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Towards an Explainable Approach: Hybrid Residual Network and SVM for Automated Brain Tumor Detection and Classification

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Abstract: The abnormal growth of brain cells leads to tumor formation, which can be fatal if not detected and treated promptly. Given the complexity of brain tumors, early detection is critical in healthcare. Traditional radiology-based tumor detection is prone to human error and delays. Hence, a computer-assisted method is needed for accurate and efficient diagnosis. With the rapid advancements in the medical science; integrating machine learning, deep learning, artificial intelligence demonstrated great potential in diagnosing diseases and overcome the existing drawbacks while focusing on appropriate treatment plans and improved patient outcomes. A pre-trained model namely Residual Network i.e., ResNet101V2 has been leveraged in the proposed model to extract significant features following supervised algorithm for differentiating different brain MRI scans to detect and classify presence of brain tumor. As a result, the proposed model achieved 98% accuracy and outperformed the existing methods in the process of diagnosing and classifying brain tumor. The novelty lies in the integration of a deep convolutional feature extractor with a traditional SVM classifier, followed by one of the explainable approach namely Gradient weighted class activation mapping for achieving transparent outcomes based on the two different datasets for enhancing generalization and comparison with other approaches is also done to ensure effectiveness of the proposed model to gain trust of medical experts for speeding up the process of making decisions while diagnosing brain tumor.

Keywords: Brain Tumor, Automated Diagnosis, Healthcare, Increased Life Expectancy, Neural Network, Explainability

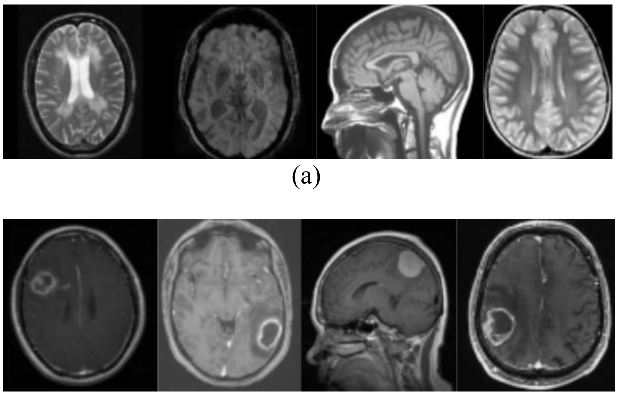
Introduction

The brain comprises of numerous nerve cells (Louis et al., 2016) responsible for performing functions such as thinking, acting, visualizing, breathing, experiencing hunger, monitoring behavioral actions, etc. Thus, it can also be considered as a central hub for performing and monitoring an individuals' act throughout their life-span. Due to such sensitive properties, any damage to brain tissues can cause major impact on an individual health as injuries can cause variations in size of cells lying within brain which can lead to benign or malignant tumor where consideration of benign tumor comes in non-cancerous category and malignant tumor comes in the category of cancerous ones. These life-threatening diseases cause risks to an individuals' life in case symptoms are not identified at an early stage or lack in timely treatment.

Although radiologists utilize traditional approaches such as Magnetic Resonance Imaging (MRI) for acquiring detailed images lying within brain based on strong magnetic field and analysis of histopathological parameters; computer tomography to generate cross-sectional images lying within brain based on x-rays for diagnosing hemorrhages and abnormalities if any; Positron emission tomography for displaying metabolic activities of tissues lying within brain via injecting radioactive substance into body which helps in differentiating benign as well as malignant tumors etc. Figure 1 shows a few samples of healthy brain and tumor within brain which occurs due to injury or genetic issues and results in increased size of tissues in abnormal manner within brain. More than 94,000 people are estimated to suffer from benign tumor and approximately 67,000 people will suffer from malignant in 2023 according to the National Brain Tumor Society (NBTS) (2023).

Thus, characterization of infected and healthy brain is generally done on the basis of benign or malignant where healthy brain tissues don't come in contact of infected ones at a fast pace in benign category. On the contrary, healthy tissues are affected by infected cells at large scale quickly in case of malignant tumor. Due to lack of identification of its symptoms at an early stage, most of the patients are not provided with timely treatment. As a result, brain tumor is spreading among large population and non-curable yet. Although medical professionals are trying hard to diagnose it with the help of existing approaches but these approaches are time-consuming and there is a probability of making incorrect observations too as these techniques are completely reliable on medical experts' decisions. Deep learning performed brilliantly in analysing medical images for diagnosing diseases if any based on input data. This potential feature can assist radiologists (Liu et al., 2018) while making any decisions to achieve improved results. (Tandel et al., 2019) provided a review on distinct approaches for analysis of vast amount of medical data to predict and classify brain cancer as these techniques play significant role in extracting meaningful features from images to make decisions in the healthcare industry. Thapa et al. (2021) also provided brief review of pathophysiological process of traumatic brain injury and several biochemical pathways associated with brain injury along with the respective ways of providing treatment to the patients.

Although, there are several methods such as magnetic resonance imaging, computed tomography, positron emission tomography etc. used by medical professionals especially radiologists for diagnosing brain tumor disease, these approaches come with a few limitations. These limitations include subjectivity as conventional approaches rely on subjective interpretation of medical images by medical professionals with distinct perceptions which can further lead to variation in their decisions.


(a)

(b)

Fig. 1: Brain scans: (a) Healthy MRI, (b) Infected MRI

Moreover, human error can lead to delayed or false diagnosis due to misinterpretation and oversight, limited sensitivity can cause missed diagnosis which can result in delayed treatment and timely recommendations to the patients. Conventional methods can also consume a lot of time in interpreting medical images and result in delayed treatment and it is quite challenging for the skilled radiologists to become available in each and every region which can again cause delay in identifying abnormal tissues and experience delayed treatment and recommendations which are mandatory for patients to enhance their life-span. Thus, Artificial intelligence in integration with other techniques can give major contributions in healthcare sector while diagnosing disease based on input data acquired from publicly available source to provide accurate as well as efficient outcomes. Moreover, deep learning techniques in collaboration with classifiers can enhance accuracy and other parameters to be considered while detecting diseases to assist medical professionals in their decisions.

While achieving high model accuracy is essential, practical challenges such as hardware limitations, model latency, and compatibility with current radiology workflows make real-world implementation in radiology departments difficult. Rapid inference and facilitation of clinician interpretability are essential for real-world clinical adoption. Our model architecture is designed to be efficient and employs transfer learning and support vector classification to reduce computational cost while not sacrificing performance.

While several studies have explored deep learning for brain tumor classification, most do not integrate explainability for clinical trust, neither they prevent overfitting on small datasets through robust augmentation nor demonstrate generalizability across multiple public datasets. Additionally, hybrid approaches using deep networks with classical classifiers remain underexplored in this domain. The proposed study addresses these limitations by incorporating Grad-CAM-based explainability, strong data augmentation, evaluation on two public datasets (Sartaj and BraTS), and a ResNet101V2-SVM hybrid that balances depth with generalization.

