

Brain Tumor Segmentation Using the Hybrid CNN & LSTM Model

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Abstract— The present study offers a convolutional neural network (CNN) architecture with tumor segmentation using a hybrid CNN & LSTM model. The study makes use of a split dataset, where the training data is utilized for the training test information is utilized for model assessment of methods after preliminary processing. Utilizing the training dataset, together with additional models based on Gaussian Naive Bayes, Random Forest, and Logistic Regression, the proposed hybrids CNN & LSTM model was trained. These additional models—Gaussian Naive Bayes, Random Forest, and Logistic Regression serve as benchmarks for comparing and assessing the efficacy of the proposed hybrids CNN & LSTM model applying a variety of performance metrics. The F1score of 97.66%, accuracy of 98.4%, precision of 96.34%, recall of 97.9% & recall of 97.9% are impressive findings that show the efficiency of the suggested hybrid CNN & LSTM approach. These results surpass the performance of previous models, highlighting the effectiveness of the hybrid CNN & LSTM architecture considering tumor segmentation. Additionally, a VGG UNet architecture is employed for segmentation purposes, enhancing the accuracy of the segmentation process.

Keywords: Hybrid CNN & LSTM, Tumor Segmentation, Logistic Regression, Random Forest & Gaussian Naive Bayes, VGG UNet.

I. INTRODUCTION

Because of its unpredictable character, cancer continues to be a social disease despite advances in biology and human knowledge over the last several decades having triumphed over other illnesses. Malignant brain tumors are among the deadliest and fastest-growing medical conditions. Largest and most intricate organ in the human body is the brain. Among the many processes governed by the nervous system are breathing, muscle contraction, and sensory perception[1]. Each cell is different, capable of growing in many ways depending on the circumstances. Some cells develop normally, expand beyond their potential, or resist. Generous aggregates of atypical cells that constitute tissue are known as tumors. Aberrant and uncontrolled brain cell development is the cause of cancerous brain tumors. Among the most deadly and deadly cancers is this one[2].

Over the years, there has been a substantial advancement in the processes for assessing tumors. Though regrettably, we do not yet have the means to treat brain tumors, we are moving closer to our goal thanks to our diagnostic technologies. Brain tumors may be detected and treated in conjunction with magnetic resonance imaging (MRI). Since brain tumors may be

easily identified by these pictures, we employ MRI scans for high-quality imaging. They help detect and locate tumor components more rapidly. All processes are currently dependent on individuals' interpretation, which might lead to inaccurate results. When these tumors are still small, it might be difficult to find them sooner. Medical professionals cannot get accurate findings from imaging procedures like CT and MRI[3].

As a result, they will wait and carry out the imaging process again. If someone predicts incorrectly there isn't a tumor there, the tumor will grow and pose a threat to their lives. Compared to conventional techniques, machine-based identification and evaluation could be simpler and more lucid [4]. Tumors that were not present when the item was registered may be addressed using tumor-growth modelling. For this, two different models of tumor formation were investigated. Even though a limited tumor development model calculated more rapidly, More comprehensive tumor-growing models has shown a greater ability to provide deeper and distinctive separation [5]. The two techniques are now part of a unified framework for evaluating brain images with tumors that typically uses all available imaging data in lab settings [6]. Based on latest studies regarding to identification & segmentation currently, there's a brain tumor no universally adaptable approach for identifying cancers that is not dependent on the location, type, [7]. Many algorithms for classifying brain tumors and extracting features have been reported in recent study. GLCMs, or grey-level co-occurrence matrices, are often used in low-level feature extraction [8]. In an attempt to address the complex texture of a brain tumor, further feature extraction approaches include Bag-of-Words (Bow), Fisher Vector, & Neural Network [9].

A new research found that the three forms of brain cancers that may be identified with an accuracy range from 71.39 to 94.68% by combining the fisher vector approach with efficient site pooling include meningioma, pituitary astrocytoma, and glioma[10]. With the help of this segmentation system, radiation evaluation, analysis, identification, treatment planning, and monitoring may be enhanced[11].

