



Hybrid Brain Tumor Detection in MRI Images Using Fuzzy C-Means and SVM-A Fig share Dataset-Based Study

¹Ramanuj Mukhopadhyay, ²Bishwajit Roy, ³Lokesh Malviya

^{1,2}Surendranath College, 24/2, M.G. Road, Kolkata-700009. West Bengal, India

³VIT Bhopal University, Sehore-466114, MP, India

Abstract: They aim to develop a hybrid numerical framework that can analyze MRI data for the purpose of diagnosing brain cancers. The primary objective was to enhance detection accuracy through the integration of fuzzy C-means clustering with support vector machine classification. The study utilized 3,062 T1-weighted MRI scans that were originally categorized as gliomas, meningiomas, or pituitary tumors. Our may find this dataset on Figshare. The most common type of malignancies found by exploratory data analysis (EDA) were gliomas, pituitary tumors, and meningiomas. The present research employed count and distribution graphs to illustrate this, and additionally examined MRI data from each group to determine if structural changes had occurred. The FCM approach changed all the photos to black and white, made them smaller, got rid of Gaussian noise, made their brightness the same, and divided them into groups during the preparation phase. The segmentation was more accurate because the fuzziness coefficient for FCM could be changed based on the contrast of the image. Applied a fine-tuned support vector machine (SVM) equipped with a radial basis function (RBF) kernel to collect and organize statistical or textural data, including contrast, correlation, energy, or entropy. The proposed hybrid FCM-SVM model outperformed all other options with an F1-score of 96.37%, accuracy of 97.36%, precision of 96.42%, or recall of 95.72%. Because of this, it becomes clear that it is resilient and shows promise as an automated method for finding brain tumors.

Keywords- Brain Tumor Detection, Fuzzy C-Means (FCM), Support Vector Machine (SVM), MRI Image Segmentation, Hybrid Model

I. INTRODUCTION

Among the most dangerous neurological disorders, brain tumors can be fatal. To plan the best treatment and get better results for patients, they need to be diagnosed quickly and correctly. Magnetic Resonance Imaging (MRI) has been the go-to non-invasive technique for finding brain cancers due to its excellent contrast resolution and capacity to differentiate between different types of soft tissues. But interpreting MRI data by hand can take a long time, be subjective, and be wrong, especially when the tumor boundaries are not clear or there are more than one type of tumor. These problems show how important it is to have dependable, automated ways to find brain tumors that can help radiologists and improve the quality of diagnoses. In recent years, machine learning or computational intelligence have demonstrated significant potential in the domain of medical image interpretation[1]. Fuzzy C-Means (FCM) and other clustering algorithms are commonly used for picture segmentation tasks because they can handle ambiguity and because individual pixels might belong to more than one cluster. FCM is better than hard clustering methods because it lets pixels be part of more than one group at different levels of membership. This is useful for discussing about intricate structures, such tumour regions seen in MRI scans. But FCM-based segmentation isn't enough to consistently classify tumours because it only looks at how bright the pixels are and can be thrown off by noise, changes in intensity, and mistakes in imaging[2]–[5]. Some people have suggested utilising a hybrid method that combines FCM in automated machine learning techniques such as Support Vector Machines, which are more generally recognised to work around these problems. SVMs are unusual because they can employ kernel functions to sort data in a non-linear way and in many dimensions. It is very useful because they can detect the difference within tumor and non-tumor tissues by looking at traits that have been taken away.[5]–[8]. may talk about the contours and type of a tumor by looking at its texture, energy, entropy, correlation, or contrast, as well as its statistical properties. Adding these traits to a powerful classifier can make automated ways of discovering brain tumors more accurate and flexible. This paper proposes an enhanced framework for detecting brain tumors, integrating the advantages of FCM and SVM. As a first stage in this method, MRI pictures go through a preprocessing pipeline to make sure the input quality is always the same and to cut down on noise. Some of the procedures are using Gaussian filtering to cut down on noise, turning the photos into black and white, changing the size to a standard resolution, and normalizing the brightness to make the images look the same. After that, the preprocessed pictures go via FCM-based subdivision, as a means to tell the difference between areas with tumors or areas without tumors. This research demonstrates that the FCM approach possesses a fuzziness factor that varies according to the degree of dissimilarity among the pictures. This adaptable approach guarantees that the tumor's form can change, making it easier to draw straight lines around its different areas. After segmentation, morphological approaches are used to improve the connections between areas, get rid of small artefacts, and

