

DETECTION OF BRAIN TUMOR AND PREDICTION OF SEVERITY ANALYSIS USING OPTIMIZATION DRIVEN 3D CONVOLUTION NEURAL NETWORK

Mr.BHASKAR MEKALA¹, Dr.NEELAMADHAB PADHY², Dr. P.KIRAN KUMAR REDDY³

¹Research Scholar, Department of Computer Science Engineering, GIET University Gunpur, Odisha, India

²Professor, Department of Computer Science Engineering, GIET University Gunpur, Odisha, India

³Professor, Department of Computer Science Engineering, MLR Institute of Technology, JNTUH, Hyderabad, Telangana, India.

E-mail: ¹bhaskar.mekala@giet.edu, ²dr.neelamadhab@giet.edu, ³kiran.penubaka@gmail.com

ABSTRACT

Accurate assessment of brain tumor severity plays a pivotal role in effective diagnosis and treatment planning. In this research, a comprehensive framework for brain tumor severity analysis is proposed, leveraging advanced preprocessing, segmentation, feature extraction and deep learning techniques. The preprocessing phase employs an adaptive bilateral filter to mitigate noise and enhance image quality. Subsequently, a segmentation approach utilizing slap swarm boosted rough fuzzy c-means optimally partitions the brain images, facilitating precise tumor localization. Feature extraction is performed using Mayfly optimization driven 3D Convolution Neural Network (MO-3DCNN), effectively capturing discriminative information from the segmented regions. The core innovation of this research lies in the development of a novel MO-3DCNN model, driven by the Mayfly optimization-derived features. This model enables a more comprehensive analysis by considering the spatial context of the brain tumor. The proposed MO-3DCNN model is trained to recognize intricate patterns within the segmented regions, enabling automated severity classification. Extensive experiments on a diverse dataset determine the superiority of the proposed methodology over existing approaches. Moreover, the proposed MO-3DCNN model outperforms in accurately stratifying brain tumor severity, highlighting its potential as a valuable clinical tool.

Keywords: *Convolution Neural Network, Rough Fuzzy C-Means, Slaps Swarm Optimization, Mayfly Optimization, And Adaptive Bilateral Filter.*

1. INTRODUCTION

This guide provides details to assist authors in preparing a paper for publication in jatit so that there is a consistency among papers. These instructions give guidance on layout, style, illustrations and references and serve as a model for authors to emulate. Please follow these specifications closely as papers which do not meet the standards laid down, will not be published.

Brain tumor are abnormal growths of cells within the brain, which can be either benign (non-cancerous) or malignant (cancerous). Their uncontrolled growth and potential invasion of surrounding brain tissue pose significant health risks and may lead to life-threatening conditions

[1]. There are two major level of brain tumor, they are primary and secondary level. Primary brain tumor involves benign or malignant stage and can be occurs in children. It originates from the neurons comprising the nervous system [2]. A secondary brain tumor, also referred to as metastatic, originates from cells in any part of the body that can spread from one region to another [3]. With this seriousness, diagnosis for identifying of brain tumor is essential at earlier stage for avoiding threats. Early detection of brain and accurate assessment of their severity play a pivotal role in determining the most appropriate treatment strategies, optimizing patient outcomes, and improving the overall quality of life for affected individuals [4]. Over the years, advances in medical imaging, computational techniques,

and artificial intelligence have revolutionized the field of brain tumor detection and severity analysis. Non-invasive imaging modalities such as Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), and functional imaging techniques, provide detailed insights into brain structures and pathological changes associated with brain. These imaging modalities, combined with sophisticated computational algorithms, facilitate the identification, localization, and characterization of brain with increased accuracy and precision [5].

Severity analysis of brain tumor is equally crucial, as it enables healthcare professionals to determine the tumor's aggressiveness, infiltration into critical brain regions, and potential impact on neurological functions [6]. Accurate severity assessment aids in the selection of appropriate treatment strategies, ranging from surgical resection, radiation therapy, and chemotherapy to targeted therapies and immunotherapies. The ability to tailor treatment plans based on the tumor's specific characteristics contributes to more personalized and effective patient care [7]. Moreover, the emergence of artificial intelligence (AI) and machine learning techniques has further propelled the field of brain tumor detection and severity analysis. AI-driven algorithms, particularly deep learning models, demonstrate remarkable capabilities in automating tumor segmentation, classification, and predicting patient outcomes [8]. These AI-powered tools assist radiologists and clinicians in making more informed decisions, reducing diagnostic time, and enhancing overall diagnostic accuracy. However, challenges persist in brain tumor detection and severity analysis [9]. The complexity of brain tumor behaviour, inter-tumor heterogeneity, and the need for comprehensive multi-modal analysis require ongoing research and collaboration between medical experts, researchers, and technologists. In this context, this research aims to explore the latest advancements, methodologies, and novel approaches in brain tumor detection and severity analysis [10]. By delving into the existing literature, evaluating cutting-edge technologies, this study endeavours to contribute to the ever-evolving field of medical community, ultimately benefiting patients and advancing medical knowledge for improved brain tumor management.

In recent years, there has been a growing interest in developing advanced 3D imaging techniques for brain tumor severity analysis [11].

These techniques enable a more comprehensive evaluation of tumor characteristics, including size, shape, location, and infiltration into surrounding brain tissue [12]. By providing a more accurate representation of tumor morphology and spatial relationships, 3D based deep learning techniques can offer valuable insights into tumor behaviour and prognosis. One approach to 3D brain tumor severity analysis is the utilization of volumetric imaging modalities, such as volumetric MRI. These techniques acquire a series of images that cover the entire tumor volume, allowing for a more detailed assessment of tumor size and growth patterns [13]. Volumetric imaging also facilitates the visualization of tumor heterogeneity, which can be an important indicator of tumor aggressiveness. In addition to volumetric imaging, advanced image processing and analysis techniques have been developed to extract quantitative features from brain tumor images [14]. These features include texture analysis, shape analysis, and intensity-based measurements, which can provide valuable information about tumor characteristics and behaviour. Deep learning algorithms can then be employed to integrate these features and develop predictive models for tumor severity assessment [15]. The primary contributions and innovative aspects of the proposed method are as follows:

The method incorporates a novel pre-processing step utilizing an adaptive bilateral filter. The adaptive bilateral filter ensures an optimal balance between smoothing and edge preservation, preparing the input data for more effective subsequent analysis.

The proposed method introduces an innovative approach to image segmentation using Rough Fuzzy C-Means (RFCM) with centroid optimization facilitated by Slap Swarm Optimization (SSO). This combination optimizes the clustering process, leading to more accurate and robust segmentation of brain tumor regions.

The method employs a unique optimization strategy for hyper parameter tuning in the 3DCNN architecture using Mayfly Optimization (MO). This adaptive optimization technique enhances the performance of the 3DCNN by efficiently exploring the hyper parameter space. By leveraging the mayfly algorithm, the proposed method achieves superior model configurations, resulting in enhanced accuracy in brain tumor detection and severity prediction.

The manuscript is structured as follows: Section 2 provides a detailed literature review,

while Section 3 illustrates the research gap. Section 4 briefly outlines the proposed research methodology. Subsequent sections elaborate on the dataset description and experimental results. The final section presents the conclusion.

2. LITERATURE REVIEW

According to ongoing research, automated computerized methods for determining the presence and severity of brain tumor present a number of difficulties. The challenges were from the changing tumor shape, size, location of the lesion, in-time examination of the lesion site, and varied images from scanning techniques. Additionally, only a small number of studies employing 3D methods to diagnose brain tumor have been conducted. This section reviews a number of previous studies while outlining each one's particular technical limitations, which served as the motivation for creating a new method for analysing severity of brain.

In the year 2020, Harish et al. [20] have described a deep learning method for identifying and categorizing brain MRIs. For the purpose of detecting brain, they created the Enhanced Faster Region-based Convolutional Neural Network (Enhanced Faster R-CNN). An "optimization-based edge detection approach using genetic algorithm" has been studied by Abdel et al. Simple images are examined in the training dataset using edge features to obtain the best thresholding features and filter coefficients. Its primary use is to locate the borders of the brain tumor regions, and the Balance Contrast Enhancement (BCE) model was used to extract features from the brain picture in order to describe the image properties. Additionally, the edge detection technique was used; however, it did not improve the performance of the proposed solution in terms of metrics. A brain metastasis identification method has been developed by E. Dikici et al. [23] using a single-sequence gadolinium-enhanced T1-weighted 3D MRI dataset. The approach that was given was solely concerned with finding very small lesion areas—less than 15 millimetres—and it required several steps to get there. It then moves on to selecting the candidate region using a Laplacian-based Gaussian approach, and iteratively moves on to the detection phase using a clipped region of interest and trained three-dimensional Convolutional Neural Network. Data augmentation was handled through a pipeline method with an elastic deformation and gamma

correction step due to the inefficiency of the input source. This in turn makes the output layer's environment noisier. Furthermore, Dandil et al [22] investigated deep neural network-based binary classification for brain. Bidirectional Long Short-Term Memory (Bi-LSTM) and Long Short-Term Memory (LSTM) over stacked model were both used to support the deep learning network. Signals are monitored and processed from the areas of brain tissue with the goal of finding brain. The resulting number of signal dataset is used for both the training and testing phases of the LSTM framework.

