IJE TRANSACTIONS C: Aspects Vol. 38, No. 12, (December 2025) 2819-2833

International Journal of Engineering

Journal Homepage: www.ije.ir

Enhanced Segmentation of High-Grade and Low-Grade Brain Tumors Using Advanced 3D U-Net++ with Hybrid Lion-Spider Monkey Optimization

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PAPER INFO

Paper history:
Received 07 November 2024
Received in revised form 14 February 2025
Accepted 03 March 2025

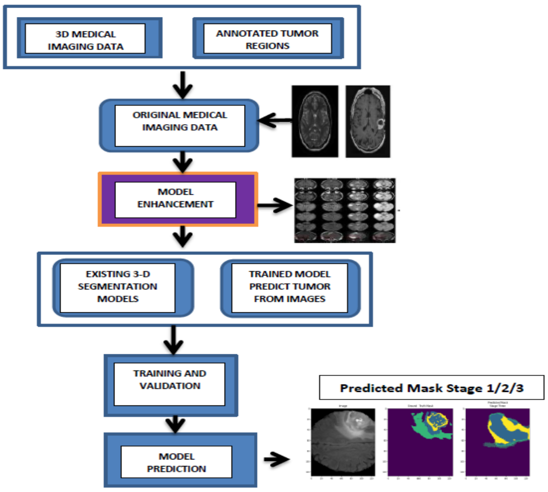
Keywords:
Brain Tumor Segmentation
MRI Imaging
3D U-Net++
Medical Image Analysis
Neuro-Oncology

ABSTRACT

Appropriate segmentation of brain tumors from MRI images is crucial for accurate evaluation and treatment management. This paper presents an enhanced approach to segment high- and low-grade gliomas by optimizing the 3D U-Net++ architecture using the Hybrid Lion-Spider Monkey Optimization Algorithm (LSMA). The LSMA integrates the Lion-Spider Monkey Algorithm (LSMA) to improve parameter tuning and feature extraction, significantly enhancing the segmentation process. The study utilizes the BRATS 2020 dataset, which includes T1-weighted, T2-weighted, and FLAIR MRI scans, capturing the distinctive features of the tumors. Preprocessing steps involve estimating image noise tiers and applying the Frost clear out to reduce clutter even as keeping essential details. The modalities are blended into a unified dataset and standardized to make sure regular depth throughout images. Data augmentation strategies, such as rotation and deformation, are employed to increase set of rules resilience. In terms of network structure, the 3-D U-Net++ model features an encoder-decoder shape with dense connections for effective information transmission and characteristic extraction. Deep supervision with auxiliary outputs similarly refines gradient float and improves segmentation accuracy. The model is to start with pretrained on downscaled images to capture large-scale capabilities, accompanied via first-class-tuning on complete-decision pictures for stronger aspect detail. Evaluation on a separate test set demonstrates that the LSMA-optimized 3-D U-Net++ achieves an outstanding accuracy of 99%, surpassing previous methods. This advanced architecture, applied in Python, gives a fairly correct and flexible answer for brain tumor segmentation, offering precious support for clinical practitioners in making informed remedy choices and planning.

***doi**: 10.5829/ije.2025.38.12c.01*

Graphical Abstract



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Please cite this article as: Sajjanar R, Dixit UD. Enhanced Segmentation of High-Grade and Low-Grade Brain Tumors Using Advanced 3D U-Net++ with Hybrid Lion-Spider Monkey Optimization. International Journal of Engineering, Transactions C: Aspects. 2025;38(12):2819-33.

1. INTRODUCTION

Brain tumor identification and detection constitute one the hardest tasks in modern medicinal Science, due to its complexity and critical outcomes for the health of sufferers. Tumors of the brain are a massive category of cerebral tumors that encompass either cancerous or benign kinds. Tumors like those expand from a couple of styles of neurons inside the brain or unfold from diverse cancers within the human organism. The consequences for the wellness of patients are significant.

