Classification of Brain Tumors using Fuzzy C-means and VGG16

V Ramakrishna Sajja^{a}, **and Hemantha Kumar Kalluri**^{b}

^{a,b}Department of Computer Science and Engineering, VFSTR Deemed to be University, Vadlamudi, Guntur, AP, INDIA.

Article History: Received: 10 January 2021; Revised: 12 February 2021; Accepted: 27 March 2021;

Abstract: Brain tumor is a treacherous and pernicious type of cancer detected in grown-ups and kids.It is critical to pinpoint the primary and precise brain tumors in the recovery process. Abnormal cell development within the skull is a brain tumor. With direct effects such as cognitive impairment and poor quality of life, malignant brain tumors are among the most dreadful forms of cancer. Brain tumors are a lethal cancer, and because of the heterogeneous nature of the tumor cells, their classification is a difficult challenge for radiologists. Stratifying the Brain Tumors (BT) is a pivotal assignment for tumor diagnosis and proper care. Several imaging techniques are in use to identify tumors in the brain. Because of its unrivaled image clarity and the fact that it does not rely on ionizing radiation, Magnetic Resonance Imaging (MRI) is commonly utilized for such a mission. In medical imaging field, the importance of Artificial Intelligence (AI) in the context of Deep Learning (DL) has paved the way for extraordinary advances in categorizing and predicting intricate pathological diseases, such as brain tumors, etc. Deep learning has proven and shown an amazing presentation, particularly in segmenting brain tumors and classifying them. In this study,AI-based classification of BT using Deep Learning Algorithms for stratifying different brain tumor kinds is suggested using publicly available datasets. These datasets classify(malignant and benign) BTs. The datasets contain 696 images for research purposes on T1-weighted images. The predicted arrangement produces a noteworthy efficiency of 99.04 percent for the highest precision. The result obtained reflects the potential of the proposed algorithm to identify brain tumors.

1. Introduction

In brain cells, brain tumors can be identified as unnatural and unregulated development. Consequently, as the person's cranium is hard and capacity bounded, any sudden development will affect human functions based on the portion of the brain involvement and the cancer may also spread to other parts of the body. As stated by WHO, World Cancer Report; Cerebrum disease represents under 2% of human malignant growth; anyway, serious toxicity and complicacy are generated (B. W. Stewart 2014). In the United Kingdom, It is estimated that annually around 5,250 deaths are recorded due to actions of brain, Central Nervous System (CNS), and other intracranial tumors (Brain, 2019).

Brain tumors can be grouped in a variety of methods, including major, minor tumors. About 70% of all mind malignant growths are essential tumors, while 30% are auxiliary tumors. This classification is based on the origin of tumors; for example, primary tumors are those that begin in the brain. Tumors, then again, start in another piece of the body and afterward spread to the mind, most of which are guileful (A. Behin, 2003). Brain tumors can be detected using a variety of imaging methods. Diffusion tensor imaging (DTI) and Magnetic resonance imaging (MRI) are two minimally invasive diagnostic procedures. Rather than ionizing radiation, a MRI examine utilizes non-intrusive difference specialists and an assortment of imaging boundaries, two of which are more explicit in delicate tissue (A. Drevelegas, 2007; G. Litjens, 2017).

Gliomas are the extremely well-known kind of cerebrum tumor that begin in the glial cells of the mind (M. L. Goodenberger, 2012). Gliomas are available in 30% of all brain and central nervous system tumors and in 80% of threatening cerebrum tumors. Gliomas are arranged by the World Health Organization into four sorts, going from type I to type IV (D. N. Louis, 2016). Evaluation I tumors are non malignant and have a surface that is fairly near that of typical glial cells, grade II tumors have a surface that is generously unique, grade III tumors are malignant with unusual tissue appearance, and grade IV tumors have the most serious level of unaided eye representation of gliomas and tissue defects (L. M. De Angelis, 2001). Meningioma is a considerate tumor that grows gradually inside the human skull on the layer that covers the brain and spinal cord. Most of meningioma tumors are non malignant (D. N. Louis, 2016). Nonetheless, the pituitary tumor begins with the pituitary glands, which control hormone production and body functions. It is common for it to be benign, bone-expanding, or malignant.