II. RELATED WORK

[12] The idea is to use MRI imaging to include a new, fully automated technique that would segregate the whole cerebral venous system based on anatomical, morphological, and relaxometry data. Utilizing brain, the use of magnetic resonance imaging numerical findings indicate the effectiveness Among

the suggested approach with an accuracy of around 98.51% at differentiating between ill and normal tissue. [13] The study's authors suggest a proprietary Mask RCNN, a densenet-41 core-based convolutional neural network based on regions, has been precisely taught via transferable knowledge to separate and classify brain tumors. With division & categorization accuracy of 96.3% & 98.34%, respectively, the suggested model outperformed the most advanced techniques in terms of resilience. [14] Within the selected MR image collection, meningioma, pituitary, and glioma are the three primary forms of brain tumors. The Hybrid CNN & LSTM architecture serves as the foundation for each of the classifier network and the region recommendation network in the proposed methodology. An average of 75.18%, 89.45%, and 68.18% for meningiomas, gliomas, and pituitary tumors were found to be detected by the algorithm throughout its detection and classification phases. Performance-wise, the algorithm performed with a mean average accuracy of 77.60% across all classes.

[15] 3064 T1 graded Brain MR pictures improved by contrast were graded (classified) into 3 categories (meningioma, pituitary tumor, and glioma) applying Convolutional Neural Network also known as CNN is a commonly used neural network architecture. With sensitivity accuracy 98.18% and 98.93% to trimmed tumours, 99% & for uncropped lesions, 98.52%; for segmented lesion images, 97.62% and 97.40%, the suggested CNN classifier is an all-around strong tool. [16] highlighted three studies that used VGGNet-based convolutional neural networks, Random Forest & Gaussian Naive Bayes, using Logistic Regression to detect brain cancers, including pituitary, glioma, and meningioma. As stated by the proposed study, the optimized hybrid CNN & LSTM architecture had the highest classification & detection accuracy (98.69). [17] In contrast to conventional techniques that depend on trial and error, this strategy uses GA to update CNN architecture. by following pre-existing frameworks. Additionally, one ensemble strategy to reduce the volatility of the prediction error is the bagging procedure the best model produced by the GA. 3 Glioma grades were identified with 90.9% accuracy in a case study. According to research, the accuracy rate for classifying pituitary tumors, meningiomas, and lymphomas was 94.2%. [18] The objective is to address this problem and offer a block-wise transfers learning-based fine-tuning technique using sophisticated CNN technique using already received instruction. The CT imaging that is T1-weighted and contrast-enhanced (CE-MRI) reference collection is used to assess the suggested technique. approach is more broadly applicable since it doesn't rely on manually created characteristics, needs less preparation, and after five cross-valid phases, can achieve a median accuracy of the 94.82%. [19] detailed the process of applying a convolutional neural network (CNN) to identify cancers in brain images obtained from magnetic resonance imaging (MRI). CNN was first used to apply images. 98.67% accuracy was maintained by the Soft Max Fully Linked layer throughout the picture categorization process. Additionally, the CNN attains 94.34% accuracy when splitting using radial basis functions (RBF) and 94.24% accuracy when applying a Decision Tree (DT) classifier. [20] A study of the free tumor database was complete the demonstrate the effectiveness of the suggested CNN technique. An empirical analysis reveals that the suggested CNN achieves

a total accuracy level of 89.93% in the absence of data augmentation. The diagnosis accuracy of meningiomas, gliomas, and pituitary tumors increased to 91.81%, 91.03%, and 98.67%, respectively, when data augmentation was included. The diagnosis' overall accuracy was 93.83%.

III. BACKGROUND

In this part, background details on algorithms like CNN, Random Forest, Gaussian Naïve Bayes, and logistic regression is provided.