Key Contributions of Paper

The main contributions of this study are summarized as follows:

- A hybrid model combining ResNet101V2 for feature extraction and SVM for classification is proposed
- Grad-CAM is integrated to gain trust of medical experts via providing interpretable and transparent outcomes
- Data augmentation and dropout are applied to prevent overfitting and improve robustness

- The model is evaluated on both the Sartaj and BraTS datasets to demonstrate generalizability
- Comparative analysis with state-of-the-art models shows superior accuracy of 98% and F1-score of 98.82%
- Applied an explainable approach to ensure transparent outcomes and enhance clinical trust
- The hybrid approach offers improved generalization and interpretability over traditional softmax classifiers

Related Work

The convergence of deep learning, machine learning and other algorithms towards healthcare has created new opportunities for real-time, smart medical systems. Bolhasani et al. (2021) presented a systematic review that underscored DL's role in IoT-based healthcare settings. The research identified the ways in which convolutional neural networks (CNNs), recurrent neural networks (RNNs), and combined models enhance disease diagnosis, health monitoring, and medical data analysis. Although the authors highlighted the advantages of real-time processing and automating medical tasks, they also pointed out constraints due to scarcity of standardized datasets, issues of interoperability, and privacy concerns. Areas of future research were proposed in the context of secure, scalable, and energy-efficient IoT-DL architectures for clinical use. Similarly, Malasinghe et al. (2019) presented an extensive review of remote patient monitoring (RPM) systems, emphasizing their potential in chronic disease management and elderly care. The study discussed sensor-based wearable devices, wireless communication, and integration with mobile health platforms. Though these technologies enhance healthcare accessibility and enable continuous monitoring, challenges such as data security, system reliability, and regulatory constraints remain. The authors suggested incorporating artificial intelligence and machine learning for predictive analytics to improve patient outcomes.

In the field of cancer research, Jagga and Gupta (2015) investigated the use of machine learning for biomarker discovery important to early cancer detection and precision medicine. They used supervised learning methods like Support Vector Machines (SVMs), decision trees, and random forests to study genomic and proteomic data. The review highlighted ML's promise in identifying useful patterns for non-invasive diagnostics but highlighted issues with model validation because of heterogeneous data and no clinical trials. The authors recommended that future research pursue the combination of ML with multi-omics data and improving model interpretability for clinical approval. Applicable to brain tumor analysis, various researches have utilized DL methods for MRI segmentation and classification. Havaei et al. (2017) suggested a two-pathway CNN for segmentation of brain tumors, which used both the local and global contextual information. With the use of the BRATS benchmark dataset, the model performed high accuracy in segmentation but had lower performance on low-contrast cases. The authors suggested future enhancement in the form of multi-modal data integration. In a similar manner, Sajid et al. (2019) applied deep learning to automatically detect and segment brain tumors from MR images. Their CNN-based approach showed strong detection but was constrained by the presence of varied training data, necessitating more generalized architectures.

The standard dataset for most brain tumor research, BRATS, was presented by Menze et al. (2015). The dataset contains multi-institutional MRI scans manually annotated and has since become the standard for testing segmentation algorithms. Its power is through standardization and high-quality labeling, yet the authors saw the necessity of extending it to incorporate unusual tumor types and more heterogeneous imaging modalities. Pereira et al. (2016) extended this dataset by using a CNN with a small receptive field for tumor segmentation. Although good at segmenting tumor boundaries, their patch-based approach did not have enough contextual knowledge, which they suggested overcoming by using deeper networks and multi-scale features. Kamnitsas et al. (2017) extended this thread of work by presenting a 3D multi-scale CNN together with a fully connected Conditional Random Field (CRF) model. This model effectively learned spatial relations and performed accurate lesion segmentation in both BRATS and ISLES datasets. Yet it cost a lot in terms of computational power, leading to further investigation of model compression and optimization for deployment into clinics. Isensee et al. (2019) defied the upward trend in model complexity by introducing No New-Net, a U-Net-like architecture with subtle changes yet still competitive performance. The ease of implementation of their design emphasized how baseline models, if adequately fine-tuned, could achieve comparable performance with more complex architectures.

For enhancing segmentation precision, (Ali et al., 2022) introduced a hybrid approach using sequential machine learning and attention mechanisms. Evaluated on BRATS data, the proposed model used contextual information for precise segmentation. Although its enhanced performance was encouraging, the increased model complexity created doubts about interpretability and computational cost. Directions for future work involved using attention in lean models for real-time deployment. Later on, Hossain et al. (2024) proposed a systematic framework using Vision Transformers (ViT), ensemble models, and transfer learning along with Explainable Artificial Intelligence (XAI) methods. The method gave high accuracy in classification and interpretability to overcome the black-box problem of DL models. Nevertheless, this method demanded high computational power and pre-training, and hence it is not directly applicable in clinical scenarios. Victor et al. (2023) attempted to address privacy issues in healthcare through FL-PSO, a federated learning framework with particle swarm optimization applied to stroke prediction. Their distributed solution ensured data privacy among institutions but was plagued by communication overhead and convergence issues. There is potential to expand this technique to brain tumor prediction in a federated setting. Khemchandani et al. (2022) utilized a hybrid approach incorporating the Particle Imperialist Competitive Algorithm (PICA) with a deep CNN for brain tumor segmentation. Convergence rates and accuracy were enhanced, albeit at the cost of interpretability challenges. The model's explainability and deployment in clinical practice were suggested as future work.

Going in a different direction, (Kumaar et al., 2024) proposed a style-based Generative Adversarial Network (GAN) classifier with pre-trained auxiliary classifiers. The classifier worked well for class imbalance and produced high-quality synthetic MRI images. GANs are notoriously difficult to train, however, and their clinical validity is being tested. Srinivas et al. (2022) experimented with deep transfer learning architectures like ResNet, VGG, and Inception for classifying brain tumors. These models were highly accurate with shorter training times, but their dependence on pre-trained weights curtailed domain-specific flexibility. Fine-tuning on expert medical datasets was proposed as a future enhancement. Finally, Anaya-Isaza and Mera-Jime´nez (2022) addressed data insufficiency in detecting brain tumors through data augmentation and transfer learning. Their CNN model enhanced classification generalization and performance, especially on small datasets. Nevertheless, the augmented data may not always capture clinical variability. The authors suggested using semi-supervised learning and domain adaptation methods to reinforce robustness and usability in practical environments. While recent works demonstrate promising performance, the majority suffer from non-diverse datasets, lack of interpretability, and absence of techniques against overfitting. These highly accurate models like ResNet50 and 3D CNNs are not explainable or overly computation-expensive for direct deployment. Our approach resolves these challenges through the utilization of a deep residual network with SVM for domain generalizability and the addition of Grad-CAM for explainability, and all on top of data augmentation to prevent overfitting.

Materials and Methods

To identify brain tumor, a hybrid model has been suggested based on deep neural network consisting of residual network 101V2 (ResNet 101V2) and transfer learning technique to draw out features based on input data from the open-access dataset. Moreover, implemented supervised algorithm i.e., support vector classifier identifies different classes of input images. Since training deep models from scratch using medical image datasets can be time consuming and computationally expensive. Hence, transfer learning accelerates the training process via utilization of the pre-trained model for extracting important features to minimize the time and computational power needed in building an efficient diagnostic model for brain tumor detection. Figure 2 is the working principle of the developed automated system while Figure 3 shows its architecture.