Early identification and stratification of brain tumors is a critical chore regardless of the knowledge described above in case evaluation and therefore, assist in choosing the most Convenient form of therapy to rescue sufferer's lives. Also, the stratification stage can be a disappointing and redundant job in some difficult situations for surgeons or radiologists. These cases require specialists to focus on the localization of the tumor, Comparing tumor tissues with neighboring areas, applying filters Whenever needed, on the picture; to make it more clear for people Vision, and in the end finish up; assuming, in addition, it's a tumor If available, their grade and type. Relatively absorbed by this assignment Time, and that's why a computer aided diagnosis (CAD) is needed for the early identification of brain tumors in certain short time devoid of human being interference.

The algorithmic analyzation and mathematical structures is nothing but Machine Learning (ML) which is utilized as opposed to depending on patterns to execute a given task without using direct instructions (Ranjeeth, S., 2020). ML algorithms are commonly used as part of artificial intelligence in the field of medical imaging [6]. It is separated into two primary, supervised, and unsupervised groups. In supervised techniques, a function is developed using an algorithm for mapping Input variables and it's corresponding output labels are used to forecast labels for new topics. The primary objective is to use algorithms such as K-Nearest Neighbors (KNN), Support Vector Machine (SVM), and Artificial Neural Network (ANN) to learn intrinsic patterns within the training results. Unsupervised learning, then again, depends just on input factors, such as k-means and fuzzy c-means. In order to create learning, there is a necessity of extracting the training data's characteristics that are normally texture , statistical, and grayscale features and may include segmentation of the tumor before the extraction stage in most cases. These features are referred to as handcrafted features that involve a specialist with good experience and the ability to work out the most important features. In addition, this work requires a lot of time and is vulnerable to errors when juggling large data.

Deep Learning (DL) is an ML subdivision focused on representations of Hierarchical Feature Learning and learning data. Algorithms in Deep Learning use various levels of nonlinear identity analysis for the extraction of features. Each sequential layer's output is the next layer's input, and as we go deep inside the network, that helps in data abstraction (L. Deng, 2014). Convolution Neural Network (CNN) is DL class which is widely utilized for visual imaging research and is structured to involve limited preprocessing. It is driven by genetic functions in the human brain and is used to treat multi-array data. In the last century's last years , a deep neural network " lenet ",developed by Lecun was utilized in applications of text recognition, first use of the deep CNN with a similar shape to its current one in the year 1998. After several years, a deep CNN to categorize images (ImageNet LSVRC-2010), using a model named (VGG16), it became far more common. Compared to additional network structures used at this point, VGG16 shows excellent performance. Afterwards, its popularity led to successive achievements in the deep learning culture of CNNs.

CNNs key benefits are limitless precision and feature learning rather than machine learning and conventional vanilla neural networks, which can be accomplished by escalating training datasets, leading to a more stable and precise model [6]. The convolutionary filters function as extractors of characteristics in the CNN architecture, and more complex characteristics(structural and spatial information) are observed as we dwell in. Function extraction occurs by integrating tiny filters with the input patterns Subsequently, the most distinguishing characteristics were chosen and then the classification network started training.

2. Related Work

Afar et al. introduced a classification system for brain tumours. They recommended a single convolutionalance layer with 64 function charts. They were accurate, to a measure of 86.56 percent. According to the company, their model was found to be 72.13% accurate in the same study to be that in replicating CNN (Afshar, P.,2018).

In their study Saxena et al. have been classifying brain tumour data using the Vgg16, InceptionV3, and Resnet50 models. They attained the greatest accuracy in the Resnet50 model utilising methods of transfer learning with 95% in this sample (Saxena, P., 2019).

Shahzadi et al. used the Cnn - Lstm hybrid structure to categorize cells of the brain tumour. They claim that Alexnet-Lstm has defined the network with 71% precision, VggNet-Lstm with 84% precision and 71% precision. In VggNet-Lstm, they had the maximum precision score of 84 percent (Shahzadi, I.,2018).

Using the single value decomposition method, El Abadi and his colleagues explored the tumour results. With 20 daily and 50 irregular data sets, they tested their methods. They said they achieved a 96,66% accuracy rate, a 90% sensitivity rate and a 98% specificity rate (Latchoumi, T. P.,2019).

A modern model for classifying data from brain tumours utilising profound learning processes, Mohsen et al. suggested (DWT). The model they developed obtained a 93.94% hit rate. This model was compared with the Deep Learning and Kernels frameworks (Loganathan, J.,2017).