A. Logistic Regression

Machine learning (ML) methods such as logistic regression are not mysterious; rather, we know exactly how they operate. Higher-end variations, such an exceptionally deep neural network (DNN), are often referred to as black box models. Either 0 or 1 might be the outcome of a binomial logistic regression. We know precisely how logistic regression works, making it one of those machine learning (ML) approaches that is not mysterious. Higher-performing iterations, such an extraordinarily deep neural network (DNN), are often represented using black box models. A result of 0 or 1 may be obtained when applying binomial logistic regression. What comes next is figuring out whether a certain occurrence will provide a 1 or a 0. 1-p denotes the chance that it won't, given p is the probability of a 1. A specific kind of binomial distribution, the Bernoulli distribution, is exemplified by this. Logistic regression aims to represent the issue using an adjusted linear regression model.

$$\hat{y} = \beta_0 + \beta_1 x_1 + \dots + \beta_n x_n \quad (1)$$

The sigmoid function may appear as:

$$P = \frac{1}{1 + e^{-\hat{y}}} \quad (2)$$

From here, logistic regression may be represented by a single-layered neural network (NN) using a sigmoid activation function. Stated differently, we may estimate the weight parameters by minimizing the cross-entropy loss function provided by the standard stochastic gradient descent (SGD) technique:

$$l(p, y) = -y \log(p) - (1 - y) \log(1 - p) \quad (3)$$

where $y \in [0, 1]$

Consequently, the multinomial logistic regression's only feasible result is an increase in the layer's sigmoid neuron count. Furthermore, instead of using the logistic function as the activation function, we might use the SoftMax to keep the output as a probability distribution. In the multinomial logistic regression situation, the loss is transformed into the log likelihood loss using a SoftMax.

B. CNN

Neural networks with convolutions (CNNs) are most prevalent popular kind of Artificial Neural Network (ANN) utilized by profound understanding methods for analyzing visual images. An alternative moniker for it is a convolutional neural network (CNN). Convolution neural networks have three layers: layer of input, layer of hidden layer, and layer of final output. Given that their sources and products are concealed in

to the final convolution & activating function, the intermediate levels of a feed-forward neural network are also known as hidden layers. Within a convolutional neural network's hidden layers are layers known as convolutional or convolution-executing layers.

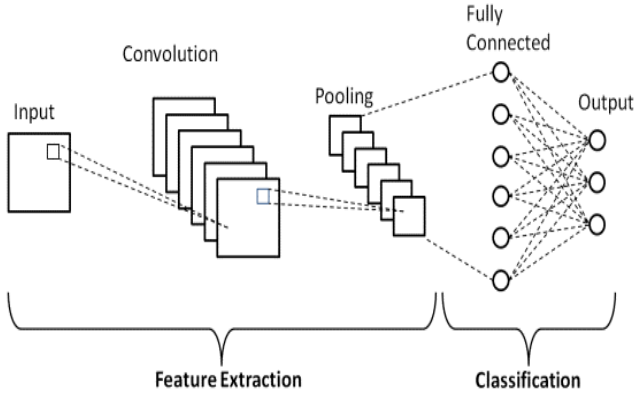


Fig. 1. CNN Architecture

C. Random Forest

Several When Random Forests (RF) are trained, they generate unique decision trees. Putting the average forecast together with the class mode yields the final prediction for regression or classification. For this reason, ensemble techniques are named so because they utilize a variety of results to arrive at an answer. The procedure of categorizing data using random forest is as follows: Within Scikit-learn, every decision tree uses to assess a node's Gini Importance, importance, assuming there are only 2 child nodes (a binary tree):

$$im_j = wsn_j mp_j - wsn_{left(j)} mp_{left(j)} - wsn_{right(j)} mp_{right(j)} \quad (4)$$

Were

$im_j \rightarrow$ Significance of the protocol for nodes J

$wsn_j \rightarrow$ The test number was weighted and reached node

$j.mp_j \rightarrow$ an assessment of the node j's impurity level

$left(j) \rightarrow$ The kid node on the left broke from node j.

$right(j) \rightarrow$ Subsidiary junction at the intersection of junction J and the division to the right.