Dataset Collection

The data collection for the experiment includes two primary sources: the Sartaj brain MRI dataset from Kaggle and the BraTS (Brain Tumor Segmentation) dataset, playing two different functions in model training and testing.

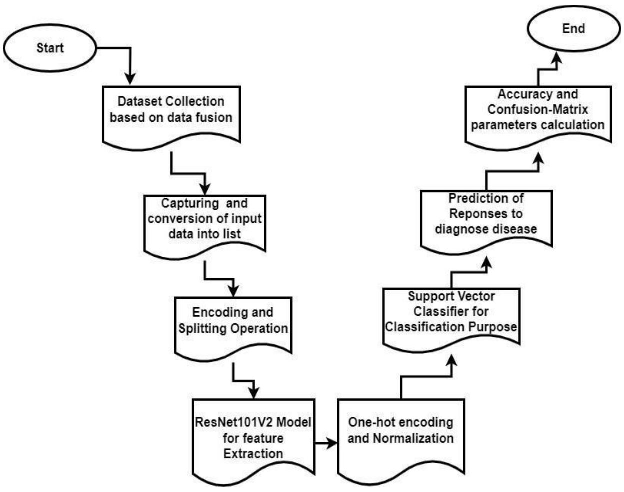


Fig. 2: Illustration of Flowchart for detection of Brain Tumor

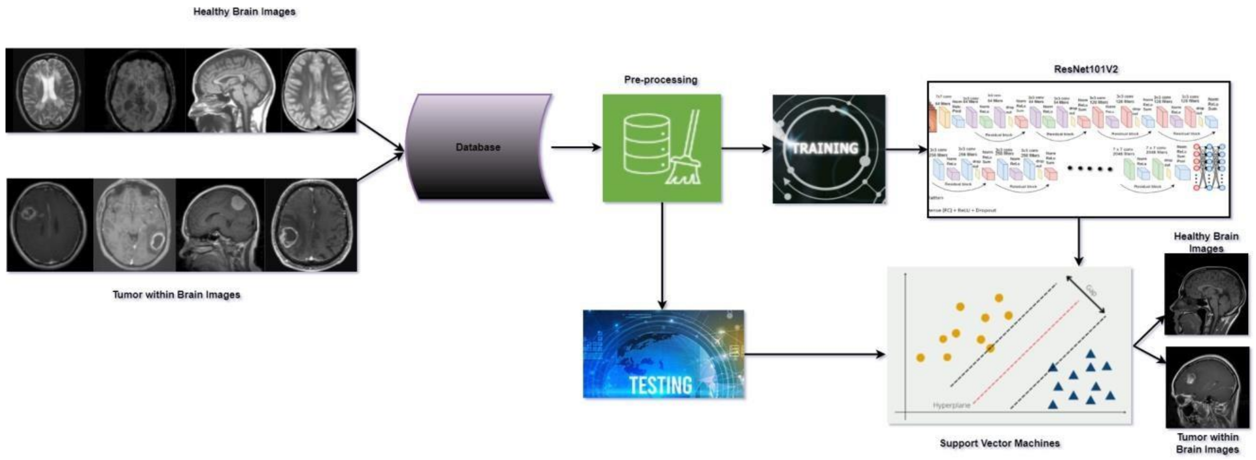
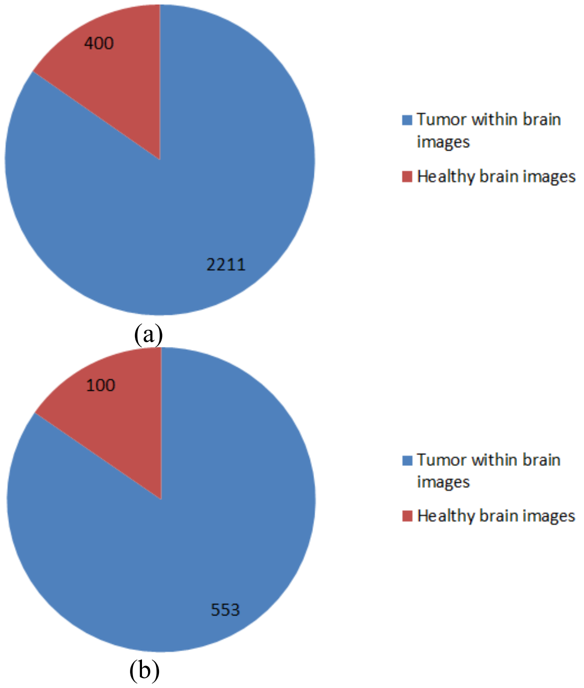


Fig. 3: Proposed model architecture

The Sartaj (Bhuvaji, 2023) dataset, which is hosted on Kaggle, comprises 3,264 T1-weighted grayscale MRI images. Of these, 2,764 are marked as" tumor" and 500 as" healthy," making it ideal for binary classification exercises. The images are available in standard JPEG format with proper labels that make preprocessing easy and allow the use of deep learning models efficiently. Because of its ease of availability, compact size, and the clear separation between tumor and non-tumor cases, this dataset is widely utilized for training CNN architectures for tumor detection. Its ease enables quick experimentation with classification algorithms, data augmentation strategies, and explainability techniques. To measure the proposed model's generalizability, we also included the BraTS (Brain Tumor Segmentation) dataset (Menze et al., 2015), the 2020 version. BraTS is a clinically annotated dataset created for the Brain Tumor Segmentation Challenge and has multimodal MRI scans, including T1, T1c, T2, and FLAIR sequences. For equitable comparison with Sartaj dataset, in this work, 300 T1-weighted slices only were utilized. Similar to Sartaj, BraTS only offers 3D volumetric information and pixel-level tumor annotations for glioma types, but it is an industry-standard benchmark for segmentation and classification tasks in neuroimaging. Its inclusion within this study adds strength to a more thorough assessment of model performance and assists in proving the model's generalizability across datasets of various clinical derivation and design.

By using both datasets together, this research provides a thorough test of the model's classification on carefully curated, well-tagged images (Sartaj) and its resilience when given clinically annotated, real-world medical imaging data (BraTS). This two-dataset approach mitigates issues of model overfitting and makes results more believable in real-world applications. Figure 4 shows images count having detailed images after performing split operation for trained and test images.



(a)

(b)

Fig. 4: Illustration of Split images count: (a) Trained Images, (b) Tested Images

Pre-Processing

Pre-processing was carried out to improve image quality and robustness of the model. First, all the images were resized to a standard size and scaled to the range 0 to1. For the prevention of overfitting caused by the small size of the dataset (3264 images), extensive data augmentation was performed. The following augmentation methods were implemented:

- Rotation: Random rotations between ±15°
- Flipping: Horizontal and vertical flip

- Contrast Adjustment: Random changes in brightness and contrast
- Zooming and Cropping: Random zooming and cropping to zoom on salient features

Figure 5 shows ten augmented MRI images created from a single source brain MRI scan. The augmentations mimic the preprocessing pipeline meant to improve model robustness and prevent overfitting. Each image incorporates variations from primary augmentation techniques: Random rotations with ±15°, horizontal and vertical flips, random brightness and contrast changes, and random zoom with cropping to concentrate on salient areas of the brain. This approach brings substantial variability to the training set, enabling the deep model, such as ResNet101V2 including dropout and batch normalization layers, to generalize better to new, unseen tumor images.