Brain lesions can impair important cognitive functions by squeezing or invading tissue in the brain, causing a variety of indications. Signs may include migraines, epileptic fits, intellectual or behavioural abnormalities, neurological disorders, as well as perceptual difficulties. The particular signs felt are determined by the tumor's precise position as well as dimensions, which could differ significantly (1). For example, tumors in the anterior region may influence behaviour as well as making choices, but one in the cortex can hamper balance and motor skills. Furthermore, most of these tumors grow aggressively, quickly expanding their scope as well as aggressiveness. Tumors with malignant cells, like glioblastomas, are well-known for their fast development and refusal to respond to therapy (2). They frequently penetrate neighboring tissue of the brain, making total removal by surgery challenging and raising the risk of relapse. The invasive nature of malignant cancers needs urgent and accurate detection procedures to start therapy soon (3).

Prompt and precise identification of tumors in the brain is critical for several reasons. For starters, the initial discovery can significantly enhance the individual's outlook. For several cancers, early identity opens up extra remedy choices, which might also prove as less intrusive. For instance, if a tumor is tiny and constrained, elimination by using surgery is far more likely to be powerful. Also, speedy identity may be beneficial in arranging the management of more remedies which consist of radiology and radiation treatment, possibly stopping most cancers and increasing the hazard of surviving. Correct identification is also vital for making informed therapy picks (4). Management of tumors in the brain requires an integrative approach that includes neurologists, cancer experts, radiographers, as well as other experts. Accurate evaluation, which includes knowing the tumor's kind, level, all genetic features, guides your choice of the best possible therapies (5). This personalized strategy can increase the effectiveness of therapy, reduce negative reactions, and improve patients' general level of care of life.

Also, the proper analysis of brain tumors impacts over-time treatment for sufferers. After initial therapy, people regularly need continuing surveillance to become aware of Recurrences or examine treatment efficacy. Sophisticated diagnostic exams can offer comprehensive statistics to help on-going treatment and model techniques of remedy as required. At the end, the complexities of tumors within the brain as well as their grave outcomes on health spotlight the significance of active and accurate diagnosis. Developments in healthcare imaging as well as diagnostic technology offer the capability to beautify outcomes, yet there remain troubles in successfully integrating these advancements in medical settings (6). The modern-day article will check out those improvements and their ability to revolutionize the identification of brain tumors and diagnostics. Advances in the healthcare imaging era have altered the technique used for mind cancer detection. With these improvements, interpreting information from snapshots is still a hard enterprise that requires the talents of psychiatrists and neurological specialists (7). This reliance creates volatility in addition to individuality, emphasizing the significance of unbiased, reliable, and robot strategies for testing. In the beyond few years, the utility of neural networks and device studying in healthcare imaging has come to light as an ability prospect. These techniques have a risk of enhancing the precision and efficacy of brain cancer diagnosis by automatically studying pictures, finding tiny systems, and turning in qualitative findings (8).

The novelty of the study comes from integrating two metaheuristic algorithms—Lion Optimization and Spider Monkey Optimization .AI algorithms, mainly deep getting-to-know strategies, display exceptional ability to stumble on and classify intricate tendencies in clinical statistics with relative precision. This examination examines the latest breakthroughs in brain tumor identity, with an emphasis on the use of present-day AI and ML tactics (8). Researchers will investigate different computational closer, ranging from conventional visual processing methods to cutting-edge neural network models, including assessing their efficacy in clinical scenarios. Furthermore, the presentation will address the problems and limits presented by these devices, such as the accessibility of data, forecast clarity, and how they fit into traditional clinical practices. By giving an in-depth evaluation of present developments and prospects in tumor discovery this study hopes to contribute to continuing efforts to increase precision in diagnosis, decrease testing delays, and, eventually, improve outcomes for patients. The combination of healthcare imaging and AI has enormous potential and knowing both its strengths and weaknesses is critical for reaping its benefits in healthcare (9).

