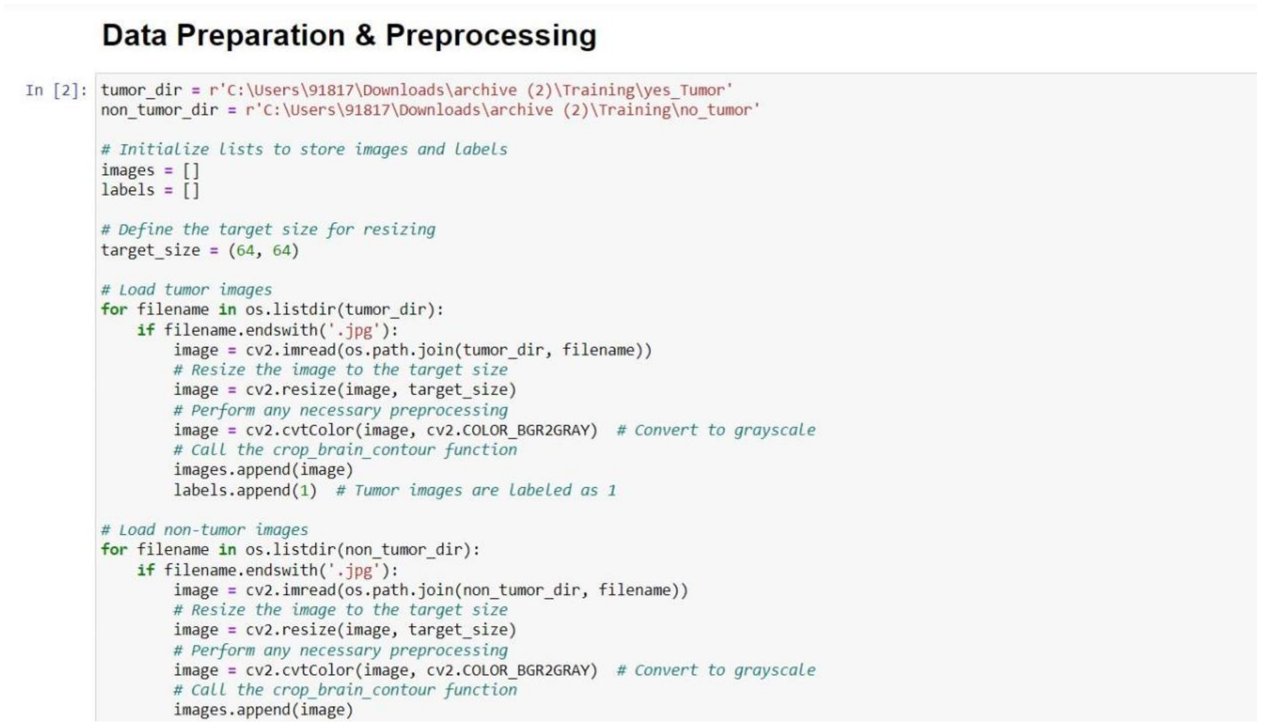
About the Brain MRI Images dataset:

The dataset contains 2 folders: yes and no which contains Brain MRI Images. The folder yes contains 827 Brain MRI Images that are tumorous and the folder no contains 395 Brain MRI Images that are non-tumorous.

Import necessary libraries

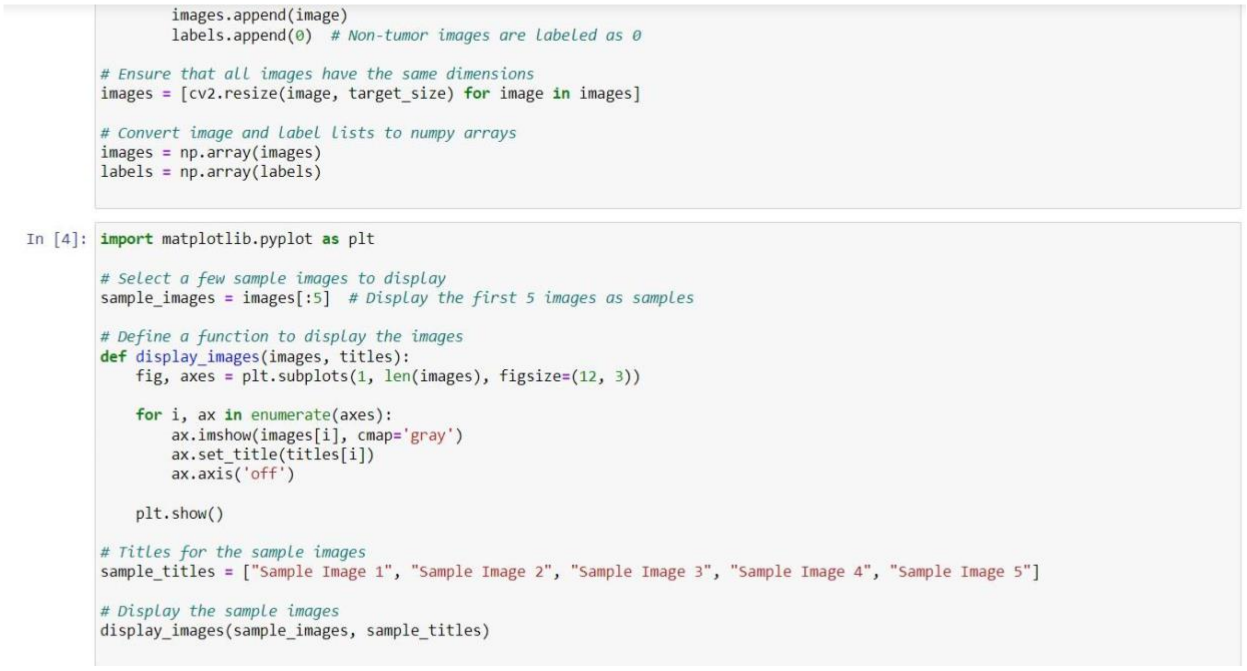
In [1]:

```
import numpy as np
import os
import cv2
from skimage.feature import hog
from sklearn import svm
from sklearn.model_selection import train_test_split
from sklearn.metrics import roc_curve, roc_auc_score, auc
from sklearn.metrics import f1_score
import matplotlib.pyplot as plt
from skimage.feature import hog
from skimage import exposure
import imutils
from matplotlib import pyplot as plt
from sklearn import svm
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
```

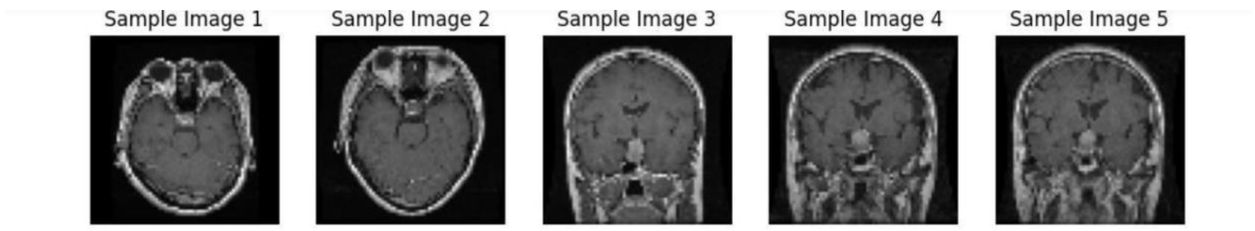


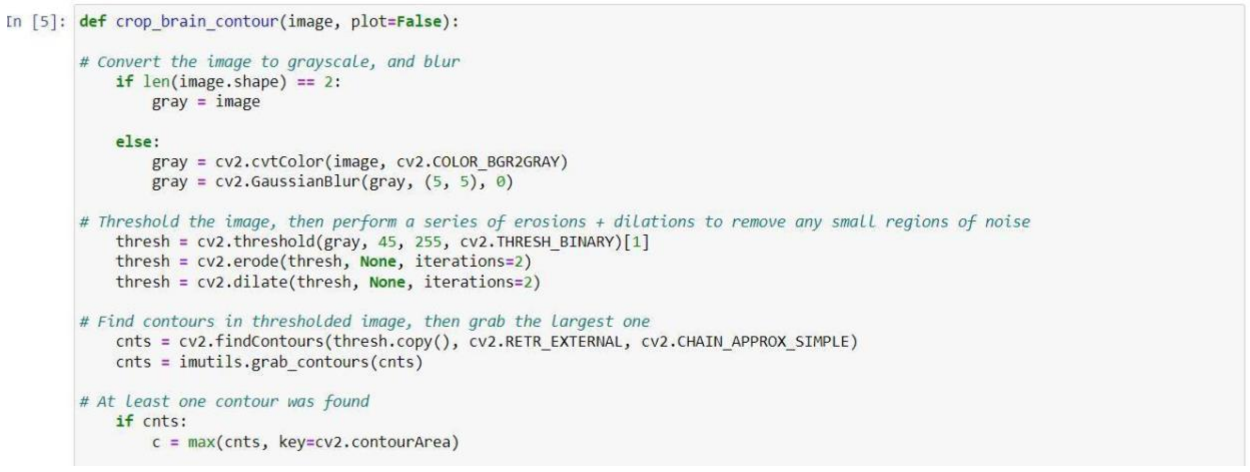
Data Preparation & Preprocessing

```
In [2]: tumor_dir = r'C:\Users\91817\Downloads\archive (2)\Training\yes_Tumor'
        non_tumor_dir = r'C:\Users\91817\Downloads\archive (2)\Training\no_tumor'

        # Initialize lists to store images and labels
        images = []
        labels = []

        # Define the target size for resizing
        target_size = (64, 64)

        # Load tumor images
        for filename in os.listdir(tumor_dir):
            if filename.endswith('.jpg'):
                image = cv2.imread(os.path.join(tumor_dir, filename))
                # Resize the image to the target size
                image = cv2.resize(image, target_size)
                # Perform any necessary preprocessing
                image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)  # Convert to grayscale
                # Call the crop_brain_contour function
                images.append(image)
                labels.append(1)  # Tumor images are labeled as 1

        # Load non-tumor images
        for filename in os.listdir(non_tumor_dir):
            if filename.endswith('.jpg'):
                image = cv2.imread(os.path.join(non_tumor_dir, filename))
                # Resize the image to the target size
                image = cv2.resize(image, target_size)
                # Perform any necessary preprocessing
                image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)  # Convert to grayscale
                # Call the crop_brain_contour function
                images.append(image)
```

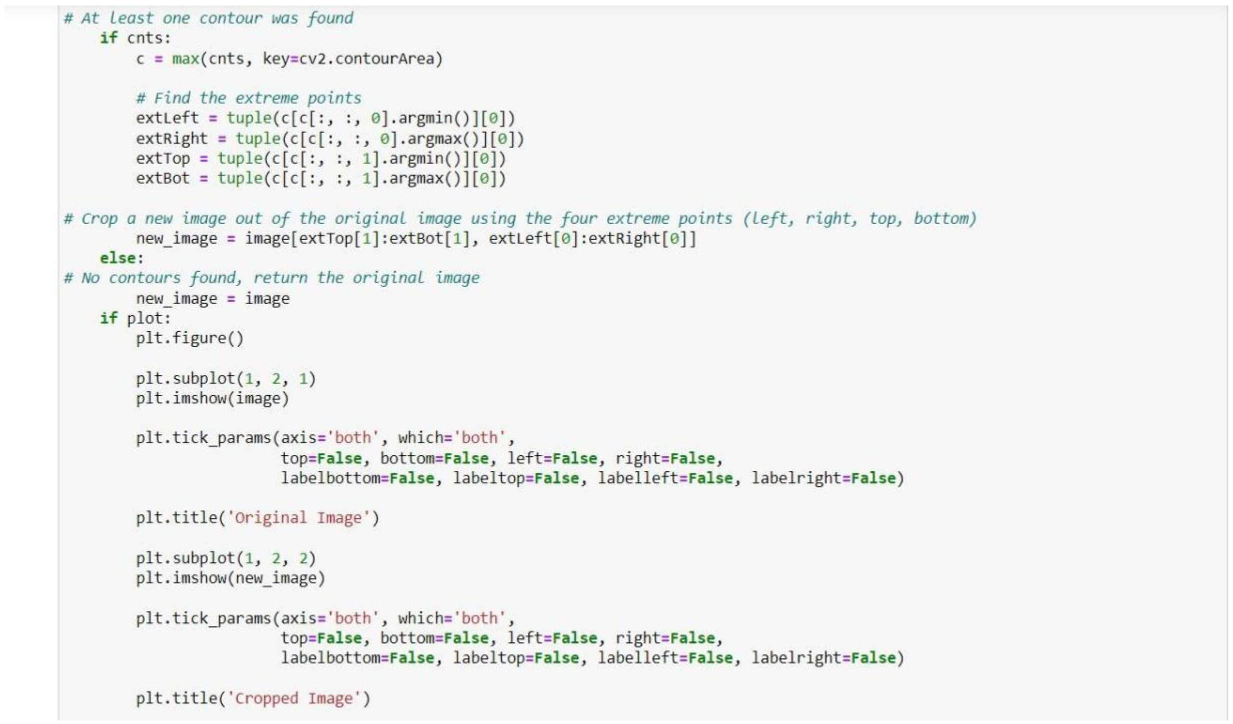


```
                images.append(image)
                labels.append(0)  # Non-tumor images are labeled as 0

        # Ensure that all images have the same dimensions
        images = [cv2.resize(image, target_size) for image in images]

        # Convert image and label lists to numpy arrays
        images = np.array(images)
        labels = np.array(labels)

In [4]: import matplotlib.pyplot as plt

        # Select a few sample images to display
        sample_images = images[:5]  # Display the first 5 images as samples

        # Define a function to display the images
        def display_images(images, titles):
            fig, axes = plt.subplots(1, len(images), figsize=(12, 3))

            for i, ax in enumerate(axes):
                ax.imshow(images[i], cmap='gray')
                ax.set_title(titles[i])
                ax.axis('off')

            plt.show()

        # Titles for the sample images
        sample_titles = ["Sample Image 1", "Sample Image 2", "Sample Image 3", "Sample Image 4", "Sample Image 5"]

        # Display the sample images
        display_images(sample_images, sample_titles)
```



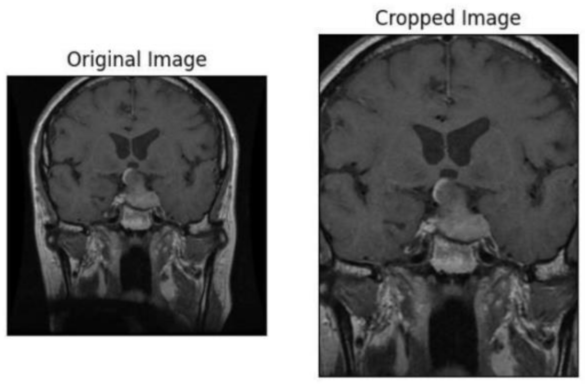


```
In [5]: def crop_brain_contour(image, plot=False):

        # Convert the image to grayscale, and blur
            if len(image.shape) == 2:
                gray = image

            else:
                gray = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
                gray = cv2.GaussianBlur(gray, (5, 5), 0)

        # Threshold the image, then perform a series of erosions + dilations to remove any small regions of noise
            thresh = cv2.threshold(gray, 45, 255, cv2.THRESH_BINARY)[1]
            thresh = cv2.erode(thresh, None, iterations=2)
            thresh = cv2.dilate(thresh, None, iterations=2)

        # Find contours in thresholded image, then grab the largest one
            cnts = cv2.findContours(thresh.copy(), cv2.RETR_EXTERNAL, cv2.CHAIN_APPROX_SIMPLE)
            cnts = imutils.grab_contours(cnts)

        # At least one contour was found
            if cnts:
                c = max(cnts, key=cv2.contourArea)
```



```
# At least one contour was found
    if cnts:
        c = max(cnts, key=cv2.contourArea)

        # Find the extreme points
        extLeft = tuple(c[c[:, :, 0].argmin()][0])
        extRight = tuple(c[c[:, :, 0].argmax()][0])
        extTop = tuple(c[c[:, :, 1].argmin()][0])
        extBot = tuple(c[c[:, :, 1].argmax()][0])

# Crop a new image out of the original image using the four extreme points (left, right, top, bottom)
        new_image = image[extTop[1]:extBot[1], extLeft[0]:extRight[0]]
    else:
# No contours found, return the original image
        new_image = image
    if plot:
        plt.figure()

        plt.subplot(1, 2, 1)
        plt.imshow(image)

        plt.tick_params(axis='both', which='both',
                        top=False, bottom=False, left=False, right=False,
                        labelbottom=False, labeltop=False, labelleft=False, labelright=False)

        plt.title('Original Image')

        plt.subplot(1, 2, 2)
        plt.imshow(new_image)

        plt.tick_params(axis='both', which='both',
                        top=False, bottom=False, left=False, right=False,
                        labelbottom=False, labeltop=False, labelleft=False, labelright=False)

        plt.title('Cropped Image')
        plt.show()

    return new_image
```

```
In [6]: ex_img = cv2.imread(r'C:\Users\91817\Downloads\archive (2)\Training\yes_tumor\p (88).jpg')
        ex_new_img = crop_brain_contour(ex_img, True)
```