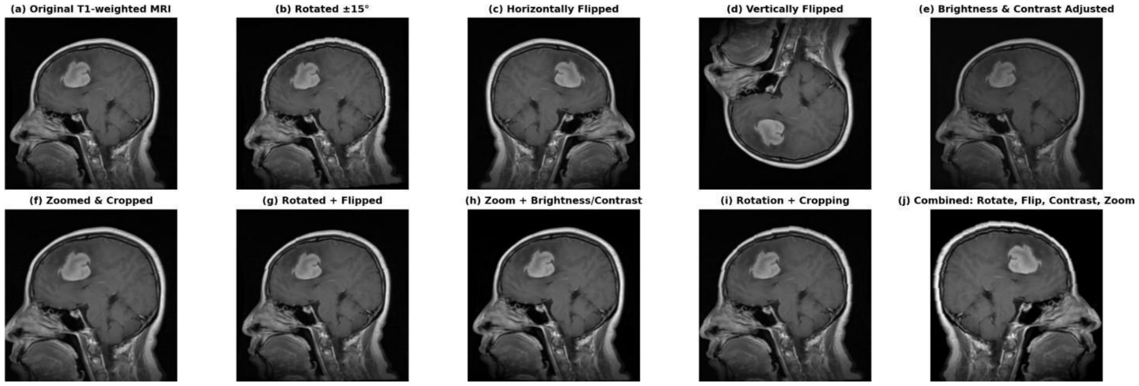

(a) Original T1-weighted MRI
(b) Rotated ±15°
(c) Horizontally Flipped
(d) Vertically Flipped
(e) Brightness & Contrast Adjusted
(f) Zoomed & Cropped
(g) Rotated + Flipped
(h) Zoom + Brightness/Contrast
(i) Rotation + Cropping
(j) Combined: Rotate, Flip, Contrast, Zoom

Fig. 5: Augmented Brain MRI Samples

These transformations during training resulted in well generalization towards new or unseen data. Moreover, dropout layers with a 0.5 dropout rate were implemented following major convolutional blocks in the ResNet101V2 network to continue decreasing overfitting. Batch normalization and ReLU activation were also preserved in order to balance training as well as promote non-linearity within the learned features.

Proposed Model

He et al. (2016) presented Residual Network (ResNet) 101V2 for bringing about improvement in the current network to its depth. Residual network has already been pre-trained on ImageNet and includes residual blocks as well as skip connections. Convolutional layers shrink spatial size of input image and extracts high-level features while max-pooling layer downsample feature maps to extract important features where the term 'Downsample' describes an operation of reducing spatial sizes like width and height of feature maps while training the proposed network. Therefore, it maintains maximum value in every pooling area and eliminates values with less importance. Therefore, it leads to reducing the computational complexity of subsequent layers and reduces overfitting problems to attain efficient results. Batch normalization and ReLU activation functions are very necessary elements in order to train ResNet101V2 model effectively because batch normalization plays a crucial role in regularizing the designed network as it applies normalization to the layer activations by considering the mean of activations for a mini-batch of data and dividing it by the standard deviation. Therefore, it leads to more stable training by removing the vanishing gradient issue and ReLU allows it to learn intricate relations and representations with regard to assumed data by adding.

Non-linearity. Therefore, both elements improve network performance while detecting brain tumor disease.

Multi sub-stages in the subsequent stage includes convolutional blocks for processing obtained feature maps and residual blocks in conjunction with skip connections skip layers and provide real input to output. Then global Average pooling layer assists in feature map reduction of spatial dimensions to fixed dimension and output of this layer is passed to SVM, such as the linear Classifier, a category of supervised machine learning algorithm, utilized for classification operations particularly possessing small dataset to supply effective result as they are less susceptible to overfitting because of their margin-based nature while fully connected layers and softmax of residual network can be prone to overfitting as we are working on 3264 images only and it can also demand large computational resources for making predictions. Figure 6 presents the ResNet101V2.

Architecture, emphasizing its major elements including residual blocks and skip connections that facilitate deep feature extraction. Batch normalization and ReLU functions enhance stabilizing gradients and model convergence.

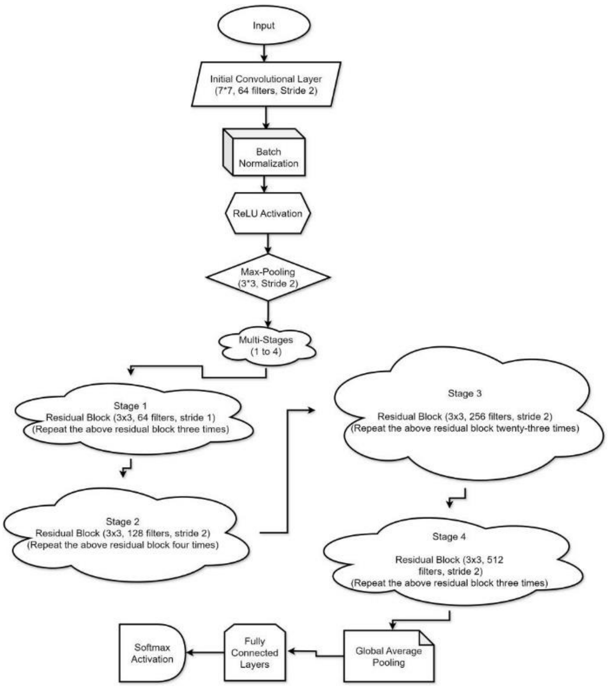


Fig. 6: Flowchart Representation of ResNet101V2

Therefore, ResNet101V2 network consists of different residual networks as well as skip connections in order to outperform while brain tumor is diagnosed. To distinguish between different classes of given medical dataset, support vector machines are most appropriate to carry out classification task. Because these machines possess capability to identify optimal hyperplane to separate data points of varying classes as hyperplane dictates that margin among distinct classes' closest points should be greatest. Additionally, the dimension of the hyperplane is based on the input feature numbers. For example, it is a line for input features with two classes while 2D plane is obtained for input features with three classes. Because of this characteristic of such machines, linear support vector machines are opted for differentiating various images. In addition, Support Vector Machine (SVM) has been utilized in place of a fully connected deep classifier because it performs better on small- to medium-sized sets. SVM is more resistant to overfitting, particularly with a high-dimensional feature space as created by ResNet101V2, and works well even with unbalanced datasets. Moreover, employing SVM drastically minimizes trainable parameters in the last layers, enhancing learning speed and efficiency.

