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ENHANCED BRAIN TUMOR DETECTION IN MRI: A COMPARATIVE STUDY OF MACHINE LEARNING MODELS

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Abstract

Image processing is essential and attractive in the medical and healthcare. Digital image processing identifies diverse pathological methods, like identifying, classifying, evaluating, and testing brain tumors through microscopic images. Many machine-learning methods are recognized in the era of the AI century for detecting brain tumors through Magnetic Resonance Imaging (MRI). MRI is a recognized image processing method through three-dimensional examination, which identifies unambiguous images of the infection or tumor. The paper aims to offer supervised machine-learning algorithms for brain tumor detection in MRI images through a comparative analysis of different models. Considering the specific features of the tumor and surrounding infected tissues of the brain through analysis supports us in estimating the accuracy of the models and recognizing the optimal operative method. In this paper, four supervised machine learning models are considered: Logistic Regression (LR), Neural Network (NN), Stochastic Gradient Descent (SGD), and Support Vector Machines (SVM). MRI images can quickly identify brain tumors or infections by comparing these models. Furthermore, a model is developed using the Visual Geometry Group (VGG-19) embedder and the Kaggle dataset. The result section shows that the proposed model outperforms the benchmark schemes by attaining high proximity accuracies.

INTRODUCTION

The current modern era technology is a core factor in making procedures simple, particularly in medicine, along with Patient outcomes that can be improved by lowering healthcare expenditures by using Artificial Intelligence [61][25], Machine Learning, and Blockchain [64] in the medical domain and the Internet of Medical Robotic Things (IoMT), etc. [62]. However, the use of machine learning concepts in the healthcare industry still needs to be improved. Brain tumors, caused by the uncontrolled proliferation of cells [1], have the potential to disrupt typical brain operations and pose a significant risk to an individual's survival [2]. Multiple challenges like age, geographic location, and gender have crucial importance in the growth of brain tumors, increasing the death rate [3]. A brain tumor is very dangerous and non-treatable at times. The Glioma tumor is divided into High-Grade Glioma (HGG) and Low-Grade Glioma (LGG). LGG spreads very silently and slowly, but HGG tumors proliferate and are considered a deadly disease. The paper [4] on the Canadian population from 2009-2013 shows that the endurance rate for ages 20-44 is 19% with treatment after 14 months. Figure 1 shows many types of brain tumors with survival rates.

Figure 1 illustrates the relative 5-Year Survival Rate in the United Kingdom for different age groups and genders, demonstrating that brain tumors occur across all age ranges, with peaks in childhood and old age. They are the third topmost reason related to cancer death among males aged 15-54 and the fourth-leading cause among females aged 15-34, emphasizing their high mortality rate [5]. Symptoms of brain tumors can include headaches, vomiting, vision problems, and cognitive abnormalities. Current treatment approaches involve a combination of surgery, radiotherapy, and chemotherapy [6].

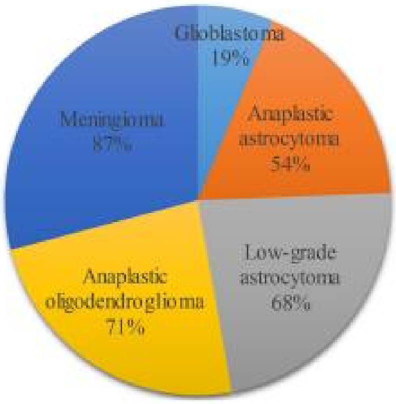

Figure 1. 5-Year Survival Rate in the United Kingdom

The application of artificial intelligence (AI) to medical imaging is increasing in terms of image interpretation and processing [63]. Magnetic resonance imaging (MRI) scans are a valuable tool for diagnosing brain tumors when they are still in the early stages. Deep learning models have been widely applied to medical image processing [40]. Neurologists often cannot detect or diagnose many brain tumors before symptoms manifest. Therefore, magnetic resonance imaging (MRI) is utilized to guide the accurate administration of radiotherapy, which is the most effective treatment for brain tumors [7]. MRI is commonly employed in the diagnosis and prognosis of various neurological disorders, including brain tumors. By analyzing visual characteristics and soft tissue contrast texture, standard MRI sequences are frequently employed to differentiate between different types of brain tumors [8]. Consequently, MRI has gained popularity in the medical field, particularly in brain imaging, as it enables the detection of tumor growth and facilitates appropriate treatment responses.

To comprehensively analyze brain tumors, high-resolution and high-contrast brain images are obtained in three orientations: axial, coronal, and sagittal, providing a three-dimensional perspective of the tumor [9]. Various approaches have been employed for identifying and classifying brain tumors, with the classification stage being particularly critical, encompassing statistical methods and machine learning-based models [10]. Previous studies have utilized numerous machine-learning models for brain tumor detection. Applying these models to MRI images makes early and accurate brain tumor prediction possible, facilitating effective patient treatment. Radiologists can utilize these predictions to make timely decisions [11-12].

Many lives around the world are saved by early and accurate diagnosis of the type of brain tumor, which is essential to the treatment process. Tumor identification is commonly accomplished with non-invasive magnetic resonance imaging (MRI) scans, which spare patients from having an uncomfortable biopsy [65]. Detection and initial assessment are essential for better treatment and planning of patient health. The significance of brain tumor comparative analysis through supervised machine learning algorithms lies in its potential to enhance diagnostic capabilities. By comparing and assessing the performance of different models, medical professionals can better understand which algorithms are more reliable and capable of correctly identifying brain tumors in MRI images [13].

Furthermore, MRI images can identify supervised machine-learning models that excel in brain tumor identification. Healthcare practitioners can develop tailored treatment plans for individual patients by selecting the most accurate and reliable models. This ensures that the treatment approach aligns with the specific characteristics and requirements of each patient's brain tumor, leading to improved treatment outcomes and patient care [14].

The remainder of this paper explains the literature review in Section 2. Section 3 describes the data and methodology in detail, elucidating machine learning models. Section 4 summarizes the results and analysis. Finally, Section 5 provides the conclusion and future work in the study.

2. Related Work

The identification of brain tumors is a crucial application of medical image processing. According to the literature review, most previous approaches have overlooked poor picture quality, such as noisy images or low brightness, and some competitive machine-learning techniques. Data is collected from multiple databases, including cloud storage, libraries, and big data platforms, accessed through wired and wireless networks [15-16][17-19].

In their study, Omar Sedqi Kareem et al. conducted an SLR for segmentation algorithms and classification in MRI images. They explored diverse approaches, including interbreeding, to achieve their objectives. The review evaluated segmentation techniques, such as thresholding, region growing, edge-based, watershed, K-nearest neighbor, support vector machines, random forests, artificial neural networks, clustering with K-means, active contour models, and hybrid techniques. The findings highlighted that combining wavelet with fully convolutional neural networks (FCNN) and auto-encoder enhanced tumor segmentation performance [20].

Neha Bhagat and Gurmanik Kaur presented a segmentation approach that combines the K-means algorithm with the Swarm-based Grasshopper Optimization method (SGHO). Brain tumor images were processed using the Speeded Up Robust Feature (SURF) method to extract relevant features, which were selected using an SGHO-based approach. The tumor images were classified using an SVM classifier. The proposed system showed improved efficiency in terms of performance metrics [21].

