Original Article
DOI: https://doi.org/10.70749/ijbr.v3i12.2722

INDUS JOURNAL OF BIOSCIENCE RESEARCH
https://ijbr.com.pk
ISSN: 2960-2793/ 2960-2807

Improving Brain Tumor Diagnosis Accuracy: A Machine Learning Approach with CNN, RNN, and PCA

Sahil Kumar[1], Nadeem Ahmed[2]

[1]DePaul University, United States.
[2]Professor of Computing at Iqra University.

ARTICLE INFO

Keywords: Brain Tumor Diagnosis, Convolutional Neural Networks, Machine Learning, Medical Imaging, Principal Component Analysis, Recurrent Neural Networks.

Correspondence to: Sahil Kumar, DePaul University, United States.
Email: skumar46@depaul.edu

Declaration
Authors' Contribution
Both authors equally contributed to the study and approved the final manuscript.

Conflict of Interest: No conflict of interest.

Funding: No funding received by the authors.

Article History
Received: 28-10-2025 Revised: 13-12-2025
Accepted: 21-12-2025 Published: 30-12-2025

ABSTRACT

Effective and efficient brain tumor classification from MRI scans is of critical importance as medical diagnostics in detecting early signs of the disease and treating the disease as early as possible. The focus of this paper is to propose a novel method to classify the brain tumors into 4 types of glioma, meningioma, notumor, and pituitary tumors using a combination of RNN based LSTM with PCA and SVM. To extract features from the MRI images, we use VGG19 a pre trained Convolutional Neural Network (CNN) and because the data is sequential, LSTM is utilized to process the sequential nature of the data so that the model learns the temporal relationship between multiple MRI slices. They are then applied to an SVM classifier with Principal Component Analysis (PCA) for dimensionality reduction and improved efficiency for classification. To further enhance model robustness, we combine three prominent brain MRI datasets, ensuring a diverse set of training examples. The experimental results show that the proposed LSTM-based SVM model gives 97% accuracy in all the tumor categories with high precision, recall and F1 scores. The model's performance dominates the existing CNN based models especially in term of generalization where training and validation accuracy exhibit little change implying good overfitting prevention. Two main contributions are identified to address the problem with a hybrid approach consisting of both Deep Learning and traditional ML techniques: (a) both methods achieve high accuracy and (b) results are interpretable and scalable.

INTRODUCTION

Brain tumors are globally among the leading causes of morbidity as well as mortality and have an important impact on patients' quality of life. Based on the statistics reported by the American Cancer Society (2025), it is estimated that in 2025 there will be approximately 25,000 cases of new brain and spinal cord tumor diagnoses on the American territory, emphasizing the need for accurate and early detection of brain and spinal cord tumors [1].

Brain tumors are difficult to diagnose because the disease is heterogeneous, meaning it presents with substantial variation of tumor types, locations as well as factors shape and size [2]. Due to these complexities, identification and classification of tumors is difficult and, hence, heavily rely on traditional diagnostic methods of medical professionals (radiologist) to diagnose various tumors. Despite their expertise, human error and subjectivity in interpreting medical images remain prevalent, especially considering the large volume of imaging data, leading to inconsistencies in diagnoses [3].

The two imaging modalities used to identify and evalu- ate brain tumors are Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans. All of these must be done, but do not come without their limitations. The problems that radiologists often encounter include identify- ing subtle abnormalities, separating benign and malignant tumors and differentiating tumor recurrences from post treat- ment changes [4].

Moreover, the growing amount of medical image data and the necessity to make a prompt diagnosis in critical care situations have stressed the demand for improved and more accurate automated diagnosis systems.

In recent years Machine Learning (ML) techniques have proven to be great tools for helping to automatically analyze medical images in a way, which can potentially help to improve diagnostic accuracy and consistency. Furthermore, there have been exceptional results achieved by applying ML models, more specifically deep learning methods in- cluding, Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), and Principal Component Anal- ysis (PCA), in examining and diagnosing complex medical imaging data with high accuracy, consistency, and autonomy [5]. For example, brain tumors can be classified using MRI scans using CNNs

that successfully learn features often hard to detect by humans [6]. Since RNNs excel in learning sequential data, they are capable of analyzing temporal changes in imaging data over time and understanding the tumor progression [7]. For example, PCA, a statistical dimen- sionality reduction technique, has also been used to reduce the complexity of data itself so that it would be easier for the ML models to process and identify the most important key features [8].

The purpose of this paper is to investigate how CNNs, RNNs and PCA can enhance the accuracy of brain tumor diagnosis. In this work, we review the state of research done in the area and examine the current methods used in brain tumor detection, identify the short comings of the state of the art approaches and propose a hybrid machine learning model which is a combination of existing techniques, improving the performance of proposed models as compared to the existing approaches.