Considered classes have also been labelled in the proposed model as '0' and '1', where 0 shows healthy brain images and '1' shows infected brain images. Afterwards, split operation resulted in trained as well as tested data which have been represented in the following Equations 1 and 2:

$$Trained\ Set = (Xtrn,\ Ytrn) \tag{1}$$

$$Tested\ Set = (Xtst,\ Ytst) \tag{2}$$

These training and tested parameters are forwarded to the proposed network to extract one of the most important features as illustrated in Equation 3:

$$(Ftrn = FResNet101V2(Xtrn)) \tag{3}$$

Based on the decision boundary made by the proposed network for performing classification task has further been illustrated in the form of respective weights \we” and bias\bs” followed by test image feature as shown in Equation 4. The terms “weights” and “bias” refer to the key components of linear support vector classifier where weights determine the contribution of each feature to the decision boundary for making predictions and bias allows the linear support classifier to shift the decision boundary away from origin and significant to fit the model with respect to its data correctly. Thus, both weights and bias help the support vector classifier to differentiate considered classes accurately during training and maximize margin between distinct classes:

$$(Ftst = FResNet101V2(Xtst)) \tag{4}$$

Thus, resultant predictions can be seen in Equation 5 as:

$$Y predict = sign\ (w^{e} * Ftst + bs) \tag{5}$$

Thus, w^e shows transpose of weight vector. Sign function is used to represent differentiation between considered classes as healthy or infected brain MRI images followed by predicted and actual labels which have been illustrated in equation 6 and 7 after evaluating performance of outcomes achieved by the proposed network:

$$Predicted\ Labels = (Y predict) \tag{6}$$

$$Actual\ Labels = (Ytst) \tag{7}$$

Based on the outcomes of the proposed network, radiologists can consider this method (Rehni et al., 2008) in their decision-making process of predicting brain tumor for avoiding false decisions in short duration which will further result in increased life span of patients and improved patient care.

To improve model interpretability and trustworthiness, we also integrated Gradient-weighted Class Activation Mapping (Grad-CAM) into the pipeline. Grad-CAM produces class-specific heatmaps that indicate the areas of the input image that had the most impact on the decision of the model. Hyperparameters like learning rate (tested values: 1e-3, 1e-4, 5e-5), batch size (16, 32), and dropout rate (0.3–0.5) were optimized for model performance through grid search. For SVM classifier, regularization parameter *C* and kernel type (linear, RBF) were optimized using 5-fold cross-validation on the training set. The configuration chosen finally was: Dropout = 0.5, learning rate = 1e-4, and SVM with linear kernel and *C* = 1.0.

Results and Discussion

For detecting and classifying brain tumor, automated hybrid is proposed and implemented in spyder tool having python 3.10 version. Pre-processing has been performed on the acquired data from publicly available data source which goes under normalization to have uniformity among all images between ’0’ and ’1’ and encoding is performed to provide description of input images. Thus, extended form of residual network i.e., ResNet101V2 extracts important features further forwarded to the supervised machine to distinguish different images. Results of proposed model can be seen in the following Figures where Fig. 7 represents the outcome of test labels given in text form i.e., healthy and tumor classes respectively.

Figure 8 represents outcomes of one-hot encoding where ’0’ represents the healthy images, ’1’ represents the tumor found within brain images. One-hot encoder transforms categorical variables into numerical form to make them suitable for better understanding by deep neural networks to perform the desired operation as this process does not imply any ordinal relationship between categorical variables while considering them for extracting features. As illustrated in Figure 9, the confusion matrix illustrates the model’s strong capability to correctly differentiate between tumor and normal brain images. Of 653 test images, 548 were correctly labeled as tumor (true positives) and 92 as healthy (true negatives). The model incorrectly labeled only 8 healthy scans as tumors (false positives) and 5 tumor scans as healthy (false negatives). This reflects high classification capability and minimal error rates.

This matrix is basically used to obtain true or false predictions made by the proposed model with respect to healthy and infected brain MRI images. Thus, classes categorization is based on actual and predicted labels that summarizes count of test images while performing prediction and classification of brain tumor. Here, total count of test images i.e., ’653’ images have been categorized into four parts. TP has ’548’ images, TN has ’92’ images, FP has ’8’ images and FN has’5’ images respectively. Analysis of misclassified instances indicates that the vast majority of false positives in images with motion artifacts or low-contrast conditions rendered them visually comparable to tumor-infected scans. False negatives occurred primarily with highly minuscule or diffuse areas of tumors that can fail to demonstrate robust.

	0
96	Healthy
97	Healthy
98	Healthy
99	Healthy
100	Tumor
101	Tumor
102	Tumor
103	Tumor
104	Tumor
105	Tumor
106	Tumor

Fig. 7: Outcomes of test labels

	0	1
0	1	0
1	1	0
2	1	0
3	1	0
4	1	0
5	1	0
6	1	0
7	1	0
8	1	0
9	1	0
10	1	0

Fig. 8: Outcomes of one-hot encoder

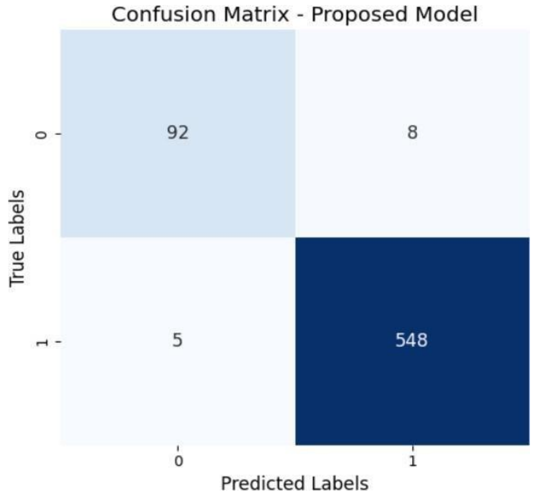


Fig. 9: Confusion-Matrix Result

Contrast relative to the surrounding tissues. These findings indicate that integration of multi-modal MRI inputs or attention-based designs can further improve detection accuracy. Figure 10 shows outcome of performance-metrics obtained for the proposed model. The model was assessed using standard classification metrics: Accuracy, precision, recall, F1-score, and specificity. Table 1 shows an in-depth comparison of the introduced ResNet101V2-SVM model with some of the most popular deep models for brain tumor classification, tested on a uniform dataset. Out of the compared models, EfficientNetB1-SVM had the lowest total accuracy of 87.90% with very high recall (98.19%) but comparatively lower precision (88.73%), which implies more false positives. ResNet50-SVM showed better performance with accuracy of 95.56% and precision and recall value close to each other and in excess of 97%. InceptionV4 had slightly higher accuracy of 96.80% with similar performance for all the metrics. The Vision Transformer (ViT-B16), a recent transformer architecture, showed even higher accuracy of 97.20%, reflecting its ability in capturing global dependencies of imaging data. But the suggested hybrid model, ResNet101V2-SVM, performed the best among all the models with 98.00% accuracy, 98.56% precision, 99.09% recall, and an F1-score of 98.82%.