G. Ramkumar et al.. introduced the Deep Convolutional Neural Network Algorithm (DCNNA), a novel systematic approach that thoroughly examines various 3×3 kernel sections. Their proposed method yielded satisfactory results with similarity coefficient metrics ranging from 0.886 to 0.773. The segmentation process incorporated fuzzy-based techniques to enhance the accuracy of the DCNNA and nonlinear approaches, effectively capturing variations from classical outcomes. The proposed algorithm effectively summarized the features, and the segmented component of the system utilizing DCNNA for brain tumor detection achieved an accuracy exceeding 95% by combining fuzzy logic with the proposed nonlinear technique [22].

S. Rinesh et al.. studied tumor localization within the brain using hyperspectral images and other techniques. The proposed optimized mapping approach significantly improved outputs across various aspects, effectively mapping molecules in spectral medical photos. A comparison was made between the proposed model and other methods, including K-Nearest Neighbor (K-NN), Deep Neural Network (DNN), Particle Swarm Optimization (PSO), Lagrangian Support Vector Machine (LSVM), and DCNN. The proposed model achieved an accuracy of 96.47% and demonstrated superior performance compared to previous strategies [23].

In their research, R. Nanmaran et al.. explored the potential of image fusion. The study employed a contrast-limited adaptive histogram equalization technique to preprocess input images, including MRI and Single-Photon Emission Computerized Tomography (SPECT) scans. Subsequently, a fusion method based on discrete cosine transform was utilized to generate fused images representing benign and malignant brain tumor classes. The results were compared to those obtained using individual input images. The SVM classifier achieved the highest accuracy of 96.8% when utilizing features extracted from the fused images, surpassing the performance of both K-NN and Decision Tree classifiers [24].

Javeria Amin et al. introduced an unsupervised clustering approach for tumor segmentation in their research. Their methodology involved the utilization of a fused feature vector that combined Gabor Wavelet Features (GWF), Histograms of Oriented Gradient (HOG), Local Binary Pattern (LBP), and Segmentation-based Fractal Texture Analysis (SFTA) features. The Random Forest (RF) classifier was employed to differentiate between three sub-tumoral regions: entire tumors, enhancing tumors, and non-enhancing tumors. To mitigate overfitting, the study implemented fivefold and 0.5 holdout cross-validation techniques. The proposed technique was tested on various MRI modalities, including DWI, FLAIR, T2, T1, and T1c. The evaluation encompassed feature-based outcomes as well as pixel-based outcomes. The results demonstrated the effectiveness of the proposed method in achieving accurate segmentation results, surpassing the performance of existing approaches [1].

Ahmet Safa Karakoc and Ahmet Yasir Cilvez applied Glioma and Meningioma tumor MRI scans to two separate data sets. The accuracy rate indicates that the algorithm correctly detects the tumor type according to the algorithm's results. It was found that the rate is, however, lower than expected. Many low-quality images in the collection are one likely cause of this problem. Enhancement, image filtering, and segmentation are employed in the image processing aspect of the research, while support vector machines are used in the machine learning aspect. Because of this study, test images are classified into two groups with a 62 % accuracy rate of at least [26].

G.Hemanth et al. investigated various risk factors identified in brain tumor surveillance systems. Furthermore, they developed a highly efficient and accurate brain tumor detection, classification, and segmentation technique. The study introduced an automated segmentation method that utilizes Convolutional Neural Networks (CNN) to identify small 3 x 3 kernels. By combining this single approach, segmentation and classification were accomplished. The results indicated that the CNN method was remarkably effective in detecting brain tumors. The proposed approach was applied to multiple images, yielding the best and most precise output [27].

The main objective of this paper is to provide researchers with a comparison of brain tumor detection significance using magnetic resonance imaging and machine learning models like logistic regression and stochastic gradient descent. These machine-learning models have yet to be explicitly employed in brain tumor classification and MRI image prediction. After the comparisons, an important outcome has been achieved. To get evidence-based recommendations from supervised machine learning algorithms, the analysis helps medical practitioners decide about brain tumor identification. As a result, it will guide us in improving the accuracy of the diagnosis and treatment methodologies. This paper uses a Kaggle dataset and augmentation of MRI images to generalize the results.

A good classifier should have a precision of 1 (high) only when TP = TP +FP does precision become 1. This also implies that FP is zero. As FP increases, the precision value decreases, which is undesirable. A good classifier should have a recall of 1 (high). Only when TP = TP +FN does recall become 1. This also implies that FN is zero. As FN increases, the recall value decreases, which is undesirable [28-29]. A periodic comparison table (see Table 1) succinctly summarizes all the major factors of each study or article previously presented in this domain. The results collected have been highlighted for precise analysis.

Table 1. Comparative Analysis with Other Approaches

Reference	Year	Methodology/Approach	Dataset	Result
[30]	2019	CNN+ Softmax / CNN+ RBF / CNN+ DT	Private dataset comprising 1892 images	Above 90% accuracy
[31]	2019	6 Multiple Classifiers	BRATS 2015, 2016, 2017 datasets	Above 80% accuracy
[32]	2020	Recurrent neural network RNN	Private dataset comprising 1000 images	Classification 96% Specificity 98% Sensitivity 97%
[33]	2020	Convolutional neural network (CNN)	Kaggle dataset	Above 90% accuracy

[34]	2021	5 Multiple models of CNN	Figshare public brain tumor data set with 3,064 images	Above 90% accuracy
[35]	2021	Fuzzy wavelet neural network (FWNNet)	BraTS dataset	100% accuracy
[36]	2021	CNN with VGG-16	Kaggle dataset	99% accuracy
[37]	2022	Naïve Bayes / BoVW-based SVM / CNN	Harvard \Medical School dataset	Above 90% accuracy
[38]	2022	CNN / VGG-16 / Ensemble Model	Brain MRI Images for Brain Tumor Detection dataset with 253 images	Above 90% accuracy
[39]	2022	ResNet50	Cancer Genome Atlas Low-Grade Glioma (TCGA-LGG) dataset with 110 images	F1 92.34%
Proposed Models	2023	SGD, LR, NN, SVM with VGG-19	Kaggle dataset with 2065 images	90% to 100% accuracies

3. Data and Methodology

Data and methodology are crucial elements in any research or analysis. They form the foundation for reliable and valid conclusions. Figure 2 shows the details of the data used in the applied methodology.

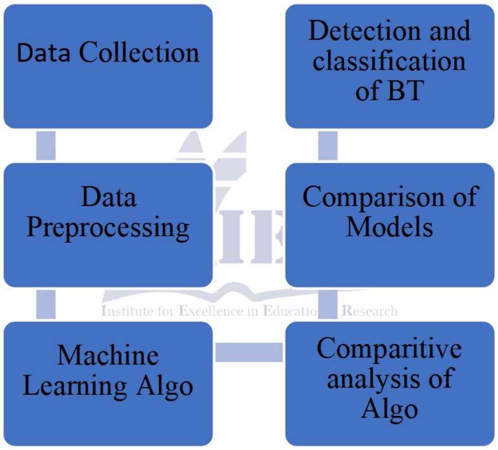

Figure 2. Proposed Workflow

3.1. Data Augmentation and Pre-Processing

This research focuses on optimizing brain tumor classification accuracy and evaluating and comparing the outcomes of several existing approaches, as shown in Figure 3.

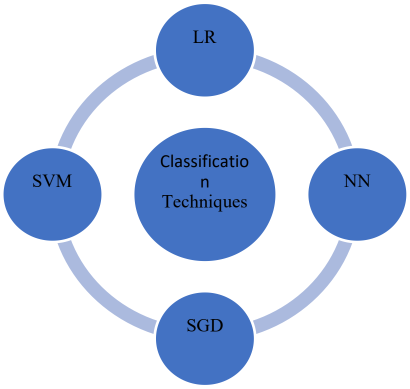

Figure 3. Classification Techniques

We will review these classifier findings in depth and draw conclusions based on them [3]. For comparative analysis, MRI images are acquired (http://kaggle.com. 2022). The dataset comprised 253 brain MRI images and was then re-modified into two classes: Have Tumor and No Tumor. There are 155 tumorous brain MRI images classified as Have Tumor and 98 non-tumorous brain MRI images classified as No Tumor. The Orange software autonomously selects the features at the back end of image analytics.