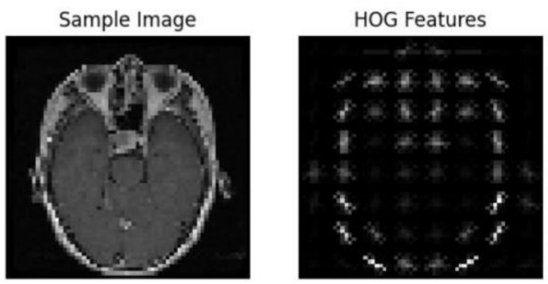
Extracting hog features

```
In [7]: from skimage.feature import hog
        from skimage import exposure
```

```
In [42]: def extract_hog_features(images):
             features = []
             for image in images:
                 # Resize and convert to grayscale if needed
                 image = cv2.resize(image, (64, 64))
                 if len(image.shape) == 3:  # Ensure grayscale
                     image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)

                 # Extract HOG features parameters
                 feature_vector = hog(image, pixels_per_cell=(8, 8), cells_per_block=(2, 2), visualize=False)

                 features.append(feature_vector)
                 # return the feature matrix
             return np.array(features)

         # Define X and y based on dataset and extracted features
         X = extract_hog_features(images)  # X should be the feature matrix
         y = labels  # y should be the corresponding labels
```

```
In [9]: sample_image = images[100]

        # Check if the sample image is valid and its shape contains the expected dimensions
        if sample_image is not None and len(sample_image.shape) == 2 and sample_image.shape[0] > 0 and sample_image.shape[1] > 0:
            # Adjust these parameters based on image size
            pixels_per_cell = (8, 8)
            cells_per_block = (2, 2)

            # Calculate HOG features
            fd, hog_image = hog(sample_image, pixels_per_cell=pixels_per_cell, cells_per_block=cells_per_block, visualize=True)

            # Plot the HOG features
            fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(6, 3), sharex=True, sharey=True)
            ax1.imshow(sample_image, cmap=plt.cm.gray)
            ax1.set_title('Sample Image')
            ax1.axis('off')
            ax2.imshow(hog_image, cmap=plt.cm.gray)
```

```
    ax1.set_title('Sample Image')
    ax1.axis('off')
    ax2.imshow(hog_image, cmap=plt.cm.gray)
    ax2.set_title('HOG Features')
    ax2.axis('off')
    plt.show()
else:
    print("Invalid sample image or dimensions.")
```



Splitting into training and testing dataset

```
In [10]: # Ensure that X is a 2D array
         if len(X.shape) == 1:
             X = np.array([x.flatten() for x in X])

         # Split the dataset into training and testing sets
         X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

```
print("X_train shape:", X_train.shape)
print("y_train shape:", y_train.shape)
```

```
X_train shape: (977, 1764)
y_train shape: (977,)
```

```
In [11]: print ("number of training examples = " + str(X_train.shape[0]))
         print ("number of test examples = " + str(X_test.shape[0]))
         print ("X_train shape: " + str(X_train.shape))
         print ("Y_train shape: " + str(y_train.shape))
         print ("X_test shape: " + str(X_test.shape))
         print ("Y_test shape: " + str(y_test.shape))
```

```
number of training examples = 977
number of test examples = 245
X_train shape: (977, 1764)
Y_train shape: (977,)
X_test shape: (245, 1764)
Y_test shape: (245,)
```

Implementing SVM

```
In [12]: scaler = StandardScaler()

         #Standardization data and involves scaling features to have a mean and standard deviation .

         X_train = scaler.fit_transform(X_train)
         X_test = scaler.transform(X_test)
```

```
In [14]: from sklearn.model_selection import GridSearchCV
         # Define the parameter grid for hyperparameter tuning
```

Hyperparameter Tuning

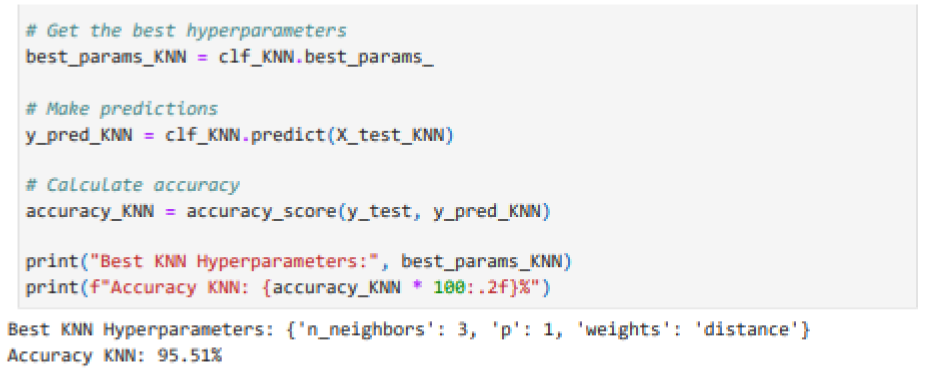
In [15]:
```
# Train the SVM with hyperparameter tuning
clf.fit(X_train, y_train)

# Get the best hyperparameters
best_params = clf.best_params_
print(f"Best hyperparameters: {best_params}")

# Make predictions on the test set
y_pred = clf.predict(X_test)
y_prob = clf.predict_proba(X_test)[:, 1]  # Probability of class 1 (tumor)

#Evaluate the model using ROC
fpr, tpr, thresholds = roc_curve(y_test, y_prob)
roc_auc = auc(fpr, tpr)
# Evaluate the SVM model
accuracy_SVM = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy_SVM * 100:.2f}%")
```

```
Best hyperparameters: {'C': 10, 'gamma': 0.001, 'kernel': 'rbf'}
Accuracy: 98.78%
```

In [16]:
```
'''
The C parameter is the regularization parameter in an SVM.
The gamma is kernel coefficient that control shape of decision boundary
The kernel maps input data in multi-D shape, rbf (radial basis fn)
'''
```

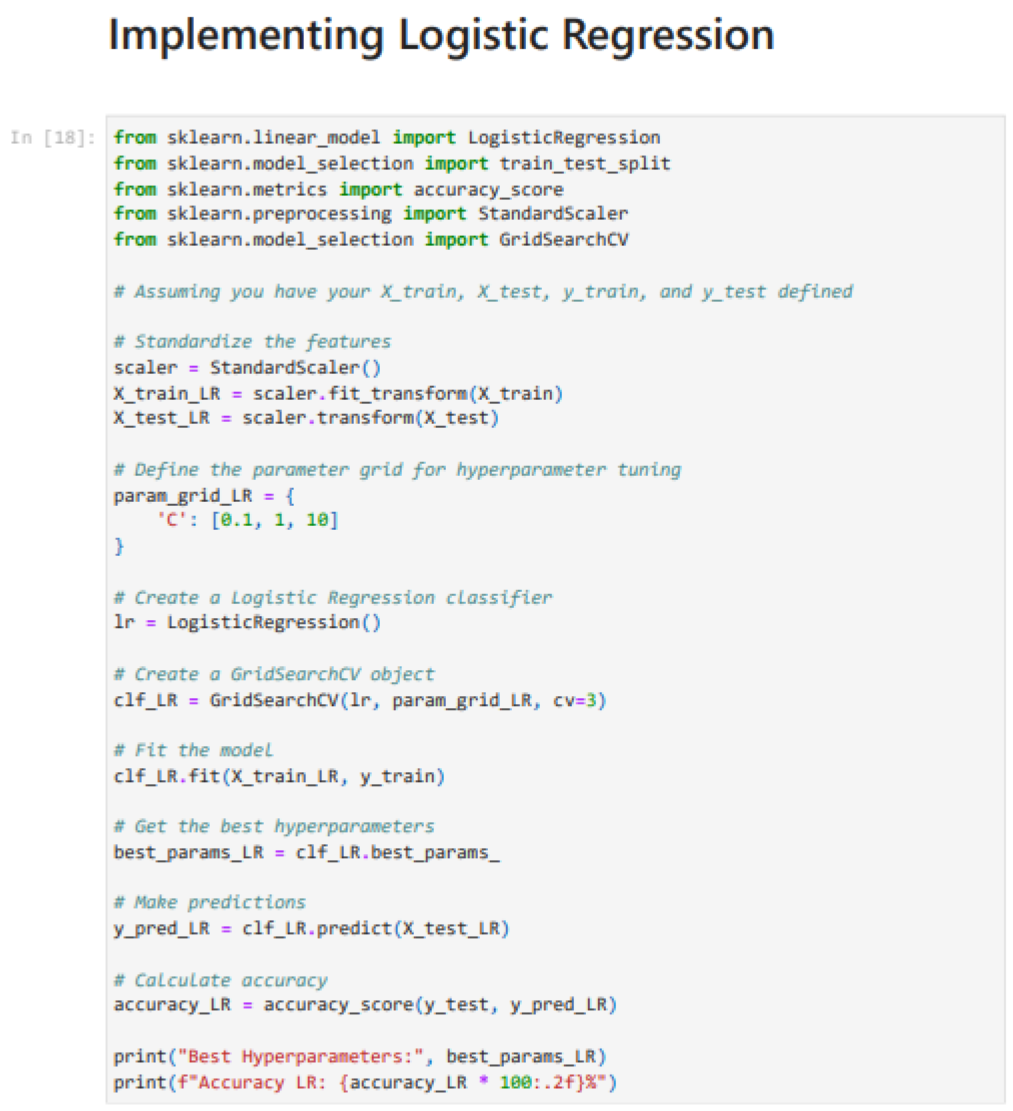
Implementing KNN

In [17]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV

# Assuming you have your X_train, X_test, y_train, and y_test defined

# Standardize the features
scaler = StandardScaler()
X_train_KNN = scaler.fit_transform(X_train)
X_test_KNN = scaler.transform(X_test)

# Define the parameter grid for hyperparameter tuning
param_grid_KNN = {
    'n_neighbors': [3, 5, 7, 9],
    'weights': ['uniform', 'distance'],
    'p': [1, 2],  # 1 for Manhattan distance, 2 for Euclidean distance
}

# Create a KNN classifier
knn = KNeighborsClassifier()

# Create a GridSearchCV object
clf_KNN = GridSearchCV(knn, param_grid_KNN, cv=3)

# Fit the model
clf_KNN.fit(X_train_KNN, y_train)

# Get the best hyperparameters
best_params_KNN = clf_KNN.best_params_
```



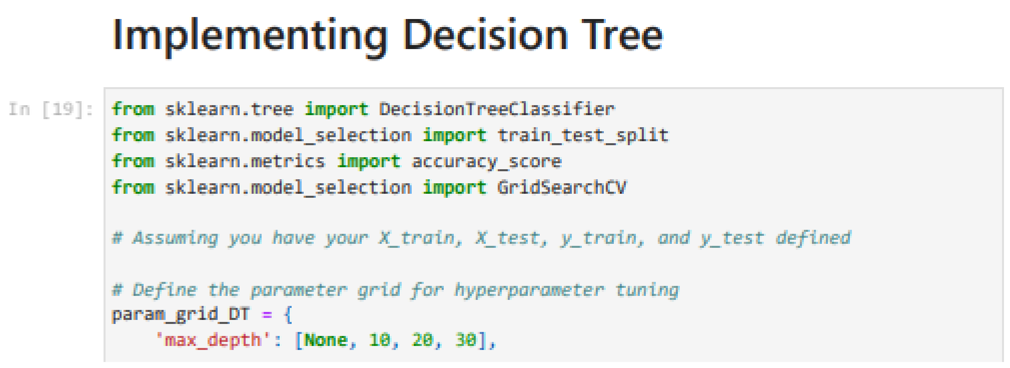
```
# Get the best hyperparameters
best_params_KNN = clf_KNN.best_params_

# Make predictions
y_pred_KNN = clf_KNN.predict(X_test_KNN)

# Calculate accuracy
accuracy_KNN = accuracy_score(y_test, y_pred_KNN)

print("Best KNN Hyperparameters:", best_params_KNN)
print(f"Accuracy KNN: {accuracy_KNN * 100:.2f}%")
```

```
Best KNN Hyperparameters: {'n_neighbors': 3, 'p': 1, 'weights': 'distance'}
Accuracy KNN: 95.51%
```



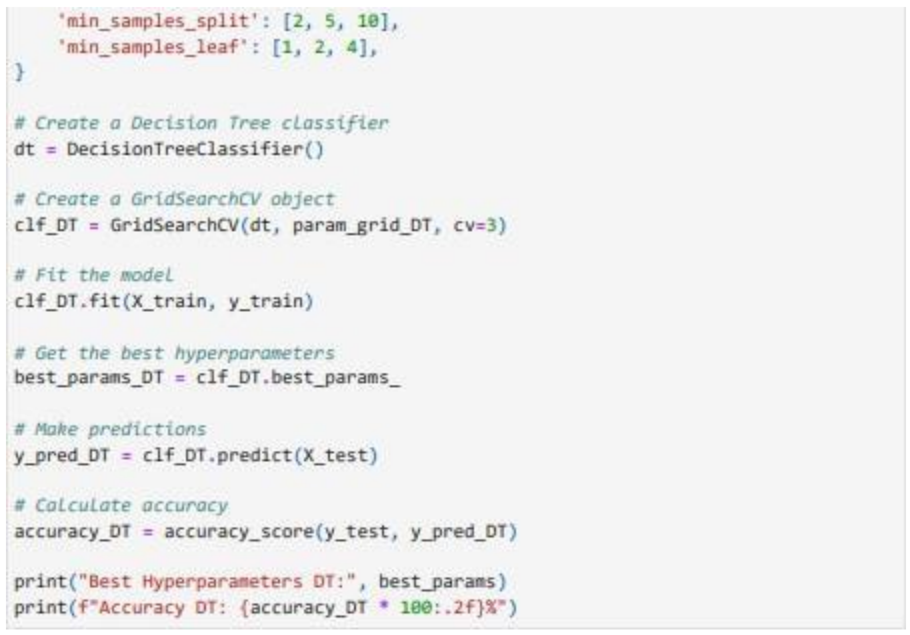
Implementing Logistic Regression

```
In [18]: from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV

# Assuming you have your X_train, X_test, y_train, and y_test defined

# Standardize the features
scaler = StandardScaler()
X_train_LR = scaler.fit_transform(X_train)
X_test_LR = scaler.transform(X_test)

# Define the parameter grid for hyperparameter tuning
param_grid_LR = {
    'C': [0.1, 1, 10]
}

# Create a Logistic Regression classifier
lr = LogisticRegression()

# Create a GridSearchCV object
clf_LR = GridSearchCV(lr, param_grid_LR, cv=3)

# Fit the model
clf_LR.fit(X_train_LR, y_train)

# Get the best hyperparameters
best_params_LR = clf_LR.best_params_

# Make predictions
y_pred_LR = clf_LR.predict(X_test_LR)

# Calculate accuracy
accuracy_LR = accuracy_score(y_test, y_pred_LR)

print("Best Hyperparameters:", best_params_LR)
print(f"Accuracy LR: {accuracy_LR * 100:.2f}%")
```