LITERATURE REVIEW

Over the past few years, Deep Learning (DL) has led to a rapid change in the way medical images are being analyzed, and has greatly improved the diagnosis of brain tumor in the last decade with integration of machine learning techniques. Convolutional Neural Networks (CNNs) have been one of the key components in these advancements, as CNNs have be- come the 'go to' architecture for automating the classification of brain tumors in medical imaging. Feature extraction tasks involving complex tasks such as Magnetic resonance imaging (MRI) analysis can be performed accurately without doing manual feature engineering using CNNs [9]. These models work best in classifying the tumor types using features that could not easily be extracted manually [10].

Besides CNNs, Capsule networks (CapsNets) are also pointed out by recent studies as a potential diagnosis model for brain tumors. CapsNets are very resistant to spatial transformations like rotations and scalings and can be applied to spatial hierarchies, unlike traditional CNNs, Hinton et al., [11]. This is a property that makes CapsNets appropriate for medical image analysis in which the transformations are often present due to patient positioning or different image acquisition protocols. CapsNets also appear to outperform CNNs in the case of limited training data, as early studies show that they can outperform CNNs with limited amount of training data [12] and offer value for a particular application with medical datasets that are small and imbalanced.

One big advancement of interest in the brain tumor diag- nosis field is the introduction of Vision Transformers (ViTs) [13]. Already well established for natural image analysis tasks, ViTs have shown better performance in medical image analysis by capturing long range dependencies among pixels because of the image. Their integration with CNNs has given rise to hybrid architecture which adds to the ability of feature extraction leading to the improvement in brain tumor detection.

Although these advancements are promising, there are still various issues to be dealt with. For example, CapsNets have promising results, yet are not commonly used in clinical settings as their scalability in large datasets has been under studied. Moreover, ViTs face the hurdle of needing large labeled datasets for effective training since such datasets are often lacking in medical imaging tasks [14]. Additionally, these models still require generalization across different patient populations and imaging conditions.

In automated brain tumor detection, Convolutional Neural Networks (CNNs) have become a dominating force, with many well defined architectures obtaining very good results in medical image analysis. Azaharan, Ton Komar, et al. [15] studied that AlexNet model is performing perfectly well on a brain tumor dataset with accuracy of 96.10%. The same research revealed that VGG-16 detected the classification accuracy of 98.69% in the brain tumor using the MRI images.

Hybrid Approaches with RNNs that also integrates CNNs with Recurrent Neural Networks (RNNs), such as AlexNet- LSTM (71%) and VGGNet-LSTM (84%), have been studied in brain tumor classification [16].

while CNN architectures like AlexNet and VGGNet reach high accuracy, their computation demands might render them unusable in the clinical domain because of their inability to suit a clinical environment burdened with limited hardware capabilities. Also, small dataset models tend to overfit. Be- cause of this, there is a need for developing more lightweight CNN architectures or incorporating the more advanced regu- larization techniques in the field.

For a study of lightweight CNN Architectures, Ganguly, Priyam, and Akhilbaran Ghosh [17] introduce a novel lightweight CNN model using separable convolutions and global average pooling that reaches a validation accuracy of 99.22% and a test accuracy of 98.44% in brain tumor classification.

Regularization Techniques, Dropout, weight decay or early stopping are some of the regularization methods to prevent overfitting in CNN models on the grounds of limited data in medical imaging.

Traditionally, Recurrent Neural Networks (RNNs) have been applied to time series data and are thus well suited to analysis of sequential brain imaging data, where they can continue to track changes in MRI scans over time. Traditional CNNs process frames independently, whereas RNNs preserve the frame history in some kind of a memory token, allowing to use the frame history to capture temporal dependencies. In this regard, RNNs are very useful for such time monitoring tasks, such as following the progression of gliomas, or determining whether there are slight changes in brain tissue from treatment [18].

There has also been some promise in integrating RNN with CNN to improve tumor detection. For instance, in studies that involve analyzing MRI sequence with CNNs can deal with the spatial feature of the images and the pool of RNNs can capture temporal relationship between successive frames [19]. This hybrid approach has resulted with enhanced diag- nostic accuracy, specifically in longitudinal studies where a patient is imaged multiple times for tracking tumor growth.

However the use of RNNs for brain tumor detection is not mature yet. However, annotated time-series datasets for training RNN models are still highly scarce [20]. In

addition, RNNs are computationally expensive and may fail to handle extremely large datasets like in medical imaging [12].