Since the dataset was limited, more samples were needed to train the supervised machine learning models. So, data augmentation is applied because it has proved effective in mitigating the data imbalance problem. Data augmentation applies random transformations to our training samples (contrast/brightness, crops/scales, flips, rotations, shifts, and so on) to create images our model has yet to observe while keeping the original sample labels [41]. We then train on these transformations, improving our model's generalizability (performing better on hidden data) [42].

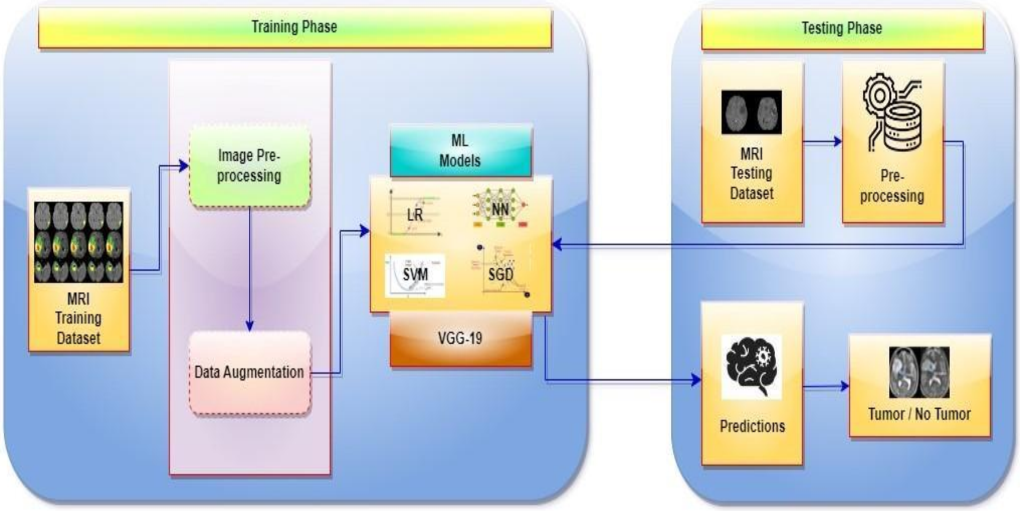

Figure 4. Methodology used to classify a dataset of brain tumors

Figure 4 illustrates the implementation of ML models for analyzing a brain tumor MRI dataset. In Figures 5 and 6, the Receiver Operating Characteristics (ROC) analysis for each target class or label, i.e., "Have Tumor" and "No Tumor," is now presented. The ROC curve is one of the key measures for assessing a classification model's performance. In a graphical representation, ROC curves show the relationship/trade-off between clinical sensitivity and specificity for each possible cut-off for a test or a combination of tests. Furthermore, the area under the ROC curve reveals the utility of considering the test(s). ROC curves are used to establish the optimum appropriate cut-off for a test. The optimal cut-off has the lowest rate of false positives and the highest rate of true positives. The area under an ROC curve is used to compare the efficacy of tests since it measures a test's overall utility, with a greater area implying a more beneficial test.

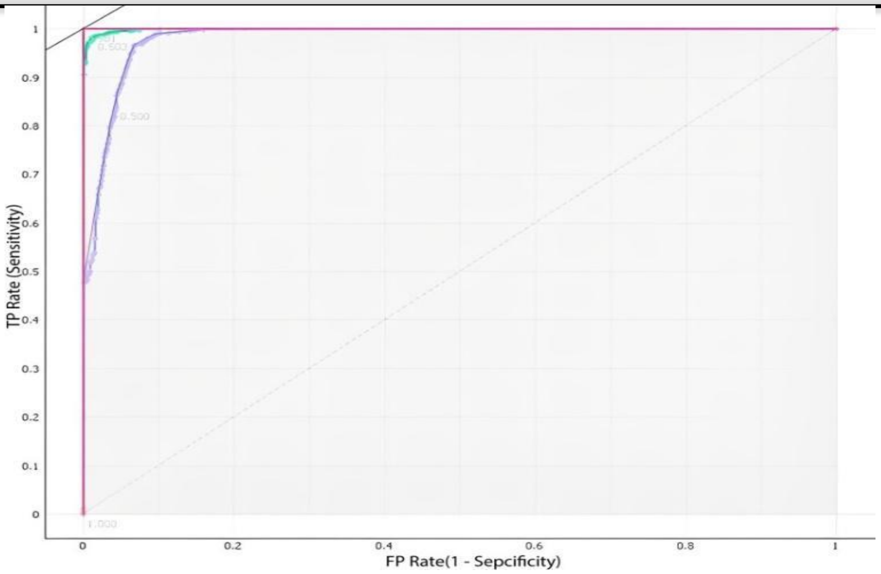

Figure 5. ROC Curve Analysis of Class Have Tumor

The dotted line in the middle represents the ROC curve of any model, and the colored ROC curve corresponds to the input model [43-44]. The performance line in Figure 5 is positioned between 0.9 and 1.0, indicating that the models performed ideally with a prior probability of 53% for the class or label "Have Tumor." The performance line in Figure 6 is also positioned between 0.9 and 1.0, indicating that the models performed ideally with a prior probability of 47% for class or label "No Tumor."

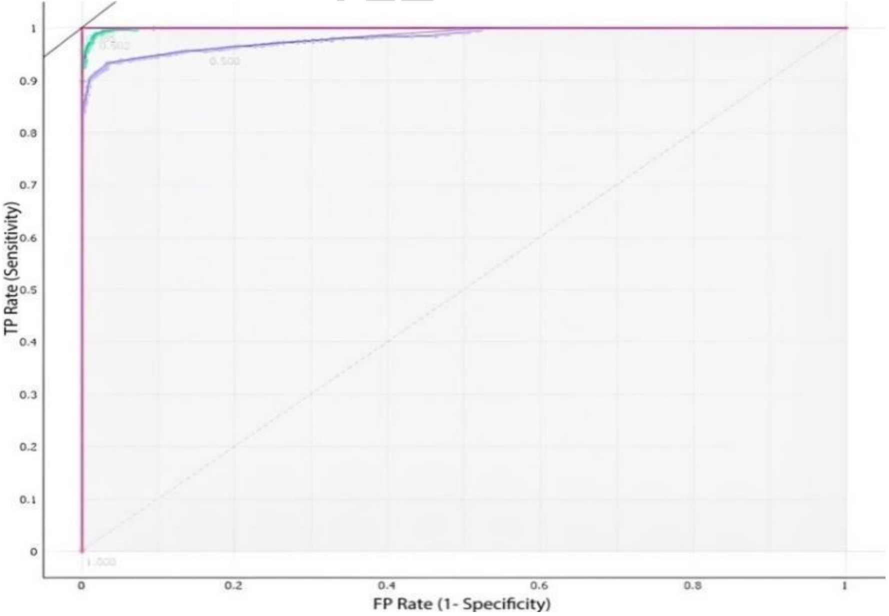

Figure 6. ROC Curve Analysis of Class No Tumor

After data augmentation, the dataset now contains 1085 tumorous (see Figure 7) and 980 non-tumorous (see Figure 8) images for 2065 sample images. However, it is essential to note that there are 253 original images among the 2065 samples. After performing data augmentation, pre-processing is the initial stage in tumor identification; it improves the image and removes noise to detect the objects of interest. The accuracy of MRI scans is compromised when they are affected by noise [45].