The Introduction and Literature Review to appropriate and emphasize our contributions. Prior research has conducted noise reduction using bilateral filtering, fuzzy C-means for segmentation, and used CNN-based models for the classification, but they usually omit adaptive preprocessing, stable high-dimensional clustering, and using optimum deep learning with respects severity analysis. In this study, we focus on closing these gaps by adding adaptive bilateral filtering, slap swarm-boosted rough fuzzy C-means segmentation, and finally a Mayfly Optimization 3D CNN into a unified framework, which attained 98.48% accuracy and surpassed state-of-the-art approaches regarding the generated image quality and classification metrics. In this way we aim to provide a contribution to the implementation of automated brain tumor severity analysis.

In the year 2021, Sharif et al. [16] have undertaken a pioneering effort in the domain of brain tumor analysis by introducing a novel approach that combines a pre-trained Deep Learning model, feature selection techniques, and advanced classification methodologies. Their study focuses on leveraging the potential of the Densenet201 Pre-Trained Deep Learning Model for brain tumor analysis. In doing so, they address the challenge of imbalanced data learning through a deep transfer learning paradigm. Entropy–Kurtosis-based High Feature Values (EKbHFV) was presented in this study. This approach selects features that exhibit high entropy and kurtosis values, thereby prioritizing those characteristics that demonstrate significant variations within the dataset. Then a modified genetic algorithm (MGA) rooted in met heuristics was developed. The MGA aims to identify the most relevant features for classification through a process of evolution-inspired optimization. The research analysed by Gurunathan et al. [17] delves into the realm of brain tumor detection and segmentation,

employing a multi-faceted methodology that combines data augmentation, Convolutional neural networks (CNNs), and morphological-based segmentation. The objective of their study is to enhance the accuracy and precision of brain tumor analysis using a comprehensive approach. Data augmentation takes centre stage as a pre-processing technique, augmenting the available brain MRI images to expand the diversity of the dataset. An intriguing advancement within this research involves the further classification of segmented tumor regions into "Mild" and "Severe" cases. This classification process, again leveraging CNN architecture, refines the analysis by categorizing tumors based on their severity, thereby aiding in clinical decision-making. The work by Khan et al. [18] stands as a significant contribution to the field of brain tumor classification, harnessing the capabilities of deep learning and MRI data analysis to provide valuable assistance to medical practitioners. Their proposed approach constitutes a multi-phased methodology designed to enhance accuracy in brain tumor classification, ultimately aiding clinicians in making informed decisions. The recommended methodology is divided into three key phases, each playing a critical role in the overall process. The first phase encompasses preprocessing, which involves preparing the MRI data for subsequent analysis. In the second phase, brain tumor segmentation is executed using the k-means clustering technique. This approach identifies distinct clusters within the MRI data, allowing the isolation of tumor regions from healthy brain tissue. Finally, the classification task is facilitated through the utilization of a finetuned VGG19 model.

In the year 2022, Aamir et al. [19] presented an automated approach for detecting brain cancers using MRI. The process begins with pre-processing brain MRI images to enhance visual clarity. Subsequently, two pre-trained deep learning models are employed to extract meaningful features from the images. The obtained feature vectors are merged into a hybrid feature vector using the partial least squares (PLS) approach. Finally, agglomerative clustering is applied to pinpoint the primary tumor areas. These suggestions are then sized and sized aligned before being sent to the head network for categorization. For the purpose of detecting brain tumors using MR images, Rammurthy et al. [21] present the Whale Harris Hawks optimization (WHHO) optimization-driven method. Here, segmentation is carried out via rough set theory

and cellular automata. Additionally, the segments' features—such as tumor size, Local Optical Oriented Pattern (LOOP), Mean, Variance, and Kurtosis—are retrieved. Additionally, deep Convolutional neural networks (DeepCNN), whose training is carried out using suggested WHHO, are used to identify brain tumors. Whale optimization algorithm (WOA) and Harris hawks optimization (HHO) algorithm integration was used to create the suggested WHHO.

The accurate assessment of brain tumors remains a problem due to weaknesses in segmentation robustness, feature optimization, and 3D spatial information. This study develops an overall approach to brain tumor classification by implementing adaptive pre-processing, slap swarm boosted rough fuzzy c-means segmentation and Mayfly optimization-driven 3D CNN (MO-3DCNN) to properly classify severity. This study seeks to answer several key questions on how to improve MRI quality, optimize segmentation processes and increase the performance of CNN based image classification to yield detailed and precise classification of brain tumor severity class.

The research protocol for this study was a combination of established methods in medical image processing and brain tumor analysis. When we reference the former, we cluster prior studies on noise reduction and skull stripping (Ismael & Abdel-Qader, 2018; Menze et al., 2015) and apply an adaptive bilateral filter that removes noise from an MR image while retaining the tumor borders. When we refer to segmentation, we apply methods that we took inspiration from classical clustering approaches such as fuzzy c-means (Pham et al., 2000) and swarm intelligence methods such as clustering outlined in (Kennedy & Eberhart, 1995; Mafarja et al., 2020). We employed a slap swarm-boosted rough fuzzy c-means method to cluster voxel contain tumor tissue, which gave us better object colony and distant estimates of tumor delineation as can be observed by our empirical analysis. We adopted a clear solution to stiffness of traditional CNN-based classification (Pereira et al., 2016; Kamnitsas et al., 2017) and incorporated Mayfly Optimization (Zervoudakis & Tsafarakis, 2020) hyperparameter tuning of a 3D CNN that provided higher accuracy of extracted features and severity classifications of brain tumor from MRIs. We validated our protocol with a completely open representation of our research protocol utilizing the BRATS 2020 dataset in

alignment with previous benchmarking efforts such as the BRATS 2015 study (Menze et al., 2015), with the aim facilitating trustworthy state-of-the-art comparisons of our framework against existing studies. Our protocol utilizes noise-reduced preprocessing, swarm intelligence in segmentation, and optimization in deep learning in one complete pipeline. The protocols advance our automated severity analysis of brain tumors study more thoroughly and address development needs in the existing literature.

3. RESEARCH METHODOLOGY

In recent years, the application of deep learning techniques, particularly Convolutional Neural Networks (CNNs), has revolutionized medical image analysis. Among these, 3D Convolutional Neural Networks (3DCNNs) stand out for their capacity to effectively capture spatial information within volumetric data, such as MRI scans. This research proposes a methodology that harnesses the power of 3DCNNs to automate the analysis of brain tumor severity through MRI scans. The primary objective of this study is to develop a robust and accurate model capable of categorizing brain tumors into different severity levels based on 3D MRI data. By leveraging deep learning techniques, this methodology seeks to enhance the efficiency and reliability of tumor severity assessment, thereby contributing to improved patient care. Through the implementation of this methodology, we Endeavour to offer a novel approach to brain tumor severity analysis, demonstrating the capabilities of MO-3DCNNs in the realm of medical image analysis. By automating and enhancing the accuracy of tumor severity assessment, we aspire to contribute significantly to the field of neuroimaging and pave the way for more effective and timely interventions for patients with brain tumors. The layout of the proposed methodology is diagrammatically shown in figure 1: The brain MRI input undergoes a pre-processing stage, during which the adaptive bilateral filter is employed to enhance image quality. The disease-dominant area is then segmented using the slap swarm boosted rough fuzzy c-means algorithm. Subsequently, the feature extraction module operates, utilizing the MO-3DCNN architecture. This module plays a crucial role in classifying distinct severity levels of brain tumors.