Principal Component Analysis (PCA) is a widely used tech- nique for dimensionality reduction, particularly in the context of medical image processing. PCA projects high dimensional data into a smaller dimensional subspace to obtain the most relevant features with discarding of noise and redundant fea- tures. Medical imaging is a crucial application since the data can be large and noisy, masking important features [21]. It has been proved that integrating Principal Component Anal- ysis (PCA) with Convolutional Neural Networks (CNNs) can improve detection of brain tumors' classification accuracy by improving feature selection and reducing the computational complexity. Shoaib, Mohamed R., et al. [22] showed that by combining PCA with each of the pre trained CNN models (DenseNet201, EfficientNetB5, InceptionResNetV2), 100% accuracy can be reached on one data set and 98% on another, demonstrating that this is an effective integration. Moreover, PCA has been reported to improve the processing time and the accuracy of classifications by employing it to reduce image dimensionality prior to feeding the MRI images to CNNs, indicating that PCA and CNN are complementary in the medical image analysis [23]. PCA has been used for denoising purpose in medical images, where it is a necessary step to prevent missing tumors in the presence of irrelevant features [24]. PCA is a good dimensionality reduction tool, but it must be tuned very well so that beneficial features are not chopped away. By reducing dimensions too much, critical information will be lost, while reducing too little can lead to larger computation. The performance of PCA when used in models can be improved with a more adaptive approach, perhaps use of machine learning techniques to dynamically select number of principal components [21].

Finally, a great progress is made in deep learning and machine learning approaches for brain tumor detection; how-ever, some challenges are still remain. On the other hand, promising results are shown by models like CNNs, CapsNets, and ViTs, but they need to be improved in the sense that they are too computationally inefficient. also, they have low generalization capabilities on various patient populations and they depend on very large annotated datasets. In addition, hybrid models that utilize CNNs along with RNNs and PCA have exhibited the potential to enhance tumor detection. These models can only be practically used in clinical settings if challenges such as availability of data and computational resources can be tackled. Further advancement of automated brain tumor detection will need the continued development of more efficient models, more adequate regularization tech- niques, and further advancement of methods of adaptive dimensionality reduction.

PROPOSED METHODOLOGY

Dataset Description for Brain Tumor Detection

The brain tumor detection dataset that we are using in this research is a mixture of three renowned datasets namely Figshare [25], SARTAJ [26] and Br35H [27]. It contains 7,023 human brain MRI images grouped into four different classes: glioma, meningioma, no tumor, pituitary. The images that would be used for training machine learning models were carefully curated to ensure that they were of the best quality and accuracy. The following provides a breakdown of the source and class distribution of the dataset:

Figshare Dataset

The Figshare dataset is a publicly available database of MRI images that includes images having different classes of brain tumor. To study the image classes like glioma, meningioma, and pituitary tumor, we use the images of this dataset. This dataset is central to the current compilation, given images of high quality and the relatedness to the task.

SARTAJ Dataset

We are using SARTAJ dataset images for the meningioma and pituatary classes only to add diversity and enhance the size of the dataset for brain tumor detection and classification purpose.

Br35H Dataset

Non tumor class images of the current dataset are obtained from the Br35H dataset. They are well labeled images and serve as a strong basis for training the model to identify whether the given brain MRI image is of tumor or non tumor.

Data Preprocessing

Several preprocessing steps are implemented to prepare the data before training a CNN model on that data. There are 3 steps, image resizing, normalization, and label encoding.

Figure 1

Multiple classes of brain tumor

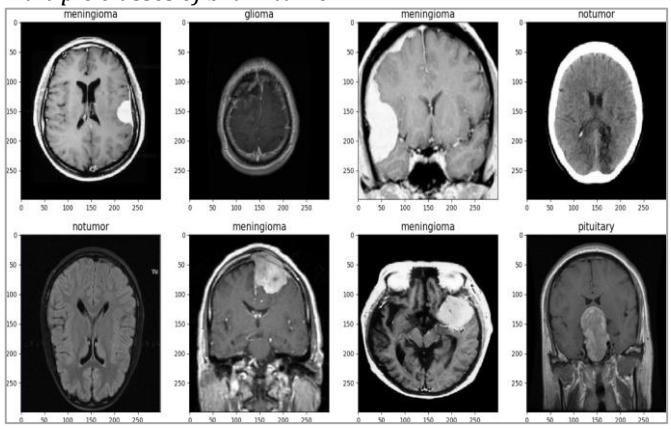


Image Resizing

Resizing serves the purpose of having all the images at the same size and all input dimensions to a CNN are fixed, hence resizing is critical for feeding the images into our neural network. The images have been resized to fixed dimension of 224x224 by using resizing function in the image processing libraries. This is imperative since CNNs necessitate inputs of the same size.

Normalization

Normalizing helps for faster convergence, and prevents an input value to be too large for the learning process. The standardization of features makes the training of the model more stable. The pixel values of the images are

normalized in the range of 0 to 1 by division by 255 (the pixel values lie between 0 to 255). To perform this, a normalization function is used within the preprocessing pipeline.

Encoding Labels

It defines the use of Label encoder to encode the categorical labels into a numeric form. For instance, in the dataset, glioma is encoded as 0, meningioma is encoded as 1, no tumor as 2, and pituitary as 3. The reason why this is done is that the class labels of the CNN models should be used as inputs to the loss function which expects numeric labels.