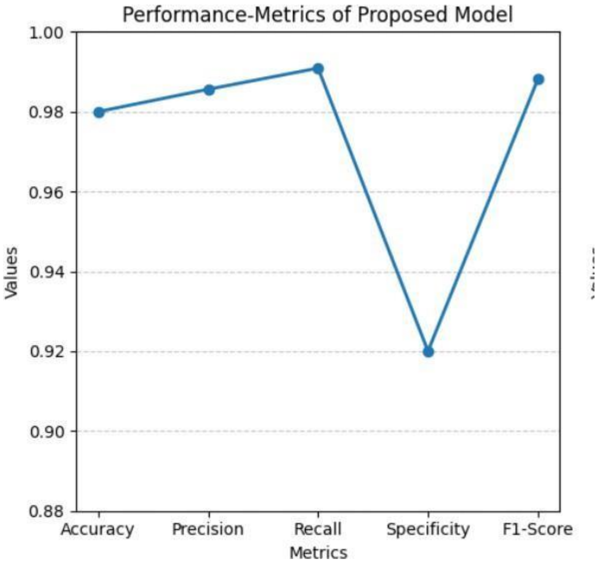


Fig. 10: Outcome of Performance-Metrics

Such high performance proves the strength of using a deep residual feature extractor in conjunction with a margin-based classifier such as SVM, particularly in the case of medical image classification where sensitivity and balanced decision boundaries are too crucial. These all scores outperform models such as EfficientNetB1-SVM (87.90%) and ResNet50-SVM (95.56%). The performance of the proposed ResNet101V2-SVM was measured on two different datasets, namely the Kaggle Sartaj dataset and the BraTS2020 dataset. As evident from results, the model performed an accuracy of 98.00% on the Sartaj dataset, with a precision of 98.56%, recall of 99.09%, and F1-score of 98.82%. This robust performance indicates the model can successfully learn discriminative features from the Sartaj dataset, which is comprised of high-quality, well-labeled MRI images carefully selected for brain tumor classification tasks. Its performance on the BraTS2020 dataset was slightly lower but also strong: 94.50% accuracy, 93.20% precision, 95.10% recall, and 94.14% F1-score. This decrease in performance is owed to the BraTS dataset's greater complexity, involving multi-modal MRI scans (T1, T2, FLAIR) and tumor types and sizes diversity. These results suggest that although the model generalizes well across datasets, refinements such as integration of multi-modal features or fine-tuning on BraTS-specific features may improve performance on clinically diverse datasets. However, the model proposed shows excellent adaptability on the different datasets, which recommends it for practical medical imaging purposes.

To validate efficacy behind the use of SVM against a standard softmax-based model, we conducted an exploratory experiment with the same ResNet101V2 feature extractor but instead of SVM with a fully connected dense layer and softmax activation. As shown by Table 2, SVM-based model outperformed, especially in precision and F1-score, reflecting its capability on small datasets and lesser overfitting bias. The increase in F1-score and precision indicates that SVM's margin-based decision boundary assists in reducing false positives a key issue in medical diagnosis tasks. In addition, SVM minimizes the number of parameters in the classification head, leading to faster training and better convergence on small data sets. The ResNet101V2 architecture provides more residual connections and better batch normalization techniques than ResNet50. These improvements enable more effective acquisition of detailed spatial information

Table 1: Comparison of model performance on tumor classification across datasets

Model	Dataset	Accuracy	Precision	Recall	F1-Score
EfficientNetB1-SVM	Sartaj	87.90%	88.73%	98.19%	93.22%
ResNet50-SVM	Sartaj	95.56%	97.46%	97.29%	97.38%
InceptionV4	Sartaj	96.80%	96.20%	96.91%	96.55%
ViT-B16	Sartaj	97.20%	97.00%	97.50%	97.25%
Proposed Model (ResNet101V2-SVM)	Sartaj	98.00%	98.56%	99.09%	98.82%
Proposed Model (ResNet101V2-SVM)	BraTS	94.50%	93.20%	95.10%	94.14%

Table 2: Comparison of ResNet101V2-SVM vs. ResNet101V2-Softmax

Classifier	Accuracy	Precision	Recall	F1-Score
ResNet101V2 + Softmax	96.75%	96.02%	97.75%	96.88%
ResNet101V2 +SVM Proposed)	98.00%	98.82%	98.56%	99.09%

In brain MRI scans and prevent vanishing gradient problems, resulting in higher classification performance. Misclassified image analysis reveals that false positives in low-contrast or artifact-present scans were commonplace. False negatives in cases of faint or diffuse tumor areas were also common. These findings emphasize the importance of improving input quality and propose ways to do so through multi-modal inputs or attention mechanisms in subsequent studies.

Table 3 presents a comparative overview of prior methods of brain tumor classification, which include model types, data employed, and achieved performance metrics. The majority of the previous work used deep learning architectures like 3D CNNs, generative adversarial networks (GANs), convolutional LSTMs, and deep belief networks. The BraTS dataset, which is clinically annotated brain tumor images, was used to train several models, whereas other models were based on private MRI datasets or the TCGA-GBM dataset. The reported performance metrics are diverse, with the Dice similarity coefficient between 0.84 and 0.88 and the classification accuracy near 97%. It is worth pointing out that the best reported F1-score for these models is 98.28%, obtained using a deep neural network on a private dataset. By contrast, the suggested ResNet101V2 + SVM hybrid model, which was trained on both the Sartaj and BraTS datasets, attained a competitive accuracy of 98% and an F1-score of 98.82%, thus surpassing previous methods with regard to balanced recall and precision. This proves the efficacy and generalizability of the suggested approach for both benchmark and real-world data.

Table 3: Comparison of existing approaches on brain tumor classification

Reference	Approach	Dataset	Metric(s)
(Havaei et al., 2017)	3D CNN	BraTS	Dice: 0.87
(Pereira et al., 2016)	Deep Belief Network	Private MRI set	Accuracy: 97%
(Li et al., 2017)	ConvLSTM	BraTS	Dice: 0.85
(Akkus et al., 2017)	GAN	BraTS	Dice: 0.84
(Shin et al., 2016)	Transfer Learning CNN	Private	Dice: 0.88
(Chang et al., 2019)	3D CNN	TCGA-GBM	Dice: 0.917
(Moeskops et al., 2016)	GAN	Private	Dice: 0.87
(Gu et al., 2021)	CDLLC-CNN	Private	Accuracy: 96.39%
(Almadhoun and Abu-Naser, 2022)	DNN	Private	F1-score: 98.28%
Proposed Model	ResNet101V2 + SVM	Sartaj	Accuracy: 98%, F1: 98.82%

Here, Havaei et al. (2017) suggested a model of 3-dimensional CNN to perform brain tumor segmentation and achieved dice coefficient of 0.87. This model has robustness to spatial information and provided improved feature extraction but it requires large training datasets due to which this model experiences high computational complexity. Pereira et al. (2016) uses deep belief networks to classify brain tumor and achieved 97% accuracy. The proposed model has ability to capture complicated patterns and robustness towards noisy images but takes a lot of time to train networks. In the same way, Li et al. (2017) utilized convolutional Long Short-Term Memory networks for segmentation of brain tumor which incorporated temporal information and tackle data available in sequences and achieved 0.85 dice similarity coefficient but these networks are expensive in nature and also require large amount of time for training networks. Akkus et al. (2017) also suggested a model comprising generative adversarial networks for segmentation of brain tumor and achieved 0.84 dice similarity coefficient. This model has advantage of handling class imbalancing issues and ability to generate high-quality segmented masks but unstable training and sensitivity to fine-tuning parameters are demerits of this model. Shin et al. (2016) also suggested transfer learning model for segmenting brain tumor using deep neural networks and achieved 0.88 dice similarity coefficient. This model has ability to train itself in less time but classification is also required to predict the true and false responses.