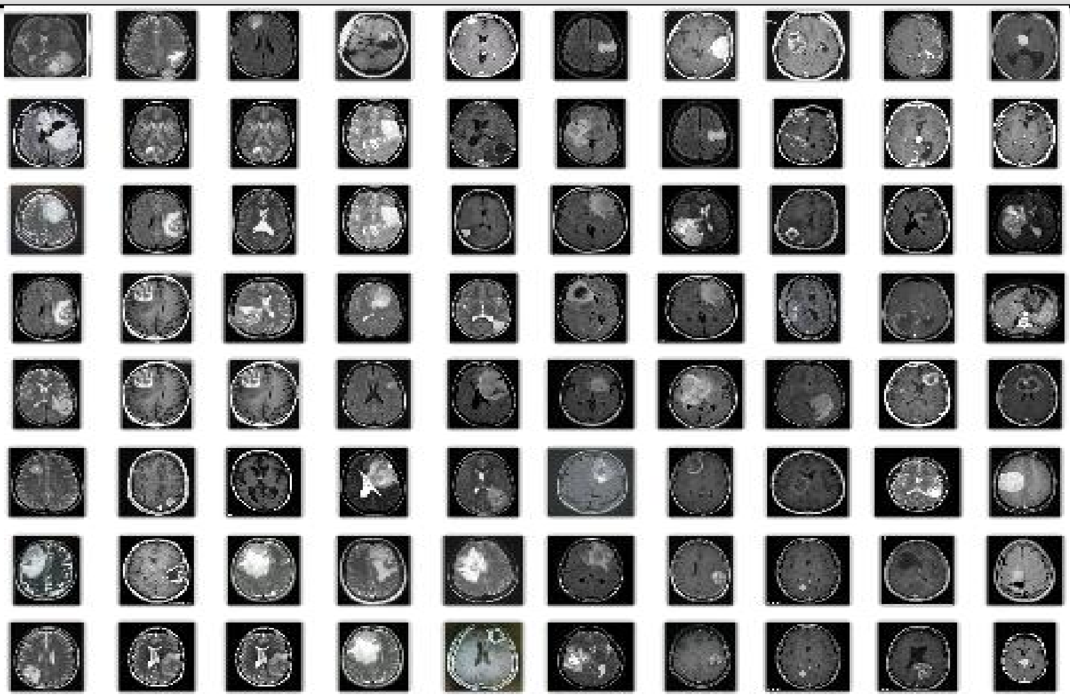

Figure 7. Samples of Grid Visualization of Tumorous Images

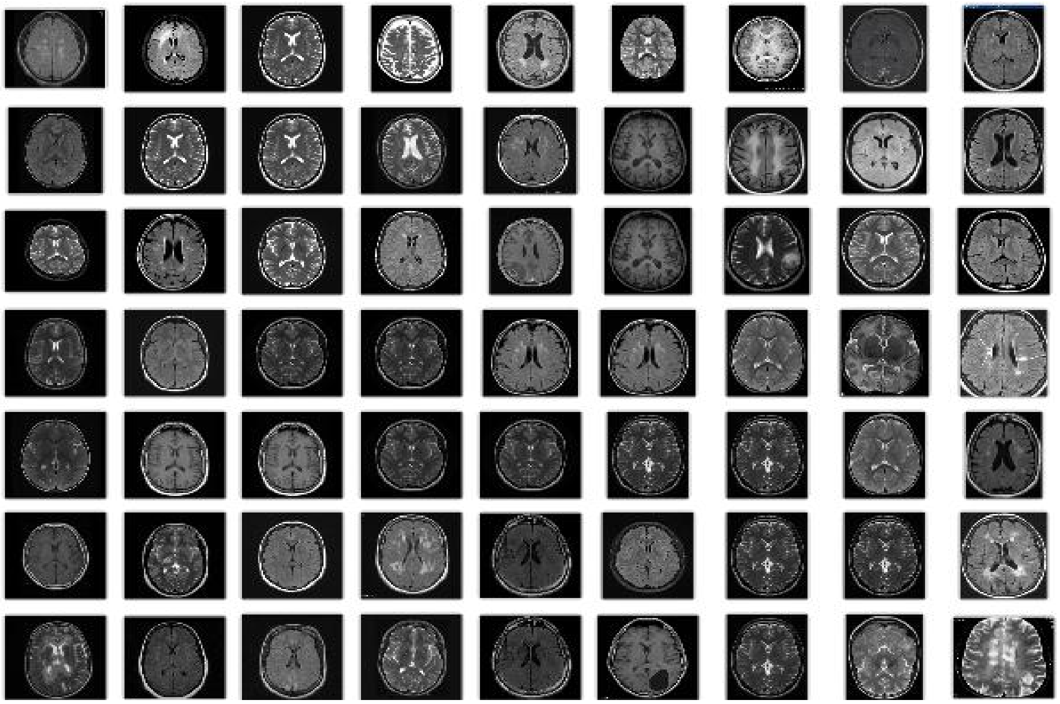

Figure 8. Samples of Grid Visualization of Non-Tumorous Images

Noise reduction is a fundamental step in every preprocessing step. The dataset in concern has already been pre-filtered for noise. As a result, we use our customized noise reduction approach to preprocess all the images. The collection contains some opaque images, which necessitates the use of an image enhancement approach. The inhomogeneity aberrations in MRI data are removed using a thresholding-based approach [3].

- The following preprocessing steps were performed on each image:

- The image is cropped to retain only the central portion, specifically the brain, while excluding surrounding areas.
- To address the varying sizes of images within the dataset, the images are resized to a consistent shape of (240, 240, 3), representing the image width, height, and number of channels. This ensures that all images conform to the same shape, allowing them to be effectively utilized as input for the models.
- Normalization is implemented to rescale the pixel values, ensuring they fall from 0 to 1.

3.2. Research Methodology

Many methodologies for tumor classification and detection on MRI images have been proposed. In contemporary diagnostic science, automatic brain tumor classification is critical since it establishes the patient's initial diagnosis and treatment options. An MRI image has been used as input in tumor classification, and trained classifiers have been used to determine whether the MRI image is tumorous or non-tumorous. After augmentation and pre-processing, 1085 MRI tumorous images and 980 MRI non-tumorous images are chosen from the dataset for tumor classification [11]. The Image Embedding process involves ingesting and processing images, which can be done either by uploading them to a remote server or evaluating them locally on the user's computer. Image Embedding consists of multiple embedders, each trained to perform specific tasks. The images are transmitted to a server or processed locally, generating vector representations. In this study, a VGG-19 embedder, which is a convolutional neural network with 19 layers, is utilized. To leverage a pre-trained version of the network, trained on a vast collection of over a million images, the ImageNet database can be employed [46]. Then, we applied four supervised machine learning models with binary classification using random sampling with stratified sampling, having a 70% training set size with 1445 images and a 30% testing set size with 620 images to solve the problem. The ML algorithm learns to extract features while training automatically. The entire training and testing process is repeated ten times with stratified random sampling using an Orange image analytics tool. The following are the four supervised machine learning models employed in this study.