Data Augmentation

Data augmentation is a technique which artificially increases the training dataset by applying random transformations to images that help make the model more robust to changes in the input data. The following augmentations are applied before training CNN model.

Rotation

The images are randomly rotated in the range of of the specified angle from −30 to +30 degrees. This can be done with ImageDataGenerator for preprocessing. Tumors in MRI scans may occur at different angles. The model will learn features despite the tumors being set any way in the image.

Width and Height Shift

The images are subjected to random horizontal and vertical shifts, thus it makes the model to learn from slightly trans- lated versions of the same image. If the brain tumor has an appearance at different locations in the MRI scan. The shifting of the image helps the model learn spatially invariant features that enable the model to detect tumors, not based on the spatial location of the tumor.

Zoom

Random zoom is used on the images so that the model could observe the tumors at different scales. Tumors can be any size, depending on the stage and type of tumor. The model is used to detect tumors of different sizes by changing the scale of input image in the training.

Flipping (Horizontal Flip)

The images are randomly flipped horizontally to simulate variations to the inputs. Tumors can occur on the left or right side of the brain, and flipping helps the model to detect tumors on either side.

Train-test Split

The model is trained using the training set, and the testing set establishes how well the model generalizes. If there is no properly defined test set, it could lead for the model to overfit the training data and thus inadequately perform on unseen new data. The dataset has an 80–20 ratio of train set and testing set. Both sets should have similar number of images in each class (glioma, meningioma, pituitary, and no tumor). The goal is to make sure that this model generalizes well on new, unseen data.

CNN Model Architecture

In our proposed methodology, we first train a multi layer CNN for the classification of brain tumor in one of four classes. The optimizer plays the role of updating the weights when training. Adam optimizer is used to computes adaptive learning rates for each parameter, and it is composed of two other extensions of the stochastic gradient descend (SGD), namely AdaGrad and RMSProp. A brief detail of training processes and their respective details is presented in Table 1.

Use of LSTM In the Brain tumor classification

Recurrent Neural Networks (RNN) that are specialized to process a sequence of data are known as Long Short-Term Memory (LSTM). Temporal dependencies and sequences, in which the past information is needed to predict the future outcome, are very suitable for LSTMs. In this case, however, the role of LSTM is hidden since we are working with the image data MRI scans. A few of the aspects that shows its usefulness will be discussed in this context:

Sequential Feature Processing

The major idea of using LSTM in this situation is to consider MRI images as sequences. For example, The sequence of images comprised in a 3D MRI scan can be viewed as a sequence of images, with each image representing a slice of a particular part of the brain. A spatial temporal sequence is formed out of these slices. Such sequential slices can be processed by LSTM in order to capture spatial dependencies among the slices. It learns how to make use of changes in the features extracted by VGG19 from one slice to the next, i.e., it learns how to make use of temporal or sequential relations of these features.

When we have several MRI slices of a brain tumor then us- ing LSTM enables the model to learn how features of a tumor change between slices or time and this can potentially result in better classification performance by adding a sequential aspect to the image features.

Sequential Feature extraction and representation

VGG19 is used to extract features from individual MRI images, which is then passed to LSTM. These features are normally 2D (e.g., vectors of pixel activations), but may fail to capture the sequence in the data.

LSTM learns the temporal dynamics between slices, see- ing how information propagated from one slice to the other, This is achieved by treating the MRI slices as a sequence. The idea is to enrich the brain tumor classification by adding a temporal dimension to it, whereby the network shall try to capture how the shape, position, and size of the tumor evolve across the slices. It's useful to use LSTM here if the spatial structure of the brain tumor changes drastically across slices, or if you are reading in a video like sequence of MRI scans in time e.g. many MRI scans at different time intervals.

Basically, the temporal aspect, how features change across each slice is captured by LSTM, so that the model can understand how to use features extracted by VGG19 from respective slices in order to improve prediction.

Use of Principal Component Analysis (Pca)

PCA is frequently applied as a dimensionality reduction algorithm which selects a subset of features to uphold maxi- mum data variance. When VGG19 derives features from MRI images the outcome creates an extensive dimensional space where you obtain various image characteristics through large vectors. Feature vectors

consist of mostly unused dimensions that carry repetitive values. PCA analysis reduces the number of features by transforming them into a smaller space which preserves the primary data information. The feature reduction technology accelerates learning while preventing memory exploration problems which enables models to concentrate on essential characteristics. The high-dimensional features that VGG19 extracts from brain tumors need to undergo dimension reduction through PCA because noisy or unessen- tial information might negatively impact the following SVM classifier results. PCA functions to identify important fea- tures which leads to an improved performance of the clas- sifier model.