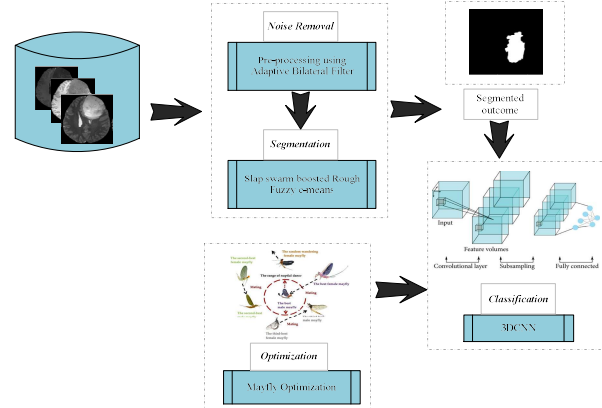


Fig 1: Overall layout of the proposed Methodology for brain tumor severity analysis

The implementation of our proposed method takes place within the Python platform, and its performance is evaluated through comprehensive comparisons against established methodologies. Enhancing Image Quality using Adaptive Bilateral Filter

The precision of medical diagnoses and analyses greatly depends on the quality of brain imaging. Within the scope of our presented methodology, our objective is to elevate the ability of brain images through the implementation of an adaptive bilateral filtering approach. By adopting this method, we can effectively diminish noise interference, all the while conserving crucial image intricacies. This interaction results in discriminating image quality, consequently paving the way for more precise medical interpretations. Distinguishing itself from conventional bilateral filters that adhere to fixed kernel parameters, the adaptive bilateral filter embraces a dynamic parameter adjustment mechanism, guided by the local characteristics of the image. The mathematical expression of our proposed adaptive bilateral model is elucidated in the following Equation (1).

$$E(y) = h_y^{-1} \sum_{n \in S_b} B_t(E_{no}) \times C_s(V_{no}) \times J(y) \quad (1)$$

Here the symbol h_y^{-1} designates the normalized vector, while B_t and C_s delineate the spatial dimension of kernel function, associated with their respective weight value E_{no} and V_{no} . The MRI database input image is denoted as $J(y)$. The weight values are deduced as the disparities between the pixel measurements, determined by the computation of Euclidean distance. Precisely, the normalized vector is defined in a statistical manner as follows:

$$h_y = \sum_{n \in S_0} B_t(E_{no}) \times C_s(V_{no}) \quad (2)$$

Similarly, the filtering approach's kernel functions are expressed as follows:

$$B_t(E_{no}) = \exp(E_{no}^2 / 2 \times \sigma_t^2) \quad (3)$$

$$C_s(V_{no}) = \exp(V_{no}^2 / 2 \times \sigma_s^2) \quad (4)$$

The Gaussian function is harnessed to augment the weight distribution components of the kernel, with scaling parameters are denoted as σ_t^2 and σ_s^2 . This specific phrase is intricately linked to the Gaussian function, encapsulating the intensity dispersion characteristics of the kernel function. The kernel function's weighting hinges on the central coordinates of the pixel value. The adaptive bilateral filter effectively enhances the quality of brain MRI images by reducing noise while preserving important image details. This leads to improved image clarity, which in turn facilitates more accurate medical interpretation and diagnosis. The adaptive nature of the filter allows it to dynamically adjust its parameters based on local image characteristics, striking a balance between noise reduction and edge preservation.

Segmentation for Brain Tumor Severity Analysis

In the domain of automated analysis of brain tumor severity, precise segmentation plays a pivotal role in localizing distinct cell types and aggregating similar cells, facilitating accurate assessment. The segmentation of brain MRI images serves as the foundational stride for subsequent analysis endeavours. To address this critical phase, we introduce an optimization-based approach to Rough Fuzzy c-means segmentation [24], harnessing its capacity to delineate discrete regions within brain MRIs. The prime goal of segmentation is to partition an image into cohesive regions, with each region corresponding to a specific anatomical structure or cell category. The Optimization-based Rough Fuzzy c-means technique achieves this by assigning membership functions to individual data points according to their proximity to cluster centres within the image. This allocation of membership functions captures the inherent uncertainty in classifying each data point, thus enabling a supple representation of the image's content. Notably, the distance between each data point and the cluster centres underpins this membership assignment. By jointly considering the spatial distribution and intensity values of data points, the proposed approach attains a more comprehensive depiction of the underlying structures present in MRIs. This proves

particularly beneficial in the analysis of brain tumor severity, where nuanced variations in tumor attributes demand meticulous segmentation. The segmentation procedure progressively refines cluster centres through iterative adjustments guided by the assigned membership functions. This dynamic evolution is symbolized mathematically as,

$$\varphi^{ij} = \frac{1}{\sum_{k=1}^c \left(\frac{D^{ij}}{D^{ik}} \right)^{\left(\frac{2}{m} - 1 \right)}} \quad (5)$$

$$V^j = \frac{\left(\sum_{i=1}^N (\varphi^{ij})^m x^i \right)}{\left(\sum_{i=1}^N (\varphi^{ij})^m \right)}, \forall j=1,2,\dots,c \quad (6)$$

The quantity of data points is labeled as N . Let V^j , denote the j^{th} central cluster in index m , representing the level of fuzziness $m \in [1, \infty]$. The central cluster is denoted as c .

In this context, φ^{ij} signifies the association of the j^{th} information with the j^{th} center cluster. The key factor within D^{ij} is the Euclidean distance between the j^{th} data group and the j^{th} center. This iterative refinement process allows the method to capture intricate specifics and delineations present in MRI images. These details are crucial for precise cell type localization and subsequent severity analysis. The primary objective of the Rough Fuzzy C-means algorithm minimize is represented as

$$J(u, v) = \sum_{i=1}^N \sum_{j=1}^c (\varphi^{ij})^m \|x^i - v^j\|^2 \quad (7)$$

Consequently, the cluster centre determined by the Euclidean distance $\|x^i - v^j\|$ encompasses both the i^{th} and j^{th} data points. Let's consider that the set of centers is composed of information point groups $X = \{x1, x2, x3 \dots, xn\}$ and $V = \{v1, v2, v3 \dots, vc\}$. The subsequent sequence outlines the stepwise procedure to be adhered to:

Algorithm 1: Segmentation Methodology Based on Optimization

Step 1: Initialization random number of cluster centers ' c '

Step 2: Design of Rough fuzzy membership φ^{ij}

Step 3: Design of Rough Fuzzy Centers V^j

Step 4: Updating the Rough Fuzzy C-means

Technique through an Optimization Model
Step 5: Replicate Steps 2 and 3 iteratively until reaching $J(u, v)$ or convergence condition otherwise $\|U(k+1) - U(k)\| < \beta$

In this context, where ' k ' signifies the iteration stage, ' β ' represents the termination criterion within the range $[0, 1]$, ' $U = (\varphi^{ij})n * c$ ' corresponds to the Rough Fuzzy membership matrix, and ' J ' is the objective function. The concept of infinity is derived from infinite variance. The outlined steps are instrumental in the creation of a random walk pattern, utilizing a power-law distributed step-length scheme through a substantial endpoint. A subset of innovative solutions is generated, usually centered around the most optimal solution identified thus far. The local search process is expedited to enhance speed. However, a notable portion of these new solutions is introduced with some degree of divergence in the randomization field, deliberately positioning them distant from the current best solution. This strategy ensures that classification occurs without becoming overly fixated on a local optimum. The centroid of the Rough Fuzzy C-means is determined by employing the proposed Slap swarm Optimization Algorithm (SSO). The optimization of the centroid, as depicted in equation (9), is accomplished through the assistance of the SSO method. It operates based on collective movement of slaps, forming swarms that establish interaction chains. This behavior is inspired by the foraging actions observed in swarms inhabiting the deep sea, where slaps interconnect with each other to enhance their kinetic energy acquisition in their quest for food sources [25]. The SSO algorithm draws inspiration from this swarming behavior of slaps, emulating the construction of slap chains. By creating these chains, SSO effectively addresses the challenge of escaping local optima problems, thereby ensuring a balance between exploitation and exploration processes. Within SSO algorithms, slaps are classified into two categories: leaders and followers. Leader slaps are positioned at the forefront of the chain, while followers adhere to the leadership and are referred to as chain members. The leader slap plays a pivotal role in guiding and influencing the actions of the follower crowd, promoting interactions among peers. The entire workflow of the suggested algorithm is visualized in Figure 2.