The key contributions of this article are:

- The research employs Frost filtering and normalization methods in enhancing MRI image quality for accurate tumor segmentation.
- It uses a complex 3D U-Net++ model with dense skip connections and deep supervision, enhancing

segmentation accuracy and resilience.

- Through the use of data augmentation techniques such as rotation, scaling, and deformation, the model generalizes better across heterogeneous MRI data and tumor variations.
- The use of deep supervision with side outputs improves gradient flow, which is responsible for improved segmentation, particularly in tumor boundary detection.
- The model is superior to past approaches, with an impressive 99% accuracy in brain tumor segmentation as measured by the Dice coefficient on an independent test dataset

This paper formulates a thorough methodology for improved segmentation of low-grade and high-grade brain tumors based on a sophisticated 3D U-Net++ architecture coupled with a hybrid Lion-Spider Monkey Optimization algorithm. The research initiates with the review of available literature (section 2) and then elaborates on prominent challenges and knowledge gaps in available segmentation methods in the problem statement (section 3). In section 4, we introduce a new approach that blends the 3D U-Net++ model with hybrid optimization methods for higher accuracy and better efficiency in tumor segmentation. Section 5 presents the outcome of the suggested model, demonstrating its better performance compared to conventional methods. Section 6 concludes by summarizing the findings and indicating future research directions to enhance the functionality of this method further for brain tumor segmentation.

2. RELATED WORKS

Zheshu developed a Fully Automated Hierarchical Segmentation for the segmentation of brain tumors using deep learning methods. Their method attempted to overcome the difficulties related to identifying, categorizing, and retrieving areas of cancer using MRI scans. By combining fundamental, shape, and relaxometry characteristics, the algorithm segmented the brain's vascular circulation with excellent consistency. Also, researchers used Extreme Learning Machines and stochastic deep neural network categorization to teach and evaluate the precision of tumor identification in magnetic resonance imaging scans. Their findings revealed an amazing accuracy rate of roughly 98.51% in discriminating between diseased as well as normal brain tissues, demonstrating the effectiveness of their suggested approach. It makes major improvements to the discipline of healthcare imaging by providing an exciting answer to the challenging undertaking of assessing MRI data for tumor appearance along with position, which might decrease the pressure on radiologists while clinicians as growing accurate diagnosis and patient satisfaction.

Khan et al. (10) developed a system with intelligence for finding and categorizing brain cancers that use an ordered neural network algorithm that greatly assists clinicians by utilizing the clinical processing of images. Their work centers around classifying malignancies in the brain into glioma, meningioma, and pituitary kinds using a CNN. The suggested technique, known as Hierarchical Deep Learningbased Brain Tumor classification, uses CNN to undergo training on picture parts to effectively classify malignancies into four types: glioma, meningioma, pituitary, and no tumor. This approach outperformed prior methods for identifying brain tumors and segmentation, with an accuracy of 92.13% and a miss rate of 7.87%. The new component of their job is its hierarchical categorization strategy, which improves detection efficiency as well as efficacy, so greatly helping the prompt detection and management of brain cancers. The idea put forward has tremendous promise in offering therapeutic support and enhancing success in the biomedical area.

Dahab et al. (11) presented an improved imaging segmentation technique in MRI imaging for automated brain tumor categorization. They used advanced picture and data processing methods to improve the accuracy of the PNN classifier. Effectiveness was measured based on training accuracy, proficiency in classification, and computing efficiency. Simulation findings displayed that the updated PNN performed speedy and excellent designation, beating traditional imaging processing systems and previously presented PNN algorithms. Particularly, if the distribution value was set to 1, the suggested LVQ-based PNN systems achieved a perfect score in identifying brain tumors while also reducing processing time by around 79% as compared to existing PNN approaches. The results presented demonstrate the promise of the suggested approach for in-vivo diagnosis and verification, with significant increases in both precision and productivity.