PCA benefits data analysis by maintaining the complete most essential data variability while keeping the features which represent fundamental class differences. The vital informa- tion which helps tumor classification such as its shape or texture stays present within the dataset post-dimensionality reduction. PCA reduces the data dimensions by using prin- cipal components with greatest variance so the information remains useful for tumor classification.

Support Vector Machine (SVM) As Final Classifier

In our proposed methodology, Support Vector Machine (SVM) is used as the final classification layer after the feature extraction using VGG19 and sequential modeling via LSTM. SVM is a supervised machine learning algorithm and its operation is mainly for classification. The idea behind it is to find this optimal hyperplane or decision boundary that sepa- rates data points of other classes in a high dimensional feature space. The main underlying idea is to find support vectors, that is, the data points closest to the decision boundary and maximize the margin between the classes.

SVM is one of the advantages when it comes to working with high dimensional feature spaces, thereby this can be an ad- vantage in working with features extracted from deep neural network, such as VGG19. As PCA dimensionality reduction is performed prior to feeding the data into SVM, it prevents the latter one from taking into account irrelevant information and hence performs both efficiency and reduction of the risk of overfitting.

VGG 19 extracts a high-dimensional features i.e. high dimen- sional vectors of different characteristics of MRI images and SVM is highly effective in such spaces. SVM can effectively perform even when the decision boundary is not linear, and this ability is due to the kernel trick in SVM that enables it to work well even on non linear decision boundaries, which can be especially useful in image classification tasks that are complex,and there may be no linear separability in the raw feature space.

The feature space dimension is reduced using Principal Com- ponent Analysis (PCA). Deep learning models, like CNNs, can learn directly from raw data e.g. pixels in an image, but can be computationally expensive, or more expensive, as what we face in high dimensional feature spaces. PCA enables a manageable number of features for the use of SVM classifier. This is because the SVM can perform bet- ter by concentrating only on the most important principal components since it does not over fit to large feature spaces. Compared to more complex models such as CNNs, SVMs are quite simpler in terms of architecture and training. With the model trained, it is easier to interpret the decision boundary created by the model which was directly connected to the support vectors and the margin. The interpretability of this model can be helpful in medical situations in which it is vital to comprehend why the model came to a certain decision to predict the presence of tumor.

Table 1

Model Training Details

Process	Details
Training Process	The model is trained on the training dataset in batches. The model learns to minimize the loss function over multiple epochs.
Loss Function	**Categorical Cross-Entropy** (for multi-class classification) Measures the difference between predicted labels and actual labels.
Optimizer	**Adam Optimizer**: Computes adaptive learning rates for each parameter. It combines advantages of AdaGrad and RMSProp.
Hyperparameters	Key hyperparameters include: - **Learning rate** - **Batch size** - **Number of epochs** These are adjusted to optimize the model's performance.
Overfitting Prevention	- **Early Stopping**: Monitoring the validation set to stop training when performance degrades. **Dropout**: Randomly dropping neurons to prevent overfitting.

Model Evaluation

After training, the model's performance is evaluated on the test dataset Figure 3, which is separate from both the training and validation datasets. Evaluation typically involves calcu- lating:

Figure 2

Classification results of brain tumor using RNN based LSTM model with PCA and VGG19

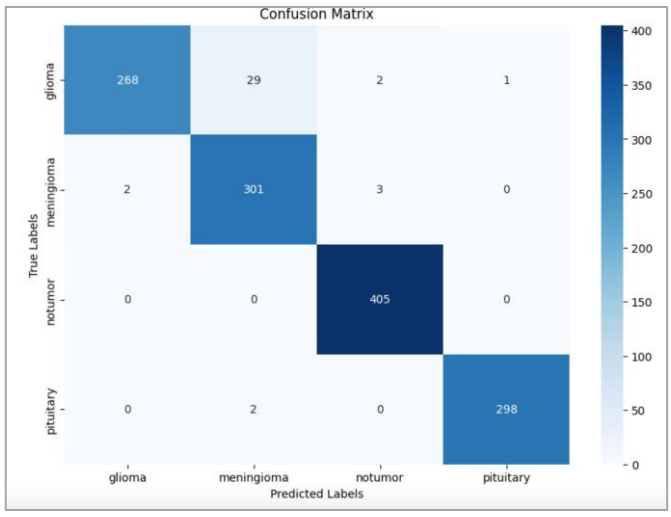


Table 2

Classification results of brain tumor using RNN based LSTM model with PCA and VGG19