Charfi et al. , created a CLASSIFICATION OF BRAIN IMAGING. In the machine learning system he suggested using the histogram equalisation method for the segmentation of images. Then he used PCA to compact his collected info. Finally, a feedback back propagation neural network has been used for the categorization process. He had an accuracy rate of 90 percent in the photographs he categorised as ordinary and irregular. He says that this precision rate is "highly fine" (Charfi S, 2014).

Vani et al used an SVM to detect brain tumour samples. It was calculated that they were right on their predictions when they claimed that they just made 82% of the good ones and yet slightly wrong on the negative ones The researchers found that MRI scans were helpful in classifying Brain tumour. DWT, PCA, and SVM are used for data clustering A 80% success rate, an 84% precision, a 92% sensitivity, and a speciality, respectively. They believe their studies can be included in a clinical setting, they say (Vani, N., 2017).

Citak et al. found that they used three distinct machine learning techniques in their tumour study. multi-layered SVM, single-layered multi-perceptrons, and logistic regression Although they could produce 93% accuracy, 86.7% precision, and 94% accuracy by using this method (Ezhilarasi, T. P., 2020).

Discussion and Discussion on the methodology and the third part of the report was covered in the paper. These elements are all listed in this segment: Deep learning, Cnn, and the Cnn Layers Then the better one was unveiled. You will find the application and results in the fourth line. This theory has been tested and all the data was collected for potential research..

3. Materials and methods

Objective of this work is identification of brain tumors in MRI images. MRI images of the considered dataset is segmented using fuzzy c means algorithm. Then assign the labels, partition the data into training and testing. Dataset consists of 577 images includes normal images of 290 and tumor images of 287. VGG16 network has prepared with normal images of 210 and tumor images of 185. Then trained model is tested with normal images of 80 and abnormal images of 102. VGG16 is a high-performance network and each image is processed through input layer, convolution layer, max pooling layer, drop out layer, fully connected layer, soft max function and then classification layer.

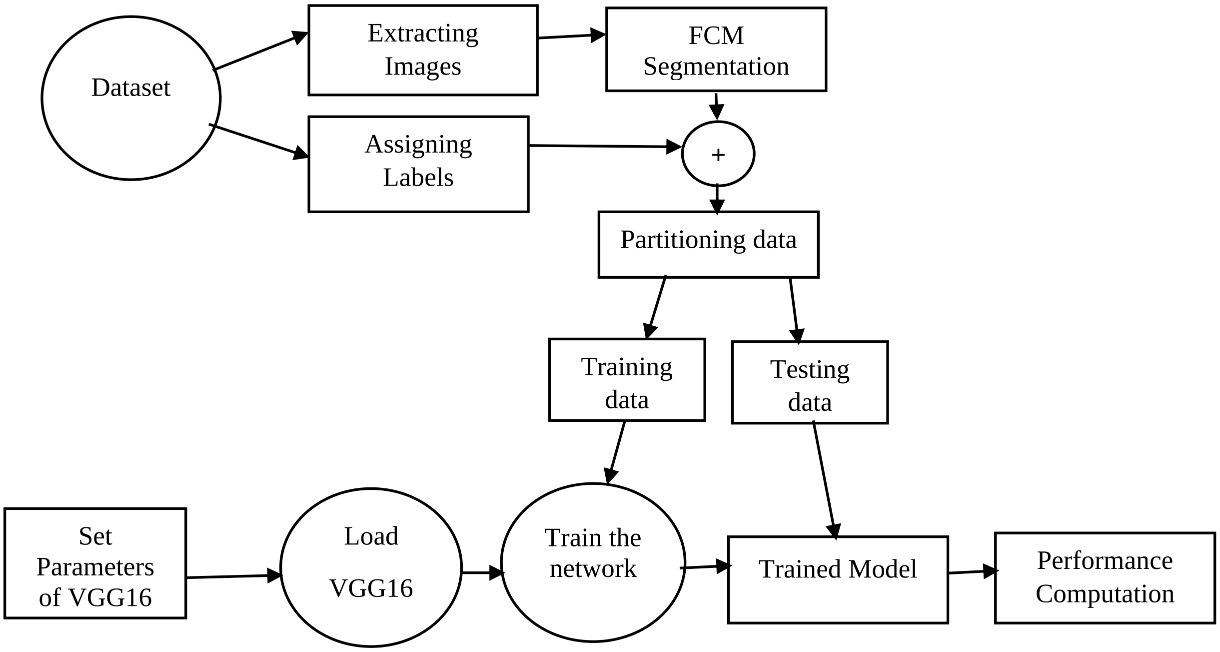

Fig. 1. Architecture of proposed model

3.1 Dataset

In this study, BRATS dataset[19-21] is considered for experimentation. It consists of 577 images includes normal images of 290 and tumor images of 287. Normal images of 210 and tumor images of 185 are used for training. Normal images of 80 and tumor images of 102 are used for testing. Then labels are assigned to 2 each image.