Let us define the following mathematical symbols for the four algorithms or models:

- Let X be the input matrix of size (m x n), where m is the number of samples and n is the number of features.
- Let y be the output vector of size (m x 1), where each element corresponds to detecting the existence or non-existence of a brain tumor.
- Let $f(X;\theta)$ be the supervised machine learning model, where θ represents the model parameters.
- Let $h\theta(x)$ be the predicted output for a single input sample x, given the model parameters θ.
- Let $J(\theta)$ be the objective function that measures the difference between the predicted output and the proper labels.
- Let α be the learning rate, which determines the step size for each iteration of the optimization algorithm.
- Let L be the regularization parameter, which controls the complexity of the model.

3.2.1. Logistic Regression

The Least Absolute Shrinkage and Selection Operator (LASSO) (L1) or ridge (L2) regularization method is used in the logistic regression classification process. It is solely helpful for classification tasks. Logistic Regression performs default pre-processing when no other pre-processors are specified [47]. The following is the sequence in which it is executed:

- Removing instances with target values that are not known.
- Keeping categorical variables in a continuous state (with one-hot-encoding).
- Removing empty columns.
- Blaming the missing values with the mean of the values.

This study employs the ridge (L2) regularization type for binary classification. The mathematical model for logistic regression is given below:

$$h\theta(x) = g(\theta^T x) = 1 / (1 + \exp(-\theta^T x))$$
$$J(\theta) = -1/m * [\sum y*\log(h\theta(x)) + (1-y)*\log(1-h\theta(x))] + (L/2m) * \sum \theta^2$$
$$\nabla J(\theta) = (1/m) * X^T (h\theta(x) - y) + (L/m) * \theta$$
$$\theta := \theta - \alpha * \nabla J(\theta)$$
(1)

3.2.2. Neural Network

A neural network imitates brain activity and reacts to the environment to attain the ideal state. Artificial neurons process and transmit input signals from one to the other, moving through multilayer hidden networks to obtain the proper output from the final layer. In this model, the data is normalized by centering the data on the mean and scaling it to a standard deviation of 1 [20]. The model parameters are set in this study: The number of Neurons per hidden layer is set to 100, which is the number of neurons in the ith hidden layer represented as the ith element. The activation function for the hidden layer is set to Rectified Linear Unit (ReLu), the rectified linear unit function. The solver for weight optimization is set to Adam, a stochastic gradient-based optimizer with 200 maximum number of iterations. The mathematical model for neural networks with one hidden layer is given below:

$$h\theta(x) = g(\theta^T z2) = 1 / (1 + \exp(-\theta^T z2))$$

$$z2 = g(\theta1^T x) = 1 / (1 + \exp(-\theta1^T x))$$

$$J(\theta) = -1/m * [\sum y*\log(h\theta(x)) + (1-y)*\log(1-h\theta(x))] + (L/2m) * (\sum \theta^2 + \sum \theta1^2)$$

$$\nabla J(\theta) = (1/m) * X^T (h\theta(x) - y) + (L/m) * \theta$$

$$\nabla J(\theta1) = (1/m) * (h\theta(x) - y) * \theta^T * g'(\theta1^T x) * X$$

$$\theta = \theta - \alpha * \nabla J(\theta)$$

$$\theta1 = \theta1 - \alpha * \nabla J(\theta1)$$

(2)

3.2.3. Stochastic Gradient Descent

The Stochastic Gradient Descent (SGD) decreases a loss function to a linear function. The technique approximates an actual gradient by evaluating one sample at a time while updating the model based on the loss function's gradient. It returns predictors as sum minimizers, i.e., M-estimators, for regression and is particularly beneficial for large-scale and sparse datasets [48]. In this study, the loss function parameters are set such that classification is the hinge loss function in a linear SVM, Regression is set to the Squared Loss function, and Regularization is set to Ridge (L2). Optimization parameters are set such that the Learning Rate is Constant, i.e., all epochs have the same learning rate (passes). The mathematical model for stochastic gradient descent is given below:

$$\theta = \theta - \alpha * \nabla J(\theta, xi, yi) \qquad (3)$$

Where xi and yi are randomly selected from dataset X and y.

3.2.4. Support Vector Machine

The Support Vector Machine (SVM) is a machine learning algorithm that employs a hyperplane to separate the attribute space, maximizing the margin between different classes or class values. This method often delivers excellent performance in predictions. SVM utilizes ε-insensitive loss for regression tasks to perform linear regression in high-dimensional feature space. The estimation accuracy relies on the proper configuration of parameters such as C, ε, and the kernel. In classification and regression tasks, cost is a penalty term for loss. For the epsilon-support Vector Regression (SVR) model, ε-regression is a task-specific parameter with no penalty applied to predicted values within a certain distance from the actual values. The kernel is a function that transforms the attribute space into a new feature space, allowing the construction of models using Linear, Polynomial, Radial Basis Functions (RBF), and Sigmoid kernels [49-51]. Here, the Kernel function is set to RBF with 100 iterations. The mathematical model for support vector machines is given below:

$$\text{minimize } (1/2) ||\theta||^2$$

$$\text{subject to: } y(i) (\theta^T x(i) + b) >= 1, \text{ for all } i = 1, 2, \ldots, m$$

$$J(\theta) = (1/2) ||\theta||^2 + C * \sum \max(0, 1 - y(i) (\theta^T x(i) + b)) \qquad (4)$$

C is the regularization parameter, which controls the trade-off between the margin and the classification error.

Next, the scatter plots for each supervised machine-learning model are displayed. In these plots, points represent the values of two numerical features. The position of each point on the horizontal and vertical axes corresponds to the respective values. Scatter plots are utilized to visualize the relationships between different classes or labels. A scatter plot can be used to see if two classes or labels have a correlation or relationship. Below are 2-dimensional scatter plot representations for each machine learning model (see Figures 9-12). The data is represented as a set of points, with the x-axis attribute indicating the horizontal axis position relative to the class "Have Tumor" and the y-axis attribute indicating the vertical axis position relative to the class "No Tumor."

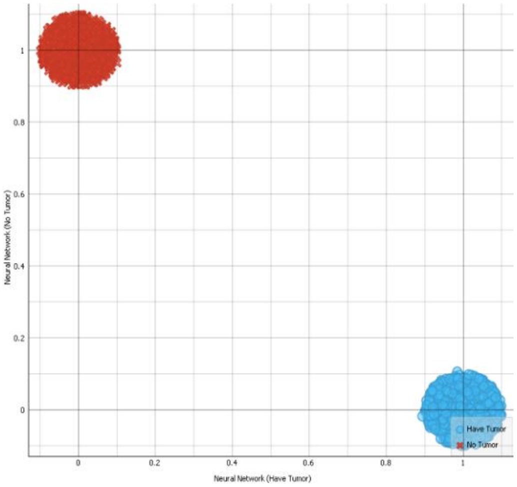

Figure 9. Scatterplot Visualization of Neural Net Model

Figures 9 and 12 show two perfect segments or groups of visualization according to the classes Have Tumor and No Tumor based on how tightly sets of points clusters are together as the data points are split into two groups. As both Neural Net and SGD models have achieved 100% classification and prediction accuracy, there are no misclassified data points overlaid into each other. A red cross shape indicates the non-tumorous instances, whereas a blue circle shape indicates the tumorous instances. A null or no relationship exists between the two classes' points classification [52].