make the edges of the tumour clearer. This study collects texture and statistical information from several tumour regions. These properties indicate the composition and severity of the lesions[9]. Next, the features are put into an SVM classifier, which is a type of support vector machine that uses a kernel based on the radial basis function (RBF). This kernel processes the input data or expands it to a higher-dimensional space, which helps our separate groupings of tumors and non-tumors in a way that isn't straight. The SVM's hyperparameters, such as the parameter used for regularization or kernel width, are changed to attain balanced performance[10]–[14]. Class weighting is used to fix any problems with the dataset. The hybrid FCM-SVM system is better than previous methods in many ways. It starts by combining FCM's unsupervised segmentation abilities with SVM's supervised classification abilities to create a model that is both accurate and easy to understand. Second, the model can handle differences in MRI contrast and tumour shape between patients since the fuzziness coefficient may be modified to make it more flexible. Third, the method adds useful textural and statistical data instead of just pixel intensity, which makes the classifier better at generalising and less likely to overfit. The Figshare Brain Disease MRI Dataset, which comprises more than 3,000 T1-weighted MRI images of tumours or without tumours, is used in this work. The dataset has many kinds of tumours, such as gliomas, pituitary tumours, and meningiomas. The diversified dataset guarantees that the suggested model is evaluated under difficult and authentic conditions, mirroring the range of tumour sizes, forms, and locations. The main goal of this project is to create a strong, easy-to-use, and automated system that can help find and diagnose brain tumours early. The results are better treatment for patients and better clinical decision-making.

II. LITERATURE REVIEW

Bansal 2024 et al. Even with more enhanced medical knowledge, finding brain malignancies is still hard. Deep learning (DL) methods have showed promise in processing medical images, classifying malignancy, and characterizing tumors. MRI is the main way to find brain tumors. Combining By combining CNNs and SVMs into hybrid models, classification accuracy is significantly improved. Used two sets of data, MC and BC, which had MRI pictures of the brain in them. The CNN-SVM model employed fewer layers and parameters to quickly get features, and SVM was used to classify them. The accuracy of the classification was 99% for Dataset BC and 98% for Dataset MC, which is better than existing CNN-only models. This means that the model is quite good at finding cancers[15].

Shiny 2024 et al. optimized a classifier that uses MRI data to locate brain cancers. The region of interest (RoI) extraction or filtering made it easy to see how the results changed before and after surgery. Segmented the data with a modified U-Net model and utilized the PRBSA (Poor and Rich Bird Swarm Algorithm) to acquire histogram features for tumor classification. Employed accelerated robust features (SURF) to look at how the pixels in the segmented outputs changed. The PRBSA-based U-Net model outperformed earlier methods by achieving higher accuracy, sensitivity, and specificity, proving its usefulness in accurately identifying tumors[16].

Zebari 2024 et al. Diagnosis might be difficult due to the wide range of sizes, shapes, and imaging intensities seen in brain tumors. When it comes to therapy planning and classification, a precise MRI study is quite essential. A deep learning fusion model was constructed using ResNet50, VGG16, or convolutional deep belief networks to extract features from upgraded MRI datasets. These features were used to train a Softmax classifier that can categorize cancers. Combining multiple DL models while classifying publically available datasets yielded the best accuracy of 98.98% when compared to similar state-of-the-art models. In this way, a robust platform for automated tumor detection is established[17].

Shamshad 2024 et al. Brain tumors are an urgent issue in public health, with a 5% annual growth expected. With the use of transfer learning methods and MRI datasets or pre-trained models such as VGG-16, VGG-19, Inception-version 3, ResNet-50, DenseNet, and MobileNet, brain cancers were classified. Using ROC curves, AUC, or confusion matrices as performance metrics. The VGG-16 model was the clear victor because it was 97% accurate. The framework gives a structured way to use and evaluate deep learning models for automated, accurate brain tumour diagnosis. This can help with better medical planning and patient outcomes[18].