After that, these after criteria are used to determine each characteristic's importance on a decision tree:

$$f_i = \frac{\sum_{j: \text{node } j \text{ splits on feature } i} ni_j}{\sum_{k \in \text{all nodes}} ni_k} \quad (5)$$

f_i sub(i)= the significance of characteristic i

ni sub(j)= Node J's significance

After that, to normalize to a range of 0 to 1, The sum of all features significant values may be used to split them. Q

$$normf_i = \frac{f_i}{\sum_{j \in \text{all features}} f_j} \quad (6)$$

A characteristic's ultimate significance is determined by averaging it across every tree in the Random Forest. Each tree's total feature significance value is split by the

$$\text{overall quantity of trees: } RFf_i = \frac{\sum_{j \in \text{all trees}} normf_{ij}}{T} \quad (7)$$

RFfi sub(i)= With the use of information from each tree in the Random Forest framework, I calculated the feature's significance.

norm sub(ij)= The 3 j's accepted characteristic significance i
T = represents all among the tree.

D. Gaussian Naïve Bayes

If the continuous values associated with each class, follow a normal distribution is standard procedure when working with continuous data. This is because this kind of data analysis is more straightforward. It is believed that the traits might be

$$P(x_i | y) = \frac{1}{\sqrt{2\pi\sigma_y^2}} \exp\left(-\frac{(x_i - \mu_y)^2}{2\sigma_y^2}\right) \quad (8)$$

Occasionally, accept variance

- Does not rely on Y (i.e., σ_i),
- or apart from Xi (that is, σ_k)
- or the two (that is, σ)

IV. METHODOLOGY

A. Dataset Description

We used the website below to gather data for these studies:

<https://www.kaggle.com/datasets/leaderandpiller/brain-tumor-segmentation>. From this collection, we have selected brain tumor images for segmentation.

B. Pre-processing

The aim is to demonstrate the variation in accuracy that occurs when several popular Pre-processing techniques are utilized for simple convolutional neural networks. Several pre-processing methods are listed below.

- Read image
- Resize image-
- Remove noise

Read image: We initially created a way of loading groups combining pictures in arrays by first keeping the address of the A field containing an image collection, which allowed us to retrieve the photo.

Resize image: To make the differences visible to you at this resizing step, design two strategies for present the photos. 1 technique will show you one picture, whereas the other will show you two images. We then develop an approach that we refer to as processing, and it only accepts images as input.

Remove noise: To silence the commotion A Gaussian blur may be produced by applying the Gaussian function to an image. To lessen visual noise, this popular graphics programmed effect is often utilized. Another pre-processing method that computer vision algorithms utilize to improve visual structures at various sizes is called Gaussian smoothing.

Segmentation

Segmentation is crucial in medical imaging for tasks like tumor detection, organ delineation, and treatment planning, providing valuable information for healthcare professionals.

Segmenting brain tumor images using the VGGUnet methodology involves employing Hybrid CNN & LSTM as an encoder, integrated with a U-Net decoder. The dataset, comprising brain MRI images and corresponding tumor masks, is divided for training, validation, and testing.

The Proposed VGG-UNet is a deep learning framework that combines the benefits from the Hybrid CNN & LSTM & U-Net models [21]. Figure 1 illustrates how the Hybrid CNN & LSTM model can be a powerful feature extractor, but the U-Net model was an architecture best suited for image segmentation.