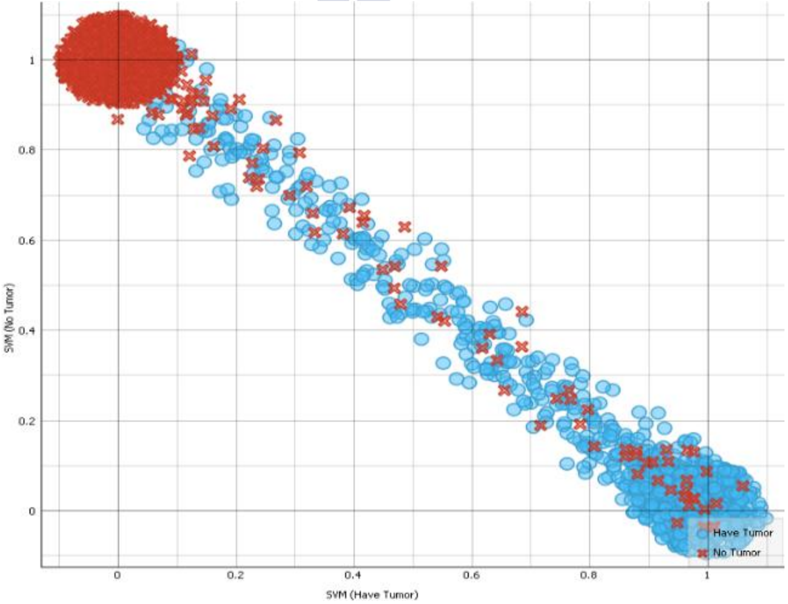

Figure 10. Scatterplot Visualization of SVM Model

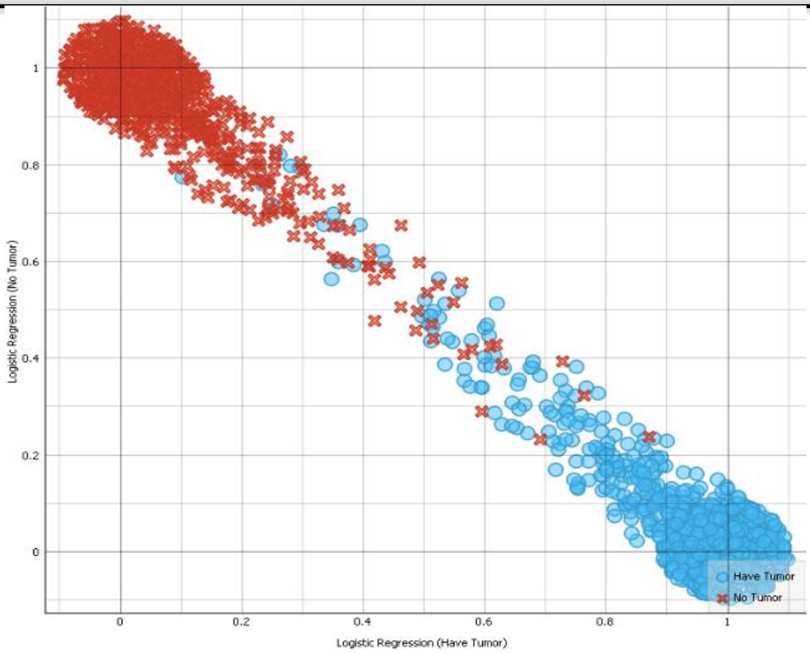

Figure 11. Scatterplot Visualization of Logistic Regression Model

Figures 10 and 11 show the positive linear relationship between the two classes as the data points are overlaid. This indicates that the logistic regression and SVM models misclassify the data points. Hence, scatter plots are frequently employed to identify correlations between variables. In such scenarios, the objective is to determine a reliable prediction of the vertical value given a specific horizontal value. The class or label displayed on the horizontal axis is commonly referred to as an independent variable, while the class or label shown on the vertical axis is referred to as a dependent variable in the context of the plots.

We want to analyze individual data points from a high-dimensional data collection in a lower-dimensional space so that the best pattern recognition can do the heavy work. When analyzing a two- or three-dimensional data collection, one can see patterns based on how close the points are to one another. As a result, we need to depict the points so that their distances significantly change as little as possible. This is known as linear projection in general. A Principal Component Analysis (PCA) projection is a representation that is created by computing the principal components and then leveraging them to produce a linear projection, as shown in Figure 13. According to binary classes, the two principal components separate the models per class or label [51]. The figure shows that the Logistic Regression, Neural Network, and SGD models are perfectly projected separately in classes or labels “Have Tumor” and “No Tumor,” respectively. However, the SVM model is not distinctly projected separately into two classes or labels.

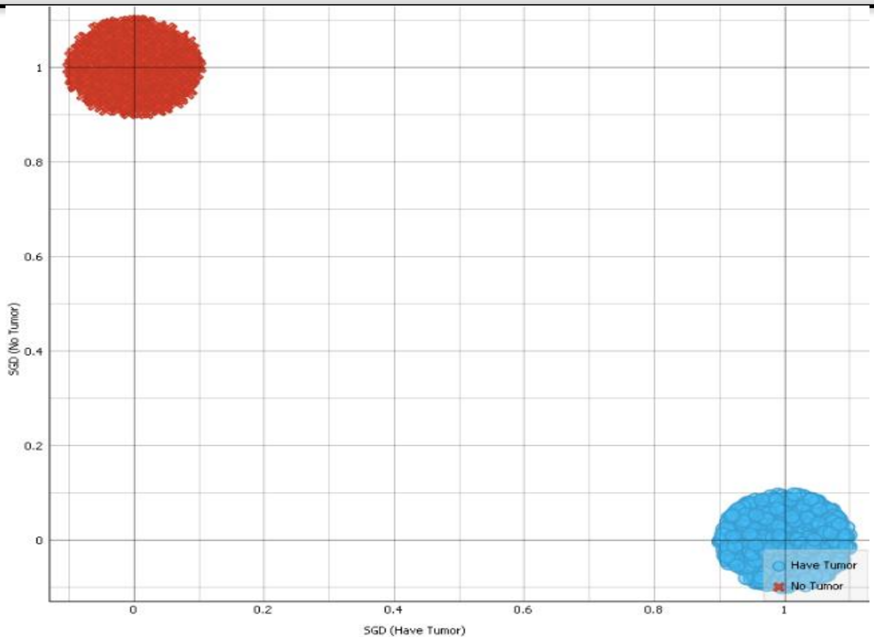

Figure 12. Scatterplot Visualization of SGD Model

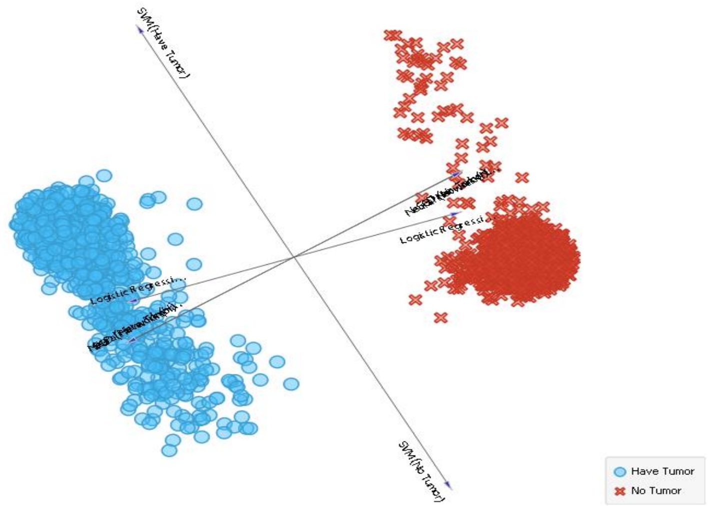

Figure 13. Linear Projection Representation of Machine Learning Models

3.3. Feature Extraction

Although the Orange tool autonomously extracts the features in the images. Texture analysis has been employed as a feature extraction method in medical image processing to identify subtle changes in texture patterns that may indicate specific diseases or abnormalities. In brain tumour identification, texture analysis could extract features such as entropy, contrast, and homogeneity from the MRI images. A widely used approach involves utilizing texture features derived from a grey-level co-occurrence matrix (GLCM). The GLCM captures the occurrence frequency of pixel intensity values that co-occur at a specific offset within an image [53].

