

GENETIC ALGORITHM AND CNN METHODS IN BRAIN TUMOR SEGMENTATION

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Abstract –

A correct diagnosis is the foremost step in receiving quality medical care. Vast information provided by medical imaging technology presents the interpreting physician with problems and probability. Diagnosis is a complex process that combines technical tools, patient history, practical reasoning, and the collective expertise in the field to interpret and connect the results of a specific examination procedure. Although it is challenging to design a completely computerized system for processing data on this variability, there are some situations in which a computerized system could provide helpful diagnostic assistance. Computer-aided systems are excellent at managing vast amounts of data and completing complex, time-consuming tasks quickly. Thus, the integration of a digital system and a human interpreter improves.

***keywords* – CNN Classifier, MR Image, Wrapper based GA**

I. INTRODUCTION

The intracranial malignancy fractionation challenge aims to assess advanced methods for segmenting cerebral malignancies using multi-parametric tomography technology. Since its inception, it has served as a publicly available dataset and a benchmark for testing. Pre-operative tomographic images are used to analyze intracranial malignancies, particularly focusing on glioma fractions, which are inherently diverse in appearance, shape, and

cytology. Additionally, BraTS 2018 emphasizes tumor patient survival prediction through integrated analyses of radiomic features and machine learning (ML) techniques, ensuring alignment with the practical requirements of the fractionation process. The BraTS dataset, which is continuously updated and expanded annually, contributed significant resources for this work.

Today's MRI systems can provide images of organs with up to 65,535 gray levels. Unquestionably important data obtained from the MRI scan cannot be reviewed using human eyes. This paves the path for the implementation of a computer-aided diagnosis system (CAD), which can thoroughly assess both high and low resolution MR images. CAD allows a radio surgeon to clearly examine the abnormal location of the damaged tissue structure. These characteristics have made image processing unavoidable, allowing millions of lives to be saved through timely and precise diagnosis. The initial stage of tumor segmentation and characterisation is characterized as the first discovery of the tumor in order to estimate its position for brain tumor diagnosis.

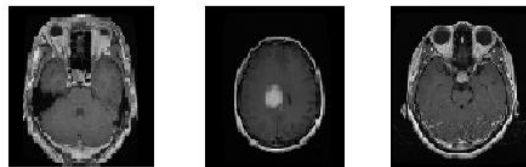


Figure 1: Brain Tumor Images.

II. RELATED WORK

Priyanka [1] demonstrated a Filter norm to remove impulsive noise from the input photos. The median filter maintains an image's edge while simultaneously reducing random noise. Ramalakshmi and JayaChandran [2] suggested an improved version of an isotropic norm that removes distortion while preserving the border points present. Vidyarthi and Mittal [3] developed a brain tumor extraction algorithm based on Otsu threshold segmentation. Preprocessing occurs during the early stage. The second phase defines the segmentation stage, in which the system employs threshold segmentation in addition to the watershed method. The goal is to simplify the description, which makes the image more relevant for processing. Threshold segmentation is one of the simplest ways of segmentation.

Vishal and Chaudhari [5] developed an autonomous malignancy detection system based on area growth. In this technological effort, the traditional region-growing method is used for segmentation. The seed selection technique is influenced by challenges related to automated seed creation. Automatic seed point selection is accomplished using the fuzzy c means method. It describes the region growth method and fuzzy c means method, as well as the design.

Arulselvi et al. [6] developed AdaBoost SVM-based brain tumour picture segmentation. They are noise removal and classification, texture formulation, and segmentation using multifractal features. Fisher SVM technique is better suited for segmenting complicated tumors. Zhanget al. [7] developed a new segmentation method based on AI and a hierarchical dice loss. Wang et al. [8] investigated automated malignancy bifurcation using the integration of deep CNN,

with regularization performed using a graph cut. The system analyzes various deep convolution network that are used in semantic and medical picture segmentation. Vidyarthi and Mittal [9] created an innovative texture-based feature extraction method to identify and extract relevant features from the brain.