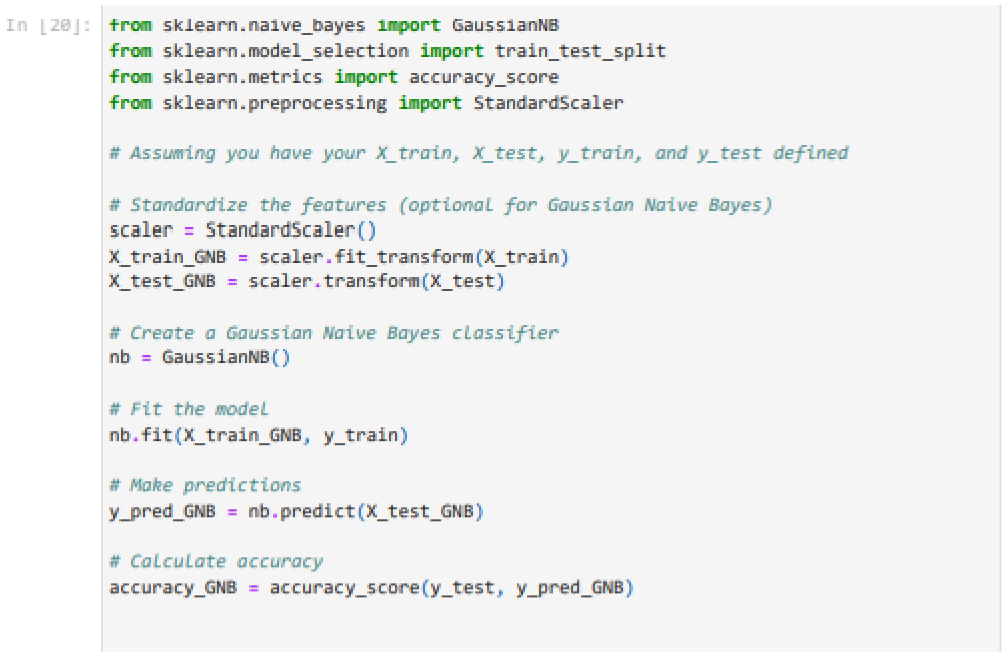
Implementing Decision Tree

```
In [19]: from sklearn.tree import DecisionTreeClassifier
         from sklearn.model_selection import train_test_split
         from sklearn.metrics import accuracy_score
         from sklearn.model_selection import GridSearchCV

         # Assuming you have your X_train, X_test, y_train, and y_test defined

         # Define the parameter grid for hyperparameter tuning
         param_grid_DT = {
             'max_depth': [None, 10, 20, 30],
```



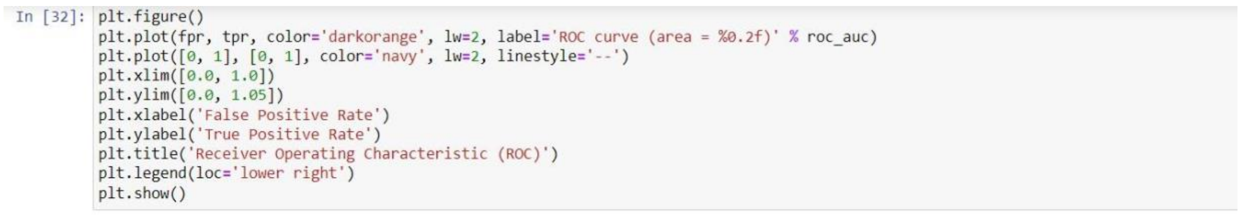
```
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4],
}

# Create a Decision Tree classifier
dt = DecisionTreeClassifier()

# Create a GridSearchCV object
clf_DT = GridSearchCV(dt, param_grid_DT, cv=3)

# Fit the model
clf_DT.fit(X_train, y_train)

# Get the best hyperparameters
best_params_DT = clf_DT.best_params_

# Make predictions
y_pred_DT = clf_DT.predict(X_test)

# Calculate accuracy
accuracy_DT = accuracy_score(y_test, y_pred_DT)

print("Best Hyperparameters DT:", best_params)
print(f"Accuracy DT: {accuracy_DT * 100:.2f}%")
```

Implementing Naive Bayes

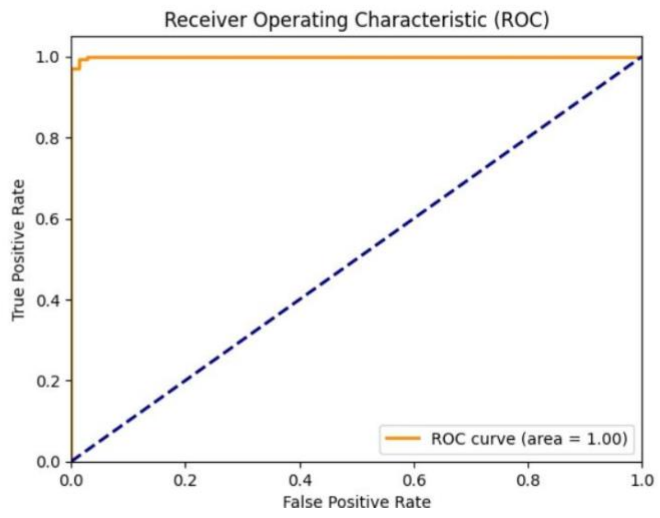


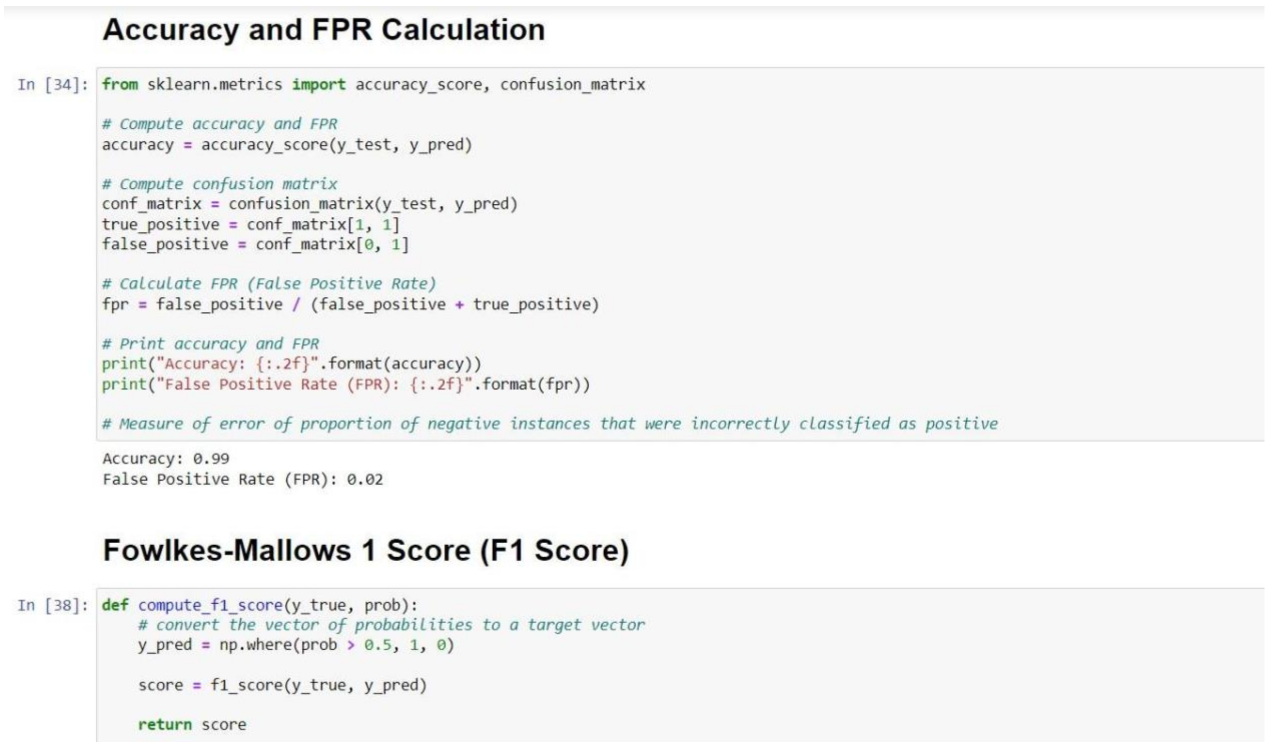
```
In [20]: from sklearn.naive_bayes import GaussianNB
         from sklearn.model_selection import train_test_split
         from sklearn.metrics import accuracy_score
         from sklearn.preprocessing import StandardScaler

         # Assuming you have your X_train, X_test, y_train, and y_test defined

         # Standardize the features (optional for Gaussian Naive Bayes)
         scaler = StandardScaler()
         X_train_GNB = scaler.fit_transform(X_train)
         X_test_GNB = scaler.transform(X_test)

         # Create a Gaussian Naive Bayes classifier
         nb = GaussianNB()

         # Fit the model
         nb.fit(X_train_GNB, y_train)

         # Make predictions
         y_pred_GNB = nb.predict(X_test_GNB)

         # Calculate accuracy
         accuracy_GNB = accuracy_score(y_test, y_pred_GNB)
```

Plot the ROC curve



```
In [32]: plt.figure()
         plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
         plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
         plt.xlim([0.0, 1.0])
         plt.ylim([0.0, 1.05])
         plt.xlabel('False Positive Rate')
         plt.ylabel('True Positive Rate')
         plt.title('Receiver Operating Characteristic (ROC)')
         plt.legend(loc='lower right')
         plt.show()
```





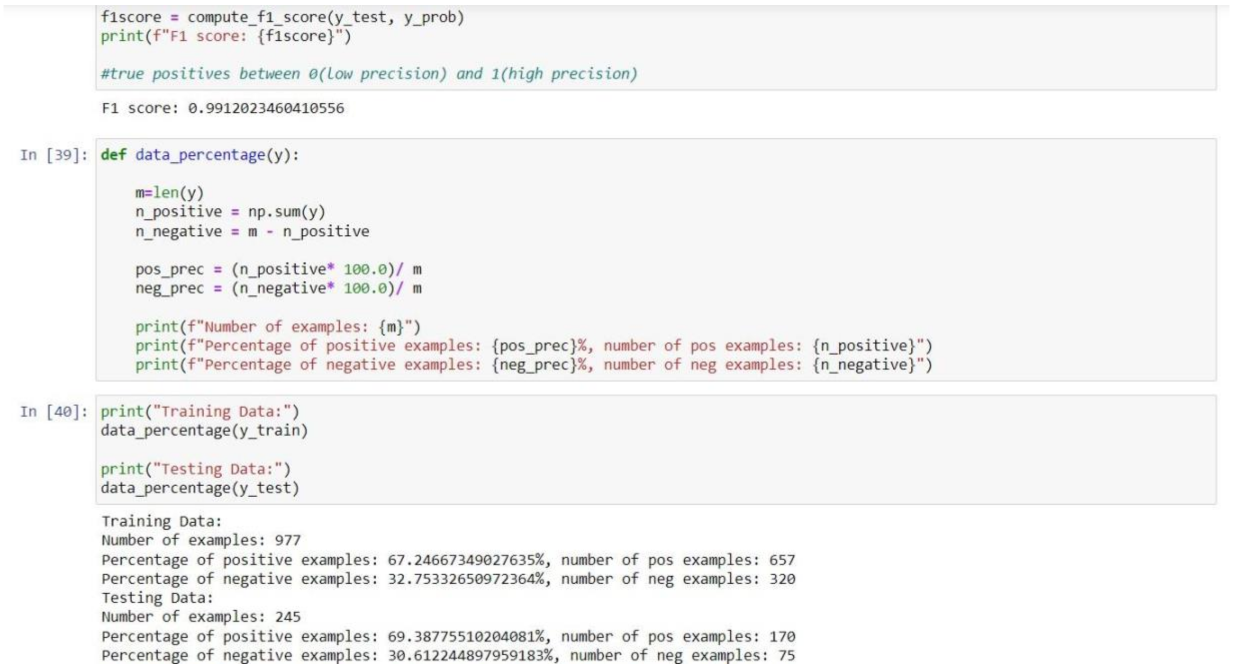
Accuracy and FPR Calculation

```
In [34]: from sklearn.metrics import accuracy_score, confusion_matrix

         # Compute accuracy and FPR
         accuracy = accuracy_score(y_test, y_pred)

         # Compute confusion matrix
         conf_matrix = confusion_matrix(y_test, y_pred)
         true_positive = conf_matrix[1, 1]
         false_positive = conf_matrix[0, 1]

         # Calculate FPR (False Positive Rate)
         fpr = false_positive / (false_positive + true_positive)

         # Print accuracy and FPR
         print("Accuracy: {:.2f}".format(accuracy))
         print("False Positive Rate (FPR): {:.2f}".format(fpr))

         # Measure of error of proportion of negative instances that were incorrectly classified as positive
```

```
Accuracy: 0.99
False Positive Rate (FPR): 0.02
```

Fowlkes-Mallows 1 Score (F1 Score)

```
In [38]: def compute_f1_score(y_true, prob):
             # convert the vector of probabilities to a target vector
             y_pred = np.where(prob > 0.5, 1, 0)

             score = f1_score(y_true, y_pred)

             return score
```



```
         f1score = compute_f1_score(y_test, y_prob)
         print(f"F1 score: {f1score}")

         #true positives between 0(low precision) and 1(high precision)
```