Let us consider a texture feature such as Contrast, which measures the contrast intensity between neighbouring pixels. The mathematical equation for computing the Contrast feature using the GLCM is:

$$\text{Contrast} = \sum_{i,j}(i-j)^2\,P(i,j) \quad (5)$$

Where i and j are the intensity values of two neighboring pixels, P(i,j) is the GLCM value at the corresponding offset, and the sum is computed over all pairs of neighboring pixels in the image.

Another commonly used texture feature is Entropy, which measures the amount of disorder in the texture. The mathematical equation for computing Entropy using the GLCM is:

$$Entropy = -\sum_{i,j} P(i,j) \log_2(P(i,j)) \quad (6)$$

P(i,j) is the GLCM value at the corresponding offset.

To apply supervised machine learning models to the brain tumor detection Kaggle dataset using texture features, we can extract multiple texture features from each image using GLCM and other methods and then use these features as input to the machine learning models. The choice of machine learning models depends on the specific task and the dataset's characteristics.

Brain tumor detection also involves analyzing the tumor's shape from magnetic resonance imaging (MRI) scans. Shape analysis is another critical feature extraction method for medical image analysis. Shape analysis could extract features such as tumor size, shape, and location in brain tumor identification. This information could help differentiate between different types of brain tumors. Supervised machine learning models can be trained on the Kaggle dataset to classify whether an MRI scan contains cancer. Shape features are geometric properties of the tumor that can be extracted from the MRI scans that have also been used. Examples include volume, surface area, sphericity, and compactness [60]. These features can be calculated using mathematical equations such as:

$$\text{Volume: } V = \iiint dx\,dy\,dz \quad (7)$$

Where (x,y,z) are the coordinates of the points inside the tumor, and dx, dy, and dz are the infinitesimal volume elements.

$$\text{Surface area: } A = \iint dS \quad (8)$$

Where dS is the infinitesimal surface area element.

$$\text{Sphericity: } S = (\pi^{(1/3)} (6V)^{(2/3)})/A \quad (9)$$

Where V is the volume, and A is the surface area of the tumor.

Compactness: $C = V/(D^2)$, where D is the maximum diameter of the tumor.

4. Results and Analysis

This section explains the analysis of supervised machine learning models with performance metrics by analyzing and comparing models or classifiers' performance in terms of accuracy, precision, recall, and F1-score. It also analyzes the confusion matrix of the models to depict the proportions of the predicted and actual classes related to brain tumor detection using tumorous and non-tumorous MRI image classification obtained using the Orange tool.

Four robust supervised machine learning models for binary classification are used, and the results are compared with performance evaluation metrics presented in Table 2. Samples for training and testing are selected at random. The images must be appropriately processed, and the models must be devised so that the models can proactively train more about the features. Analyzing a model's robustness might be more accessible by looking at its performance outcomes during the training and testing phases. This is commonly performed using a performance metric, whether assessing the type of error, the strength of model fit, or some other mechanism. To improve the robustness of our models and avoid over-fitting, we use a 70% training set with 1445 images and a 30% testing set with 620 images using a VGG-19 embedder [54]. These results are achieved during training or validation, as shown in Table 2.

Table 2. Comparative Analysis with Other Approaches

Models	Accuracy	F1-score	Precision	Recall
Logistic Regression	98.40%	98.40%	98.40%	98.40%
Neural Network	100%	100%	100%	100%
Support Vector Machine	91.90%	91.90%	92.10%	91.90%
Stochastic Gradient Descent	100%	100%	100%	100%

Consider the challenge of detecting whether a person has a brain tumor. If the MRI test is diagnosed positive (+ve), the person expects cancer. If, on the other hand, the MRI test is diagnosed negative (-ve), the person has no tumor. We seek TRUE POSITIVE (TP) and TRUE NEGATIVE

(TN); however, we may inevitably end up with FALSE POSITIVE (FP) and FALSE NEGATIVE (FN) owing to misclassifications. As a result, determining whether a person has a tumor might be difficult. The machine-learning model needs to be impeccable [55].

$$\text{Accuracy} = \frac{TN+TP}{TN+FP+TP+FN} \qquad (i)$$

$$\text{Precision} = \frac{TP}{TP+FP} \qquad (ii)$$

$$\text{Recall} = \frac{TP}{TP+FN} \qquad (iii)$$

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \qquad (iv)$$

The number of correctly classified data instances divided by the total number of data instances is known as the model's or classifier's accuracy. If the dataset is unbalanced, accuracy may not be a suitable parameter. The comparison of the machine learning model is shown in Figure 14 in terms of accuracy achieved. The number of data instances in the negative and positive classes differs. Only when accuracy and recall are both one does the F1 score become 1. Only when both accuracy and recall are high can the F1 score increase. The F1 score is a better metric than accuracy since it is the harmonic mean of precision and recall [27].

In this research, Table 2 compares the most modern machine learning approaches. The best outcomes achieved by the ML techniques are presented and analyzed in terms of accuracy and performance. Classification and prediction were significant strategies for evaluating and analyzing the MRI brain images to classify the brain tumor. Figure 14 shows the comparative accuracies of ML models for brain tumor detection using MRI images. Nearly all the ML models used in this study are robust in their performance.

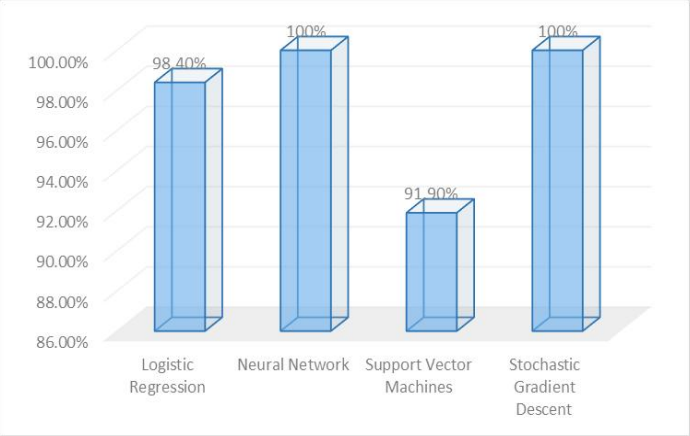

Figure 14. Comparison of Machine Learning Model Accuracy

In this case study, we will examine the confusion matrices of four supervised machine learning models. These are applied to measure the machine learning model's accuracy in classifying input into its labels. The predicted outcome (tumor +ve or -ve) using a machine learning model is called the expected label. In contrast, the actual outcome (as determined by the medical or expert record) is called the actual label. So, the confusion matrix C is a square matrix in which Cij denotes the number of data samples that belong to group i (actual label) and are predicted to belong to group j (predicted label).

Applying machine learning (ML) using conventional methodologies has significantly transformed the traditional practices of healthcare systems [56-57]. ML utilizes statistically validated algorithms that fall into various categories, such as Regression, Classification, and Clustering. These algorithms collectively contribute to developing intelligent systems that manage disease and automate healthcare operations [58-59]. Figure 15 demonstrates the performance of a Neural Network model, accurately classifying all 1085 tumorous images out of the total 1085 images. Similarly, all 980 non-tumorous images are correctly classified as non-tumorous, highlighting the model's precise classification capabilities.