.Rasel Ahmmed et al. [11] created an AI-powered model that includes steps such as picture preprocessing, fractioning, attribute isolation, SVM classification, and malignancy stage classification. Three contrast improvement approaches are utilized in pre-processing: adaptive thresholding, graphical picture representation, and minimal mean square filtering. After preprocessing and segmentation, it extracts features. Then SVM classifies the brain MRI picture as benign or malignant. The ANN classifier classifies the stage of the brain tumor. The number of statistics used for each MR image of a benign or afflicted tumor, with benign tumor obtained from 39 images. The brain MR pictures included 3 normal, 9 benign, 17 malignant I, 6 malignant II, 3 malignant II, and 1 malignant IV stage tumors.

Gaurav Gupta and Vinay Singh [12] devised a brain tumor prediction system that combines SVM and FCM. This algorithm improves the image using enhancement tactics such as contrast improvement and mid-range stretch. Double thresholding and morphological approaches have been for skull stripping. Fuzzy C-Means (FCM) clustering is used for image segmentation to identify suspicious spots in brain MR images. The GLRLM is used to takeout features from the image and the SVM technique is used to categorize the brain MRI images, yielding more efficient results in terms of accuracy [13].

Karim Gasmi ,Najib Ben Aoun proposed an innovative approach to brain tumor multi-classification by leveraging an ensemble learning method that combines advanced deep learning models with an optimal weighting strategy. This methodology integrates Vision Transformers (ViT) and EfficientNet-V2 models, both renowned for their powerful feature extraction capabilities in medical imaging. This model enhances the feature extraction step by capturing both global and local features, thanks to the combination of different deep learning models with the ViT model. These models are then combined using a weighted ensemble approach, where each model's prediction is assigned a weight. To optimize these weights, they employed a genetic algorithm, which iteratively selects the best weight combinations to maximize classification accuracy. Ttrained and validated ensemble model using a well-curated dataset comprising labeled brain MRI images. The model's performance was benchmarked against standalone ViT and EfficientNet-V2 models, as well as other traditional classifiers. The ensemble approach achieved a notable improvement in classification accuracy, precision, recall, and F1-score compared to individual models. Specifically, our model attained an accuracy rate of 95%, significantly outperforming existing methods [14].

Fatih CELIK, Kemal CELIK introduces an innovative approach known as the ensemble attention mechanism to address this challenge. This approach uses two networks to extract intermediate- and final-level feature maps from MobileNetV3 and EfficientNetB7. This assists in gathering the relevant feature maps from the different models at different levels. Then, the technique incorporates a co-attention mechanism into the intermediate and final feature map levels on both networks and ensembles them. This directs attention to certain

regions to extract global-level features at different levels. Ensemble of attentive feature maps enabling the precise detection of various feature patterns within brain tumor images at both model, local, and global levels. This leads to an improvement in the classification process. This proposed system was evaluated on the Figshare dataset and achieved an accuracy of 98.94%, and 98.48% for the BraTS 2019 dataset which is superior to other methods. Thus, it is robust and suitable for brain tumor detection in healthcare systems [15].

Mohamed R. Shoaib and Jun Zhao proposed a novel approach to brain tumour classification by exploring three pre-trained convolutional neural network (CNN) models: DenseNet201, EfficientNetB5, and InceptionResNetV2, combined with softmax activation for feature extraction. These features are then subjected to Principal Component Analysis (PCA) for dimensionality reduction. Subsequently, three machine learning models—Support Vector Machine (SVM), Multi-layer Perceptron (MLP), and Gaussian Naive Bayes (GNB)—are employed for classification. The results reveal that DenseNet201, when combined with SVM and MLP, outperforms the other models in terms of accuracy, recall, and precision. Specifically, DenseNet201 achieves 100% accuracy, recall, and precision on Dataset-I and 98% accuracy, recall, and precision on Dataset-II when paired with SVM and MLP [16].

Lubna Kiran, Asim Zeb introduces a cutting-edge deep-learning approach employing a binary convolutional neural network (BCNN) to address this. This method is employed to segment the 10 most prevalent brain tumor types and is a significant improvement over current models restricted to only segmenting four types. This methodology begins with acquiring MRI images, followed by a detailed preprocessing stage where images undergo binary conversion using an adaptive thresholding method and morphological operations. The segmentation identifies the tumor type and classifies it according to its grade (Grade I to Grade IV) and differentiates it from healthy brain tissue. The overall performance achieved by this model is 99.36%. The effectiveness of our model is underscored by its remarkable performance metrics, achieving 99.40% accuracy, 99.32% precision, 99.45% recall, and a 99.28% F-Measure in segmentation tasks [17].