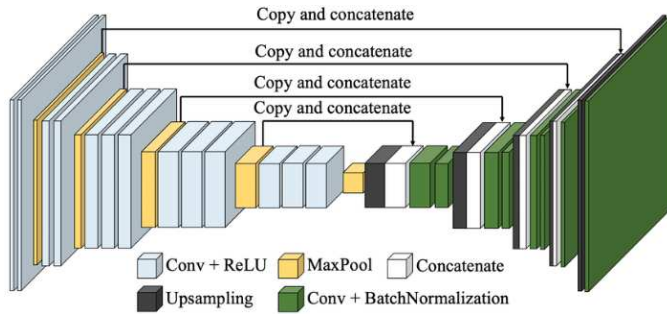


Fig. 2. Architecture of VGG-UNET

The VGG-UNet architecture's two main parts are the encoder as well as the decoder. The encoder manages the process of collecting characteristics from the input image, while the decoder generates the segmentation mask. The encoder of the proposed VGG-UNet is based on the Hybrid CNN & LSTM model. With 16 convolutional layers, the Hybrid CNN & LSTM model's maximal pooling phase comes after each of the other levels. The convolutional layers are composed of five blocks that have different numbers of filters in each block. Sized three by three, the filters in each block. For the suggested VGG-UNet decoder, the U-Net model provides the basis. What makes up the U-Net concept is a shrinking route and an increasing way. The input image must be down sampled using the contracting route, and the feature maps must be up sampled using the expanding path. The first 13 convolutional layers of the Hybrid CNN & LSTM technique make up to the contracting route of the proposed VGG-UNet. The Proposed VGG-UNet's expanding route is made up of many transposed convolutions. The feature maps are up sampled using transposed convolutions. Effectiveness for the Proposed VGG-UNet has been shown on many image segmentation tasks.

C. Train_test split

Once every step of preparation is finished, to the collection depending on a user's splitting ratio. which is also is divided in

tests and training groups. Afterwards, the models will be educated on this split train set, and the model will be assessed using the test set.

Train the network:

Training data from Random Forest, Gaussian Naive Bayes, and Logistic Regression were used to develop the suggested Hybrid CNN and LSTM models. These three methods Gaussian Naive Bayes, Random Forest, and Logistic Regression are used to compare and assess the effectiveness of the proposed model.

These One might utilize metrics. to evaluate the technique effectiveness.

D. Performance Metrics

A method's efficacy is evaluated considering the F1-score, sensitivity, accuracy, and precision of the net of misunderstanding.

Accuracy: Accuracy is the proportion of participants who, out of all subjects, had accurate identification.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (9)$$

Sensitivity: Remember sensitivity, is the proportion of exactly favorable designations that our system recognizes as headings.

$$Sensitivity = \frac{TP}{TP + FN} \quad (10)$$

Precision: To assess an outlook's accuracy, add up all of the correctly predicted events. Another name for this concept is forecast value.

$$Precision = \frac{TP}{TP + FP} \quad (11)$$

F1-Score: The F1 score is single score which includes precision and recall.

$$F1 - score = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (12)$$

Specificity : The algorithm has successfully determined the negative specificity.

$$Specificity = \frac{TN}{TN + FP} \quad (13)$$

V. RESULTS

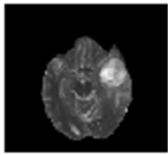
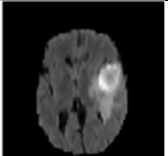
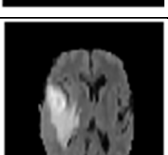
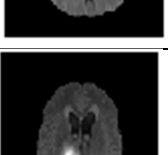
This model was created using MATLAB 2020a by utilizing image processing and deep learning toolkits

Data set:

Models are trained and assessed using data from the Kaggle Brain Tumor Data Set. Images from MRIs showing both benign and malignant tumors are used to gather data. The MRI pictures those split and improved before going to the training phase. The figure [5] illustrates the procedures used in order to segment the MRI images. These divided photos are then used to train the models. Performance measures including Specificity,

Sensitivity, and Accuracy are computed and compared with the proposed cutting edge methods for assessing the efficacy of the designs.

TABLE I. TEST IMAGES

Test images	Original	Segmented image
Test image 1		
Test image 2		
Test image 3		
Test image 4		