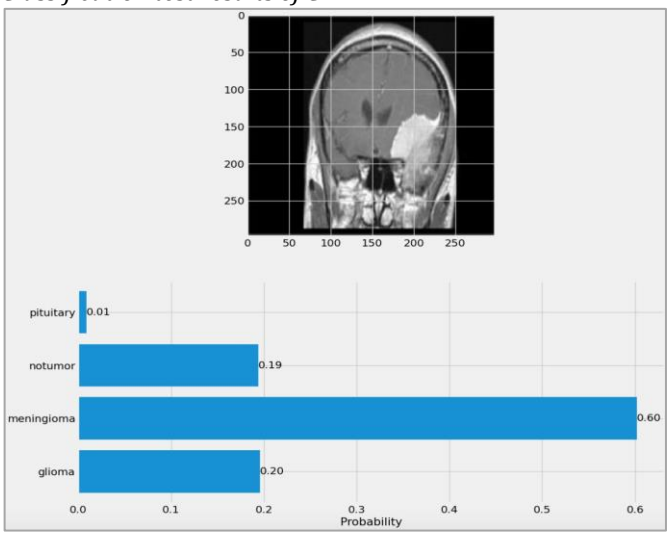
	precision	recall	f1-score
glioma	0.99	0.89	0.94
meningioma	0.91	0.98	0.94
notumor	0.99	1.00	0.99
pituitary	1.00	0.99	0.99
accuracy	0.97		

macro avg	0.97	0.97	0.97
weighted avg	0.97	0.97	0.97

Accuracy
The percentage of correct predictions out of the total predic- tions.

Precision
The ratio of correctly predicted positive observations to the total predicted positives.

Figure 3
Classification test results of CNN



Recall
The ratio of correctly predicted positive observations to the all observations in actual class.

F1-score
The weighted average of precision and recall, which is useful when dealing with imbalanced datasets.
These metrics will give you insights into how well your model performs across all the classes and helps you understand if the model is biased towards any class.

EXPERIMENTATION AND RESULTS

CNN Based Model Results Discussion

Training and validation metrics results as shown in Figure 4 over 10 epochs give the insights of the CNN model perfor- mance. First, both training loss and validation loss decrease steadily and validation loss reaches its minimum at epoch 7, which is the moment of the best generalization. In addition, training accuracy, precision, and recall keep going up during the epochs, as well as validation accuracy, precision, and recall which reach the maximum at epoch 5. This implies that the model does not generalize well to the validation set even at the point of lowest validation loss at epoch 5. From epoch 5 onwards, we can clearly see the divergence of the training vs validation metrics, with the training metrics being better than the validation ones, which means the ability to generalize is getting worse. Such results emphasize the need for monitoring during the training very carefully, and when used in conjunction with techniques like early stopping or dropout, they can help in mitigating overfitting and improv- ing the model's generalizability over unseen data.

LSTM-Based SVM Model Results Discussion

The result in the classification confusion matrix 2 and in Table 2 of LSTM based SVM classifier are outstanding. The performance of different class such as glioma, meningioma, notumor and pituitary is really good, that is they have very high precision, recall, and F1-score. For example, 0.99 for notumor and 0.94 for pituitary and 0.91 for meningioma. With a macro average accuracy of 97% and a 95% of ac- curacy for each of the classes, the model performs equally across all classes. The model is extremely good at identifying the instances of these classes high recall value, especially for notumor. We observe high F1-scores across all classes as the model is well balanced between precision and recall, which means it does not wrongly identify positives false positives and false negatives. The accuracy and classification report of the model shows that the LSTM based SVM approach can easily process multiple classes and has good generalization power over the unseen data.

In the CNN-based model, training accuracy tends to be higher than validation accuracy, and overfitting can be observed where the model performs well on training data but struggles to generalize to the validation set. In contrast, the LSTM-based SVM model demonstrates better generalization, as indicated by the close alignment between training and validation accuracy, and the lack of overfitting despite high accuracy.

The LSTM and PCA based SVM model has a stable training and validation loss as well as high precision, recall, and an F1 score for all classes and outperforms the traditional CNN model. While LSTM is better at sequential modeling and SVM for the classification, the combination of LSTM for sequential modeling and SVM for classification will give us a more robust and stable approach to the brain tumor classification. Not only does this model perform quite well, but it also generalizes very well to the unseen data, while most other CNNs tend to overfit when data is in short supply. From the above findings, it can be concluded that this LSTM-based SVM model generalizes better and is capable of handling complex data better, compared to a CNN model, which makes it a good choice compared to a CNN model for medical image classification tasks wherein both high accuracy and reliable generalization are significant.