Rahul Mapari Sangeeta Kakarwal proposed an automatic brain tumor segmentation and detection system using convolution neural network without human intervention, where an intrinsic set of features are extracted to perform the classification task. A deep learning framework is proposed to evaluate brain disease more accurately using a Black Widow Optimization driven Dense Convolution Neural Network (BW-DCNN)[18].

Sangeeta Kakarwal, Rahul Mapari introduces a novel Black Widow-Optimized Dense CNN (BW-DCNN) framework for the automated detection and segmentation of brain tumors in MRI scans, aiming to enhance early diagnosis and treatment planning. With the increasing frequency of brain tumors, early and accurate detection becomes crucial for effective treatment. Magnetic Resonance Imaging (MRI) is a diagnostic technique owing to its excellent sensitivity. However, manual MRI data analysis is time-consuming and prone to errors. Leveraging advancements in Convolutional Neural Networks (CNNs) and optimization algorithms, the proposed BW-DCNN framework utilizes a unique integration of preprocessing, segmentation enhancement, and classification techniques optimized through

Black Widow Optimization to improve diagnostic accuracy and efficiency. Evaluating the BW-DCNN framework against existing methodologies, including DCNN, DNN, and DBN, demonstrates superior performance across a comprehensive suite of metrics. These results highlight the potential of the BW-DCNN approach to significantly advance the capabilities of computer-aided diagnostic systems in medical imaging, offering a promising direction for future research and application in clinical settings [19].

P. Ashok Babu, B.V. Subba Rao introduces a work on classifying and segmenting brain tumors from MRI scan data. It aids physicians in the planning of future care or surgery. This procedure consists of four steps: image de-noising, tumor extraction, attribute extraction, and hybrid classification. In the first step of image de-noising, the curvelet transformation (CT) is used. Then, in the next stage, Artificial Bee Colony (ABC) Optimization is used in conjunction with the thresholding process to remove tumors from brain MRI scans. Another optimization approach is used to recover the learning rate of the Convolutional Neural Network for the final hybrid classification. The experiment model is assessed by using the multimodal brain tumor (BRATS) 2013 and 2015 challenge datasets from medical image computing. The outcomes of the experiment presented that the method achieved the segmentation 95.23% and 94% of accuracy, where the proposed optimized CNN achieved classification accuracy of 98.5% and 99% for both datasets [20].

A comprehensive survey was conducted in the areas of MRI brain image preprocessing, fractionation, feature extraction, feature selection, and classification. The survey clearly shows that brain tumor categorization has to be improved in terms of recognition rate, accuracy, and precision.

III. PROPOSED METHODOLOGY

In the proposed study, a wrapper-based genetic algorithm combined with CNN-based segmentation is used. The image is preprocessed to isolate the region of interest. The preprocessed image is then divided into blocks, and the textural features are extracted. The evolutionary algorithm selects relevant attributes from the feature set, while the wrapper approach optimizes these selected features. The resulting feature matrix is used to train the classifier. Figure 2 illustrates the framework of the proposed system, with each module detailed in the following section

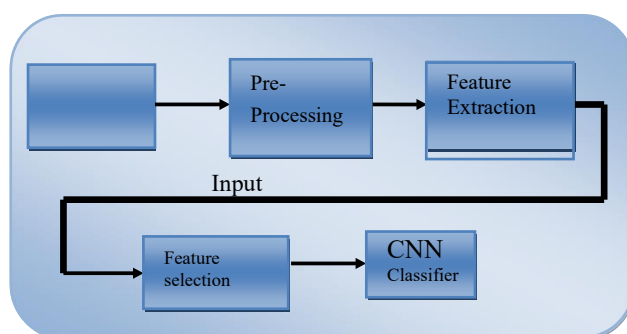


Figure2: Block diagram for the wrapper based GA using CNN for brain tumor segmentation.

A. Image Preprocessing

The suggested approach involves pre-processing the image with the goal of improving its finer shape and removing extraneous noise. Here, significance refers to background separation with the goal of attaining the area of interest (ROI). The pre-processing stage includes activities such as thresholding, region filling, morphological operations, and masking. Thresholding converts grayscale images to binary images, area filling eliminates holes in binary images, and morphological processes are mostly used to eliminate noise from the background. Finally, masking is used to encapsulate the block by hiding its underlying functionality and creating a user interface for it.