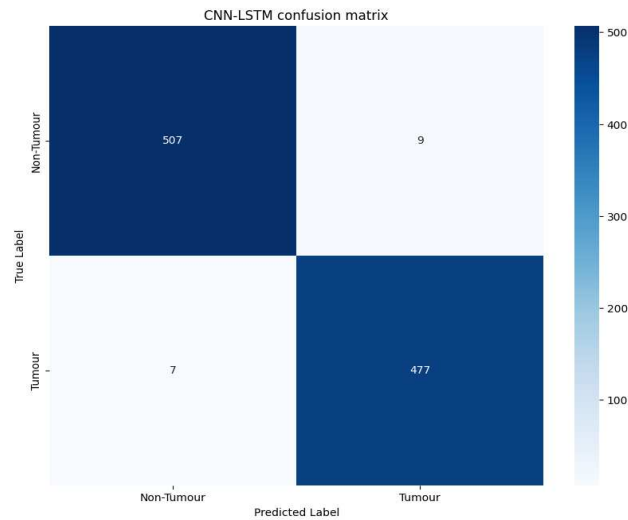


Fig. 3. Confusion Matrix of Proposed CNN-LSTM model

The above given confusion matrix for the classification task by using CNN-LSTM, Logistic Regression, Random Forest, and Gaussian Naïve Bayes shows that the rows and columns reflect the categories (Non-Tumour and Tumour). The diagonal cells of the matrix represent the number of samples that were successfully categorized. The off-diagonal cells represent the number of samples that were incorrectly categorized.

The CNN-LSTM was correctly classified as 507 non-tumour samples, while 9 misclassified. The model successfully categorized 477 tumour samples, and 7 sample was classified incorrectly. The Logistic Regression was correctly classified as 469 non-tumour samples, and 38 samples were misclassified, as well as the model correctly classified as tumour with 455 samples, while 38 samples were misclassified. The Random forest was correctly classified as 459 non-tumour samples, while 43 were classified incorrectly. And also model successfully classified as 442 tumour samples, 56 misclassifications. The Gaussian Naïve Bayes was successfully classified as 476 non tumour samples and 39 misclassifications. The model correctly classified 441 samples as tumour, while 44 samples were misclassified. The CNN-LSTM model achieves the highest accuracy of 98.4% based on overall performance. This model shows the maximum number of accurate classifications for both non-tumour and tumour samples, while demonstrating the minimum amount of misclassifications. Hence, the CNN-LSTM model demonstrates superior performance when compared to the other models.

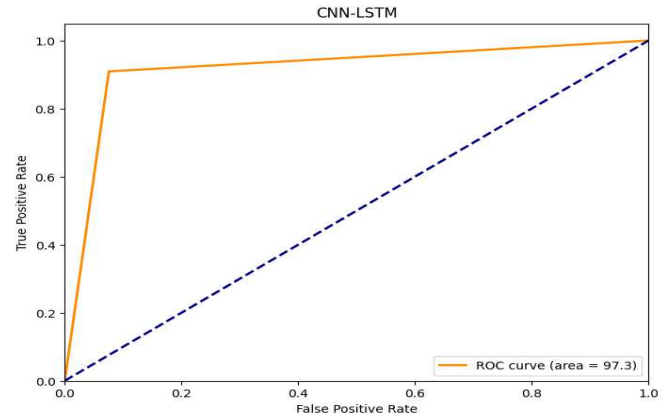


Fig. 4. ROC Curve of Proposed CNN-LSTM model

A comprehensive overview of the classification performance of the models that have been evaluated for the prediction brain tumour by the ROC curves. It is important to note that CNN-LSTM excels over the other models and has the maximum level of accuracy. A trajectory that approaches the top left corner with a high true positive rate for correctly categorized positive examples and remains close to the bottom right corner, indicating a low rate of inaccurately recognized negative instances, is depicted in the CNN- LSTM ROC curve. The Area score of the CNN-LSTM model is remarkable, surpassing that of other models such as Logistic Regression, Random Forest, and Gaussian Naïve Bayes. These are the precise area values for CNN-LSTM (Area = 0.973), & Logistic Regression (Area = 0.915), Random Forest (Area = 0.895), and Gaussian Naïve Bayes (Area = 0.90). These numerical comparisons demonstrate that CNN-LSTM performs better than other approaches.