3.2 FCM Segmentation

Second task of the proposed method is segmentation[20]. The objective of fuzzy c-means algorithm is extraction of tumored portion from normal tissue. Practical observations are depicted in figure 2.

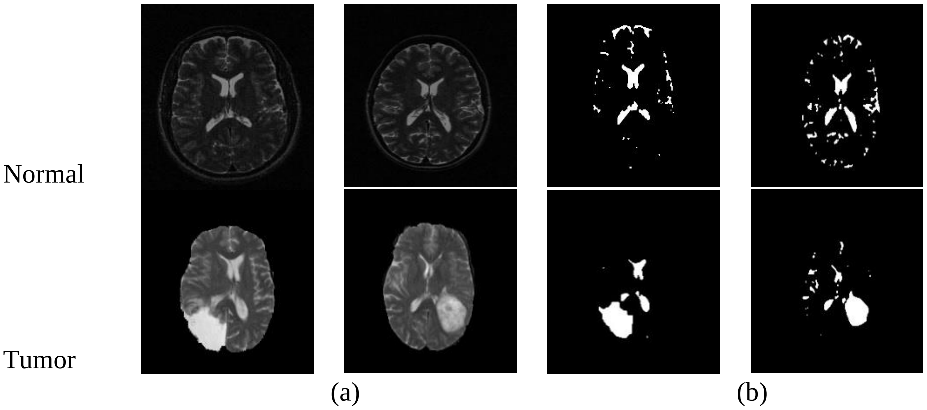

Figure. 2. Fuzzy c-means segmentation results (a) pre segmentation (b) post segmentation

Algorithm for Fuzzy c-means:

Stage 1: Determining 2D space as column-wise data with data points (for example, 4 points)

Stage 2: Set the cluster ‘c’ value and convergence of $\epsilon_L = 0.01$.

$$max_{ik}\left|\mu_{ik}^{(r+1)} - \mu_{ik}^{(r)}\right| \leq 0.01$$

Stage 3: Prepare the 1 – 3 data points in cluster 1 and 4th data point in cluster 2.

$$\mu^0 = \begin{array}{c} \begin{bmatrix} 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \end{array} \begin{array}{c} C_1 \\ C_2 \end{array}$$

Stage 4: Preliminary cluster center will be computed using equation 1

$$V_{ij} = \frac{\sum_{k=1}^{n}(\mu_{ik})^2 x_{kj}}{\sum_{k=1}^{n}(\mu_{ik})^2}\ for\ i = j = 1\ to\ c \qquad (1)$$

Stage 5: Measure the distance d_{ik} for every data point from each cluster.

Stage 6: Membership metrics have to be revised using equation 2.

$$\mu_{ik}^{(r+1)} = \left[\sum_{j=1}^{c}\left(\frac{d_{ik}^{(r)}}{d_{jk}^{(r)}}\right)\right]^{-1} \qquad (2)$$

Stage 7: Convergence has to be tested (Maximum absolute value of pairwise comparison of each value in $\mu^{(r)}\ and\ \mu^{(r+1)}$) using equation 3

$$max_{ik}\left|\mu_{ik}^{(r+1)} - \mu_{ik}^{(r)}\right| \leq 0.01 \qquad (3)$$

Stage 8: Stage 4 to 7 has to be repeated till there is no change in cluster centers.

3.2.1 Partitioning the data

Segmented images are partitioned into two different disjoint sets named as training data and testing data. Normal images of 210 and tumor images of 185 are used for training. Normal images of 80 and tumor images of 102 are used for testing. Training data is used to train the proposed model. Testing data is employed to test the trained model. Cross validation method has been applied to ensure the performance.

3.2.2 VGG16 Network

The basic VGG16 network [21] is shown in figure 3.The pretrained model of VGG16 weights are downloaded from[22]. This network consists of 5 stages of convolution layers with ReLU activation function and max pooling layer. Flatten layer transforms the data from three dimensional to one dimensional. Overfitting can be eliminated by dropout layer. Output layer is percolated by densely connected layer with sigmoid activation function. The input layer size is 256x256x3 and output layer size is 1.