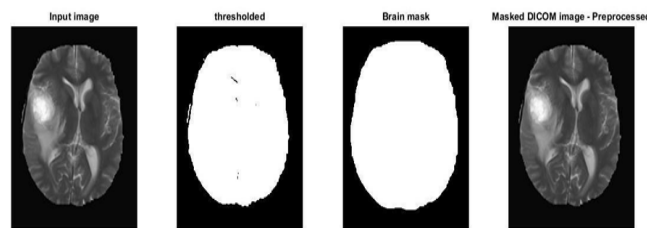


Figure3: Different stages in image Pre-processing

B. Feature Extraction

The rationale for element extraction is to reduce the first dataset by identifying a few features. This data is fed back into the classifier for image grouping and division purposes.

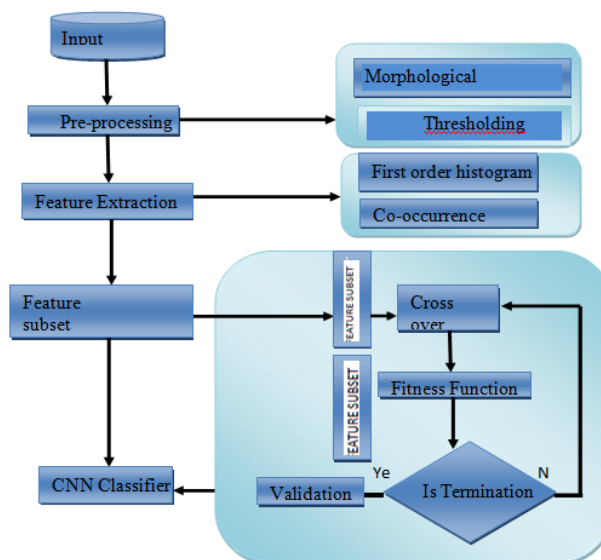


Figure4: Detailed Block Diagram for proposed Method

C. Texture based feature extraction

Features often represent characteristics such as color, shape, texture, or context. Key feature categories include transformed features, spatial features, color features, edge and boundary features, shape features, texture features, and others. In the our work texture features are derived using two methods: the first-order histogram approach and the co-occurrence matrix-based technique.

D. Feature extraction by first order histogram

Histograms give statistical data about an image. The predicted solidity of visibility of an image in terms of intensity levels is given as the ratio of the histogram's intensity level to the picture's overall pixel value.

$$P(i) = \frac{h(i)}{NM}, \quad i = 0, 1, \dots, G - 1$$

M signifies the resolution cell number, while N is the number of resolution cells in the vertical and horizontal spatial domains, respectively. G denotes the image's entire gray level. The first order histogram yields essential properties such as mean, skewness, kurtosis, energy, and entropy.

E. Feature extraction by co-occurrence matrix

Histogram-based feature extraction yields just neighborhood features, thus we employ occurrence matrix-based include extraction to account for spatial aspects. The GLCM network calculates the frequency in a predetermined spatial area using the grey level value. The number of rows and columns in a GLCM matrix represents the number of gray levels or pixel values on the image surface. The following equations define feature extraction from the provided image:

$$\text{Angular second moment (energy)} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} [P(i, j)]^2$$

$$\text{Correlation} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{ij P(i, j) - \mu_x \mu_y}{\sigma_x \sigma_y}$$

$$\text{Inertia} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (i - j) P(i, j)$$

$$\text{Absolute value} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} |i - j| P(i, j)$$

$$\text{Inverse difference} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} P(i, j) / (1 + (i - j)^2)$$

$$\text{Entropy} = H = - \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} P(i, j) \log_2 [P(i, j)]$$

$$\text{Maximum probability} = \max_{i, j} P(i, j)$$

F. Feature Selection

The proposed method uses a genetic algorithm to select characteristics. A genetic calculation is a population-based experimental search technique that removes the natural developmental history of humans. Cycles in a genetic algorithm are repeating procedures that manipulate one chromosome inhabitant (arrangement possibility) to create an original population. This is accomplished through inherited abilities such as hybrid and change. It is similar to how

Charles Darwin represented genetic recombination, propagation, and natural selection. An answer competitor's wellness is judged using a capability sometimes referred to as a fitness function.