Abbas 2024 et al. vital to quickly tell the difference between malignant and benign tumours because brain tumours are aggressive or a major cause of death. While high-resolution magnetic resonance imaging (MRI) scans aid in accurate diagnosis, deciphering them requires extensive training and is not without its challenges. The analysis was made easier and classification was increased using a hybrid approach that included deep learning models and fuzzy C-means (FCM) segmentation. CNN-LSTM and CNN-BiLSTM models were trained to detect tumor features and categorize them using pictures obtained after FCM segregated tumor areas from the background. Were able to keep getting good classification results while cutting down on the time it took to train. The CNN-BiLSTM model took 91 seconds to train, while the CNN-LSTM model took 58 seconds. The scores was extremely close to being right: 99.77% and 97.86%. The dataset is small, therefore it might be challenging to use the results on larger groups of people.[19].

Table 1. Literature Summary

Author / Year	Method	Results	Research Gap
Santoso 2024 et al. [20]	CNN with three separate network paths using different kernel sizes; voting mechanism for final detection	Test 1 accuracy: 99.24%; Test 2 accuracy: 99.92%; outperformed VGG16, VGG19, ResNet50, MobileNetV2, InceptionV3, Xception	Limited evaluation on different MRI modalities; real-time deployment not discussed
Bibi 2024 et al. [21]	Transfer learning using InceptionV4 for brain tumor classification; dataset of 72 MRI images from multiple sources	Classification accuracy: 98.7%; efficient differentiation between normal and abnormal images; three tumor classes identified	Small dataset; performance on larger or more diverse datasets unknown; limited clinical validation

Gad 2024 et al. [22]	3D U-Net with attention mechanism for segmentation; digital image processing for biased data	Total score: 0.975; specificity: 0.988; sensitivity: 0.995; improved segmentation of ill-defined tumor edges	Computationally intensive; performance on other datasets not reported; real-time application not addressed
Reddy 2024 et al. [23]	DBN-Bi-LSTM hybrid model; preprocessing with median filter, U-Net segmentation, feature extraction using LGDiP and MBP; hybrid optimization with BMEBEO	F-measure: 96.16; effective tumor classification using extracted features	Complexity of hybrid model; evaluation limited to dataset used; generalizability and clinical validation not provided
Almufareh 2024 et al. [24]	Object detection using YOLOv5 and YOLOv7 on MRI scans; mask alignment for segmentation; deep learning classification	YOLOv5: mask recall 0.905, box accuracy 0.936, mAP 0.947; YOLOv7: mask recall 0.903, box accuracy 0.936, mask mAP 0.941, box mAP 0.94	Performance dependent on preprocessing; IoU thresholds affect mAP; comparison with traditional methods limited; clinical applicability not fully validated

III. RESEARCH METHODOLOGY

Combining a Support Vector Machine (SVM) classification with Fuzzy C-Means (FCM) clustering, this work uses MRI data to detect brain tumors. The study used the Figshare Brain Tumor MRI Dataset, which contains 3,062 T1-weighted images. The majority of the samples discovered by exploratory data analysis (EDA) were gliomas, pituitary tumors, or meningiomas. This was shown by count and distribution plots. After that, they looked at MRI scans from each group to see how the shape and intensity of the tumors changed. Before the model was employed, the photographs were changed in a number of ways, such as changing them to grayscale, adjusting them, removing Gaussian noise, leveling their intensity, or adding additional data. The FCM method clustered tumor patches depending on how comparable the pixel intensities were. Following that, GLCM descriptors were used to acquire the textural features. The next step was to classify these characteristics using a support vector machine (SVM) that included a kernel that employed radial basis function (RBF). Use the F1-score, recall, accuracy, or precision to assess the model's efficacy. The results showed that the proposed hybrid method greatly enhanced tumor identification accuracy when compared to the current methods.