Fig. 3. VGG16 Architecture

i.Input layer

It is the very beginning layer where we load the data. Image data read from which is called as input layer.

ii.Convolutional layer

Instead of being a one size to fit everything, the convolution mechanism varies. Instead of the matrix multiplication, the result is calculated by convolution. With this sheet, you can get function maps[23] If you're using the approximate time convolution method, use Eq. (4)

$$\boldsymbol{s}(t) = (x * w)(t) = \sum_{a=-\infty}^{\infty} x(a)w(t-a) \qquad (4)$$

W:kernel, x:input, t:times, s:result

Eq. (5) is used for inputs that include two-dimensional data such as images.

$$S(i,j) = (I * K)(i,j) = \sum_{m}\sum_{n} I(i,j)K(i-m, j-n) \qquad (5)$$

The concepts i and j correspond to the locations of the new matrix to be obtained after the method of convolution. It is normally placed such that the filter core is at the source.

iii.Activation function

Activation functions are used to convert values learned in deep learning into non-linear terms. In multilayer artificial neural networks, activation functions are used for non-linear transformation procedures. Many activation features are available [24]. The most often used are Tanh, Sigmoid and Relu. Relu was employed in the process established and seen in equation 6.

$$Relu: f(x) = \begin{matrix} 0, x < 0 \\ 1,\ \ x \geq 0 \end{matrix} \qquad (6)$$

iv.Max Pooling Layer

In CNN the bundling layer plays a significant role to reduce the function. The output neurons in the convolutional layer should be shared by applying pooling algorithms to the neighbouring components. Max-pooling and averaging are algorithms in some cases.

Max-pooling with a 2x2 components of the entered matrix:To pick the highest function from 4 factors in the output matrix, the max-2x layer has a 2x2-dimensional kernel As input for the max-pool layer, the performance of the 2D convolution layer is given. Equation 7 is used to calculate the performance of the picture generated by the pooling layer.

$$\left[\frac{O + 2pa - 2}{st}\right] + 1 \qquad (7)$$

where O is 64×64 size of the filter (fi) is 3×3 number of stride (st) is 2, and padding (pa) is 0. So, the dimensions of the image generated from the max pool layer is 32×32 (i.e. $\left[\frac{64+0-2}{2}\right]$+ 1). All remaining paths to maxing have been exploited by the use of the same method.

v.Dropout Layer

When a model has learned a specific set of results, it has ceased to generalise. the dropout layer would drop nodes and links which are overlearned during training and avoid overtraining Because of this method, the data's data weighting is regulated. Only while in class, dropout should be used to avoid overfitting.

vi.Fully Connected Layer

Completely linked, the activation mechanism is used by the two tumour class to distinguish performance values of the two layer nodes, such as the feeder forwards. both layer nodes are fully correlated with the following layer nodes.

Increasing the number of epochs means higher classification accuracy in deep learning. Weight updates in the CNN back propagation algorithm are used during movement from epoch to epoch. The equation is shown 8.

$$w_{ij} = w_{ij} + \Delta w_{ij} \qquad (8)$$

Where $\Delta w_{ij} = (l) Err_j O_i$

vii.Softmax

At the classification layer, it is essential to provide softmax. To produce values for each class, it calculates a probabilistic sequence. In this layer we use an equation to obtain the percentages for each class (9).

$$P(y = j|x; W, b) = \frac{exp^{X^T W_j}}{\sum_{j=1}^{n} exp^{X^T W_j}} \qquad (9)$$

viii.Classification layer

This is the last convolutional layer in the last position. As we calculate the total production amount, this layer gets as many credits. To us who know it, this represents healthy tissue and non-tumor tissue, respectively.

4. Application and Results

Objective of this work is identification of brain tumors in MRI images. MRI images of the considered dataset is given for training in VGG16 network. Then some of the images are given for testing on the trained network. This work has been carried out in Jupyter Notebook with a computer which has the configuration of 8 GB Ram and i7 processor.

BRATS dataset is considered for experimentation. It consists of 577 images includes normal images of 290 and tumor images of 287. VGG16 network has trained with normal images of 210 and tumor images of 185. Then trained model is tested with normal images of 80 and abnormal images of 102. Dataset partitioning is depicted in table1.