G. Genetic algorithm based feature selection

A genetic algorithm is employed to reduce the dimensionality of the component space and improve the classifier's presentation. The important steps of genetic calculating [15] include wellness assessment, chromosome encoding, choice strategy, hereditary administrators, and condition halt emphasis. In the paired search space, genetic algorithms treat chromosomes as a piece string.

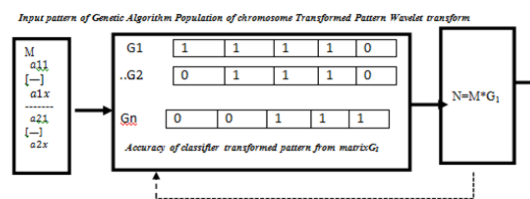


Figure5: Matrix representation of chromosome in genetic algorithm

Computation steps:

- Step 1:** Select the initial population of individuals.
- Step 2:** Evaluate the robustness and fitness of the population.
- Step 3:** Repeat the peer group process until termination criteria are met (e.g., time limit, desired fitness level)

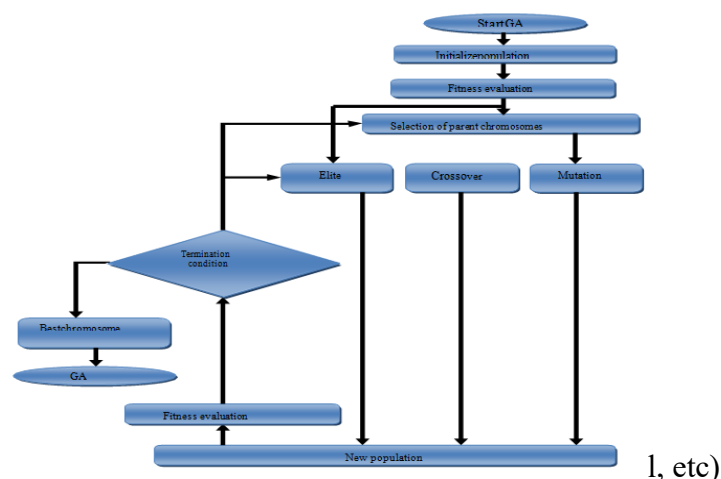


Figure 6: GA based feature selection

- ☐ The fittest individuals are selected for reproduction.
- ☐ New individuals are generated through crossover and replication processes.
- ☐ Fitness evaluation is performed for the new individuals.
- The least fit individuals are replaced with the newly generated ones.

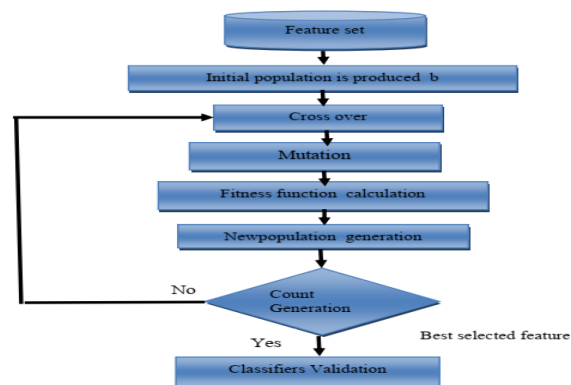


Figure7: Flowchart for optimal feature selection by Wrapper method.

H. Deep Structured Learning Method

CNNs consist of two 3x3 convolution layers grouped into a single block, utilizing the Rectified Linear Unit (ReLU) activation function. ReLU introduces nonlinearity into the network, enhancing its ability to generalize training data. The corresponding decoder block provides a skip connection to the ReLU output. Following the ReLU activation, a dropout function is applied, which randomly disables a subset of neurons. This encourages to learn new representations, promoting neuron independence and improving generalization while reducing the risk of over fitting. Finally, a 2x2 max-pooling operation is used to halve the spatial height and width of the feature maps. Figure 7 illustrates the CNN architecture..