An IoT computing platform to identify tumors in MRI scans while tackling the issues of identifying tumor grade and automating the classification procedure. Their solution blends Convolutional Neural Networks and LSTM networks, which are designed to improve the extraction of features and image classification accuracy. Using the Kaggle dataset, which contains 3264 MRI scans divided into 2870 training images and 394 testing visuals, the suggested layered LSTM-CNN construction outperformed classic CNN and Recurrent Neural Network models. Research has shown that this approach not only increased classification accuracy but also effectively handled the lengthy training procedure. It significantly advances brain tumor detection and avoidance by efficiently classifying glioma, meningioma, pituitary tumors, and benign instances, combining the benefits from both CNNs and LSTMs for improved healthcare picture interpretation (12).

Amarapur (13) suggested an effective segmentation of tumors algorithm for brain image processing, which addresses the essential job of identifying and distinguishing tumors from ambient MRI scans. For automated tumor diagnosis and division, they use Fuzzy C-Mean grouping, Gabor Wavelet-based multimodal extraction of features, and a computerized neural network classification. The scientists evaluated the suggested methodology's functionality on an assortment of 40 untrained images and 60 validated MRI scans and used confused matrix analyses to determine quality. The findings showed that the suggested approach attained the requisite reliability level of up to 85%, demonstrating its usefulness in overcoming the limits of human segmentation of tumors and improving accuracy for diagnosis in clinical imaging.

Arunkumar et al. (14) suggested an enhanced automatic brain tumor segmentation as well as classification method based on MRI images utilizing Artificial Neural Networks, to simplify the complex procedure of brain tumor detection. Their approach uses scientific methodologies for collecting features, modeling, and measuring illness images to precisely identify and distinguish between healthy and diseased brain regions.

2. 1. Research Gaps in Existing BRATS 2020 Segmentation Methods

Even with remarkable progress in brain tumor segmentation, current techniques used on the BRATS 2020 database continue to have a number of limitations. Among these shortcomings is a poor contextual representation capability since most methods, including basic U-Net and DeepMedic, have difficulty handling long-range dependencies within volumetric data. This generally leads to poor tumor border delineation, particularly in heterogeneity areas. Moreover, the class imbalance problem is still a major challenge since various tumor subregions (enhancing tumor, necrotic core, and edema) contain extremely imbalanced pixel distributions. Most segmentation models are not good at dealing with this, resulting in poor segmentation performance, especially for small tumor sub regions.

Another major limitation is feature representation and fusion strategies. Traditional 3D U-Net implementations utilize plain encoder-decoder patterns that do not have an effective way to fuse multi-scale information, and that can cause unreliable segmentation for complex cases. Moreover, most of the deep models trained on BRATS 2020 are subject to overfitting and suffer from bad generalization between varied MRI acquisition schemes and scanner inconsistencies, reducing their practical usage. Computational cost is another issue, as the latest models such as nnU-Net need considerable hyperparameter search and computational power, making them infeasible for real-world deployment in limited-resource environments. Finally, uncertainty estimation is typically overlooked, even though it is crucial for medical decision-making. Most segmentation techniques produce deterministic results without reporting any confidence, thus diminishing their applicability in healthcare.

3. PROBLEM STATEMENT

Recognizing, classifying, as well as collecting cancerous regions in MRI images offers substantial hurdles due to the intricate nature of neural networks as well as tumor features, which makes it challenging for physicians to accomplish precise and quick detection. These obstacles are solved with an innovative approach that employs sophisticated techniques from deep learning and machine learning to improve the division of brain tumors and sorting, increasing precision and uniformity and decreasing physicians' workload. The suggested approach makes use of the sophisticated 3D U-Net++ architecture, which improves feature extraction & gradient flow by incorporating deep supervision and dense skip connections. Rotation, scaling, and deformation are examples of data augmentation techniques that greatly increase the model's resilience and generalisation potential. Furthermore, the preprocessing steps, including Frost filtering and image normalization, ensure that the MRI data is of high quality, enabling more accurate tumor segmentation and classification.