Table 1. Dataset partitioning

Dataset	Normal Images	Tumor Images	Total
Testing	80	102	182
Training	210	185	395
Total	290	287	577

Confusion matrix provides the very essential values those are being used in the process of classification[25-26]. It also provides the summary of trained model. A basic confusion matrix is given in table 2.

Table 2. Confusion Matrix

Confusion Matrix	Tumor	Normal
Tumor	TP (Tumor)	FN (False Normal)
Normal	FP (False Tumor)	TN (Normal)

TP means that tumored image has been classified as tumored image. TN means that normal image has been classified as normal image. FP means that normal image has been classified as tumored image. FN means that tumored image has been classified as normal image.

Accuracy is the metric for computing the classifier performance. It results the fraction of normal and tumor images those are classified exactly using equation 10.

$$\text{Accuracy } = \frac{TN + TP}{TP + TN + FN + FP} \qquad (10)$$

Error rate is the another metric for computing the classifier misclassification rate. It results the fraction of normal and tumor images those are not classified exactly using equation 11

$$\text{Error Rate } = \frac{FN + FP}{TP + TN + FN + FP} \qquad (11)$$

Recall is the metric which measures rate of tumored images. It results the ratio of tumor cases those are exactly classified using equation 12. It is also called as sensitivity or True Positive Rate(TPR).

$$\text{Recall/ Sensitivity/ TPR} \quad = \quad \frac{TP}{TP + FN} \qquad (12)$$

Specificity is the metric which measures rate of normal images. It results the ratio of normal cases those are exactly classified using equation 13. It is also called as True Negative Rate(TNR).

$$Specificity/\ \text{TNR } = \quad \frac{TN}{TN + FP} \qquad (13)$$

Precission is the metric which measures the prediction rate. It results the ration of tumor cases those are classified correctly from the predicted tumors using equation 14.

$$\text{Precision } = \frac{TP}{TP + FP} \qquad (14)$$

F1 score is a metric which measures by combining both recall and precisions as one metric. It has been defined by by equation 15.

$$\text{F1score (F)} = \frac{2XRecallXPrecision}{Recall + Precision} \qquad (15)$$

Images that are set for testing were given to trained network to test. 182 images were tested by VGG16 trained model. It results that tumor cases of 99, normal cases of 77, false tumor cases of 3 and false normal cases of 3. This experimentation results are given in table 3. Different models against various evaluation measures are tested and results are given in table 4.

Table 3. VGG16 performance computation

Confusion Matrix	99(TP)	3 (FN)
	3 (FP)	77 (TN)
Accuracy	96.70	
Error rate	03.30	
Sensitivity	97.05	
Specificity	96.25	
Precision	97.05	
F1 score	97.05	

Table 4. Different models Performance computation

Evaluation Measures	**K Means + SVM**	**FCM + SVM**	**CNN**	**VGG16 (Proposed)**
Accuracy	92.30	94.50	96.15	96.70
Error rate	07.69	05.50	03.85	03.30
Sensitivity	94.05	96.03	97.05	97.05
Specificity	90.12	92.59	95.00	96.25

Precision	92.23	94.17	96.11	97.05
F1 score	93.13	95.09	96.53	97.05

Low misclassification rate, high classification rate, Sensitivity, Specificity, Precision and F1 score are notified by VGG16 network against existing models. Resultant values are tabulated and shown in given figure 4. Various studies performed to classify the tumor is compared with proposed model and it is given in table 5.

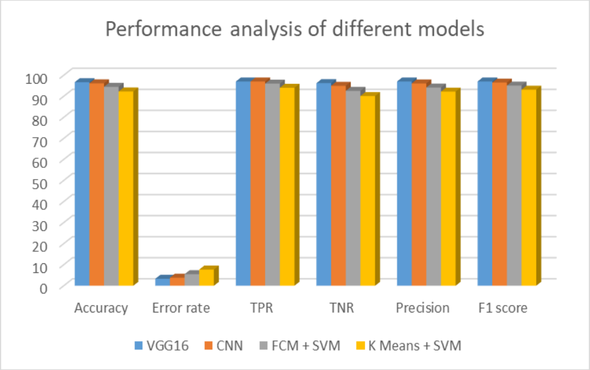

Figure 4. All models performance computation against classificatiojn metrics

Table 5. Comparison of proposed model with various existing models

Authors/Year	**Method**	**Performance**
Vani et al.[17] /2017	SVM	81.47%
Citak et al. [19] /2018	SVM and logistic regression	93.00%
Mohsen et al.[15] /2018	DWT	93.94%
V Ramakrishna et al.[20] /2019	FCM+LBP+SVM	94.80%
Saxena et al.[12] /2019	Resnet50	95.00%
V Ramakrishna et al.[27]/2020	CNN	96.15%
Proposed Method /2021	VGG16	96.70%