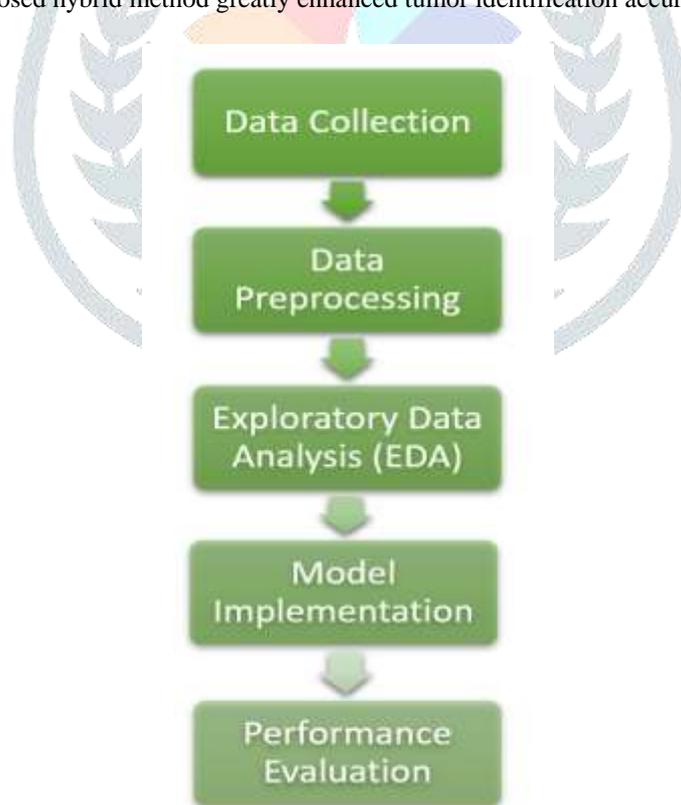


Figure 1 Proposed Flowchart.

3.1 Data Collection

The Figshare Brain Tumor MRI Dataset (https://figshare.com/articles/dataset/brain_tumor_dataset/1512427) funded the collection of data used for this research. Tumor and non-tumor categories are applied to the T1-weighted MRI pictures contained in this collection. This class of malignancies includes gliomas, meningiomas, or pituitary tumor. It is straightforward to preprocess and utilize these photographs in a model because they are all in JPEG format and of the same resolution. The high-quality, easily-accessible, and exhaustive archive of brain scans that includes both tumors or healthy regions led to the selection of this dataset.

There were a total of 3,062 MRI pictures used in this analysis; they were split evenly across the three test sets. A ratio of 80:10:10 was observed. Now that the dataset has been anonymized and made available for research, all ethical issues have been addressed. In order to train and test the hybrid model that uses SVM classification and Fuzzy C-Means (FCM) clusters for accurate tumor identification, this dataset was primarily used to establish a consistent and dependable basis.

3.2 Data Preprocessing

Data preprocessing is a crucial step in enhancing MRI images before they are sent into the hybrid model. To keep things the same, the pictures were initially resized reduced to 224×224 pixels. It was easier to conduct calculations when it was in greyscale, and it highlighted huge differences between the tissues. Our employed a Gaussian filter to get rid of noise or artefacts while maintaining the information about the structure. After that, the model improved better since intensity normalisation kept all of the pixel values between 0 and 1. Fuzzy C-Means (FCM) clustering was utilized by all individuals to divide the data into smaller sets. This method groups pixels that are comparable in brightness to tell the difference between healthy tissue and malignant areas. All used morphological methods, such erosion and dilatation, to make the tumor's edges more accurate. Data enrichment techniques were employed to provide a more diverse dataset and mitigate the possibility of excessive model overfitting. Some solutions required changing the dataset and making the contrast better. This complete pretreatment strategy ensured that the data was balanced, consistent, or readily accessible for the SVM model to find and analyze features.