To evaluate the effectiveness of such designs, performance metrics including Specificity, Sensitivity, and Accuracy are computed and presented as follows:

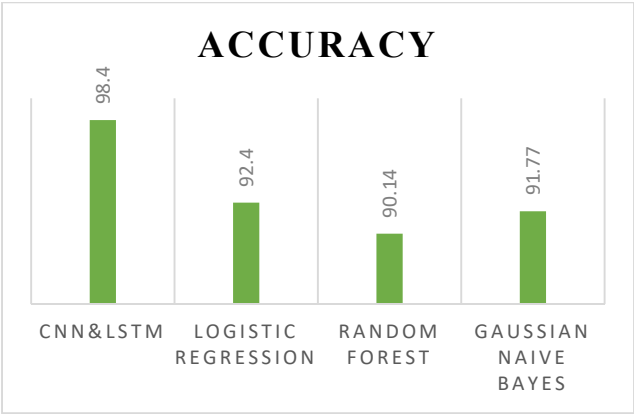


Fig. 5. Accuracy Values of Proposed and Existing Models

There is a noticeable pattern when the accuracy scores of our suggested CNN and LSTM models are compared to current models like Gaussian Naive Bayes, Random Forest & Logistic Regression. To the accuracy rate of 98.4% attained by our CNN and LSTM models is higher than that of Logistic Regression (92.4%), Random Forest (90.14%), & Gaussian Naive Bayes (91.77%). This difference indicates that our suggested models are more predictive and effective than the ones that are already their use.

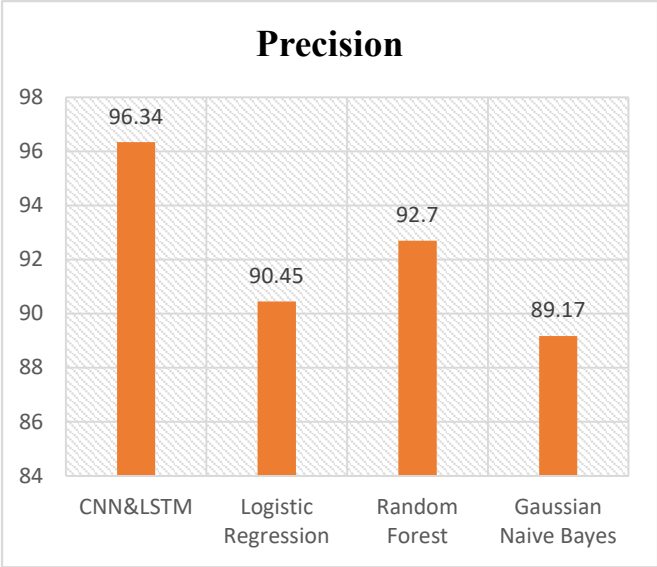


Fig. 6. Precision values of Proposed Model and Existing Models

The precision values in the comparison chart indicate that our proposed CNN and LSTM models significantly outperformed existing models like Logistic Regression, Random Forest, & Gaussian Naive Bayes. Our CNN and LSTM achieved an impressive accuracy of 96.34%, surpassing the precision of Logistic Regression (90.45%), Random Forest (92.7%), and Gaussian Naive Bayes (89.17%). This underscores the superior precision of our proposed models compared to the established ones, highlighting their effectiveness in delivering more accurate results.