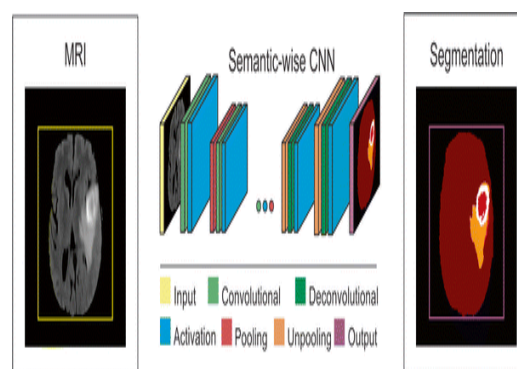


Figure8: CNN Image segmentation

A convolutional neural network model with 41 layers, including convolutions (only 3*3 size), max pooling (only 2*2 size), and fully connected layers. Figure8.

ANN is a more extensive strategy than the edge detection method. When compared to other methods, ANN [10] are particularly effective since they have a lower operating burden and provide effective benefits for reducing noise [11]. As an artificial neural network is used, it is possible to use a large number of inputs and outputs throughout the training process.

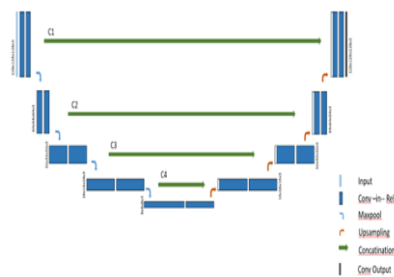


Figure9: U-net architecture

- The Sigmoid Function curve looks like a S-shape.

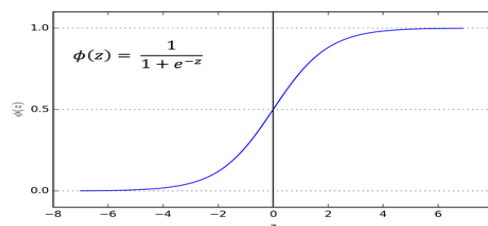


Figure10. Sigmoid function

IV. RESULTS AND DISCUSSION

This section discusses segmentation utilizing wrapper-based GA with CNN. The performance assessment took into account a set of 30 FLAIR and T2 images (23 abnormal and 7 normal); 95 of these items were used in training, while 30 were used in testing. The results are evaluated in terms of accuracy, AVME, and figure of merit. In this article, we compare the suggested work to SVM. Table 1 of Specificity shows the specificity of the Wrapper-based GA with SVM segmentation versus the existing FCM-based segmentation for both T2 and FLAIR pictures.

	FLAIR		T2	
Da ta	SVM (%)	CN N (%)	SVM (%)	CNN (%)
1	98.59 23	99.5 838	96.8602	99.883 9
2	99.00 07	99.6 829	96.8856	99.949 1
3	98.96 68	99.6 765	96.7296	99.967 1
4	99.26 18	99.6 969	96.5252	99.940 0
5	99.52	99.8	96.3061	99.994

	06	522		0
6	99.51 48	99.8 343	96.2331	99.997 0
7	99.52 10	99.7 590	96.1287	99.991 0
8	99.46 70	99.8 163	95.9441	99.991 0
9	99.12 25	99.5 867	95.8313	99.895 2
10	98.87 96	99.7 162	95.7276	99.952 2

Table1: Statistical Comparison for FLAIR and T2

	FLAIR		T2	
Data	SVM (%)	CNN (%)	SVM (%)	CNN (%)
1	98.96 41	98.58 51	96.145 8	98.9554
2	98.59 66	98.91 78	93.703 7	98.4983
3	98.46 35	98.88 31	93.454 9	98.4086
4	98.55 32	99.02 78	93.078 7	98.2002
5	98.47 22	99.18 11	92.413 2	97.9080
6	98.78 47	99.16 09	92.401 6	98.0874
7	98.75 00	99.11 75	92.326 4	98.1424
8	98.69 21	99.06 54	92.199 1	98.0150
9	98.57	98.88	92.592	98.1800

	93	31	6	
10	98.73 55	98.73 55	92.711 2	97.9514

Table2: Statistical comparison in terms of accuracy for wrapper based GA using SVM segmentation and FCM

The table above compares the accuracy of wrapper-based GA utilizing SVM segmentation and FCM. Results reveal that the GA-based SVM approach achieves an accuracy of 99.25% for FLAIR and 98.28% for T2, compared to FCM of 98.67% for FLAIR and 97.16% for T2. This result demonstrates Wrapper-based GA's accuracy with SVM segmentation. Table 3 presents a statistical comparison of FLAIR and T2 images. Tables 4 and 5 present an examination of SVM and CNN. The figure of merit for the two techniques is provided in Table 6. Volumetric analysis of manually and automatically segmented multimodality images.