5. Conclusion

Objective of this work is identification of brain tumors in MRI images. MRI images of the considered dataset is segmented using fuzzy c means algorithm. Then assign the labels, partition the data into training and testing. Dataset consists of 577 images includes normal images of 290 and tumor images of 287. VGG16 network has been trained with normal images of 210 and abnormal images of 185. Then trained model is tested with normal images of 80 and abnormal images of 102. VGG16 is a high performance network and each image is processed through input layer, convolution layer, max pooling layer, drop out layer, fully connected layer, soft max function and then classification layer. The proposed model has been evaluated with classification metrics and yields the classification rate of 96.70%, misclassification rate of 3.30%, Recall of 97.05%, Specificity of 96.25%, Precision of 97.05% and F1 score of 97.05%. Proposed model is compared with various existing model and proves that it is yielding better performance. In future, size of the data set can be increased and it will be tested against the bench mark parameters,

References

1. Afshar, P., Mohammadi, A., & Plataniotis, K. N. (2018). *Brain tumor type classification via capsule networks. In 2018 25th IEEE International Conference on Image Processing (ICIP) (pp. 3129-3133). IEEE.*
    A. Behin, K. Hoang-Xuan, A. F. Carpentier, and J.-Y. Delattre, (2003) *''Primary brain tumours in adults,'' Lancet, 361(9354), pp. 323–331.*
2. Drevelegas, (2002) *Imaging of Brain Tumors With Histological Correlations. Berlin, Germany: Springer.*
3. Arunkarthikeyan, K. and Balamurugan, K., 2021. Experimental Studies on Deep Cryo Treated Plus Tempered Tungsten Carbide Inserts in Turning Operation. In Advances in Industrial Automation and Smart Manufacturing (pp. 313-323). Springer, Singapore.
4. Balamurugan, K., Uthayakumar, M., Sankar, S., Hareesh, U.S. and Warrier, K.G.K., 2019. Predicting correlations in abrasive waterjet cutting parameters of Lanthanum phosphate/Yttria composite by response surface methodology. Measurement, 131, pp.309-318.
5. Balamurugan, K., Uthayakumar, M., Sankar, S., Hareesh, U.S. and Warrier, K.G.K., 2018. Preparation, characterisation and machining of LaPO4-Y2O3 composite by abrasive water jet machine. International Journal of Computer Aided Engineering and Technology, 10(6), pp.684-697.
6. Bhasha, A.C., Balamurugan, K. End mill studies on Al6061 hybrid composite prepared by ultrasonic-assisted stir casting. Multiscale and Multidiscip. Model. Exp. and Des. (2020). https://doi.org/10.1007/s41939-020-00083-1
7. *Brain, Other CNS and Intracranial Tumours Statistics. Accessed: (2019). [Online]. Available: https://www.cancerresearchuk.org/*
8. Charfi S, Lahmyed R, Rangarajan L. (2014) *A novel approach for brain tumor detection using neural network. Int J Res Eng Technol 2:93–104.*
9. ChinnamahammadBhasha, A., Balamurugan, K. Studies on Al6061nanohybrid Composites Reinforced with SiO_2/3x% of TiC -a Agro-Waste. Silicon (2020). https://doi.org/10.1007/s12633-020-00758-x
10. Citak-Er F, Firat Z, Kovanlikaya I, *Ture U, Ozturk-Isik E. (2018) Machine-learning in grading of gliomas based on multi-parametric magnetic resonance imaging at 3T. Comput Biol Med 99:154–60.*
11. D. N. Louis, A. Perry, G. Reifenberger, A. *von Deimling, D. Figarella-Branger, W. K. Cavenee, H. Ohgaki, O. D.* Wiestler, P. Kleihues, and D. W. Ellison, (2016) *''The 2016 World Health Organization classification of tumors of the central nervous system: A summary,'' Acta Neuropathol., 131(6), pp. 803–820.*
12. Ezhilarasi, T. P., Dilip, G., Latchoumi, T. P., & Balamurugan, K. (2020). *UIP—A Smart Web Application to Manage Network Environments. In Proceedings of the Third International Conference on Computational Intelligence and Informatics (pp. 97-108). Springer, Singapore.*
13. G. Litjens, T. Kooi, B. E. Bejnordi, *A. A. A. Setio, F. Ciompi, M. Ghafoorian, J. A. W. M. van der Laak, B. van Ginneken, and C. I. Sánchez, (2017) ''A survey on deep learning in medical image analysis,'' Med. Image Anal., 42, pp. 60–88.*
14. HK Kalluri MVNK Prasad, A Agarwal, *Palmprint identification and verification based on wide principal lines through dynamic ROI, International Journal of Biometrics 7 (1), 1-30*
15. HK Kalluri, MVNK Prasad, A Agarwal, *Palmprint identification based on wide principal lines Proceedings of the International Conference on Advances in Computing.*
16. Latchoumi, T.P., Loganathan, J., Parthiban, L. and Janakiraman, S., 2016, August. OFS method for selecting active features using clustering techniques. In *Proceedings of the International Conference on Informatics and Analytics* (pp. 1-4). https://doi.org/10.1145/2980258.2982108
17. Latchoumi, T.P. and Parthiban, L., 2016. Secure Data Storage in Cloud Environment using MAS. *Indian Journal of Science and Technology*, *9*, pp.24-29.
18. Latchoumi, T.P. and Kannan, V.V., 2013. Synthetic Identity of Crime Detection. *International Journal*, *3*(7), pp.124-129.