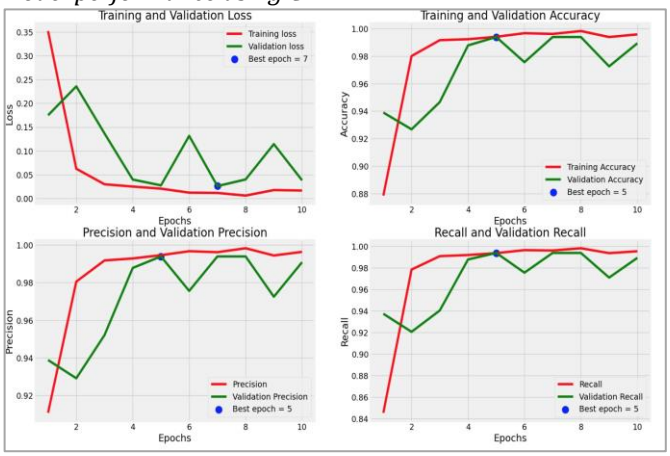
CONCLUSION

In this paper, we propose an original approach of brain tumor classification that combines LSTM for sequencing, SVM for classification and VGG19 for feature extraction along with PCA for dimensionality reduction. A major feature of this study is combining three brain MRI datasets that can be trained on a wide range of MRI scans and increase its generalization power in multiple tapes of MRI scans. The model outperforms traditional CNN based models in terms of generalization, stable and equal train and validation accuracy and minimal loss value fluctuations. We have the LSTM component accounting for temporal dependencies between the multiple slices of an MRI, and SVM and PCA help reduce the feature space and aid performance as well as avoiding overfitting. The model achieves 97% accuracy with robust precision, recall and F1 scores across all tumor types and is ready to be deployed in clinical application. Using multiple datasets

and features of deep learning and machine learn- ing techniques, this approach offers a reliable and scalable solution to brain tumor classification. Another direction to explore in future work to improve the model's performance and to conduct a more extensive evaluation includes work- ing with additional datasets and utilizing more sophisticated regularization techniques.

Figure 4

Model performance using CNN



Future Direction

In the current methodology, VGG19 is used as feature extraction model. Although VGG19 is a strong pre trained model, a newer architecture such as ResNet (Residual Networks) or DenseNet (Densely Connected Networks) may provide feature representations of deeper layers and with stronger connected forms and therefore be better suited to the task of representing brain tumor MRI scans. Such architectures can be fine tuned so as to extract better features and hence perform better in classification. LSTM is quite effective for sequential data processing, while CNNs have been perform- ing exceptionally well in extracting the spatial features. The future work may combine a CNN directly with LSTM, using CNNs to extract spatial feature from an individual slice and then send the feature into LSTM to learn the temporal dependency across multiple slices. It could take advantage of both spatial and sequential patterns in the MRI scans. These other types of medical imaging such as CT scans or PET scans are often used in combination with MRI scans to give an overall look at brain tumors. Combining features from different modalities enables fusion of multimodal data which would provide further richer information to accurately classify the future models.

REFERENCES

1. American Cancer Society. (2025). *Cancer Facts & Figures 2025*. Cancer.org. https://www.cancer.org/research/cancer-facts-statistics/all-cancer-facts-figures/2025-cancer-facts-figures.html
2. Khalighi, S., Reddy, K., Midya, A., Pandav, K. B., Madabhushi, A., & Abedalthagafi, M. (2024). Artificial intelligence in neuro-oncology: Advances and challenges in brain tumor diagnosis, prognosis, and precision treatment. *npj Precision Oncology*, *8*(1). https://doi.org/10.1038/s41698-024-00575-0
3. Zhang, L., Wen, X., Li, J., Jiang, X., Yang, X., & Li, M. (2023). Diagnostic error and bias in the Department of radiology: A pictorial essay. *Insights into Imaging*, *14*(1). https://doi.org/10.1186/s13244-023-01521-7
4. Batool, A., & Byun, Y. (2024). Brain tumor detection with integrating traditional and computational intelligence approaches across diverse imaging modalities - Challenges and future directions. *Computers in Biology and Medicine*, *175*, 108412. https://doi.org/10.1016/j.compbiomed.2024.108412
5. Lotlikar, V. S., Satpute, N., & Gupta, A. (2022). Brain tumor detection using machine learning and deep learning: AReview. *Current Medical Imaging Formerly Current Medical Imaging Reviews*, *18*(6), 604-622. https://doi.org/10.2174/1573405617666210923144739
6. Seetha, J., & Raja, S. S. (2018). Brain tumor classification using Convolutional neural networks. *Biomedical and Pharmacology Journal*, *11*(3), 1457-1461. https://doi.org/10.13005/bpj/1511
7. Vankdothu, R., & Hameed, M. A. (2022). Brain tumor MRI images identification and classification based on the recurrent convolutional neural network. *Measurement: Sensors*, *24*, 100412. https://doi.org/10.1016/j.measen.2022.100412
8. Jhariya, A., Parekh, D., Lobo, J., Bongale, A., Jayaswal, R., Kadam, P., Patil, S., & Choudhury, T. (2024). Distance analysis and dimensionality reduction using PCA on brain tumour MRI scans. *EAI Endorsed Transactions on Pervasive Health and Technology*, *10*. https://doi.org/10.4108/eetpht.10.5632
9. Akinyelu, A. A., Zaccagna, F., Grist, J. T., Castelli, M., & Rundo, L. (2022). Brain tumor diagnosis using machine learning, Convolutional neural networks, capsule neural networks and vision transformers, applied to MRI: A survey. *Journal of Imaging*, *8*(8), 205. https://doi.org/10.3390/jimaging8080205
10. Khan, M. S., Rahman, A., Debnath, T., Karim, M. R., Nasir, M. K., Band, S. S., Mosavi, A., & Dehzangi, I. (2022). Accurate brain tumor detection using deep convolutional neural network. *Computational and Structural Biotechnology Journal*, *20*, 4733-4745. https://doi.org/10.1016/j.csbj.2022.08.039
11. Hinton, G. E., Sabour, S., & Frosst, N. (2018, February). Matrix capsules with EM routing. In *International conference on learning representations*. https://openreview.net/forum?id=HJWLfGWRb&
12. G. Nagaraju. (2024). A comparative analysis of advanced machine learning techniques for enhancing brain tumor detection. *Journal of Electrical Systems*, *20*(2s), 901-909. https://doi.org/10.52783/jes.1687
13. Poornam, S., & Angelina, J. J. (2024). VITALT: A robust and efficient brain tumor detection system using vision transformer with attention and linear transformation. *Neural Computing and Applications*, *36*(12), 6403-6419. https://doi.org/10.1007/s00521-023-09306-1
14. Willemink, M. J., Roth, H. R., & Sandfort, V. (2022). Toward foundational deep learning models for medical imaging in the new era of transformer networks. *Radiology: Artificial Intelligence*, *4*(6). https://doi.org/10.1148/ryai.210284
15. Ton Komar Azaharan, T. A., Mahamad, A. K., Saon, S., Muladi, & Mudjanarko, S. W. (2023). Investigation of VGG-16, resnet-50 and AlexNet performance for brain tumor