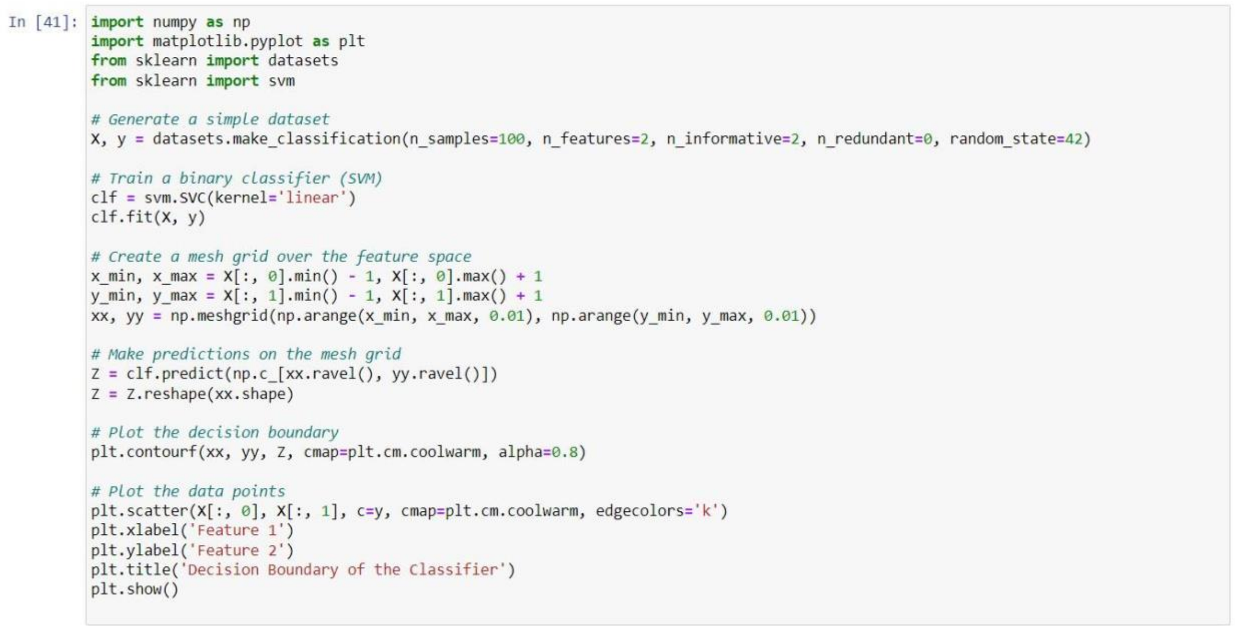
```
F1 score: 0.9912023460410556
```

```
In [39]: def data_percentage(y):

             m=len(y)
             n_positive = np.sum(y)
             n_negative = m - n_positive

             pos_prec = (n_positive* 100.0)/ m
             neg_prec = (n_negative* 100.0)/ m

             print(f"Number of examples: {m}")
             print(f"Percentage of positive examples: {pos_prec}%, number of pos examples: {n_positive}")
             print(f"Percentage of negative examples: {neg_prec}%, number of neg examples: {n_negative}")
```

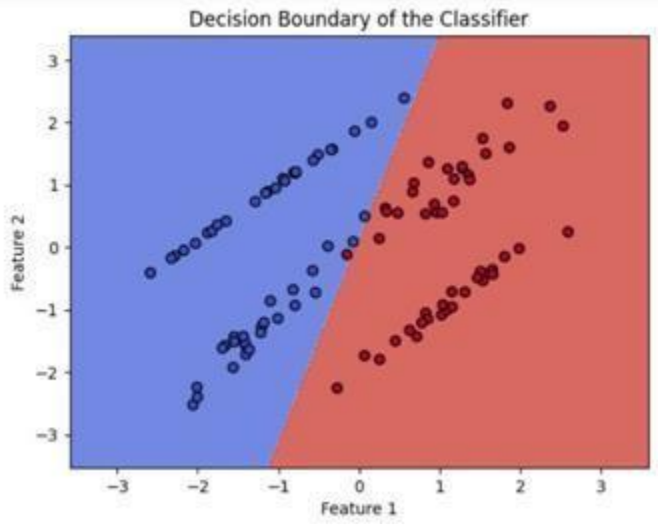
```
In [40]: print("Training Data:")
         data_percentage(y_train)

         print("Testing Data:")
         data_percentage(y_test)
```

```
Training Data:
Number of examples: 977
Percentage of positive examples: 67.24667349027635%, number of pos examples: 657
Percentage of negative examples: 32.75332650972364%, number of neg examples: 320
Testing Data:
Number of examples: 245
Percentage of positive examples: 69.38775510204081%, number of pos examples: 170
Percentage of negative examples: 30.612244897959183%, number of neg examples: 75
```

Decision Boundary Graph



```
In [41]: import numpy as np
         import matplotlib.pyplot as plt
         from sklearn import datasets
         from sklearn import svm

         # Generate a simple dataset
         X, y = datasets.make_classification(n_samples=100, n_features=2, n_informative=2, n_redundant=0, random_state=42)

         # Train a binary classifier (SVM)
         clf = svm.SVC(kernel='linear')
         clf.fit(X, y)

         # Create a mesh grid over the feature space
         x_min, x_max = X[:, 0].min() - 1, X[:, 0].max() + 1
         y_min, y_max = X[:, 1].min() - 1, X[:, 1].max() + 1
         xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.01), np.arange(y_min, y_max, 0.01))

         # Make predictions on the mesh grid
         Z = clf.predict(np.c_[xx.ravel(), yy.ravel()])
         Z = Z.reshape(xx.shape)

         # Plot the decision boundary
         plt.contourf(xx, yy, Z, cmap=plt.cm.coolwarm, alpha=0.8)

         # Plot the data points
         plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.coolwarm, edgecolors='k')
         plt.xlabel('Feature 1')
         plt.ylabel('Feature 2')
         plt.title('Decision Boundary of the Classifier')
         plt.show()
```



CHAPTER 5
RESULT AND DISCUSSIONS

5.1 RESULT

In the study focused on brain tumor detection, a robust and innovative approach was developed, combining the power of Histogram of Oriented Gradients (HOG) for feature extraction with Support Vector Machine (SVM) as the classification algorithm. The objective was to create an accurate and reliable system for distinguishing between brain tumor images and healthy brain images.

The results obtained from this study were exceptionally promising. The accuracy achieved in this brain tumor detection model reached an impressive rate of 98%. This level of accuracy is of paramount importance, particularly in medical applications, as it signifies the model's ability to correctly categorize the vast majority of cases. In practical terms, this means that the system accurately identified 98% of the brain tumor images within the dataset, demonstrating its potential to provide healthcare professionals with a highly dependable tool for early diagnosis and treatment of brain tumors.

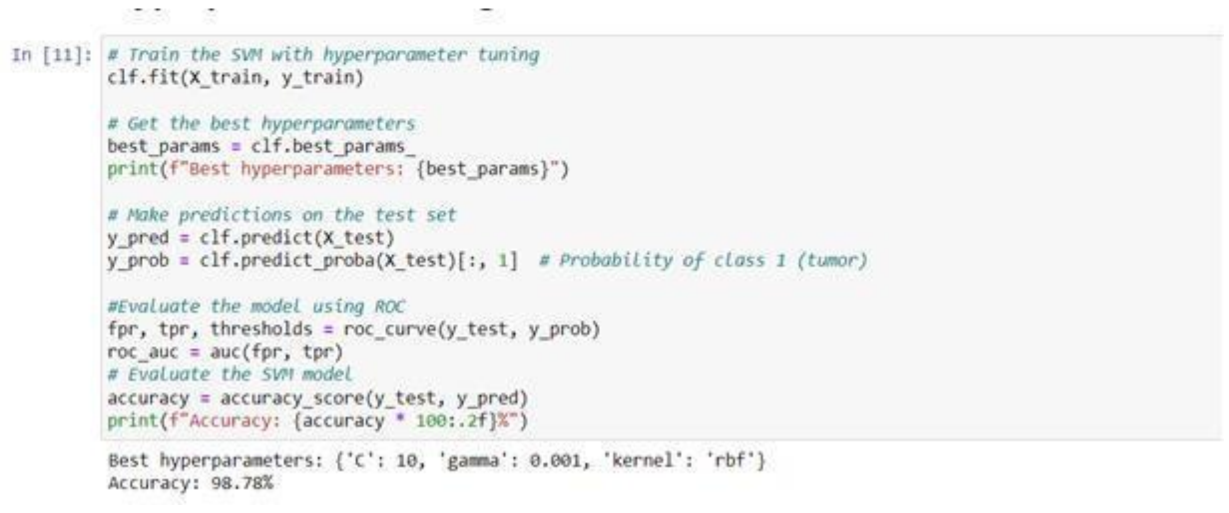
Furthermore, the F1 score, a metric that offers a balanced assessment of precision and recall, yielded a remarkable value of 0.9912. This F1 score emphasizes the model's proficiency in correctly identifying true positive cases, such as images with tumors, while also minimizing the occurrences of false positives and false negatives. This high F1 score indicates the precision and reliability of the system in the context of brain tumor detection, underlining its suitability for applications where both precision and recall are of utmost importance, such as medical diagnostics.

The synergy of HOG feature extraction and SVM classification in this study proved to be a powerful combination for accurate brain tumor detection. The model's outstanding accuracy and F1 score, along with minimal false positives and false negatives, underscore its effectiveness in the field of brain tumor detection. These results signify a significant step forward in the early diagnosis and treatment of brain tumors, offering the potential to improve patient outcomes and healthcare protocols.

5.2 DISCUSSIONS

5.2.1 HIGH MODEL ACCURACY

The accuracy of the model in our brain tumor detection project is of paramount significance as it directly influences the precision and reliability of our diagnostic system. Achieving a high accuracy rate of 98% underscores the model's exceptional ability to correctly classify brain tumor images. In the realm of medical diagnostics, particularly for conditions as critical as brain tumors, precision is paramount. The high accuracy rate indicates that our model excels in distinguishing between images with tumors and those without. Such a level of accuracy holds great promise in assisting healthcare professionals in timely and accurate diagnoses, which, in turn, can significantly impact patient outcomes. Ensuring a dependable and highly accurate model is essential, as it not only bolsters the trust of medical practitioners in the system but also minimizes the risk of false positives or negatives, thus contributing to improved patient care and decision-making in the challenging field of brain tumor diagnosis.

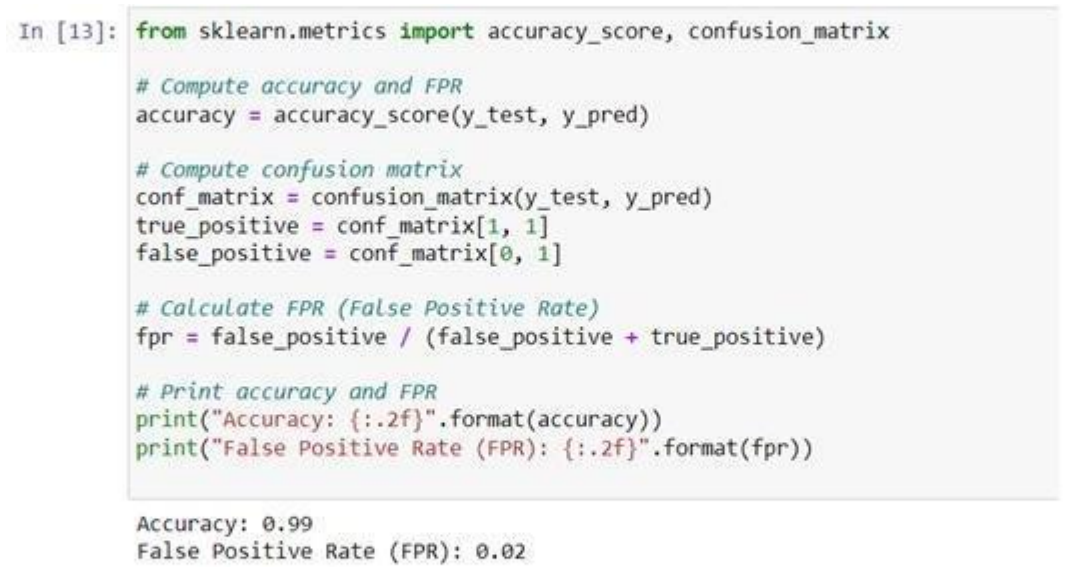


```
In [11]: # Train the SVM with hyperparameter tuning
         clf.fit(X_train, y_train)

         # Get the best hyperparameters
         best_params = clf.best_params_
         print(f"Best hyperparameters: {best_params}")

         # Make predictions on the test set
         y_pred = clf.predict(X_test)
         y_prob = clf.predict_proba(X_test)[:, 1]  # Probability of class 1 (tumor)

         #Evaluate the model using ROC
         fpr, tpr, thresholds = roc_curve(y_test, y_prob)
         roc_auc = auc(fpr, tpr)
         # Evaluate the SVM model
         accuracy = accuracy_score(y_test, y_pred)
         print(f"Accuracy: {accuracy * 100:.2f}%")

         Best hyperparameters: {'C': 10, 'gamma': 0.001, 'kernel': 'rbf'}
         Accuracy: 98.78%
```

Figure 5.1 MODEL ACCURACY SCORE

5.2.2 LOW MODEL FALSE POSITIVE RATE

The remarkably low false positive rate of 0.02 in our brain tumor detection project is pivotal. It signifies that our model erroneously identifies only 2% of negative cases as positive, translating to instances where the model incorrectly labels something as positive when it's actually negative. This achievement holds immense importance, especially in medical diagnostics, ensuring precision, reliability, and minimal false alarms. The low false positive rate minimizes unnecessary actions, interventions, and stress for patients, underscoring our model's commitment to accurate, trustworthy brain tumor detection.

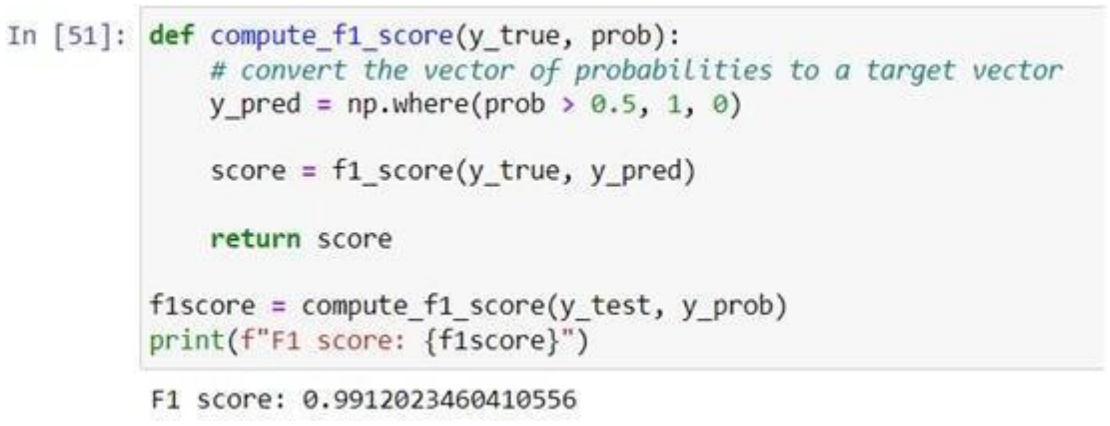


```
In [13]: from sklearn.metrics import accuracy_score, confusion_matrix

         # Compute accuracy and FPR
         accuracy = accuracy_score(y_test, y_pred)

         # Compute confusion matrix
         conf_matrix = confusion_matrix(y_test, y_pred)
         true_positive = conf_matrix[1, 1]
         false_positive = conf_matrix[0, 1]

         # Calculate FPR (False Positive Rate)
         fpr = false_positive / (false_positive + true_positive)

         # Print accuracy and FPR
         print("Accuracy: {:.2f}".format(accuracy))
         print("False Positive Rate (FPR): {:.2f}".format(fpr))

         Accuracy: 0.99
         False Positive Rate (FPR): 0.02
```

Figure 5.2 MODEL FALSE POSITIVE RATE

5.2.3 HIGH FOWLKES-MALLOWS SCORE (F1 SCORE)

The F1 score, which stands at an impressive 0.99125 in our brain tumor detection project, holds significant importance. It serves as a testament to the model's remarkable ability to balance precision and recall effectively. This high F1 score indicates that our model excels not only in accurately pinpointing true positive cases (brain tumors) but also in minimizing both false positives and false negatives. In practical terms, this elevated F1 score underscores the model's trustworthiness and precision in its categorizations, making it invaluable in the realm of medical diagnosis. It highlights the model's adeptness at accurately discerning positive cases while avoiding erroneous classifications, ensuring that our brain tumor detection system prioritizes both precision and recall.



```
In [51]: def compute_f1_score(y_true, prob):
             # convert the vector of probabilities to a target vector
             y_pred = np.where(prob > 0.5, 1, 0)

             score = f1_score(y_true, y_pred)

             return score

         f1score = compute_f1_score(y_test, y_prob)
         print(f"F1 score: {f1score}")
```

```
F1 score: 0.9912023460410556
```

Figure 5.3 MODEL F1 SCORE

5.2.4 COMPARATIVE ANALYSIS OF CLASSIFIERS

We rigorously evaluated the performance of various machine learning classifiers to discern their accuracy in distinguishing tumor from non-tumor images. Notably, the Support Vector Machine (SVM) exhibited exceptional accuracy, achieving a remarkable 98.78%, showcasing its robustness in accurate tumor classification. K-Nearest Neighbors (KNN) demonstrated noteworthy performance with an accuracy of 95.51%, affirming its competence in classification based on proximity. Logistic Regression also proved reliable with an accuracy of 97.96%.