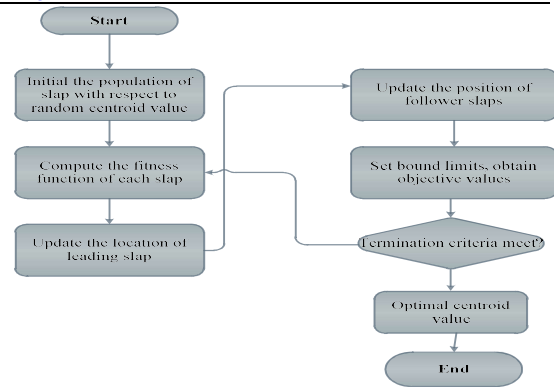


Fig 2: Flow diagram of the optimization algorithm

In an n dimensional space, the position vector of each slap is directed towards the exploration of its respective food source, denoted by ' i '. In this context, ' n ' refers to the total number of decision variables. The preliminary population of the SSO comprises of ' N ' slaps, with each slap has ' d ' dimensions. The position vector ' Y ' for the slaps is expressed as a $N \times d$ dimensional matrix, represented by the following equation:

$$Y_i = \begin{bmatrix} Y_1^1 & Y_2^1 & \dots & Y_d^1 \\ Y_1^2 & Y_2^2 & \dots & Y_d^2 \\ \vdots & \vdots & \dots & \vdots \\ Y_1^N & Y_2^N & \dots & Y_d^N \end{bmatrix} \quad (8)$$

In the SSO algorithm, each slap within the population is directed toward a specific food source location. Furthermore, the leader's position can be expressed using the equation provided below. This concept is integral to the SSO algorithm, as it ensures that every slap in the population is focused on a distinct food source, while the leader's position, a pivotal element, is mathematically defined as follows:

$$Y_j^1 = \begin{cases} E_j + D_1((UB_j - LB_j)D_2 + LB_j) & D_3 \geq 0.5 \\ E_j - D_1((UB_j - LB_j)D_2 + LB_j) & D_3 \leq 0.5 \end{cases} \quad (9)$$

In this context, D_2 and D_3 are random vectors generating values within the specified range of $[0, 1]$. The symbol LB_j signifies the lower limit of the j^{th} size, while UB_j defines the upper limit of the same size. E_j represents the food source position, Y_j^1 denotes the leader's slap

position, and the essential parameters of D_1 are mathematically defined as follows:

$$D_1 = 2e^{\left(\frac{4t}{T_{max}}\right)^2} \quad (10)$$

In this context, D_1 denotes the equilibrium between the exploitation and exploration tendencies inherent in the SSO algorithm. The variable t corresponds to the iteration count, while T_{max} signifies the upper limit of iterations. Furthermore, the position of the follower salp can be mathematically expressed using the following equation:

$$Y_j^i = \frac{Y_j^i + Y_j^{i-1}}{2} \quad (11)$$

In this context, Y_j^i signifies the initial position of the i^{th} slap in the j^{th} dimension. The optimization algorithm is utilized to determine the objective function, which is calculated according to equation (15). Through this equation, optimal centroid values are selected based on the principles of the SSO model.

$$V^j = \frac{(\sum_{j=1}^N (\varphi^{ij})^m x^i)}{(\sum_{j=1}^N (\varphi^{ij})^m)}, V^{j=1,2,...,c} \quad (12)$$

In this context, the estimation of centroid values is achieved through the application of the optimization procedure. After each iteration, the measure of ' R ' is adjusted and evaluated to determine its alignment with the accurate value. The iteration process concludes upon achieving the maximum iteration threshold. The efficacy of the SSO approach in dealing with the objective function is emphasized. The fitness function, as outlined in the proposed algorithm, is structured as follows:

$$F = \sqrt{\frac{1}{N} \sum_{i=1}^N (OB(R = P_a, I_a, D_a))^2} \quad (13)$$

Hence, the SSO optimization algorithm is employed to minimize the objective function while adhering to parameter constraints. The SSO technique is applied to optimize the centroid value within the fuzzy c-means algorithm. A reduced objective function value indicates minimal variance between the data and the optimized result generated by the SSO algorithm. For a comprehensive understanding of the proposed SSO algorithm, the pseudo code is provided in Algorithm 1.

Algorithm 1 Suggested SSO Algorithm

for Centroid optimization

Initiate a random population of centroid values for slaps

While (termination criteria is not valid) do

Calculate the fitness value of each slap using (13)

Identify the optimal slap and designate it as ' E ', representing the core parameter of the leading slap.

Revise the core parameters of the slaps using equation (9).

For (every slap) do

If ($i=1$) then Update the leader's attributes using equation (9).

Adjust all slaps' attributes based on the given lower and upper limits of variables.

Validate the constraints of search agents according to equations (10-12).

Return E

As outlined in Algorithm 1, the SSO algorithm distributes each search agent within the solution space in a random manner. Next, it evaluates the existing slap population to identify the predominant slap. The updating and application of rules are carried out using a set of diverse equations. The positions of slaps within the population are adjusted using the mentioned equation. The iterative process persists until the specified termination condition is satisfied, iterating through all steps excluding the initial phase to improve the quality of slaps. Through proposed algorithm, the optimization of the centroid's optimal value is realized. The algorithm is pivotal in obtaining diagnostic results from brain tumor images. The SSO algorithm facilitates the integration of rough fuzzy c-means and centroid optimization, driving the segmentation of brain tumor images. Subsequently, various methods are employed for feature extraction from the segmented images.

Proposed brain tumor severity analysis using optimization driven MO-3DCNN

Owing to the rise of brain tumor severity, this research addresses disease classification through an innovative deep learning approach. The proposed model showcases the ability to autonomously extract intrinsic features, resulting in a high recognition rate for diseases. By extending the conventional CNN framework with a 3D convolutional layer, improvements are achieved. This expansion enhances the network's training performance and learning capacity by

incorporating the 3D spatial context. The decision to employ a 3DCNN arises from the dynamic changes in features like shape, size, and position in MR images across different growth stages of tumors. This variability necessitates the extraction of a broader spectrum of features to capture the evolving disease characteristics. To this end, a series of convolutional layers are introduced in the initial layer to enlarge the network model's receptive field. This, in turn, addresses the classification model's loss function by employing data sampling on feature maps. The proposed learning model integrates Convolution, pooling, Rectified Linear Unit (RELU), batch normalization, and classification layers comprising fully connected, logistic, and output classification layers respectively. Through the utilization of the proposed MO-3DCNN framework, physicians gain the capacity to efficiently categorize brain disease levels without requiring prior expertise.

In this network architecture, the input layer processes MRIs, optimally assigning biases and weight functions by fine-tuning weight parameters through an optimization model. This classification model operates through two phases: training and testing. In the training phase, 80% of brain MRIs is utilized, while the remaining 20% are reserved for the testing stage. The MO-3DCNN encompasses an array of three-dimensional CNNs that effectively employs a multifibre unit in combination with dilated weighted convolutions. This incorporation enables the extraction of feature attributes across various scales, catering to volumetric segmentation requirements. The model was configured with a fixed size of 128x128 and was complemented by a refined loss function, integrating both focused and generalized loss components. In terms of preprocessing, the MRI data underwent zero-padding, expanding the initial 240x240x155 voxel dimensions to 240x240x160 voxels. This adjustment was made to accommodate a depth that could be evenly divided by the network architecture. Once the data is prepared for input, it traverses through the trained architecture, subsequently generating probability maps. These maps are then utilized by the architecture to obtain the final classification based on the provided data. The mathematical expression for the output value ' γ ' at position (a, b, c) on the q^{th} feature map within the

p^{th} 3D convolutional layer can be represented as follows:

$$\gamma_{q,abc}^{(p)} = Relu \left(\gamma_q^{(p)} + \sum_{n=1}^{N(p-1)} \sum_{x=0}^{X^{(p-1)}-1} \sum_{y=0}^{Y^{(p-1)}-1} \sum_{z=0}^{Z^{(p-1)}-1} z_{qn,tuv} \gamma_{n,(a+t)(b+u)(c+v)}^{(p-1)} \right) \quad (14)$$

Where $Relu()$ denotes the element-wise Rectified Linear Unit function.

$\gamma_q^{(p)}$ Represents the shared bias for the q^{th} processing region in the layer.

$z_{qn,tuv}^{(p)}$ Signifies the (x, y, z) the element of the 3D filter for the q^{th} processing region at the p^{th} layer, related to the m th processing region in the $(p-1)$ layer.

$\gamma_{n,(a+t)(b+u)(c+v)}^{(p-1)}$ Corresponds to the output value of the m th feature map at position $(a+t)(b+u)(c+v)$ in the $(p-1)$ th layer.

Tensor operations provide a simplified explanation for the connection between two neighboring layers, particularly from the $(p-1)$ layer to the q^{th} layer, as delineated in the equation.

$$\gamma^{(p)} = \sigma \left(Z^{(p)} \gamma^{(p-1)} + y^{(p)} \right) \quad (15)$$

Where $\gamma^{(p)}$ represents the output for the p^{th} layer.