	FLAIR		T2	
Dat a	SVM (Sec)	CNN (Sec)	SVM (Sec)	CNN (Sec)
1	0.106 44	0.687 467	0.2470 04	0.46 3591
2	0.103 34	0.701 177	0.0721 35	0.23 1283
3	0.095 835	0.683 585	0.0805 58	0.25 4667
4	0.108 671	0.652 442	0.1046 23	0.32 9427
5	0.107 736	0.960 127	0.0746 04	0.24 3118
6	0.133 56	0.980 784	0.0755 99	0.23 6125
7	0.103 878	0.740 483	0.0792 58	0.31 1487
8	0.093 298	0.819 494	0.0723 11	0.22 6894
9	0.096 376	0.677 372	0.1069 21	0.24 8339
10	0.100	0.699	0.0819	0.24

	872	691	79	2185
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Table 3: Statistical comparison of multimodality input image in terms of time elapsed.

Data	SVM(pi xels)	CNN(pi xels)
1	18432	27007
2	14679	9232
3	29742	22821
4	7623	11453
5	18789	3271
6	13654	22732
7	12957	6437
8	29394	13480
9	6327	8282
10	18432	27007

Table 4: Volume Measurement Comparison for FCM and SVM in Absolute Segmentation

Data	SVM(pi xels)	CNN(pi xels)
1	-17.35	21.102
2	20.093	-24.47
3	-2.11	-24.889
4	-21.27	18.292
5	76.754	-69.229
6	-38.77	1.9326
7	6.0051	-47.337
8	-3.255	-55.633
9	-34.65	-14.46
10	-17.35	21.102

Table 5: Quantitative Assessment of Input Images Using a Performance Metric

Data	SVM	CNN
1	0.788978	0.82651
2	0.755297	0.799067

3	0.751111	0.978903
4	0.817083	0.787337
5	0.307714	0.232455
6	0.980674	0.61226
7	0.52663	0.939949
8	0.443669	0.967449
9	0.855402	0.653481
10	0.134055	0.477234

Table 6: Volumetric analysis for multimodality image.

Image Type	Data	Manual Segmentation Method	Automatic segmentation		Absolute measurement		volume
			SVM	CNN	SVM	CNN	
FLAIR	1	22301	1843	2700	-17.3	21.102	
	2	12223	1467	9232	20.093	-24.47	
	3	30383	2974	2282	-2.1	-24.889	
	4	9682	7623	1145	-21.2	18.292	
	5	10630	1878	3271	76.754	-69.229	
T2	6	22301	1365	2273	-38.7	1.9326	
	7	12223	1295	6437	6.0051	-47.337	
	8	30383	2939	1348	-3.25	-55.633	
	9	9682	6327	8282	-34.6	-14.46	

	10	10630	1618	1425	52.277	-86.595
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Table 7: Analysis for multimodality image FLAIR and T2.

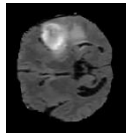
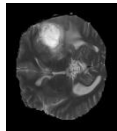
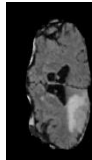
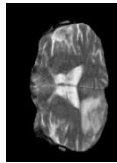
Input image (FLAIR andT2)	Segmente d output for FCM	Segmented output for SVM
		
		
		
		

Figure 11: overall efficiency of the proposed system.

In Figure 11, the first column is FLAIR and T2, the second column is the output image using the FCM algorithm, and the third column is the splitted output image utilizing wrapper-based GA with CNN. Hence, the total efficiencyis verified.

V. CONCLUSION

Computer-aided systems excel at handling large datasets and performing time-intensive, complex tasks efficiently. Combining a human interpreter with a digital system enhances diagnostic accuracy and sensitivity while minimizing errors. This work introduces a

computerized technique for identifying brain tumors using MR images. The system offers two significant advantages: first, it eliminates the need for time-consuming manual processes like tumor region demarcation; second, it come up with diagnostic support on a per-lesion basis, particularly benefiting clinicians with limited experience. The proposed system provides an optimal feature subset selection alongside a CNN classifier, enhancing its efficiency. The experimental results are also discussed..

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