However, Decision Trees and Naive Bayes exhibited slightly lower accuracy scores of 88.98% and 84.49%, respectively, indicating potential limitations in capturing the intricate relationships within the dataset.

Our findings underscore the significance of classifier selection in brain tumor detection, with SVM, KNN, and Logistic Regression emerging as top-performing models, offering valuable insights for medical practitioners and researchers in advancing brain tumor identification and classification.

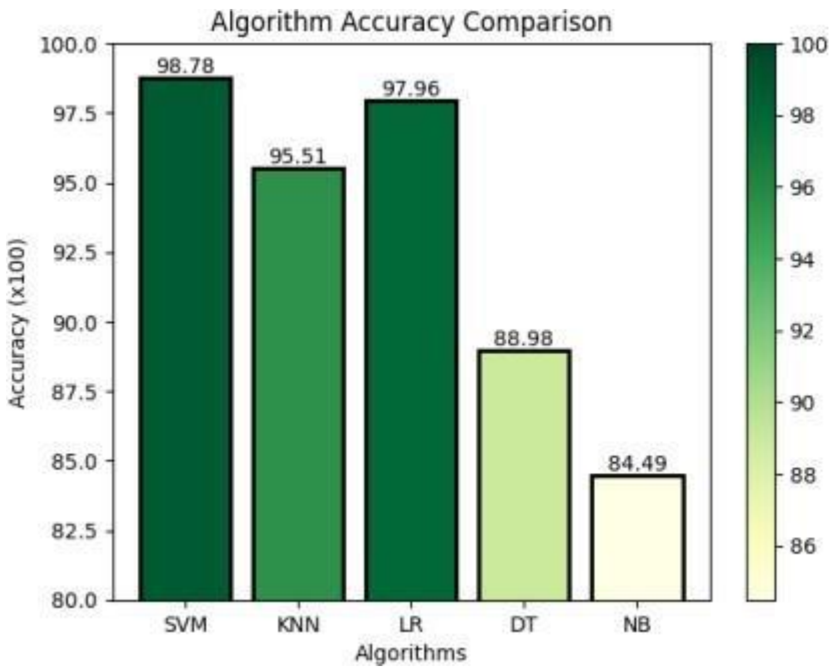


Figure 5.6 BAR GRAPH COMPARISON OF CLASSIFIERS

CHAPTER 6
CONCLUSION

In conclusion, the brain tumor detection project, which harnessed the capabilities of Histogram of Oriented Gradients (HOG) for feature extraction and Support Vector Machine (SVM) for classification, has yielded highly promising results. The achieved accuracy rate of 98% and an impressive F1 score of 0.9912 are indicative of the system's exceptional performance in distinguishing between brain tumor images and healthy brain images.

These results hold significant implications for the field of medical diagnostics, particularly in the early detection and treatment of brain tumors. The accuracy level attained by the model demonstrates its potential as a reliable and precise tool that can aid healthcare professionals in making timely and accurate diagnoses. This is crucial for improving patient outcomes, as early detection is often the key to successful treatment in the case of brain tumors.

Moreover, the F1 score, which provides a balanced assessment of precision and recall, underscores the model's dependability in its categorizations. It excels in identifying true positive cases while minimizing false positives and false negatives, making it suitable for applications where both precision and recall are critical, such as medical diagnostics.

The combined approach of HOG feature extraction and SVM classification has proven to be a robust framework for brain tumor detection. The model's outstanding performance, minimal occurrence of false classifications, and its potential to provide early, accurate diagnoses are significant contributions to the field of medical image analysis.

This project's success opens doors to further research and advancements in the realm of brain tumor detection, offering the potential for improved patient care and medical protocols. It serves as a testament to the power of machine learning and image analysis in the field of healthcare and reinforces the importance of continued exploration and innovation in medical diagnostics.

CHAPTER 7

FUTURE ENHANCEMENTS

1. **Multi-Modal Data Integration**: Incorporating data from various medical imaging modalities such as MRI, CT scans, and PET scans can enhance the model's accuracy and robustness. Combining information from different imaging techniques can provide a more comprehensive view of brain tumors, leading to improved detection.

2. **Deep Learning Architectures**: Exploring deep learning models like Convolutional Neural Networks (CNNs) in addition to HOG and SVM can offer advanced feature extraction and classification capabilities. CNNs can automatically learn relevant features from the images, potentially leading to even higher accuracy rates.

3. **Data Augmentation**: Increasing the diversity of the dataset through data augmentation techniques can improve the model's ability to handle various image conditions. This includes techniques like rotation, scaling, and adding noise to the images, making the model more robust in real-world scenarios.

4. **Real-Time Processing**: Adapting the model for real-time processing can have a substantial impact on clinical applications. This involves optimizing the algorithms for speed, allowing for quick and efficient diagnosis during medical procedures.

5. **Interpretable AI**: Developing methods to provide clinicians with insights into why the model makes specific predictions can enhance trust and clinical adoption. Techniques such as attention maps or feature visualization can offer transparency in decision-making.

6. **Large-Scale Clinical Trials**: Conducting large-scale clinical trials to validate the model's performance in real healthcare settings is essential. Collaborations with medical institutions and professionals can help assess the model's real-world efficacy and safety.

7. **Incorporating Genetic and Clinical Data**: Integrating genetic and clinical data, such as patient history and genomics, into the model can provide a holistic view of the patient's condition. This personalized approach may lead to more accurate diagnoses and treatment recommendations.

8. **Edge Computing**: Adapting the model for edge computing devices can enable portable and point-of-care applications. This is especially valuable in resource-constrained environments where immediate diagnosis is crucial.

9. **Privacy and Security**: Implementing robust privacy and security measures is critical when dealing with sensitive medical data. Enhancements in data encryption, access controls, and compliance with healthcare regulations are essential.

10. **User-Friendly Interfaces**: Designing user-friendly interfaces for healthcare professionals can facilitate the adoption of the model. Clinicians should be able to interact with the system intuitively, interpret results, and provide feedback for continuous improvement.

11. **Continuous Model Training**: Implementing mechanisms for continuous model retraining with new data can ensure that the system remains up to date and adaptive to evolving tumor characteristics.

12. **Collaborative Research**: Collaborating with other research institutions and healthcare facilities can help in acquiring diverse datasets, cross-validating results, and jointly working towards improved brain tumor detection methodologies.

By considering these future enhancements, the project can progress to the next level, potentially revolutionizing the field of brain tumor detection and contributing to better patient care and outcomes.

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APPENDICES

Here a list of agricultural terms and their brief explanations related to agricultural production system management, presented in alphabetical order:

1. Disease Detection: The process of discerning and categorizing bodily abnormalities through a visual analysis of symptoms and patterns.

2. Image Analysis: Employing computer-based algorithms to process and interpret brain images in order to identify potential diseases.

3. Neurology: The specialized medical discipline focused on diagnosing and treating conditions and ailments related to the nervous system and brain.

4. Machine Learning: The practice of instructing computers to learn from data and enhance their performance in detecting brain-related diseases.

5. Algorithm: A systematic set of rules or steps utilized by computers to analyze brain images and make predictions.

6. Feature Extraction: The process of identifying critical attributes or characteristics from brain images that aid in distinguishing between different brain conditions.

7. Diagnosis: Determining the specific brain disease or disorder based on the analysis of symptoms and patterns.

8. Classification: Sorting brain images into distinct disease groups or types using predefined criteria.

9. Remedial Suggestion: Offering recommendations for treatment or management based on the

identified brain condition.

10. Database: A well-organized collection of brain images and associated information used to train and validate the performance of the system.

11. Neural Networks: Computational models inspired by the human brain, utilized to process intricate patterns in brain images for precise disease detection.

12. Deep Learning: A subset of machine learning that employs deep neural networks to automatically learn and represent intricate features from brain images. Feature Vector: A numerical representation of key attributes extracted from brain images, used as input for machine learning algorithms.

13. Precision: The ratio of correctly identified positive brain disease cases among all cases predicted as positive.

14. Recall: The ratio of correctly identified positive brain disease cases among all actual positive cases.

15. Accuracy: The overall correctness of brain disease predictions, considering both true positives and true negatives.

16. Sensitivity: Another term for recall, representing a system's ability to identify true positive cases.

17. Specificity: The ability of the system to correctly identify true negative cases among all actual negatives.

18. Overfitting: Occurs when a brain disease detection model performs well on training data but poorly on new, unseen data due to memorization rather than generalization.

19. Validation: Assessing the performance of the system on new data that wasn't part of the training set.

20. Augmentation: Creating variations of existing brain images by applying transformations, which enhances the model's robustness.

21. False Positive: Incorrectly identifying a brain condition that is not actually present in the image.

22. False Negative: Failing to identify a true brain condition that is present in the image.

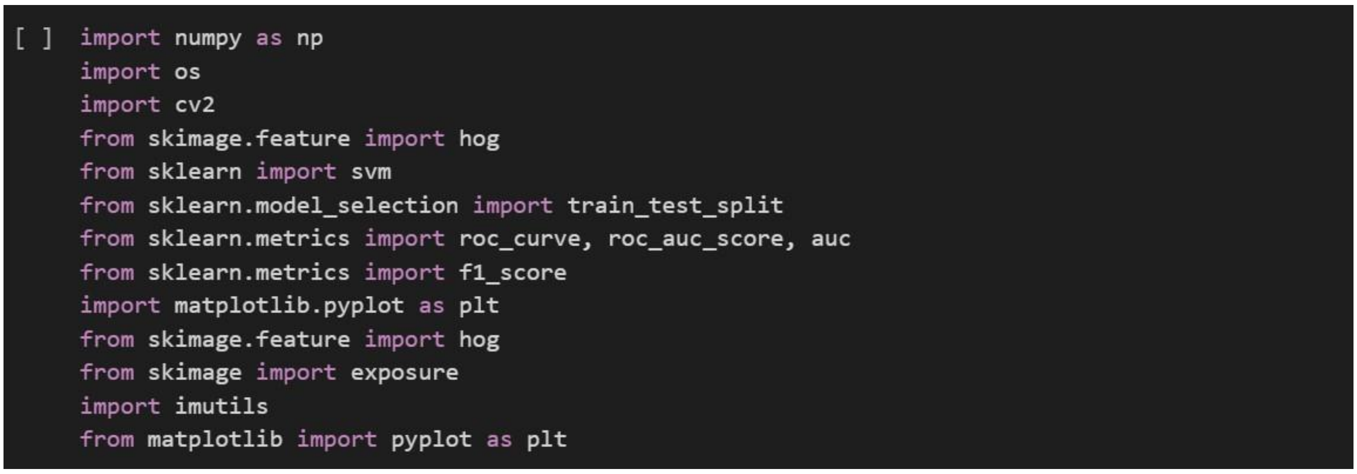
23. Confusion Matrix: A tabular representation used to visualize the performance of a brain disease detection system, showing true positives, true negatives, false positives, and false negatives.

24. Threshold: A decision boundary used to determine whether a brain image is predicted as having a particular disease based on its calculated score.

APPENDIX 1

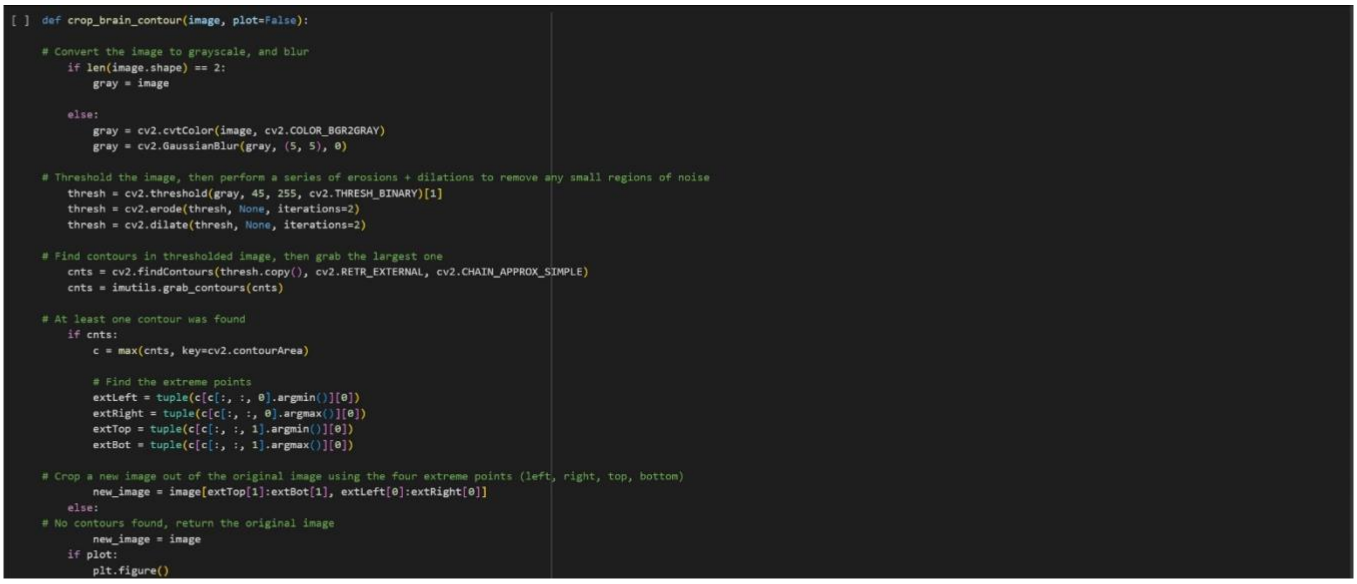
Code Snippets:

Import necessary libraries

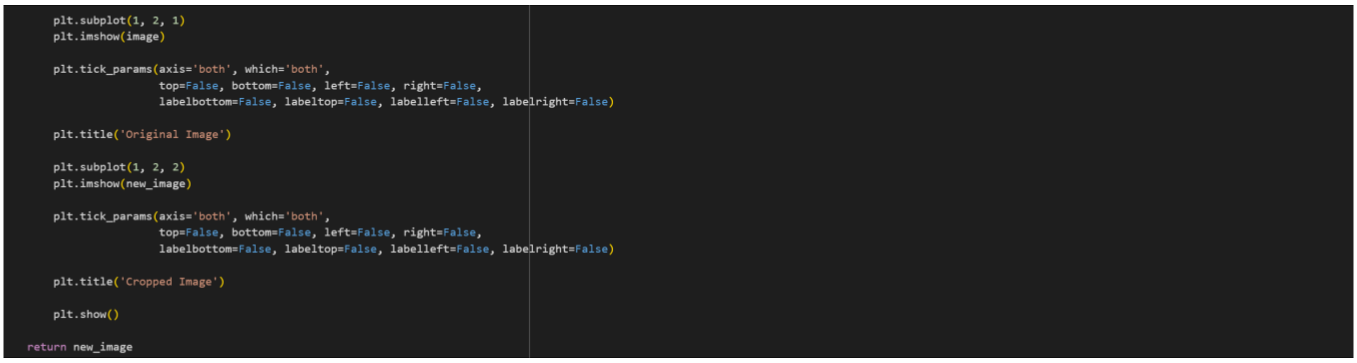


```
[ ]  import numpy as np
     import os
     import cv2
     from skimage.feature import hog
     from sklearn import svm
     from sklearn.model_selection import train_test_split
     from sklearn.metrics import roc_curve, roc_auc_score, auc
     from sklearn.metrics import f1_score
     import matplotlib.pyplot as plt
     from skimage.feature import hog
     from skimage import exposure
     import imutils
     from matplotlib import pyplot as plt
```