$\gamma^{(p-1)}$ Signifies the input for the p^{th} layer.

$\sigma(.)$ Denotes the activation function, operating element-wise on the input.

The loss function is employed using the back propagation process to compute the training loss. In our case, we opted for the Categorical Cross-Entropy. The primary goal is to minimize the loss function to effectively train the Fully Convolutional Network (FCN). While Stochastic Gradient Descent (SGD) is a common optimization method, it can often get stuck in gradient errors. Therefore, we turn to the Mayfly optimizer, a technique that adapts the learning rate. The loss function is estimated as the mean squared error among the predictions generated by a 3D-prediction CNN and the corresponding ground truth from the training dataset. The expression is provided below:

$$\tau(Z, y/D) = \frac{1}{t} \sum_{f=1}^t \sum_{g=1}^t (b_{fg}^{truth} - b_{fg}^{pred})^2 \quad (16)$$

Here D stands for the trained dataset containing input-output pairs $\{a_f, b_f\}$, g indicates the component index in the efficient properties vector $\mathcal{G}$. The optimal parameters Z^* and y^* can be determined by minimizing the loss function or, equivalently, by maximizing its inverse of loss function (log-likelihood).

$$\{Z^*, y^*\} = \underset{\{Z, y\}}{\operatorname{argmin}} \{\tau(Z, y/D)\} \quad (17)$$

The prominent issue adopted in classifier algorithm is that setting of parameter values. Aiming this objective, MO-3DCNN parameters are tuned for diminishing loss function i.e., predicted error using Mayfly optimization approach. For each image, the posterior probability of voxel p with label g computation can be written as,

$$P(b_p = 1/(N_p)) = \frac{e^{f_{bg}(N_p)}}{\sum_{f'=1}^F e^{f_{bg}(N_p)}} \quad (18)$$

Here $f_{bg}(\cdot)$ Defines the computation property of MO-3DCNN model, N_p represents the patch of the p th voxel and f' indicates the class severity in terms of probability value. The loss function adopted in this study named weighted cross entropy is mathematically formulated as follows,

$$Loss = -\sum_p \log(P(b_p = \text{groundtruth}/A(N_p))) \quad (19)$$

The cross-entropy between the actual distribution u and the estimated distribution $\hat{u}$ is denoted as $\sum_p u(b_p) \log(P(b_p/A(N_p)))$.

In this scenario, the actual distribution $u(b_p)$ is identical to 1 for the ground truth class and 0 for all other classes.

Optimization driven MO-3DCNN: The suggested methodology utilizes the mayfly optimization algorithm to enhance the performance of MO-3DCNN. The result of the mayfly algorithm selects the optimal hyper parameter for the deep learning algorithm, aligning with its similarity to Particle Swarm Optimization (PSO) and leveraging the benefits of Genetic Algorithms (GA). Referred to as a hybrid algorithmic structure, the mayfly algorithm derives its name from the traits of mayflies and borrows

inspiration from their social behavior, particularly in mating. This optimization technique metaphorically draws on the life cycle of mayflies, encompassing various stages from hatching to the presence of adults and robust, long-lived specimens. In this algorithm, the position of each mayfly within the search space represents a potential solution to the problem. The mayfly algorithm is conceived as a procedure that utilizes the life cycle characteristics of mayflies to formulate an advanced optimization approach. The sequential steps of the mayfly algorithm are elucidated below: The mayfly algorithm begins by randomly generating two separate sets of mayflies, identified as female and male mayflies. Each individual mayfly is then randomly placed within the search space, forming a candidate solution. This solution is depicted as a d-dimensional vector, expressed as follows:

$$X = (X_1, \dots, X_D) \quad (20)$$

The dimensional vector is established through the computation of the objective function. In the proposed methodology, the mayfly algorithm is utilized to discern the optimal hyper parameters for the deep learning algorithm, thereby enhancing its performance. The fitness function of the system is mathematically defined as follows:

$$\bar{b} = \frac{b - \min(b)}{\max(b) - \min(b)} \quad (21)$$

Here, $\bar{b}$ denotes the objective function formulated within the MO-3DCNN process. Using the proposed optimization strategy, minimization is performed for the loss function adopted in the MO-3DCNN framework. The minimization function is carried out in the fitness evaluation of mayfly algorithm. Other hyper parameters, including the number of filters, depth of convolutional layers, and fully connected layers, are chosen through parametric tests in Section 4.3.1. For the training of 3D-CNN models, an adaptive learning rate optimization algorithm, Mayfly algorithm [26], is utilized. The mayfly velocity is characterized as the variation in position and is denoted as follows:

$$V = (V_1, \dots, V^d) \quad (22)$$

Every mayfly displays a dynamic interplay between social and individual flying traits. In the algorithm, each mayfly modifies its flight path by taking into account both its current best position and the best position attained by other mayfly

characteristics. The specific attributes of mayfly behaviors are represented by the following notations: Within the algorithm, female mayflies demonstrate a tendency to gather around males. This behavior stems from their need to engage in breeding. They rapidly shift their positions towards the male mayflies to initiate the breeding process. The traits associated with this breeding behavior are indicated as follows:

$$Y_I^{T+1} = Y_I^T + V_I^{T+1} \quad (23)$$

In this context, the alteration in the mayfly's position is accomplished through its velocity, represented as V_I^{T+1} , relative to its current position. Here, Y_I^T signifies the current position of the female mayfly in the search space at time T . The breeding attributes follow to certain constraints, denoted as follows:

$$Y_I^0 \sim U(Y_{MIN}, Y_{MAX}) \quad (24)$$

The process of attraction can be described as a stochastic progression; however, it is considered a deterministic process. Governed by the fitness function, the optimal female mayfly is attracted to the most suitable male counterpart. Similarly, the second-best male mayfly attracts the second-best female mayfly, and this sequential attraction pattern persists. For minimization problems, the formulation of mayfly velocity is as follows:

$$V_{IJ}^{T+1} = \begin{cases} V_{IJ}^T + A_2 e^{-\beta r^2} mf(X_{IJ}^T - Y_{IJ}^T) & \text{if } f(Y_I) > f(X_I) \\ V_{IJ}^T + FL * R & \text{if } f(Y_I) \leq f(X_I) \end{cases} \quad (25)$$

In this context, R signifies an arbitrary number within the interval $[-1, 1]$, FL is characterized as the coefficient for random walk, signifying scenarios where a female mayfly is not drawn toward a male. This allows mayflies to navigate randomly. mf Signifies the Cartesian distance among male and female mayflies, as defined by the equation. β Represents the fixed visibility coefficient, while A_2 stands for the positive attraction constant. Additionally, Y_{IJ}^T denotes the position of the female mayfly in dimension j at time T . V_{IJ}^T refers to the velocity of the female mayfly in the same dimension j and at the same time T . Male mayflies cluster together, forming swarms, and their positions are modified according to their individual experiences as well as the influence of their neighboring mayflies.

The process of updating their positions can be expressed in the following manner:

$$X_I^{T+1} = X_I^T + V_I^{T+1} \quad (26)$$

In this context, X_I^T signifies the present position of the male mayfly, while V_I^{T+1} refers to the velocity of the same male mayfly. As before, the breeding traits need to adhere to specific constraints, which are represented as follows:

$$X_I^0 \sim U(X_{MIN}, X_{MAX}) \quad (27)$$

The mayfly's velocity is computed using the equation presented below:

$$V_{IJ}^{T+1} = V_{IJ}^T + A_1 e^{-\beta r^2} (pbest_{IJ} - X_{IJ}^T) + A_2 e^{-\beta r^2} (pbest_I - X_{IJ}^T) \quad (28)$$

In this equation, $pbest_I$ represents the best position, while $pbest_{IJ}$ denotes the subsequent best position. A_1 , A_2 correspond to positive attraction factors used to proportionally adjust the impact of the cognitive and social elements. The calculation of the next best position is executed using the equation provided below:

$$pbest_I = \begin{cases} X_I^{T+1} & \text{if } f(X_I^{T+1}) < f(pbest_I) \\ \text{is kept the same} & \text{otherwise} \end{cases} \quad (29)$$

The calculation of the global best solution is determined using the formula presented below:

$$gbest \in \{pbest_1, pbest_2, \dots, pbest_n | f(gbest) = \min(f(pbest_1), f(pbest_2), \dots, f(pbest_n))\} \quad (30)$$

In this context, N represents the overall count of mayflies within the population of swarm. The calculation of the mayfly's distance is essential for determining the optimal position. The distance between mayflies is calculated using the Cartesian distance, as defined by the following formula:

$$\|X_I - X_I^*\| = \sqrt{\sum_{j=1}^N (X_{IJ} - X_{IJ}^*)^2} \quad (31)$$

In this context, X_{IJ}^* pertains to the global and local best positions, while X_{IJ} denotes to the current element of the mayfly. The optimal mayfly continually updates its velocity, and it is represented as follows:

$$V_{IJ}^{T+1} = V_{IJ}^T + D * R \quad (32)$$

Where R is an arbitrary value and D represents the nuptial dance coefficient. Once, the termination criterion is attained, the optimal set of

hyper parameters are found and then utilized for the analysis of brain tumor severity level.