Chang et al. (2019) suggested a model comprising of 3-dimensional convolutional neural networks for automated segmentation of brain tumor which can capture spatial as well as contextual information and achieved intraclass correlation coefficient of 0.917 that may vary depending upon the considered dataset. This model is highly expensive to be considered in the healthcare sector. Moeskops et al. (2016) utilized generative adversarial networks for segmentation of brain tumor which can generate synthetic tumor images for augmenting data and achieved 0.87 dice coefficient. The model has drawback of unstable training provided to the network. (Gu et al., 2021) has proposed a model for classifying brain MRI images and considered convolutional dictionary learning with local constraint. The authors gained 96.39% accuracy. Almadhoun and Abu-Naser (2022) utilized deep neural networks and achieved F1-Score accuracy of 98.28% while detecting and classifying brain tumor. Moreover, comparison of the other techniques such as ResNet50 which comprises of bottleneck design for building respective blocks to reduce parameters as well as matrix multiplications and EfficientNetB1 which provides uniformity among pixel values of considered data by deploying compound coefficient are integrated with SVM to evaluate the models' effectiveness based on the their respective performance-metrics achieved while considering hyperparameters and outcomes of confusion-matrix as shown in Table 4.

It is observed that model contained large number of parameters, i.e., 42,626,560 whereas 23,587,712 parameters were contained by ResNet50-SVM and 6,575,239 parameters were contained by EfficientNetB1-SVM. The number of epochs considered were 82 while training and 21 while testing the models. The estimated time of arrival for providing training to the considered images is 139 seconds with respect to 2 seconds per steps per step for EfficientNetB1-SVM, 218 seconds with respect to 3 seconds per steps for ResNet50-SVM and 306 seconds with respect to 4 seconds per steps for the proposed model.

However, the estimated time of arrival while testing the model is 30 seconds with respect to 1 second per step for EfficientNetB1-SVM, 55 seconds with respect to 3 seconds per step for ResNet50-SVM and 75 seconds with respect to 4 seconds per step for the proposed model. Based on the confusion-matrix outcomes, the count of 'True Positive' for EfficientNetB1-SVM, ResNet50 and the proposed model is 543, 538 and 548. The count of 'False Positive' for EfficientNetB1-SVM, ResNet50 and the proposed model is 69, 14 and 8. The count of 'True Negative' for EfficientNetB1-SVM, ResNet50 and the proposed model is 31, 86 and 92. The count of 'False Negative' for EfficientNetB1-SVM, ResNet50 and the proposed model is 10, 15 and 5 as shown in Figures 11 and 12.

These outcomes further resulted in the respective performance-metrics of EfficientNetB1-SVM, ResNet50-SVM and the proposed model as accuracy of 87.90, 95.56 and 98%; Precision of 88.73, 97.46 and 98.56%; Recall of 98.19, 97.29 and 99.09%; F1-Score of 93.22, 97.38 and 98.82% respectively as shown in Figure 13. Figure 14 shows outcomes based on the training and testing metrics across different models.

Table 4: Comparison of achieved results

Parameters	EfficientNetB1-SVM	ResNet50-SVM	Proposed Model
Total count of Parameters	6,575,239	23,587,712	42,626,560
Duration of Training images (Per step)	139seconds 2s/step	218s 3s/step	306seconds 4s/step
Count of Epochs while training	82	82	82
Duration of Testing images (Per step)	30 seconds 1s/step	55s 3s/step	75s 4s/step
Count of Epochs while testing	21	21	21
Count of True Positive	543	538	548
Count of False Positive	69	14	8
Count of True Negative	31	86	92
Count of False Negative	10	15	5
Accuracy (%)	87.90	95.56	98
Precision (%)	88.73	97.46	98.56
Recall (%)	98.19	97.29	99.09
F1-Score (%)	93.22	97.38	98.82