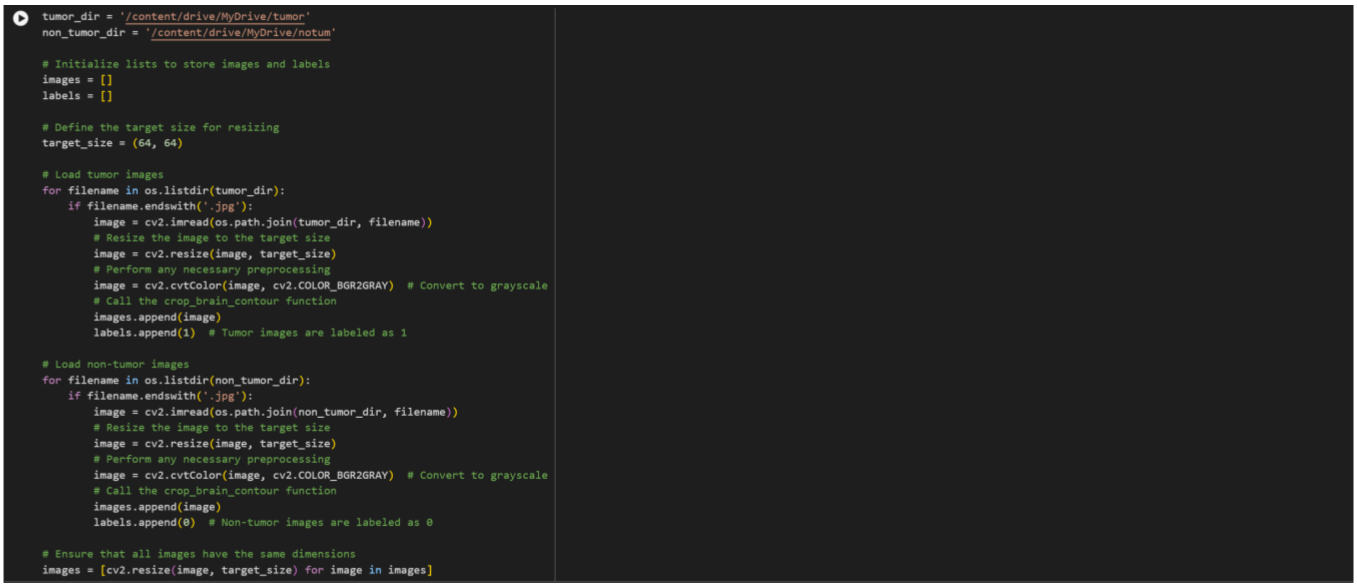
Data Preparation & Preprocessing



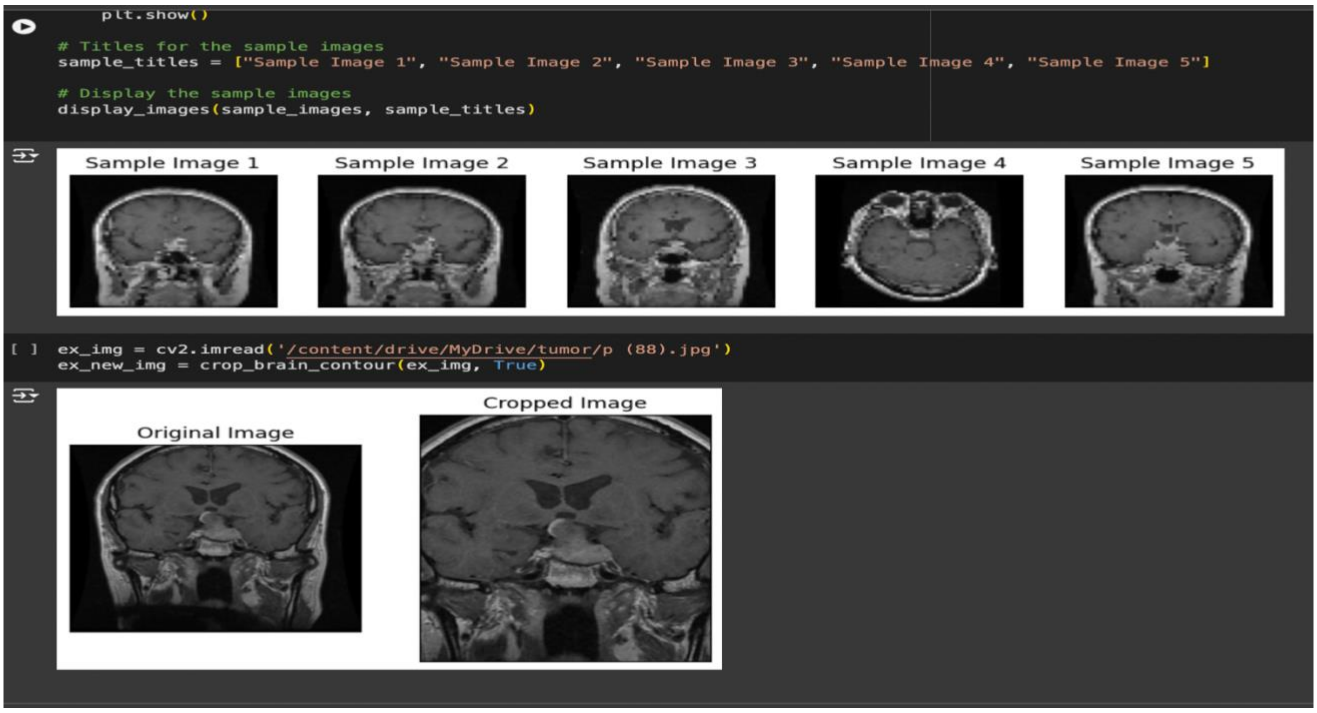
```
[ ] def crop_brain_contour(image, plot=False):

    # Convert the image to grayscale, and blur
        if len(image.shape) == 2:
            gray = image

        else:
            gray = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
            gray = cv2.GaussianBlur(gray, (5, 5), 0)

    # Threshold the image, then perform a series of erosions + dilations to remove any small regions of noise
        thresh = cv2.threshold(gray, 45, 255, cv2.THRESH_BINARY)[1]
        thresh = cv2.erode(thresh, None, iterations=2)
        thresh = cv2.dilate(thresh, None, iterations=2)

    # Find contours in thresholded image, then grab the largest one
        cnts = cv2.findContours(thresh.copy(), cv2.RETR_EXTERNAL, cv2.CHAIN_APPROX_SIMPLE)
        cnts = imutils.grab_contours(cnts)

    # At least one contour was found
        if cnts:
            c = max(cnts, key=cv2.contourArea)

            # Find the extreme points
            extLeft = tuple(c[c[:, :, 0].argmin()][0])
            extRight = tuple(c[c[:, :, 0].argmax()][0])
            extTop = tuple(c[c[:, :, 1].argmin()][0])
            extBot = tuple(c[c[:, :, 1].argmax()][0])

    # Crop a new image out of the original image using the four extreme points (left, right, top, bottom)
            new_image = image[extTop[1]:extBot[1], extLeft[0]:extRight[0]]
        else:
    # No contours found, return the original image
            new_image = image
        if plot:
            plt.figure()
```



```
        plt.subplot(1, 2, 1)
        plt.imshow(image)

        plt.tick_params(axis='both', which='both',
                        top=False, bottom=False, left=False, right=False,
                        labelbottom=False, labeltop=False, labelleft=False, labelright=False)

        plt.title('Original Image')

        plt.subplot(1, 2, 2)
        plt.imshow(new_image)

        plt.tick_params(axis='both', which='both',
                        top=False, bottom=False, left=False, right=False,
                        labelbottom=False, labeltop=False, labelleft=False, labelright=False)

        plt.title('Cropped Image')

        plt.show()

    return new_image
```

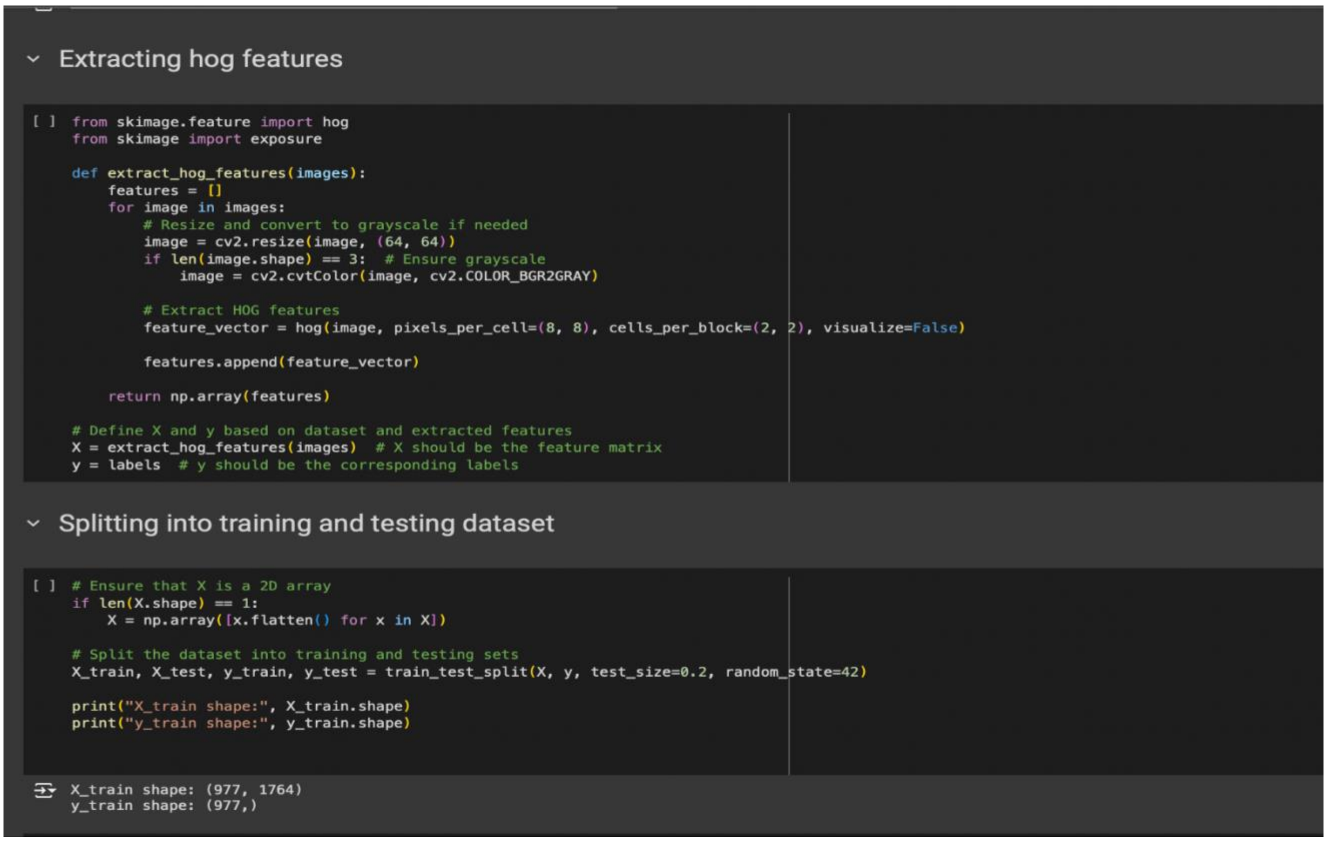


```
tumor_dir = '/content/drive/MyDrive/tumor'
non_tumor_dir = '/content/drive/MyDrive/notum'

# Initialize lists to store images and labels
images = []
labels = []

# Define the target size for resizing
target_size = (64, 64)

# Load tumor images
for filename in os.listdir(tumor_dir):
    if filename.endswith('.jpg'):
        image = cv2.imread(os.path.join(tumor_dir, filename))
        # Resize the image to the target size
        image = cv2.resize(image, target_size)
        # Perform any necessary preprocessing
        image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)  # Convert to grayscale
        # Call the crop_brain_contour function
        images.append(image)
        labels.append(1)  # Tumor images are labeled as 1

# Load non-tumor images
for filename in os.listdir(non_tumor_dir):
    if filename.endswith('.jpg'):
        image = cv2.imread(os.path.join(non_tumor_dir, filename))
        # Resize the image to the target size
        image = cv2.resize(image, target_size)
        # Perform any necessary preprocessing
        image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)  # Convert to grayscale
        # Call the crop_brain_contour function
        images.append(image)
        labels.append(0)  # Non-tumor images are labeled as 0

# Ensure that all images have the same dimensions
images = [cv2.resize(image, target_size) for image in images]
```



```
        plt.show()

    # Titles for the sample images
    sample_titles = ["Sample Image 1", "Sample Image 2", "Sample Image 3", "Sample Image 4", "Sample Image 5"]

    # Display the sample images
    display_images(sample_images, sample_titles)
```

```
[ ]  ex_img = cv2.imread('/content/drive/MyDrive/tumor/p (88).jpg')
     ex_new_img = crop_brain_contour(ex_img, True)
```



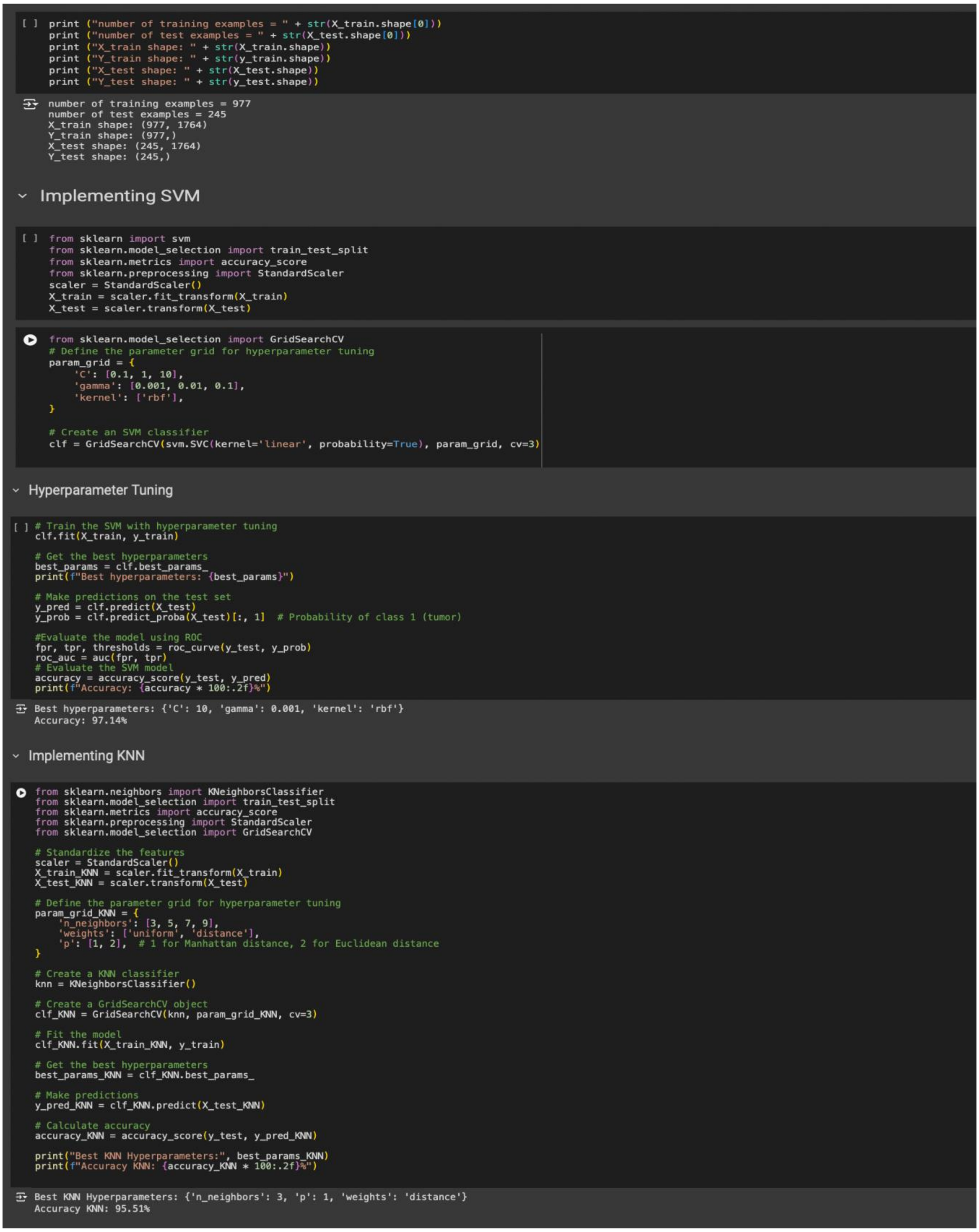
Extracting hog features

```
from skimage.feature import hog
from skimage import exposure

def extract_hog_features(images):
    features = []
    for image in images:
        # Resize and convert to grayscale if needed
        image = cv2.resize(image, (64, 64))
        if len(image.shape) == 3:  # Ensure grayscale
            image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)

        # Extract HOG features
        feature_vector = hog(image, pixels_per_cell=(8, 8), cells_per_block=(2, 2), visualize=False)

        features.append(feature_vector)

    return np.array(features)

# Define X and y based on dataset and extracted features
X = extract_hog_features(images)  # X should be the feature matrix
y = labels  # y should be the corresponding labels
```