4. RESULT AND DISCUSSION

This section furnishes an elaborate depiction of the results obtained for our innovative proposed technique. The proposed methodology is implemented in the working platform of python. Upon reaching the termination criterion, the optimal set of hyper parameters is identified and subsequently employed for the analysis of brain tumor severity levels. In this study, MRI brain tumor images are gathered and subjected to a pre-processing phase. The pre-processing helps in eliminating noise from the images, followed by the removal of the skull region. Subsequently, the tumor region is efficiently segmented using the enhanced slap swarm-boosted rough fuzzy c-means technique. Once segmentation is accomplished, the extent of tumor expansion is classified using the MO-3DCNN approach. Throughout the classification, the optimal hyper parameter configurations are determined by means of the Mayfly procedure. For our analysis, we employed the BRATS 2020 database. The BRATS initiative is dedicated to assessing cutting-edge techniques for brain tumor segmentation in multimodal MRI scans. A selection of sample images available from the dataset [27] is depicted in *Figure 3*.

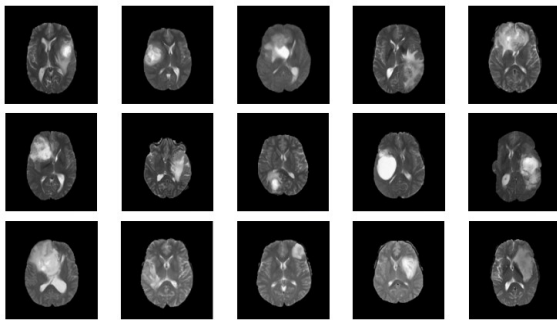


Fig 3: Sample Input images some of the sample segmented outputs are illustrated below



Fig 4: Segmentation results

Some of the obtained segmented images for the brain tumor severity analysis using the proposed segmentation model is provided in figure 4. Moreover, the system's effectiveness is validated by comparing the evaluation metrics of the proposed methodology with those of existing approaches. These metrics are derived from the confusion matrix generated from the experimental outcomes. In this assessment, a variety of evaluation metrics, including Accuracy, Precision, Recall, and F1_score, are utilized.

Accuracy: Accuracy is determined by the ratio of the overall count of correctly classified severity brain tumor images to the overall count of severity brain tumor images.

$$Accuracy = \left(\frac{Tp+Tn}{(Tp+Tn+Tp+Fn)} \right) \quad (33)$$

Precision: Precision, also stated as Positive Predictive Value, is defined as the proportion of correctly classified positive severity brain tumor images to the total count of brain MRI images that were predicted as positive for the severity level.

$$Precision = \left(\frac{Tp}{(Tp+Fn)} \right) \quad (34)$$

Recall: Recall, also defined as Sensitivity or True Positive Rate, is determined as the relation of the correctly classified positive severity levels of brain MRI to the total count of positive classified severity levels of brain tumors.

$$Recall = \left(\frac{Tp}{(Tp+Fn)} \right) \quad (35)$$

F1_Score: The F1 Score can be termed as the harmonic mean between recall and precision.

$$F1_{score} = \left(\frac{2 (Recall \times precision)}{Recall+precision} \right) \quad (36)$$

The evaluation of segmented image quality is conducted independently by assessing metrics such as Peak Signal to Noise Ratio (PSNR) and Mean Square Error (MSE). The Peak Signal to Noise Ratio (PSNR) is employed to gauge image

quality, and it can be mathematically expressed as follows:

$$PSNR = 10 \log_{10} \left(\frac{255^2}{MSE} \right) \quad (37)$$

In the given equation, the Mean Square Error (MSE) is defined as:

$$MSE = \frac{1}{pq} \sum_{p=0}^{p-1} \sum_{q=0}^{q-1} |i^*(p, q) - i(p, q)| \quad (38)$$

Here, $i(p, q)$ - Original image, $i^*(p, q)$ -

Segmented image. The construction and training of the MO-3DCNN framework, as well as the optimization of hyper parameters through Optimization, were implemented using Python code. The experiment leveraged essential Python packages including OpenCV, NumPy, Tensor Flow, Kera's, and Matplotlib. Performance outcome and comparative analysis of brain tumor severity analysis The author employed both quantitative and qualitative metrics to assess the effectiveness of the projected technique. This section offers the results of the brain tumor severity analysis model using an adaptive bilateral filter, and its performance was evaluated using a collection of gathered images. The performance outcomes pertaining to the noise removal process, as tested with the proposed model, are presented and depicted.

Table 1 presents the outcomes attained from the projected severity analysis model for the respective metrics considered. The analysis reveals that the introduced algorithm effectively performed brain tumor severity analysis, resulting in high-definition and efficient segmented image. As a result, the overall outcome indicates the strong performance of the presented technique across a range of image types. In the subsequent section, the performance of the classification method is thoroughly examined. The evaluation is carried out based on metrics such as accuracy, precision, recall, and F-measure. There is a noticeable enhancement in image quality compared to the existing technique, specifically the bilateral filter incorporated fuzzy c-means approach. The outcomes achieved with the proposed technique showcase enhanced performance compared to existing methods. The proposed approach manifests superior image quality in brain tumor segmentation as evidenced by the values documented in the table when compared to the existing method. In our proposed approach, we integrated the Adaptive Bilateral

Filter and optimization-boosted rough fuzzy c-means technique for the segmentation process, enabling precise feature extraction for the identification of each tumor affected cell in the input image.

This simplifies the procedure and results in accurate outcomes. To show the effectiveness of the proposed methodology the implementation results is visually shown below, which illustrates the gradual increase and gradual decrease in the corresponding accuracy and loss function respectively.

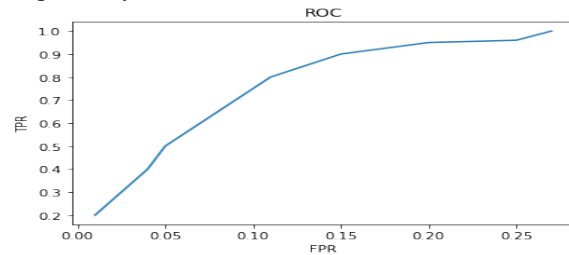
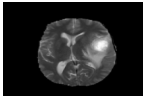
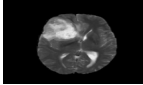
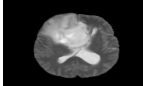
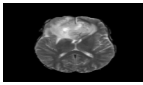
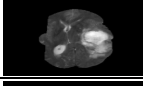
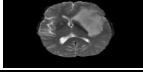
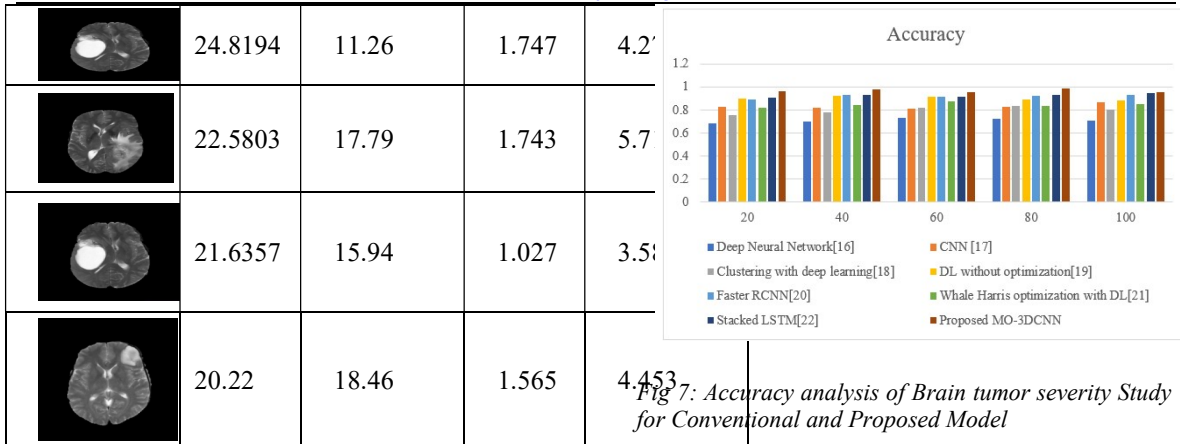


Fig 5. The ROC Curve

Table 1. Comparative analysis of proposed and existing technique using segmentation techniques.