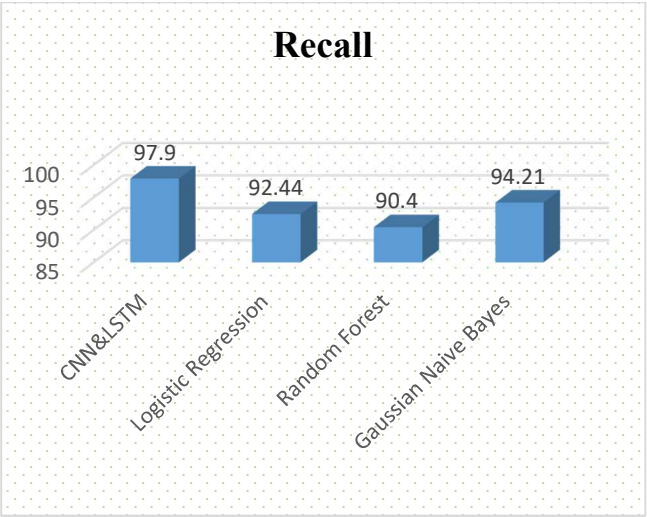


Fig. 7. Recall Values of Proposed model and Existing models

The comparison chart showcases the recall values, demonstrating that our proposed CNN and LSTM models attained superior accuracy at 97.9% compared to the recall of Logistic Regression (92.44%), Random Forest (90.4%), and Gaussian Naive Bayes (94.21%). This highlights the remarkable advantage of our suggested approaches in finding and collecting relevant events, as they exhibit higher recall rates when compared to the existing models.

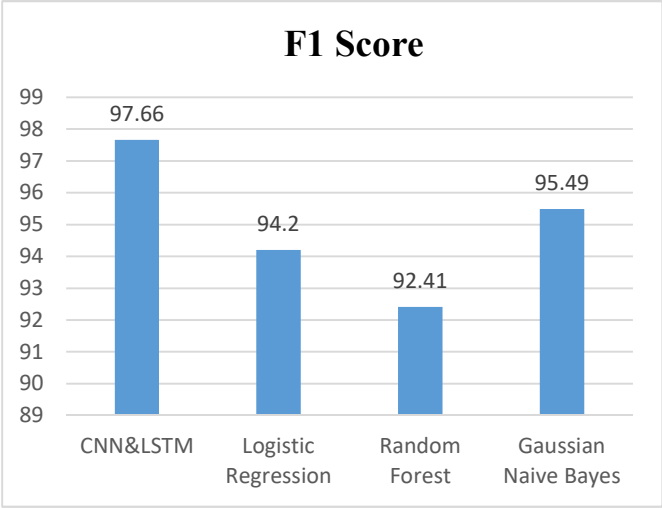


Fig. 8. F1 Score Values of Proposed Model and Existing Models

In the comparison chart, our proposed CNN and LSTM models showcased higher F1 scores, reaching an accuracy of 97.66%. This outperformed the F1 scores of Logistic Regression (94.2%), Random Forest (92.41%), and Gaussian Naive Bayes (95.49%). This indicates that our proposed models excel in achieving a balanced performance between precision and recall, resulting in a superior F1 score in contrast to the current models.

TABLE II. ARCHITECTURES AND VALUES

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 score (%)
Proposed CNN & LSTM model	98.4	96.34	97.9	97.66
Logistic Regression	92.4	90.45	92.44	94.2
Random Forest	90.14	92.7	90.4	92.41
Gaussian Naïve Bayes	91.77	89.17	94.21	95.49

VI. CONCLUSION

In in summary, this work displays the potent CNN-style methodology for tumor segmentation identification depending upon the Hybrid CNN & LSTM model. The suggested model's dependability is enhanced using a split collection for assessment and training, in addition to meticulous pre-processing. The usefulness of the Hybrid CNN & LSTM method for the analysis of medical pictures for tumor segmentation is shown by its superior performance over Logical Regression, Random Forests, and Gaussian Naive Bayes. The accuracy of 98.4% for CNN and LSTM, 96.34% for precision, 97.9% for recall, and 97.66% for F1score exceed the prior models' criteria, highlighting the importance of the suggested architecture. The incorporation of Logistic Regression, as comparison models, Random Forests & Naive Bayes Gaussian not only confirm the excellence on Hybrid CNN & LSTM but additionally provide a thorough grasp of its respective advantages and disadvantages in relation to tumor division. Additionally, the segmentation process's accuracy is increased when the VGG UNet design is used, contributing to the overall success of the proposed methodology. The outcomes of this research not only advance the field of medical image analysis but also hold promising implications for the accurate identification and delineation of tumors in clinical settings.

In future work, additional investigations could focus on optimizing the proposed model further, exploring potential enhancements or adaptations for specific types of tumors or diverse medical imaging modalities. Additionally, the integration of advanced techniques such as transfer learning or ensemble methods may offer avenues for continued improvement in performance and generalization across varied datasets.

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