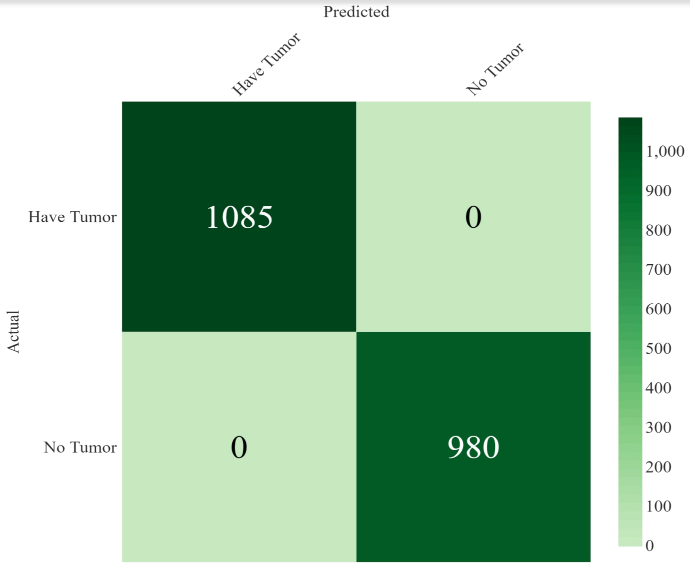

Figure 15. Confusion Matrix Representation for Neural Network

As shown in Figure 16, out of 1085 tumorous images, 969 are classified correctly, and the remaining 116 tumorous images are misclassified as non-tumorous by the SVM model.

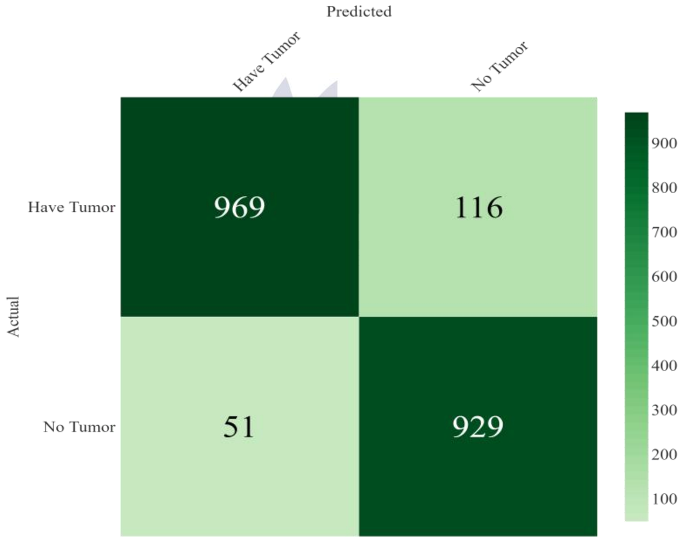

Figure 16. Confusion Matrix Representation for SVM

On the other hand, out of 980 non-tumorous images, 51 are misclassified as tumorous, and the remaining 929 are classified as non-tumorous images. As shown in Figure 17, out of 1085 tumorous images, 1065 tumorous images are classified correctly, and the remaining 20 tumorous images are misclassified as non-tumorous by the Logistic Regression model. On the other hand, out of 980 non-tumorous photos, 14 are misclassified as tumorous, and the remaining 966 are classified as non-tumorous images.

As shown in Figure 18, the SGD model correctly classified all 1085 tumorous images. Similarly, the SGD model classified all 980 non-tumorous images perfectly.

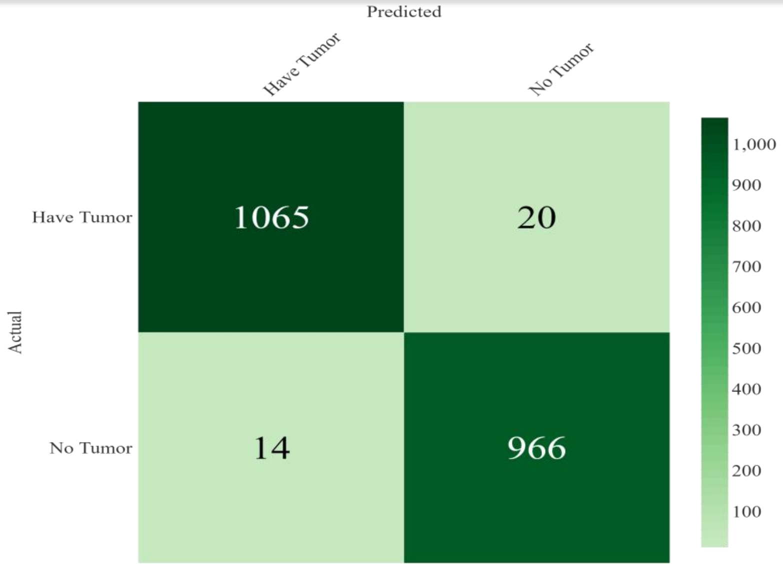

Figure 17. Confusion Matrix Representation for LR Model

Hence, the comparative analysis supports the advancement of personalized medicine in brain tumor identification. By evaluating algorithms' performance, medical professionals can tailor treatments to patients' needs, maximizing effectiveness and minimizing side effects.

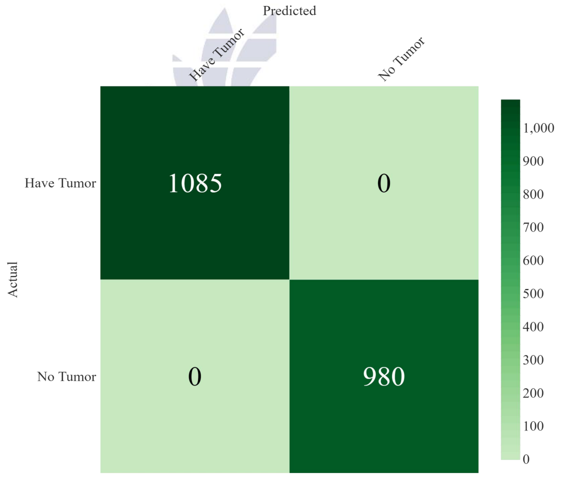

Figure 18. Confusion Matrix Representation for SGD Model

5. Conclusion and Future Work

This paper emphasizes the analysis and diagnosis of brain tumors due to the increasing number of deaths. This paper aims to detect brain tumors using machine learning models and binary classification. Machine Learning models like LR, NN, SVM, and SGD are used for brain tumor classification and prediction. Data augmentation reports the sparse dataset and resolves data imbalance issues. A customized noise reduction method, like VGG-19 embedder and a 19-layer convolutional neural network, is used for image preprocessing. Four supervised machine learning models, binary classification, and stratified sampling are used. Evaluations establish an improvement in accuracy rates; the Neural Net and SGD models achieve approximately 100% accuracy, the Logistic Regression model achieves 98%, and the SVM model achieves around 92%. The model's performance is dynamic due to the data set and features.

This paper improves the understanding of advanced machine learning models' performance in brain tumor classification and analysis. The premature finding and diagnosis of brain tumors are decisive for the professional healthcare system. The understanding increased from the comparative analysis in this study and added to developments in the field of brain tumor identification. By estimating and comparing supervised machine learning algorithms, the analysis encourages research and development, leading to better algorithms and methods in the future. In Future work, we will consider deep learning and generative models like Generative Adversarial Networks (GANs), and a comparison will be made with ML models to categorize methods for performance enhancement. Moreover, analysis can be implemented on real-time datasets using more efficient ML models for better accuracy.

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