19. Latchoumi, T. P., Balamurugan, K., Dinesh, K., & Ezhilarasi, T. P. (2019). *Particle swarm optimization approach for waterjet cavitation peening. Measurement, 141, 184-189.*

20. L. Deng and D. Yu, (2014) *''Deep learning: Methods and applications,'' Found. Trends Signal Process., 7(3–4), pp. 197–387.*

21. Liew SS, Khalil-Hani M, Bakhteri R. (2016) *Bounded activation functions for enhanced training stability of deep neural networks on visual patternre cognition problems. Neurocomputing 216:718–34. https://doi.org/10.1016/j.neucom.2016.08. 037.*

22. L. M. De Angelis*, ''Brain tumors,'' (2001) New England J. Med., 344(2), pp. 114–123.*

23. Loganathan, J., Janakiraman, S., Latchoumi, T. P., & Shanthoshini, B. (2017). *Dynamic Virtual Server For Optimized Web Service Interaction. International Journal of Pure and Applied Mathematics, 117(19), 371-377*

24. M. L. Goodenberger and R. B. Jenkins, (2012)*''Genetics of adult glioma,'' Cancer Genet., 205(12), pp. 613–621.*

25. Pei JY, Shan P. (2019) *A micro-expression recognition algorithm for students in classroom learning based on convolutional neural network. Traitement du Signal 36(6) :557–63.*

26. Ranjeeth, S., Latchoumi, T. P., & Paul, P. V. (2020). *Role of gender on academic performance based on different parameters: Data from secondary school education. Data in brief, 29, 105257.*

27. Saxena, P., Maheshwari, A., & Maheshwari, S. (2019). *Predictive modeling of brain tumor: A Deep learning approach. arXiv preprint arXiv:1911.02265.*

28. Shahzadi, I., Tang, T. B., Meriadeau, F., & Quyyum, A. (2018). *CNNLSTM: Cascaded framework for brain Tumour classification. In 2018 IEEE-EMBS Conference on Biomedical Engineering and Sciences (IECBES) (pp. 633-637). IEEE.*

29. Stewart .B .W and C. P. Wild, (2014) *World Cancer Report 2014. Lyon, France: IARC.*

30. Vani, N., Sowmya, A., & Jayamma, N. (2017). *Brain Tumor Classification using Support Vector Machine. International Research Journal of Engineering and Technology (IRJET), 4.*

31. V Ramakrishna Sajja, Hemantha Kumar Kalluri, (2020*) "Classification of Brain Tumors Using Convolutional Neural Network over Various SVM Methods", Ingénierie des Systèmes d'Information, 25(4), pp. 489-495.*

32. V Ramakrishna Sajja, Hemantha Kumar Kalluri, (2019) *"Brain Tumor Segmentation Using Fuzzy C-Means and classification using SVM", Lecture notes in Networks and Systems, Proceedings of Smart Technologies in Data Science and Communication 105, PP.197-204.*