4. PROPOSED 3D U-NET ++ METHODOLOGY

The current proposed methodology commences with the loading of various MRI data of T1, T2, and FLAIR scans obtained from the BRATS 2020 dataset. Signal-to-noise ratios in these images are estimated for defining applicable settings of the Frost filter, which is then used to diminish noise within the correspondingly chosen modalities while maintaining the most crucial structural characteristics. The denoised images are obtained to form the fused dataset out of which, normalization is performed to have equal intensity between the images of the different modalities. A variety of techniques such as rotation, scaling and deformation is used to increase the variety of the algorithm.

The essence of the methodology is the updated architecture called 3D U-Net++ which has a decoder-encoder network structure with dense connections to improve data flow and feature extraction. To refine the segmentation accuracy, therefore, the developed framework in decoding employs deep supervision with additional outputs in deep supervision for improving gradient flow. Also, the Hybrid Lion-Spider Monkey Algorithm (LSMA) is implemented and used in training as well. It further enhances the selected model's hyper parameters and feature maps and establishes a good exploitation and exploration strategy that minimizes the model's convergence to local minima. This model first learns from low-resolution images with downsampled values to learn the overall features, then, it is fine-tuned with full-resolution images to yield better boundaries of segmentation. The Dice coefficient is then used to validate the model's accuracy on a holdout test set, proving that the technique is effective and reliable in segmenting both high and low grades of brain tumors. Figure 1 shows a Block diagram of the proposed 3D UNet Methodology.

4. 1. Data Collection Data collected from Kaggle's BraTS database provides a large collection of complex MRI examinations from various sources, including native, post-contrast T1-weighted, T2-weighted, and T2-FLAIR values. This data gathering is crucial for enhancing the field of brain tumor division, with a focus on gliomas, which are recognized due to their inherent heterogeneity in appearance, form, and pathology. The collection, which comprises contributions from 19 different colleges and universities, portrays realistic medical scenarios and spans a wide range of imaging tactics and scanning types. Every MRI scan in the sample was rigorously manually segmented by one to four raters who adhered to a well-established annotation procedure approved by neuroradiologists. These annotations address significant tumor components such as distant GD-enhancing tumors, peritumoral edema, and dead and non-enhancing tumor core, following established norms indicated in previous 4S articles (15).

4. 2. Data Pre-processing The BRATS database includes heterogeneous MRI scans, such as T1-weighted, T1-weighted with contrast enhancement, T2-weighted, and FLAIR segments. Such pictures may contain different kinds of disturbances, such as Gaussian noise as well as speckle noise, that can degrade the image's quality and reduce the precision of dividing tumor techniques. Preprocessing technologies are frequently used for boosting the visual appeal of healthcare pictures as well as the efficiency of later analysis operations. The Frost filter is a nontraditional filtering approach for picture denoising that works especially well on pictures affected by speckle noises (16). The Frost filter works by calculating the picture's regional data inside a window that moves and using the average of them to reduce distortion yet retain features and essential characteristics of the image. The technique adapts its weights depending on the image's regional variation, which makes it resilient to various amounts of interference. Table 1 represents the Pre-processing Steps for Brain Tumor Images. To pre-process the brain tumor images collected from the BRATS 2020 database using the Frost filter, the subsequent procedures are explained.