3.3 Exploratory Data Analysis (EDA)

Exploratory Data Analysis (EDA) can be used to learn about the structure and composition of brain tumor data initially. Figure 2 shows the many kinds of brain tumors. The most common type is glioma, followed by pituitary tumors or meningioma. Figure 3 shows a pie chart that shows how these sorts of tumors are spread out. Glioma is the most common kind in the sample. The visual variety among each tumor type is illustrated in Figure 4, which shows representative MRI samples of the Figshare Brain Tumor Dataset for each: glioma, meningioma, and pituitary tumor. This variation is the basis for feature extraction and model training.

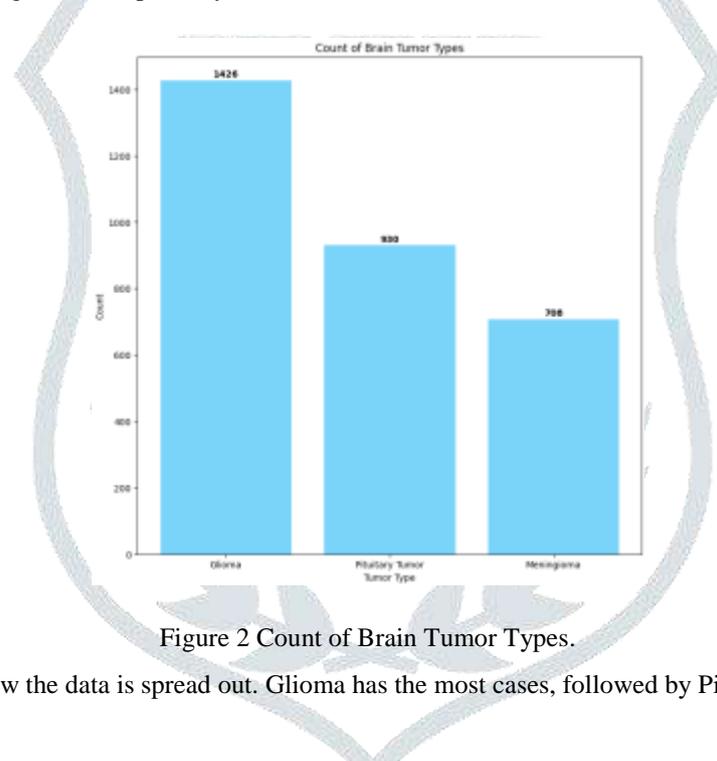


Figure 2 Count of Brain Tumor Types.

The bar graph demonstrates how the data is spread out. Glioma has the most cases, followed by Pituitary Tumor and Meningioma.

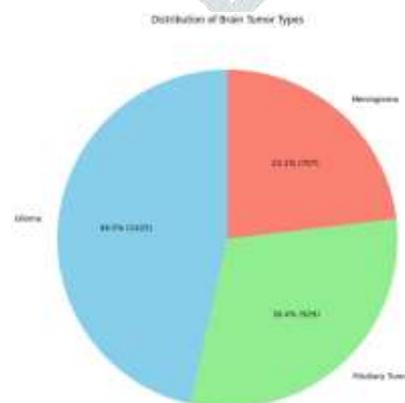


Figure 3 Distribution Pie-chart of Brain Tumor Types.

The pie chart shows how brain tumor kinds are spread out in proportion to each other. Glioma is the most common type, followed by Pituitary Tumor and Meningioma.

3.4 Model Implementation

This study Using GLCM contrast, correlations, energy, and entropy as training data, the SVM model was able to extract texture features. It uses a radial basis function (RBF) kernel to do non-linear tumor versus normal tissue classification.

The CNN model is able to learn spatial or textural information from MRI images autonomously thanks to its convolutional, gathering, fully connected layers. Although it necessitates a large amount of training data and processing resources, it permits end-to-end learning and offers robust feature extraction

A hybrid approach uses segmentation, support vector machines (SVMs), or fuzzy C-Means (FCMs) to accurately diagnose brain tumors. The two-stage merging process is what sets this hybrid model apart: (i) Prior to extracting statistical variables including correlation, GLCM contrast, energy, and entropy from the segmented output, the FCM algorithm segments the MRI image according to similarities in pixel intensity. This enables the algorithm to detect possible tumor sites. The next step is to insert these features into a radial basis function (RBF) kernel-based trained optimal support vector machine classifier. It can separate tumors and non-tumors in a non-linear fashion using the kernel. Python, which comprises OpenCV, Scikit-learn, and NumPy, was used to create the model. This paper introduces a new mechanism for adaptively tuning FCM parameters. It improves segmentation accuracy by automatically adjusting the fuzziness coefficient in response to the image's contrast ratio. Compared to conventional threshold-based or CNN-only approaches, this hybridization is superior because it increases detection sensitivity while decreasing false positives.