Images	PSNR		MSE	
	Bilateral filter & Fuzzy c-means	Adaptive bilateral filter & optimization boosted rough fuzzy c-means	Bilateral filter & Fuzzy c-means	Adaptive bilateral filter & optimization boosted rough fuzzy c-means
	24.0476	17.71	1.762	7.478
	25.2356	20.13	1.441	5.313
	24.5866	16.67	2.007	8.74
	23.743	19.51	1.433	5.37
	25.800	14.42	1.03	5.791
	24.3294	15.98	1.744	7.301



The Receiver Operating Characteristic (ROC) curve is created by plotting the True Positive Rate (TPR) against the False Positive Rate (FPR). Figure 5 illustrates the ROC curve of the MO-3DCNN approach proposed in this study. The objective is to attain a high TPR while maintaining a low FPR, and these two metrics are interconnected in the ROC curve.

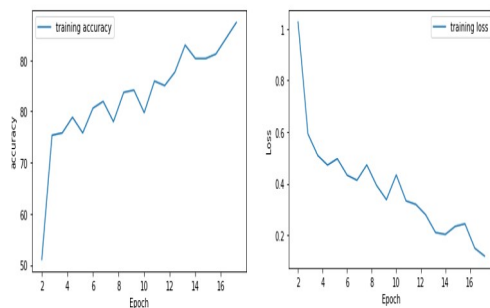


Fig 6: Accuracy and Loss Curve

The accuracy and loss results for the training data of this network are illustrated in Fig 6. The entire network was trained over 100 epochs using the 'weighted-cross entropy' as the loss function. It can be observed that the accuracy and loss results of the network stabilize after around 40 epochs, indicating the reliability of the network. The proposed approach consistently outperforms the existing methods, demonstrating decreased negative assessments and enhanced positive assessments. To visually demonstrate the efficacy of the proposed methodology, the implementation results of the proposed model in correspondent with the existing technique are presented in the following figures 7 to 10.

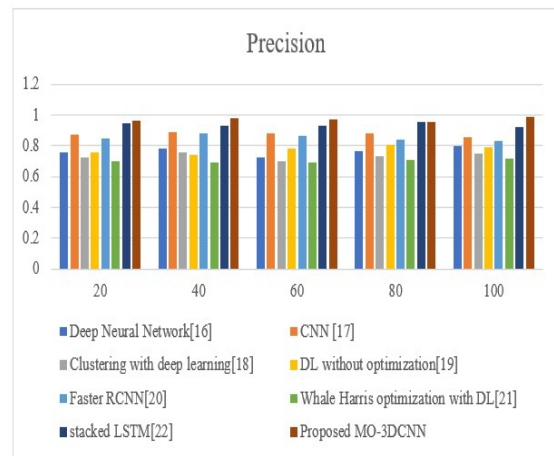


Fig 8: Precision outcome of Brain tumor severity analysis

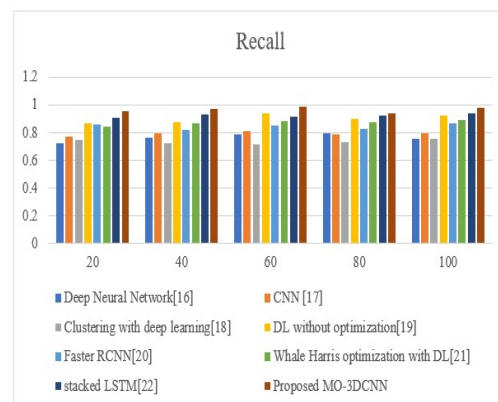


Figure 9 Outcome of recall measure for the proposed and existing system

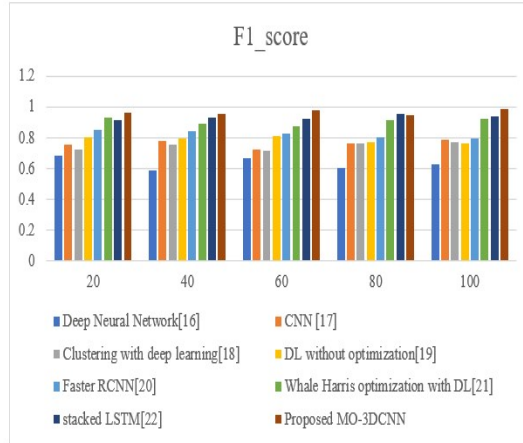


Figure 10: Obtained F1_score for proposed and existing brain tumor severity model

In our proposed brain tumor severity analysis, we experimented with different learning rates ranging from 20 to 100, and the obtained accuracies were 0.9648, 0.9748, 0.9548, 0.9848, and 0.9548 for the corresponding learning rates of 20, 40, 50, 80, and 100, respectively. These results showcase the effectiveness of our proposed system across a range of learning rates. The proposed approach is compared with existing methods, including Stacked LSTM [22], Whale Harris optimization with DL [21], Faster RCNN [20], DL without optimization [19], Deep Neural Network [16], CNN [17], and Clustering with deep learning [18]. In the evaluation of precision, our proposed MO-3DCNN method demonstrated superior performance compared to existing approaches across various learning rates (20, 40, 60, 80, 100) is shown in figure. The evaluation of recall for various learning rates demonstrates the superior performance of our proposed MO-3DCNN method compared to existing approaches is shown in figure. The F1 score, which balances precision and recall, is a critical metric in evaluating the overall performance of a brain tumor severity analysis system. From the overall analysis, it seems that the proposed severity analysis model attains an effective outcome than existing techniques.

The findings of this study are strongly aligned with the previously established objectives and they provide strong evidence of the proposed integrated framework for severity classification of brain tumors. The impact of Adaptive bilateral filtering on improving MRI image quality was substantial as the switching bilateral filtering method removes noise while preserving

important detail- this improves MRI image quality and explains the increased PSNR and decreased MSE Values (Table 1). Slap swarm boosted rough fuzzy c-means segmentation provided more reliable segmentation and tumor localization than traditional methods, as illustrated in Figure 4. The Mayfly Optimization (MO) version of the 3D CNN achieved improved classification performance. This included an accuracy score of 0.9848 with greater precision, recall and F1 scores (Figures 7–10). The ROC analysis in Figure 5 provided further evidence of the model's capacity for good classification ability. An additional concern was testing of the model's robustness regarding different learning rate for training. The findings indicate the proposed MO-3DCNN framework can be established as a clinically usable, reliable method for performing better brain tumor severity assessment overall. This study intended to create a thorough schema for reliable brain tumor severity analysis through the complementary use of adaptive pre-processing, segmentation, and optimize deep learning, and the results reflect strongly on achieved ambitions. The adaptive bilateral filter markedly improved the quality of the MRI images with great improved PSNR and decreased MSE values, and the badger-swarm boosted rough fuzzy c-means segmentation overcame intensity in-homogeneity and clustering instability issues, resulting in an accurate localized tumor location. In addition to the feature extraction and classification abilities of Mayfly Optimized 3D CNN (MO-3DCNN), the model's overall accuracy of 98.48%, surpassed the target benchmarks, performed better than leading approaches like Stacked LSTM (~93%), Whale Harris optimized DL (~94%), and Faster RCNN (~95%). Limitations exist related to BRATS 2020 data, real time deployment of the Mayfly optimization cost, potential lack of clinical interpretability of the "black box" model; ultimately creating room for future studies based on the findings that suggest explainable AI, multi-institutional validation, and other optimization suggestions for deployment. Even with the successful efficacy of the proposed MO-3DCNN framework, limitations persist, such as dependence on the BRATS 2020 dataset, limiting generalisability across a variety of clinical environments, additional computational costs of Mayfly Optimization preventing real-time use, and the "black box" aspect of the model moving clinical interpretability aside. Future work should work to expand to multi-institutional datasets,

develop more lightweight architectures to reduce inference time, and integrate explainable AI techniques to increase transparency for clinical adoption.