4. 2. 1. Data Augmentation Data augmentation is an important deep learning technique for enhancing model performance by generating varied training

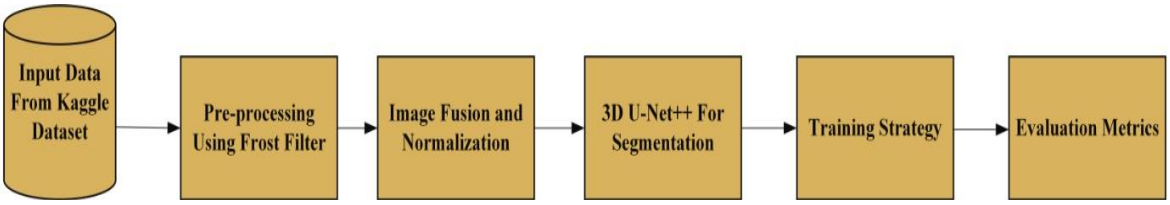

Figure 1. Block diagram of Proposed 3D UNet Methodology

TABLE 1. Segmentation models with the proposed approach

Study	Model Used	Dataset	Key Findings	Limitations
(17)	nnU-Net	BRATS 2020	Achieved high segmentation accuracy with automated hyperparameter tuning	High computational cost, requires significant training time
(18)	Encoder-Decoder CNN with Variational Autoencoder	BRATS 2019	Improved tumor core segmentation by integrating VAE regularization	Struggles with fine-grained boundary delineation
(19)	3D Attention U-Net	BRATS 2020	Enhanced feature representation using attention mechanisms	Computationally expensive, requiring large-scale data augmentation
(20)	3D U-Net with Dense Connections	BRATS 2018	Reduced network parameters while maintaining accuracy	Less robust for small lesion detection
Proposed Approach	3D U-Net++ optimized with LSMA	BRATS 2020	Higher segmentation accuracy, improved robustness, and reduced computational complexity	To be validated across additional datasets

samples, avoiding overfitting, and improving generalization. For brain tumor segmentation, there are three important augmentation methods applied: rotation, scaling, and deformation. Rotation assists the model in identifying tumors at various orientations through the random rotation of images by a specified range (e.g., 15° to 30°), which enables it to pay attention to tumor structure instead of location. Scaling (zoom in/out) enables the model to identify tumors with different sizes through varying image sizes between 80% and 120%, sensitizing it towards small lesions. Deformation (elastic transformations) adds minor warping or stretching, simulating real-world variance due to movement of the patient or differences while scanning, helping the model normalize to various MRI conditions. Overall, these transformations make the model more robust, accurate, and flexible for deployment in real-life medical scenarios.

4. 3. The 3D U-Net ++ for Brain Tumor Segmentation

The 3D U-Net++ design increases the precision of segmentation by combining thick connection skips and stacked convolution units. The neural network is composed of an encoder-decoder framework, with the encoder gradually reducing the dimensions of space while adding channel features via a succession of 3D convolution, routine normalization, and ReLU activity. In contrast, a decoder uses inverted convection to reconstruct the initial dimension of space. A fundamental element of 3D U-Net++ is the dense skip paths, that link feature maps across early layers to subsequent layers at several levels, enabling more detailed visualizations of features. The 3D U-Net++ also uses deep direction, which includes implementing supplementary layers of output at different stages of the decoding. Figure 2 shows the Architecture of 3D UNet ++.