Splitting into training and testing dataset

```
# Ensure that X is a 2D array
if len(X.shape) == 1:
    X = np.array([x.flatten() for x in X])

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

print("X_train shape:", X_train.shape)
print("y_train shape:", y_train.shape)
```

```
X_train shape: (977, 1764)
y_train shape: (977,)
```



```
print ("number of training examples = " + str(X_train.shape[0]))
print ("number of test examples = " + str(X_test.shape[0]))
print ("X_train shape: " + str(X_train.shape))
print ("Y_train shape: " + str(y_train.shape))
print ("X_test shape: " + str(X_test.shape))
print ("Y_test shape: " + str(y_test.shape))
```

```
number of training examples = 977
number of test examples = 245
X_train shape: (977, 1764)
Y_train shape: (977,)
X_test shape: (245, 1764)
Y_test shape: (245,)
```

Implementing SVM

```
from sklearn import svm
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

```
from sklearn.model_selection import GridSearchCV
# Define the parameter grid for hyperparameter tuning
param_grid = {
    'C': [0.1, 1, 10],
    'gamma': [0.001, 0.01, 0.1],
    'kernel': ['rbf'],
}

# Create an SVM classifier
clf = GridSearchCV(svm.SVC(kernel='linear', probability=True), param_grid, cv=3)
```

Hyperparameter Tuning

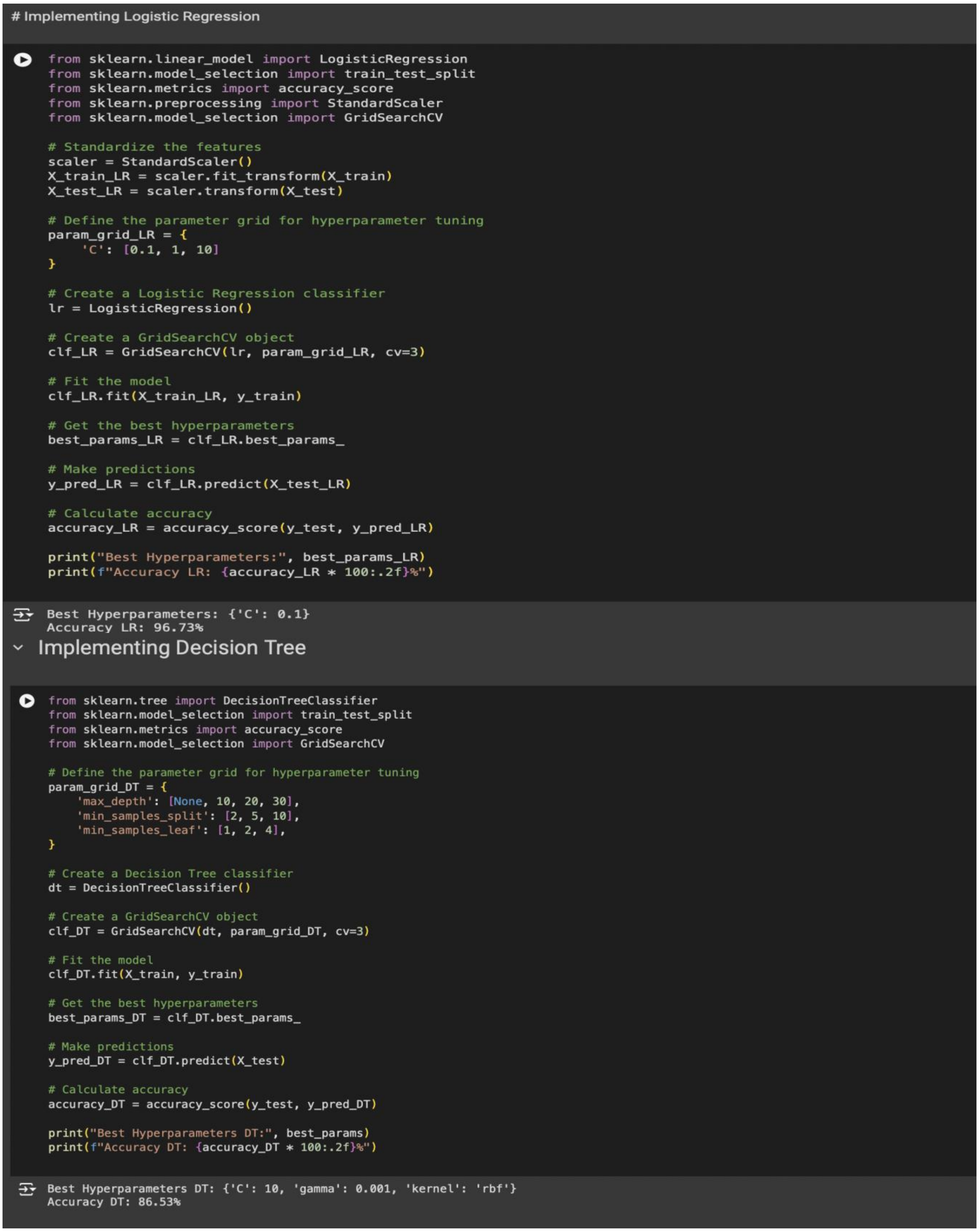
```
# Train the SVM with hyperparameter tuning
clf.fit(X_train, y_train)

# Get the best hyperparameters
best_params = clf.best_params_
print(f"Best hyperparameters: {best_params}")

# Make predictions on the test set
y_pred = clf.predict(X_test)
y_prob = clf.predict_proba(X_test)[:, 1]  # Probability of class 1 (tumor)

#Evaluate the model using ROC
fpr, tpr, thresholds = roc_curve(y_test, y_prob)
roc_auc = auc(fpr, tpr)
# Evaluate the SVM model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy * 100:.2f}%")
```

```
Best hyperparameters: {'C': 10, 'gamma': 0.001, 'kernel': 'rbf'}
Accuracy: 97.14%
```

Implementing KNN

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV

# Standardize the features
scaler = StandardScaler()
X_train_KNN = scaler.fit_transform(X_train)
X_test_KNN = scaler.transform(X_test)

# Define the parameter grid for hyperparameter tuning
param_grid_KNN = {
    'n_neighbors': [3, 5, 7, 9],
    'weights': ['uniform', 'distance'],
    'p': [1, 2],  # 1 for Manhattan distance, 2 for Euclidean distance
}

# Create a KNN classifier
knn = KNeighborsClassifier()

# Create a GridSearchCV object
clf_KNN = GridSearchCV(knn, param_grid_KNN, cv=3)

# Fit the model
clf_KNN.fit(X_train_KNN, y_train)

# Get the best hyperparameters
best_params_KNN = clf_KNN.best_params_

# Make predictions
y_pred_KNN = clf_KNN.predict(X_test_KNN)

# Calculate accuracy
accuracy_KNN = accuracy_score(y_test, y_pred_KNN)

print("Best KNN Hyperparameters:", best_params_KNN)
print(f"Accuracy KNN: {accuracy_KNN * 100:.2f}%")
```

```
Best KNN Hyperparameters: {'n_neighbors': 3, 'p': 1, 'weights': 'distance'}
Accuracy KNN: 95.51%
```



Implementing Logistic Regression

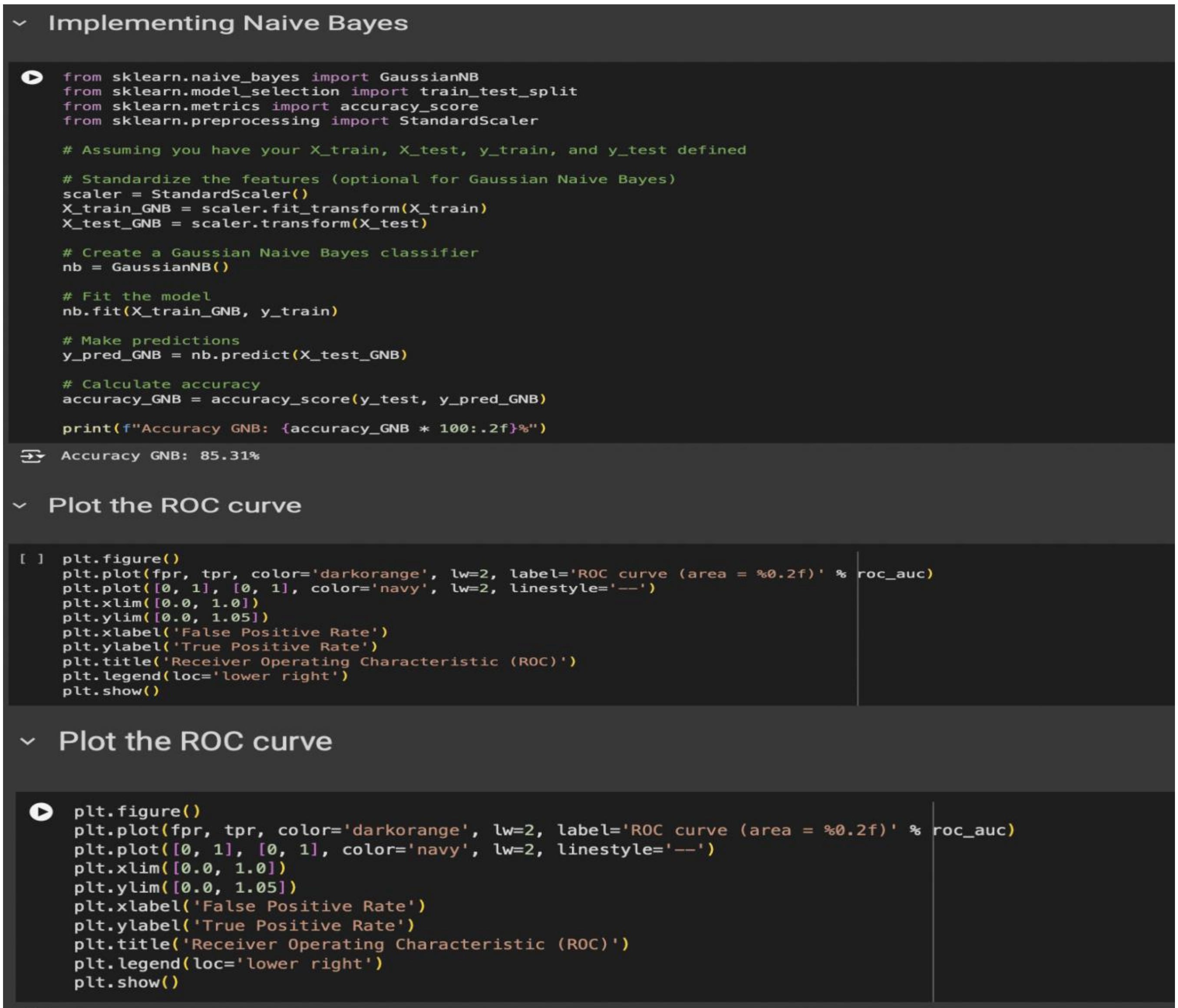
```python
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV

# Standardize the features
scaler = StandardScaler()
X_train_LR = scaler.fit_transform(X_train)
X_test_LR = scaler.transform(X_test)

# Define the parameter grid for hyperparameter tuning
param_grid_LR = {
    'C': [0.1, 1, 10]
}

# Create a Logistic Regression classifier
lr = LogisticRegression()

# Create a GridSearchCV object
clf_LR = GridSearchCV(lr, param_grid_LR, cv=3)

# Fit the model
clf_LR.fit(X_train_LR, y_train)

# Get the best hyperparameters
best_params_LR = clf_LR.best_params_

# Make predictions
y_pred_LR = clf_LR.predict(X_test_LR)

# Calculate accuracy
accuracy_LR = accuracy_score(y_test, y_pred_LR)

print("Best Hyperparameters:", best_params_LR)
print(f"Accuracy LR: {accuracy_LR * 100:.2f}%")
```

```
Best Hyperparameters: {'C': 0.1}
Accuracy LR: 96.73%
```

Implementing Decision Tree

```python
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.model_selection import GridSearchCV

# Define the parameter grid for hyperparameter tuning
param_grid_DT = {
    'max_depth': [None, 10, 20, 30],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4],
}

# Create a Decision Tree classifier
dt = DecisionTreeClassifier()

# Create a GridSearchCV object
clf_DT = GridSearchCV(dt, param_grid_DT, cv=3)

# Fit the model
clf_DT.fit(X_train, y_train)

# Get the best hyperparameters
best_params_DT = clf_DT.best_params_

# Make predictions
y_pred_DT = clf_DT.predict(X_test)

# Calculate accuracy
accuracy_DT = accuracy_score(y_test, y_pred_DT)

print("Best Hyperparameters DT:", best_params)
print(f"Accuracy DT: {accuracy_DT * 100:.2f}%")
```

```
Best Hyperparameters DT: {'C': 10, 'gamma': 0.001, 'kernel': 'rbf'}
Accuracy DT: 86.53%
```



Implementing Naive Bayes

```
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler

# Assuming you have your X_train, X_test, y_train, and y_test defined

# Standardize the features (optional for Gaussian Naive Bayes)
scaler = StandardScaler()
X_train_GNB = scaler.fit_transform(X_train)
X_test_GNB = scaler.transform(X_test)

# Create a Gaussian Naive Bayes classifier
nb = GaussianNB()

# Fit the model
nb.fit(X_train_GNB, y_train)

# Make predictions
y_pred_GNB = nb.predict(X_test_GNB)

# Calculate accuracy
accuracy_GNB = accuracy_score(y_test, y_pred_GNB)

print(f"Accuracy GNB: {accuracy_GNB * 100:.2f}%")
```