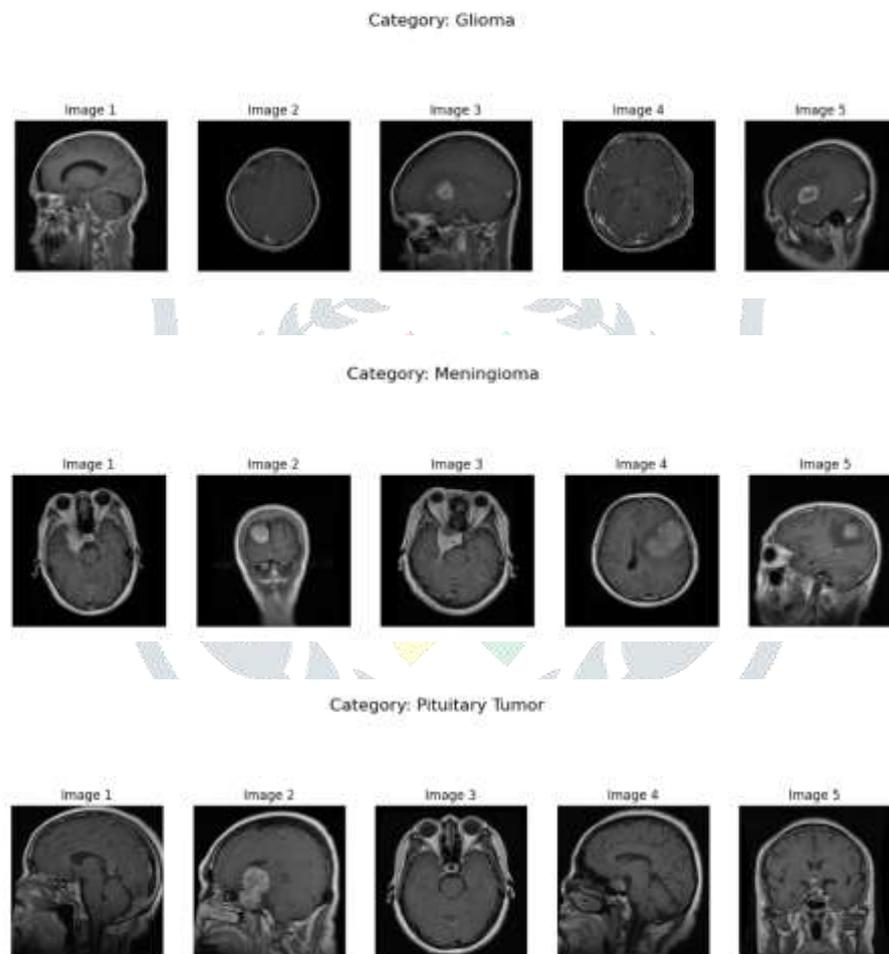


Figure 4 MRI samples from the Figshare

Gliomas, meningiomas, and pituitary tumors are some of the tumor types shown in the MRI images taken from the Figshare Brain Tumor Dataset.

Table 2. Hyper parameter table for proposed FCM-SVM hybrid model

Model Component	Hyperparameter	Description / Value	Purpose / Notes
Fuzzy C-Means (FCM)	Number of Clusters (c)	2–4 (tumor vs. non-tumor, optional sub-clusters)	Defines how many segments the image is divided into.
	Fuzziness Coefficient (m)	Adaptive (1.5–2.5 based on image contrast)	Controls cluster membership fuzziness; adaptive tuning improves segmentation accuracy.