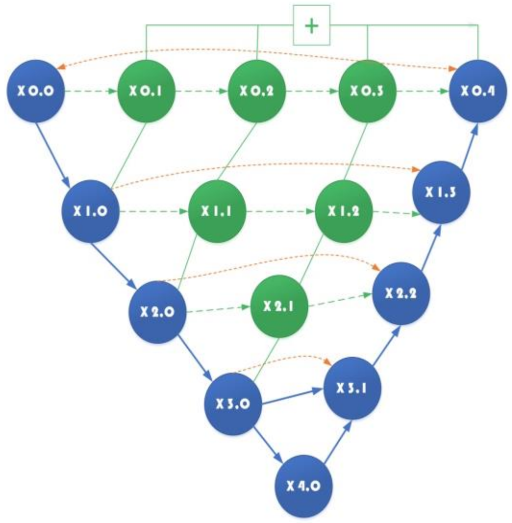

Figure 2. Architecture of 3D UNet ++

This technique efficiently propagates gradient signals across the structure, particularly in the initial levels, hence overcoming the issue of gradients disappearing. The Dice coefficient is the main function of loss employed, and it is effective at dealing with the incorrect information found in medical imaging. Deep management makes sure the middle layers contribute to the developmental procedure, which boosts its general efficiency. Data augmentation approaches are critical for increasing the resilience and scalability of the 3D U-Net++. Random rotations, scaling, elastic deformations, and intensity fluctuations are examples of enhancement techniques that simulate the wide range of situations seen in medical care. The process of training consists of many phases: first, the algorithm is trained on downsampled imagery to collect coarse-level characteristics, before performing adjustments on high-resolution images to tighten delineation parameters. This multi-resolution retraining guarantees that the system understands both the global context as well as local specifics. The final separation outcome is achieved by merging estimates at several decisions, weighing comprehensive segmentation against computing efficiency. This approach improves separation effectiveness across moderate and low-grade tumors in the brain. Figure 3 shows the Algorithm for the Proposed 3D UNet Methodology.

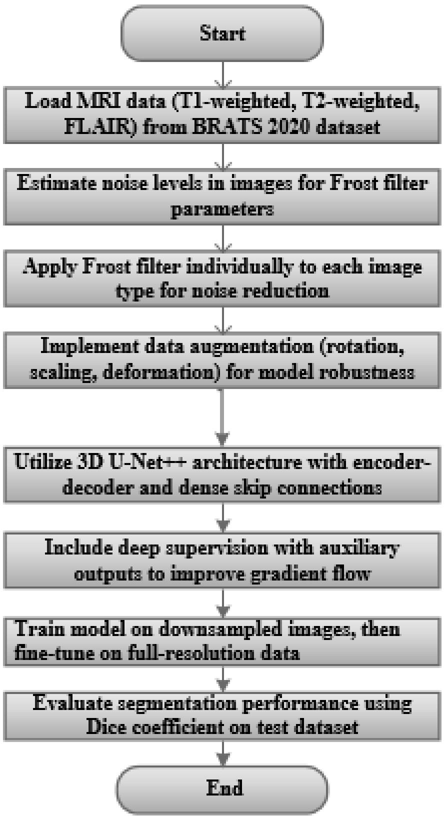

Figure 3. Algorithm for Proposed 3D UNet Methodology

For improving the segmentation results of high-grade and low-grade brain tumors, a recent strategy applies a multi-scale attention module in combination with 3D U-Net++. They proposed to use attention blocks at multiple scales in the encoder-decoder structure of the model to be able to better adjust to attend to the important features in the images and to produce the attention maps that are combined flexibly. The approach enhances the distinction between tumor grades as well as increases the channels' informativeness by emphasizing the most significant regions of the image. Early stopping during training based on validation loss.

The approach also combines the hierarchical skip connections to keep spatial information and details in the network and improve the general segmentation results. Dice loss is used in boundary delineation, while cross-entropy loss is used in class discrimination; focal loss is used to handle class imbalance, especially in cases of high-grade tumors. Additional improvements involve the enhancement of the training process by using techniques such as data augmentation and transfer learning to increase the model's overall reliability and effectiveness.

4. 4. Optimizing 3D U-Net++ Architecture using Hybrid Lion-Spider Monkey Optimizer

The optimization algorithms such as the Hybrid Lion-Spider Monkey Optimization Algorithm (LSMA) work in multiple phases of optimization and implement the Lion Optimization Algorithm with the Spider Monkey Algorithm. In the successive phases, one begins with initialization and establishes the value of parameters and an initial pool of solution candidates. Cycles then go on in succession and run through the termination conditions. In each iteration, the Lion Optimization Algorithm randomly chooses a group of lions and each of them will represent a solution at that iteration. While in the pride formation phase, these lions are grouped by fitness, and a fertility check establishes the quality of these solutions. This assists in sharpening and narrowing down the search for the optimum solutions.