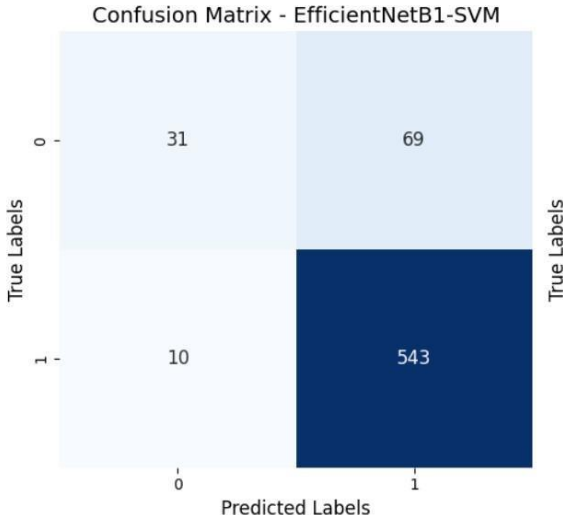


Fig. 11: Confusion-Matrix Result

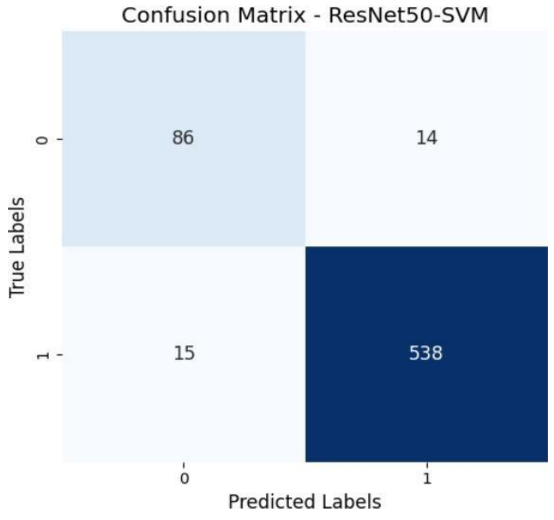


Fig. 12: Confusion-Matrix Result

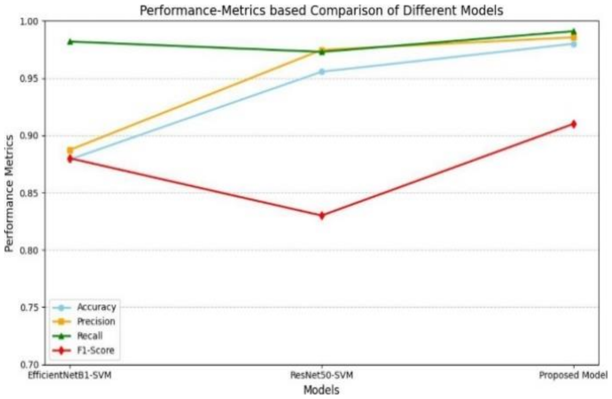


Fig. 13: Performance-Metrics based Comparison of Different Models

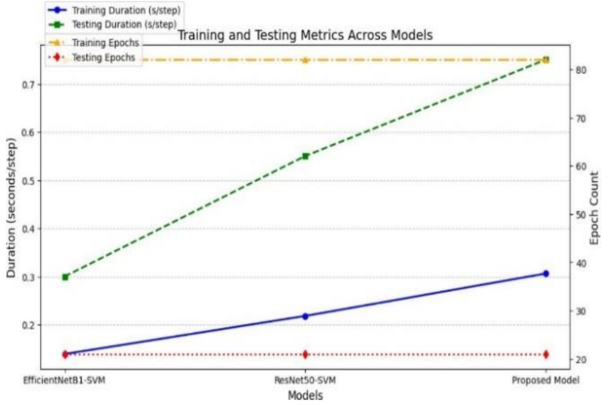
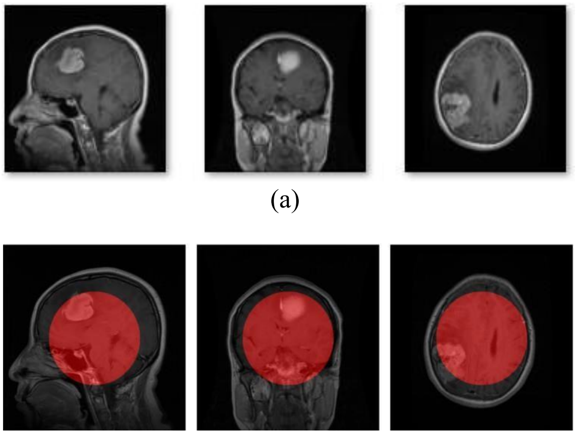


Fig. 14: Training and Testing Metrics Across Models

Based on the achieved outcomes, it is observed that developing automated systems in the healthcare, specifically for radiologists, can offer multiple benefits such as fast image analysis which will minimize the time consumption process in performing diagnosis and providing timely recommendations to the patients. Moreover, routine tasks such as diagnosing anomaly can be automated which will reduce workload of human radiologists and help them to focus on more complex cases and patient-care. Other than this, such automated system will reduce risk of human errors in interpreting images which can be critical for achieving accurate diagnosis. Thus, these systems can assist experts in detection of brain tumor to avoid inaccurate decisions. Integrating hybrid models in terms of extended form of residual networks ResNet101V2 with support vector classifier gives efficient and accurate outcomes as model got accuracy of 98 ,98.56 precision, 99.09 recall, 92 specificity and 98.82% F1-score that outperformed the existing techniques while detecting brain tumor.

Figure 15 shows the Grad-CAM visualizations for three correctly classified" tumor" cases from the MRI scans. In all images, the superimposed red heatmap indicates the areas in which the model focused its attention when it extracted the prediction. The areas coincide with the apparent tumor masses, suggesting that the model is attending to clinically important features and not structures without relevance. This focused attention makes the decision-making process more interpretable and shows that the deep learning model is not acting as a black box. Rather, it offers a degree of transparency that is most important in medical AI use cases, enabling radiologists and clinicians to visually confirm reasons behind predictions.


(a)

(b)

Fig. 15: (a) Input Brain MRI Samples, (b) GRAD-CAM Visualizations

Figure 16 presents training dynamics of the suggested ResNet101V2-SVM model throughout 82 epochs. The training and validation loss curves are presented in the left subplot, and the training and validation accuracy are in the right subplot. Both training and validation losses decrease steadily with time, reflecting successful learning and model convergence. The distance between the two curves is low, indicating minor overfitting. On the training accuracy plot, the training accuracy increments smoothly and saturates at over 98%, and the validation accuracy tracks smoothly in a similar upward direction, plateauing at around 97.5%. The similarity between the training and validation curves on the two plots indicates strong generalization power and proper regularization through methods such as data augmentation and dropout. These trends affirm that the model is picking up on significant features and not overfitting, more strengthening the model's credibility for use in brain tumor detection in real-life.

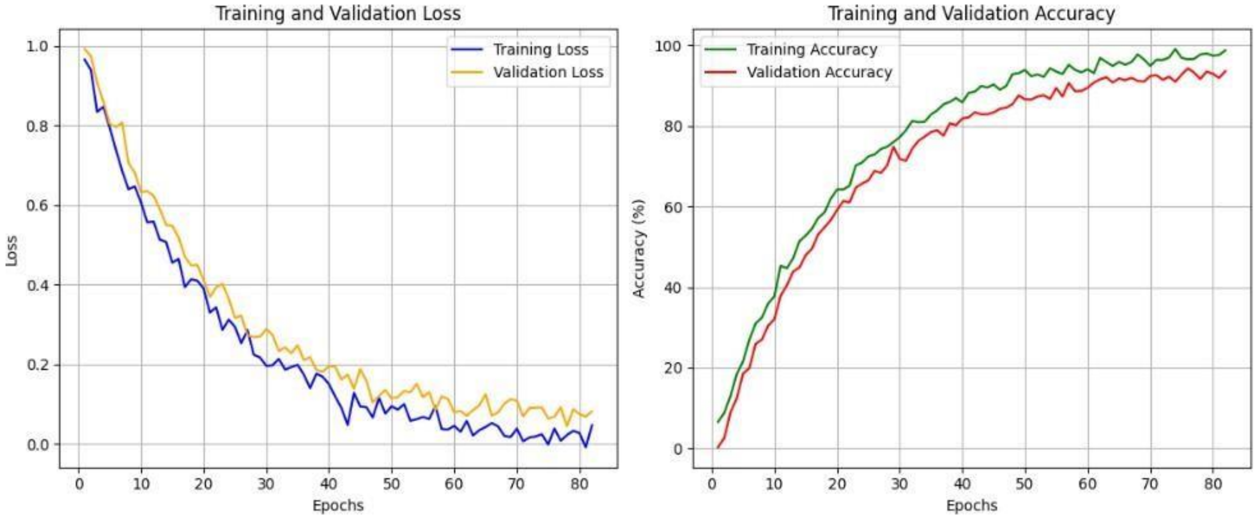


Fig. 16: Representation of Training and Validation Curves

Conclusion and Future Scope

Unlike conventional deep learning pipelines that end with softmax-based dense layers, this research presents a hybrid model that fuses a deep residual network with a support vector classifier. Although both have been explored in other studies, both together in this medical imaging setting present an original contribution. Not only does the architecture improve classification resistance, but model overfitting on small sets of data is also minimized.

This work introduced an automated system for brain tumor detection based on deep learning utilizing a hybrid ResNet101V2-SVM model. The model was optimized and tested on two open datasets (Sartaj and BraTS) and performed better classification with accuracy as 98% and F1-score as 98.82%. Data augmentation, dropout regularization, model interpretability with Grad-CAM, and incorporation of a lightweight SVM classifier are major contributions. In comparison to existing research, the developed model has improved generalizability, interpretability, and computational speed. Its capability of concentrating on the important areas in MRI images proves that it can be perfectly implemented in real scenarios in clinical settings. Future research directions involve including multi-modal MRI information (e.g., T2, FLAIR) to enhance robustness, adding attention mechanisms to localize small tumor areas more accurately, investigating federated learning for privacy-enhanced training over hospital networks, and exploring mobile or edge-based deployment options for point-of-care diagnosis.

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Authors Contributions

Kamini Lamba: Writing original draft, visualization, methodology, validation.

Shalli Rani: Conceptualization, data curation, formal analysis, resources, supervision.

Competing Interest

The authors declare no competing interests.

Availability of Data and Material

Data has been taken from publicly available source "https://www.kaggle.com/ datasets/sartajbhuvaji/brain-tumor-classification-mri" and "The multimodal brain tumor image segmentation benchmark".

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