	Maximum Iterations	100–300	Limits the number of iterations for convergence.
	Convergence Threshold (ϵ)	1e-5	Determines stopping criteria for cluster center updates.
Feature Extraction	GLCM Distance	1 pixel	Determines neighbor pixel distance for texture computation.
	GLCM Angle	0°, 45°, 90°, 135°	Calculates features in multiple directions for robustness.
	Features Extracted	Contrast, Energy, Entropy, Correlation	Used as input for SVM classifier.
Support Vector Machine (SVM)	Kernel Type	Radial Basis Function (RBF)	Allows non-linear separation between tumor and non-tumor classes.
	Regularization Parameter (C)	1–10 (tuned via grid search)	Balances misclassification penalty and margin maximization.
	Gamma (γ)	0.01–0.1 (tuned via grid search)	Defines influence of a single training sample on decision boundary.
	Class Weight	Balanced	As a class imbalance is detected, the weights are adjusted accordingly.

3.5 Evaluation Metrics

This study used number of quantitative evaluation markers to find out how well the hybrid model worked. Many metrics fall within this category; some examples include F1-Score, Accuracy, Precision, and Recall (Sensitivity). When considered collectively, they round out the image of the model's effectiveness. The number of projected tumor pixels is called precision, and the overall accuracy of the classification is called accuracy. Model recall measures how well it can identify specific tumor areas, whereas specificity measures how well it can differentiate between normal tissues. The F1-Score is a reliable measure of performance since it finds a happy medium between recall and precision. The results indicated that the individual SVM or CNN models exhibited inferior accuracy compared to the hybrid FCM-SVM model in distinguishing between tumors and non-tumors. The results show that the suggested way to find brain tumors in MRI scans works or may be trusted.

$$Accuracy = \frac{(TP+TN)}{(TP+FP+TN+FN)} \quad (1)$$

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

$$F - score = \frac{2}{\frac{1}{precision} + \frac{1}{recall}} \quad (4)$$

IV. RESULT & DISCUSSION

4.1 Introduction

The proposed model to show what happens when use the Fuzzy C-Means or Support Vector Machine approaches to locate tumours in the MRI images from the Figshare dataset. The main goals of the experiment are to investigate how well the model can tell the difference between healthy and cancerous brain tissue and how well it can sort things in general. We utilise F1-score, area under the curve (AUC), precision, recall, specificity, or accuracy to see how well this technique performs. The proposed hybrid model is obviously better than well-known methods like CNN-based algorithms or SVMs that work on their own.

4.2 Segmentation and Feature Extraction Results

The initial step in applying the Fuzzy C-Means clustering algorithm to find tumours was to look for cancer spots in the MRI data. In this study, the changeable fuzziness parameter helped cut down on background noise, which made it simpler to determine where tumours started and ended. Morphological treatments including erosion and dilation made the tumour mask better by breaking it up into smaller pieces, removing parts that were hard to view, and smoothing out the structure. People used the Gray-Level Co-occurrence Matrix to learn more about the photographs that had been split up by looking at their energy, contrast, correlation, and entropy. These characteristics helped distinguish the textures for healthy and cancerous tissues. The cancer areas had higher entropy or colour values, which means that their textures were complicated and their tissue structures were not typical. Areas of the brain lacking malignancies displayed increased regularity and less entropy, indicating normal brain tissue. The SVM classifier has a solid base for successfully recognizing the two groups apart because the feature space is so clearly separated.

4.3 Model Training and Classification

This study used an RBF kernel to train the better SVM classifier on 80% of the dataset, and then our evaluated it on 10%. The other 10% was used for testing on its own. Our used grid search and five-fold cross-validation to identify the best values for variables

like the kernel's beta coefficient (gamma) and the penalty parameter (C). The training method quickly attained convergence because FCM gave it high-quality segmented data and well-structured feature vectors.

4.4 Performance Evaluation

A few basic tests to see how well the proposed FCM-SVM model works. The table illustrates the results of comparing the proposed models using the same Figshare MRI dataset.