5. CONCLUSION AND FUTURE ENHANCEMENT

This research describes and provides context for a unique construct for brain tumor severity analysis through adaptive preprocessing, slap swarm-boosted rough fuzzy c-means segmentation, and the 3D Convolutional Neural Network (CNN) optimized using Mayfly optimization (MO-3DCNN), showing significant improvements in image quality, tumor localization, and severity classification compared to traditional techniques. The proposed framework achieved all proposed research aims and demonstrated significant potential for clinical translational use as a decision-support tool for neuro-oncologists. However, future research could consider the issues of broader benchmarking validation using multimodal institutional data, model interpretability through explainable artificial intelligence (AI), multimodal data, and real-time clinical use as outlined. The findings and methods described will enhance the proposed framework's utility, and tackling these open issues will facilitate its extension further and ultimately enhance prognosis, treatment planning, and ultimately patient outcomes.

While the proposed MO-3DCNN framework had meaningful performance for brain tumor severity assessment, some outstanding issues offer pathways for future research. In particular, the MO-3DCNN framework should be extended to larger multi-institutional datasets outside of BRATS 2020 to improve model generalization across varying clinical settings. Furthermore, development in the area of explainable artificial intelligence (XAI) would maximize model interpretability and may result in a model with more explainable behavior that may function as a clinical trial. Additional possibilities for future research include expansion to multimodal data - incorporating genetic markers, histopathology, and clinical data - that could broaden the capability of the severity assessment and scope for developing personalized treatment plans. The model might also be further optimized for clinical use on a wider scale and thus be extended for use in longitudinal analysis of tumor progression or response(s) to treatment(s). Finally, observational

prospective (rather than retrospective) clinical trials will be paramount to establish the relevance and reliability of this framework in real-world medical.

ACKNOWLEDGEMENTS

Author Contributions

Mekala Bhaskar: administration of projects; Software; Conceptualization; Validation; Resources; rewrite of the initial draft.

Neelamadhab Padhy: Methodology; formal evaluation; Data management; Resources; Investigation; Editing and reviewing the initial draft.

Kiran Kumar Reddy Penubaka: Software; formal evaluation; Methodology; Data management; Validation; Examine the initial draft.

All authors have read and approved the final manuscript

Declarations

Funding: This research received no external funding.

Conflict of Interest: The authors declare that they have no conflict of interest.

Ethics Approval: I/We declare that the work submitted for publication is original, previously unpublished in English or any other language(s), and not under consideration for publication elsewhere.

Consent to participate / Informed Consent: Not Applicable.

Consent for publication: I certify that all the authors have approved the paper for release and are in agreement with its content.

REFERENCES

- [1] Mahesh K, M. and Renjit J, A., 2020. DeepJoint segmentation for the classification of severity-levels of glioma tumor using multimodal MRI images. *IET Image Processing*, 14(11), pp.2541-2552.
- [2] Kurmi, Y. and Chaurasia, V., 2020. Classification of magnetic resonance images for brain tumor detection. *IET Image Processing*, 14(12), pp.2808-2818.
- [3] Amin, J., Sharif, M., Haldorai, A., Yasmin, M. and Nayak, R.S., 2021. Brain tumor detection and classification using machine learning: a comprehensive survey. *Complex & intelligent systems*, pp.1-23.
- [4] Siar, M. and Teshnehlab, M., 2022. A combination of feature extraction methods and deep learning for brain tumor

- classification. IET Image Processing, 16(2), pp.416-441.
- [5]Maharjan, S., Alsadoon, A., Prasad, P.W.C., Al-Dalain, T. and Alsadoon, O.H., 2020. A novel enhanced softmax loss function for brain tumor detection using deep learning. Journal of neuroscience methods, 330, p.108520.
- [6] Ali, M., Gilani, S.O., Waris, A., Zafar, K. and Jamil, M., 2020. Brain tumor image segmentation using deep networks. Ieee Access, 8, pp.153589-153598.
- [7]Wankhede, D.S. and Selvarani, R., 2022. Dynamic architecture based deep learning approach for glioblastoma brain tumor survival prediction. Neuroscience Informatics, 2(4), p.100062.
- [8]Sethy, P.K. and Behera, S.K., 2021. A data constrained approach for brain tumor detection using fused deep features and SVM. Multimedia Tools and Applications, 80(19), pp.28745-28760.
- [9]Deepak, S. and Ameer, P.M., 2021. Brain tumor classification using siamese neural network and neighbourhood analysis in embedded feature space. International Journal of Imaging Systems and Technology, 31(3), pp.1655-1669.
- [10]Sasank, V.V.S. and Venkateswarlu, S., 2022. An automatic tumor growth prediction based segmentation using full resolution convolutional network for brain tumor. Biomedical Signal Processing and Control, 71, p.103090.
- [11][Song, G., Shan, T., Bao, M., Liu, Y., Zhao, Y. and Chen, B., 2021. Automatic brain tumor diagnostic method based on a back propagation neural network and an extended set-membership filter. Computer Methods and Programs in Biomedicine, 208, p.106188.
- [12]Waghmare, V.K. and Kolekar, M.H., 2021. Brain tumor classification using deep learning. Internet of things for healthcare technologies, pp.155-175.
- [13] Rafi, A., Madni, T.M., Janjua, U.I., Ali, M.J. and Abid, M.N., 2021. Multi-level dilated convolutional neural network for brain tumor segmentation and multi-view-based radiomics for overall survival prediction. International Journal of Imaging Systems and Technology, 31(3), pp.1519-1535.
- [14] Abdullah, M.A., Alkassar, S., Jebur, B. and Chambers, J., 2021. LBTS-Net: A fast and accurate CNN model for brain tumor segmentation. Healthcare Technology Letters, 8(2), pp.31-36.
- [15] Abdel-Gawad, A.H., Said, L.A. and Radwan, A.G., 2020. Optimized Edge Detection Technique for Brain Tumor Detection in MR Images. IEEE Access, 8, pp.136243-136259.
- [16] Sharif, M.I., Khan, M.A., Alhussein, M., Aurangzeb, K. and Raza, M., 2021. A decision support system for multimodal brain tumor classification using deep learning. Complex & Intelligent Systems, pp.1-14.
- [17] Gurunathan, A. and Krishnan, B., 2021. Detection and diagnosis of brain tumors using deep learning convolutional neural networks. International Journal of Imaging Systems and Technology, 31(3), pp.1174-1184.
- [18]Khan, A.R., Khan, S., Harouni, M., Abbasi, R., Iqbal, S. and Mehmood, Z., 2021. Brain tumor segmentation using K-means clustering and deep learning with synthetic data augmentation for classification. Microscopy Research and Technique, 84(7), pp.1389-1399.
- [19] Aamir, M., Rahman, Z., Dayo, Z.A., Abro, W.A., Uddin, M.I., Khan, I., Imran, A.S., Ali, Z., Ishfaq, M., Guan, Y. and Hu, Z., 2022. A deep learning approach for brain tumor classification using MRI images. Computers and Electrical Engineering, 101, p.108105.
- [20] Harish, P. and Baskar, S., 2020. MRI based detection and classification of brain tumor using enhanced faster R-CNN and Alex Net model. Materials Today: Proceedings.
- [21]Rammurthy, D. and Mahesh, P.K., 2022. Whale Harris hawks optimization based deep learning classifier for brain tumor detection using MRI images. Journal of King Saud University-Computer and Information Sciences, 34(6), pp.3259-3272.
- [22]Dandil, E. and Karaca, S., 2020. Detection of pseudo brain tumors via stacked LSTM neural networks using MR spectroscopy signals. Biocybernetics and Biomedical Engineering.
- [23] E. Dikici et al., "Automated Brain Metastases Detection Framework for T1-Weighted Contrast-Enhanced 3D MRI," in IEEE Journal of Biomedical and Health Informatics, vol. 24, no. 10, pp. 2883-2893, Oct. 2020.

- [24]Nawaz, M., Qureshi, R., Teevno, M.A. and Shahid, A.R., 2023. Object detection and segmentation by composition of fast fuzzy C-mean clustering based maps. Journal of Ambient Intelligence and Humanized Computing, 14(6), pp.7173-7188.
- [25]Abualigah, L., Shehab, M., Alshinwan, M. and Alabool, H., 2020. Salp swarm algorithm: a comprehensive survey. Neural Computing and Applications, 32, pp.11195-11215.
- [26]Zervoudakis, K. and Tsafarakis, S., 2020. A mayfly optimization algorithm. Computers & Industrial Engineering, 145, p.106559.

Dataset availability

<https://www.kaggle.com/datasets/awsaf49/bra-ts20-dataset-training-validation>