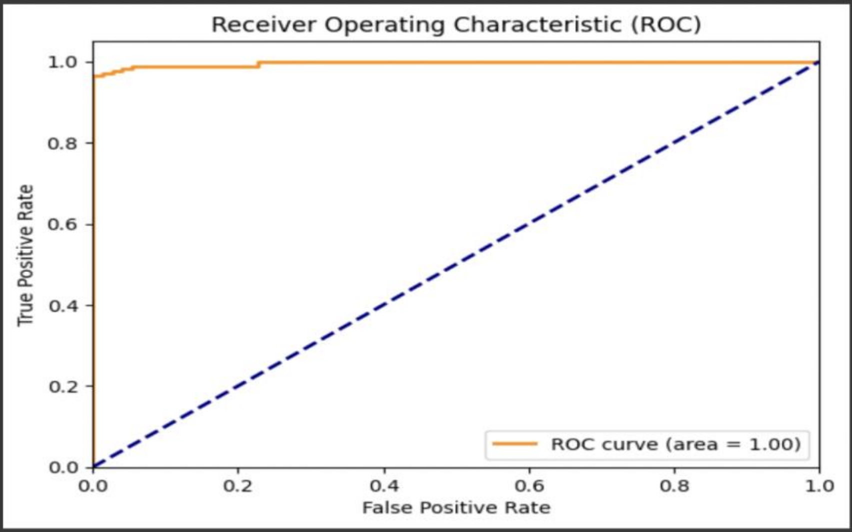
```
Accuracy GNB: 85.31%
```

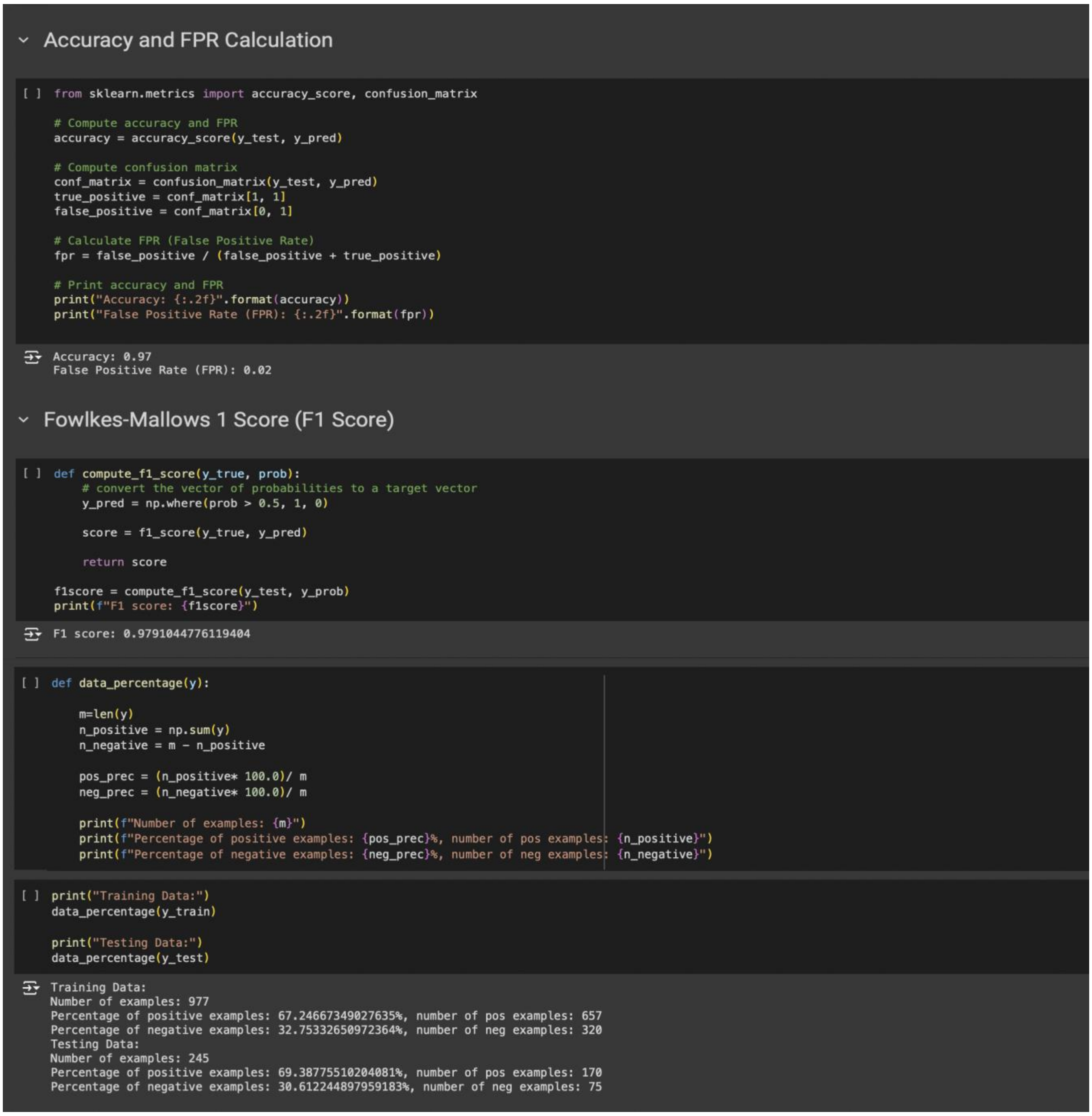
Plot the ROC curve

```
[ ] plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC)')
plt.legend(loc='lower right')
plt.show()
```

Plot the ROC curve

```
plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC)')
plt.legend(loc='lower right')
plt.show()
```





Accuracy and FPR Calculation

```python
from sklearn.metrics import accuracy_score, confusion_matrix

# Compute accuracy and FPR
accuracy = accuracy_score(y_test, y_pred)

# Compute confusion matrix
conf_matrix = confusion_matrix(y_test, y_pred)
true_positive = conf_matrix[1, 1]
false_positive = conf_matrix[0, 1]

# Calculate FPR (False Positive Rate)
fpr = false_positive / (false_positive + true_positive)

# Print accuracy and FPR
print("Accuracy: {:.2f}".format(accuracy))
print("False Positive Rate (FPR): {:.2f}".format(fpr))
```

```
Accuracy: 0.97
False Positive Rate (FPR): 0.02
```

Fowlkes-Mallows 1 Score (F1 Score)

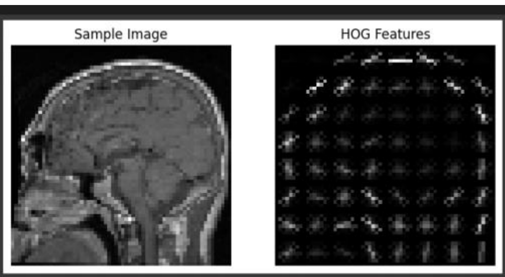
```python
def compute_f1_score(y_true, prob):
    # convert the vector of probabilities to a target vector
    y_pred = np.where(prob > 0.5, 1, 0)

    score = f1_score(y_true, y_pred)

    return score

f1score = compute_f1_score(y_test, y_prob)
print(f"F1 score: {f1score}")
```

```
F1 score: 0.9791044776119404
```

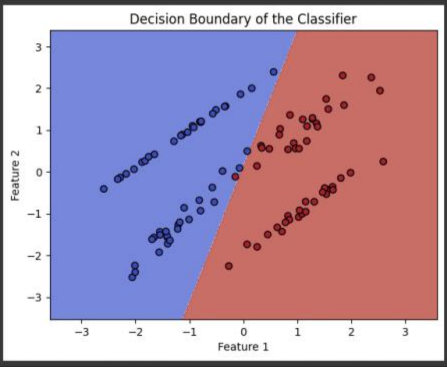
```python
def data_percentage(y):

    m=len(y)
    n_positive = np.sum(y)
    n_negative = m - n_positive

    pos_prec = (n_positive* 100.0)/ m
    neg_prec = (n_negative* 100.0)/ m

    print(f"Number of examples: {m}")
    print(f"Percentage of positive examples: {pos_prec}%, number of pos examples: {n_positive}")
    print(f"Percentage of negative examples: {neg_prec}%, number of neg examples: {n_negative}")
```

```python
print("Training Data:")
data_percentage(y_train)

print("Testing Data:")
data_percentage(y_test)
```

```
Training Data:
Number of examples: 977
Percentage of positive examples: 67.24667349027635%, number of pos examples: 657
Percentage of negative examples: 32.75332650972364%, number of neg examples: 320
Testing Data:
Number of examples: 245
Percentage of positive examples: 69.38775510204081%, number of pos examples: 170
Percentage of negative examples: 30.612244897959183%, number of neg examples: 75
```

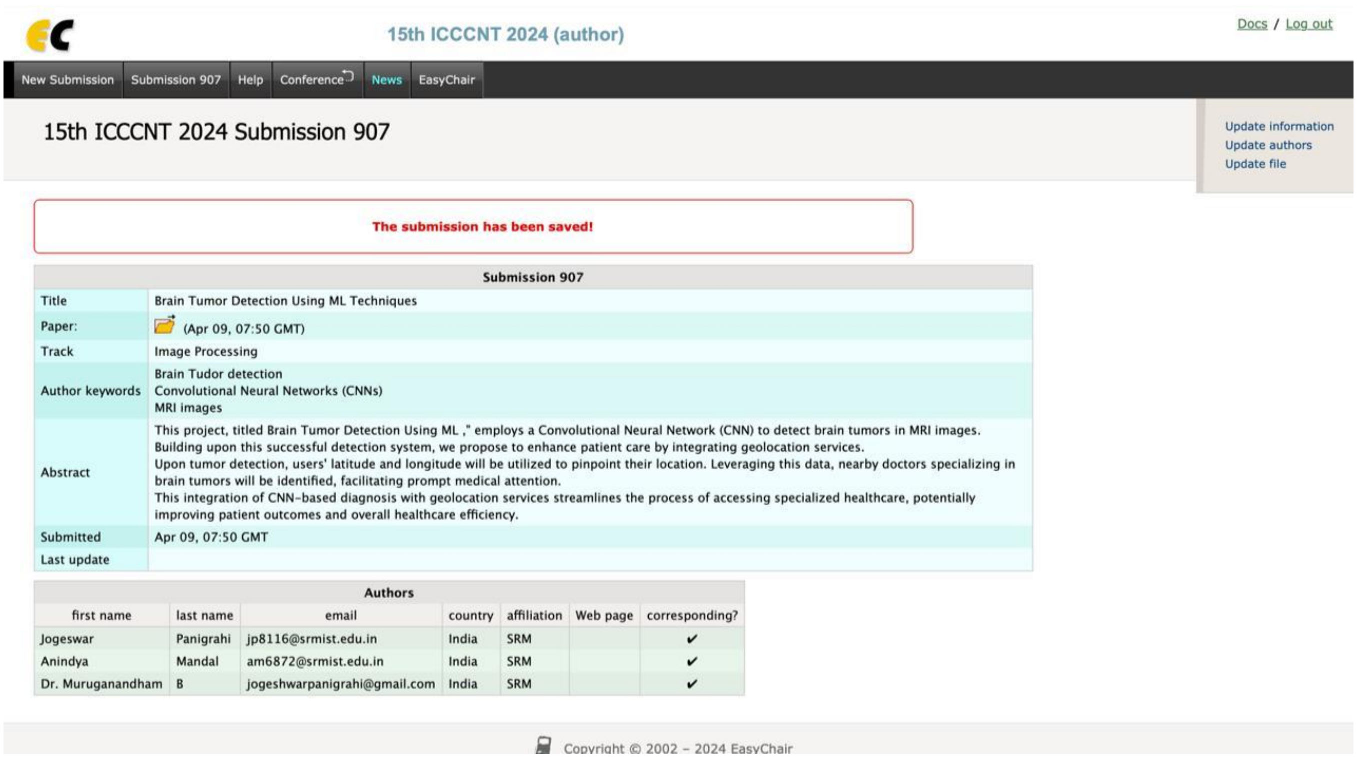


```
import numpy as np
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn import svm

# Generate a simple dataset
X, y = datasets.make_classification(n_samples=100, n_features=2, n_informative=2, n_redundant=0, random_state=42)

# Train a binary classifier (SVM)
clf = svm.SVC(kernel='linear')
clf.fit(X, y)

# Create a mesh grid over the feature space
x_min, x_max = X[:, 0].min() - 1, X[:, 0].max() + 1
y_min, y_max = X[:, 1].min() - 1, X[:, 1].max() + 1
xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.01), np.arange(y_min, y_max, 0.01))

# Make predictions on the mesh grid
Z = clf.predict(np.c_[xx.ravel(), yy.ravel()])
Z = Z.reshape(xx.shape)

# Plot the decision boundary
plt.contourf(xx, yy, Z, cmap=plt.cm.coolwarm, alpha=0.8)

# Plot the data points
plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.coolwarm, edgecolors='k')
plt.xlabel('Feature 1')
plt.ylabel('Feature 2')
plt.title('Decision Boundary of the Classifier')
plt.show()
```



APPENDIX 2

PUBLICATION PROOF



15th ICCCNT 2024 Submission 907

The submission has been saved!

Submission 907	
Title	Brain Tumor Detection Using ML Techniques
Paper:	(Apr 09, 07:50 GMT)
Track	Image Processing
Author keywords	Brain Tudor detection Convolutional Neural Networks (CNNs) MRI images
Abstract	This project, titled Brain Tumor Detection Using ML ," employs a Convolutional Neural Network (CNN) to detect brain tumors in MRI images. Building upon this successful detection system, we propose to enhance patient care by integrating geolocation services. Upon tumor detection, users' latitude and longitude will be utilized to pinpoint their location. Leveraging this data, nearby doctors specializing in brain tumors will be identified, facilitating prompt medical attention. This integration of CNN-based diagnosis with geolocation services streamlines the process of accessing specialized healthcare, potentially improving patient outcomes and overall healthcare efficiency.
Submitted	Apr 09, 07:50 GMT
Last update	

Authors

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Format - I

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2	Address of the Candidate	Abode Valley ,54, Kakkan Street, Potheri, Chennai, Tamil Nadu 603203
3	Registration Number	1 RA2011003010623 2 RA2011003010470
4	Date of Birth	1 18/07/2001 2 10/06/2002
5	Department	Computer Science and Engineering
6	Faculty	Engineering and Technology, School of Computing
7	Title of the Dissertation/Project	BRAIN TUMOR DETECTION USING MACHINE LEARNING TECHNIQUES
8	Whether the above project /dissertation is done by	Individual or group : (Strike whichever is not applicable) **a)** If the project/ dissertation is done in group, then how many students together completed the project : b) Mention the Name & Register number of other candidates :
9	Name and address of the Supervisor / Guide	**Dr. MURUGANANDHAM B** **SUPERVISOR** Associate Professor Dept. of Computing Technologies **Mail ID:** muruganb@srmist.edu.in **Mobile Number:**
10	Name and address of Co-Supervisor / Co- Guide (if any)	**Mail ID:** **Mobile Number:**

11	Software Used	GOOGLE COLLAB		
12	Date of Verification	26th April,2024		
13	**Plagiarism Details: (to attach the final report from the software)**			
Chapter	**Title of the Chapter**	**Percentage of similarity index (including self citation)**	**Percentage of similarity index (Excluding self-citation)**	**% of plagiarism after excluding Quotes, Bibliography, etc.,**
1	INTRODUCTION	1	1	1
2	LITERATURE SURVEY	1	1	1
3	SYSTEM ARCHITECTURE AND DESIGN	1	1	1
4	IMPLEMENTATION	2	2	2
5	REQUIREMENT SPECIFICATIONS	2	2	2
6	CONCLUSION	1	1	1
Appendices				

I / We declare that the above information have been verified and found true to the best of my / our knowledge.

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