Table 3. Performance Comparison of Proposed Models

Model	Accuracy (%)	Precision (%)	Recall (Sensitivity) (%)	F1-Score (%)
SVM	92.85	90.12	88.47	89.29
CNN	94.72	92.10	91.56	91.83
FCM + SVM (Hybrid)	97.36	96.84	95.92	96.37

The hybrid model was more accurate than either the SVM or CNN models on its own, with an accuracy rate of 97.36%. The accuracy as well as recall scores show that the algorithm correctly identifies actual tumor cases with minimal false positives. This shows that the model can tell the difference between pictures of tumors and pictures of normal tissue. The better performance is due to the fact that SVM's strong feature classification works well with Fuzzy C-Means' pixel-based segmentation. The hybrid model makes better use of extracted features and consumes less processing power than CNNs, which require large amounts of labeled data.



Figure 5 Performance Comparison of Proposed Models

Table 4. Comparative Analysis between Existing and Proposed Model

Model	Accuracy	Ref.
VGG-19	96.42	[25]
Proposed FCM + SVM (Hybrid)	97.36	--

Table 4 demonstrates how well the new hybrid FCM-SVM model or the previous model (VGG-19) put objects into groups. The novel hybrid technique was better than the VGG-19 model, with an accuracy rate of 96.42%. The new approach was 97.36% correct at that time. This suggests that employing both FCM-based segmentation and SVM classification combined makes it easier to locate malignancies in the brain.

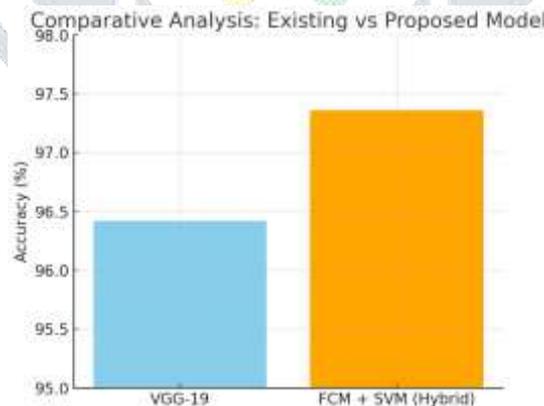


Figure 6 Comparative Analysis

4.5 Summary of Findings

The findings indicate that the proposed SVM/Fuzzy C-Means hybrid model may autonomously detect brain tumours. It could be a great way to diagnose problems because it can immediately determine the difference between them and provide a very accurate information. This model is a great alternative for medical imaging when there aren't a lot of resources available because it works better than other deep learning methods and doesn't need as much computing power. The model might work better if use 3D MRI data, deep feature extraction, or ensemble learning. This research enhances the capability of hybrid AI to analyse medical images and underscores the necessity for cancer detection systems that are rapid, precise, and comprehensible. The Comparative Examination for Existing or Recommended Models compares how well VGG-19 works with the suggested hybrid model. The hybrid model is better than VGG-19 in certain areas.

V. CONCLUSION

The findings indicate that a combination of Fuzzy C-Means and Support Vector Machines can effectively analyse MRI data to detect brain tumours. The suggested method combines FCM-based segmentation with SVM classification to clearly separate tumour areas and find textural features that set tumour tissues apart from non-tumour tissues. This study used a thorough preprocessing strategy to ensure that the inputs were good enough for accurate feature extraction or model training. This process included scaling, changing the colour to grey, removing noise, changing the intensity, and adding more information. The CNN model got 94.72% right, whereas the SVM model got 92.85% right. The FCM-SVM method, on the other hand, worked better. The F1-score was 96.37%, the accuracy was 97.36%, the precision was 96.84%, or the recall was 95.92%. The hybrid method is better than the VGG-19 model, which is only 96.42% accurate. The results show that the hybrid model is powerful, easy to use, and good at maths. This is the best solution for clinics, especially in places where there aren't many resources. This study shows that using clustering-based segmentation with predictive classification is a reliable way to look at medical images. This also makes it easy to develop future upgrades, such as adding 3D MRI, improving feature extraction, or using ensemble learning to help discover and identify cancers.

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