detection. *International Journal of Online and Biomedical Engineering (iJOE)*, *19*(08), 97-109. https://doi.org/10.3991/ijoe.v19i08.38619
16. Çinar, A., & Yildirim, M. (2020). Detection of tumors on brain MRI images using the hybrid convolutional neural network architecture. *Medical Hypotheses*, *139*, 109684. https://doi.org/10.1016/j.mehy.2020.109684
17. Ganguly, P., & Ghosh, A. (2024). Efficient brain tumor classification with lightweight CNN architecture: A novel approach. *2024 IEEE International Conference on Future Machine Learning and Data Science (FMLDS)*, 325-330. https://doi.org/10.1109/fmlds63805.2024.00065
18. Lin, K., Jie, B., Dong, P., Ding, X., Bian, W., & Liu, M. (2022). Convolutional recurrent neural network for dynamic functional MRI analysis and brain disease identification. *Frontiers in Neuroscience*, *16*. https://doi.org/10.3389/fnins.2022.933660
19. Jha, A., Singh, O., Singh, K. K., Akbari, A. S., & Takei, M. (2024). An integrated CNN-RNN-SVM framework for classification of MRI brain tumor images. *2024 IEEE International Conference on Imaging Systems and Techniques (IST)*, 1-6. https://doi.org/10.1109/ist63414.2024.10759212
20. Yang, X., Qi, X., & Zhou, X. (2023). Deep learning technologies for time series anomaly detection in healthcare: A review. *IEEE Access*, *11*, 117788-117799. https://doi.org/10.1109/access.2023.3325896
21. Nandi, D., Ashour, A. S., Samanta, S., Chakraborty, S., Salem, M. A., & Dey, N. (2015). Principal component analysis in medical image processing: A study. *International Journal of Image Mining*, *1*(1), 65. https://doi.org/10.1504/ijim.2015.070024
22. Shoaib, M. R., Zhao, J., Emara, H. M., Mubarak, A. S., Omer, O. A., Abd El-Samie, F. E., & Esmaiel, H. (2025). Improving brain tumor classification: An approach integrating pre-trained CNN models and machine learning algorithms. *Heliyon*, *11*(10), e33471. https://doi.org/10.1016/j.heliyon.2024.e33471
23. Gunasundari, C., & Selva Bhuvaneswari, K. (2025). A novel approach for the detection of brain tumor and its classification via independent component analysis. *Scientific Reports*, *15*(1). https://doi.org/10.1038/s41598-025-87934-4
24. Zhang, L., Dong, W., Zhang, D., & Shi, G. (2010). Two-stage image denoising by principal component analysis with local pixel grouping. *Pattern Recognition*, *43*(4), 1531-1549. https://doi.org/10.1016/j.patcog.2009.09.023
25. Sartaj. (2024). *Brain Tumor Classification (MRI)*. Kaggle.com. https://www.kaggle.com/dsv/1183165
26. Ahmed Hamada. Br35h: Brain tumor detection 2020. https://www.kaggle.com/datasets/ahmedhamada0/brain-tumordetection,