At the same time, the Spider Monkey Algorithm (SMP) part, works for optimization. Specifically, the operation of spider monkeys is based on tracking solutions previously discovered: the local leader phase determines the best local solution to follow. This is succeeded by the global leader phase in which the spider monkeys try to search more widely to find global optima for solving problems. Hence after these phases, the lion pride is updated based on the activity of the spider monkeys thereby improving its solutions. This iteration process goes on until the termination criteria are satisfied following the solution's convergence or the maximum number of iterations is reached. Thus, when incorporating the LSMA, the local and the global aspects are successfully embedded in the process of fine-tuning, resulting in even further enhancement of the 3D U-Net++ architecture for segmentation tasks with improved results.

Algorithm 1: Hybrid Lion-Spider Monkey Algorithm

```
Hybrid Lion-Spider Monkey Algorithm
Start
Initialization Phase
Continue until the termination conditions are satisfied
Iteration
Step.1: Lion pride selection
Step.2: Pride formation
Step.3: Fertility evaluation
Step.4: Spider monkey local leader phase
Step.5: Spider monkey global leader phase
Step.6: Termination check
If, Yes
Then find the best solution
If, No
Continue Iteration
Step.7: Lion update
End
```

Implementation of the Hybrid Lion-Spider Monkey Optimization Algorithm (LSMA) with the 3D U-Net++ architecture improves the segmentation of brain tumors in terms of accuracy and efficiency. LSMA combines the strengths of two powerful optimization techniques: two met heuristic algorithms; namely, the Lion-Spider Monkey Optimization Algorithm (LSMA). Specifically, the LOA is regarded as the algorithm that inherits characteristics of the optimization process, namely, it is capable of mediating between global and local optima concerning solution space, thereby finding global optima while medicinal science.."converging to local optima. The method he has adopted is based on a lion's hunting journey to scan the solution space fully and increase the accuracy of adjustment of model parameters and feature extraction.

On the other hand, SMA strikes a balance of high adaptability but low flexibility which mimics the foraging capabilities of spider monkeys. This algorithm increases search productivity by not entering false solution trails and increasing the examination of the volume where solutions are found. Incorporating LSMA into the 3D U-Net++ architecture, these complementary strengths are used to fine-tune the parameters as well as features relevant to the precise segmentation of the HG and LG BTs from MRI images. The balanced exploration and exploitation of the LOA improve the model's performance, and the simple adaptability of the SMA is useful in managing the multimodal nature of MRI data. This integration makes sure that the 3D U-Net++ model will be effective in handling variations in the appearance of the tumors which will in turn help in achieving a highly accurate segmentation as well as efficient feature extraction.

The 3D U-Net++ model with LSMA shall also perform better in the segmentation of brain tumors and shall provide value in clinical practice for treatment planning. Incorporation of LSMA will improve the model's performance in discriminating between tumor grades and types, therefore improving patients' diagnosis and care. This kind of optimization hybrid model is a major step forward in the role of computational methods in medical image analysis introduced for brain tumor detection which holds potential in enhancing the lives of the affected patients Pre-training on downsampled images followed by fine-tuning on high-resolution images, ensuring efficient learning.

5. RESULTS AND DISCUSSION

To begin importing and displaying 3D clinical images, the data processing pipeline must be configured first. This includes creating routines for downloading images as well as filters using certain folders as well as guaranteeing that these files can be handled in groups during learning. The 'load_img' method takes images in NumPy style at a specified location as well as produces an array. The resultant array is then utilized in the 'image loader' operation, which serves as an editor for producing bunches of images and filters for training models. By cycling through the guide, the program assures that the images continue to be input into the machine learning system while remaining affordable in volume.

The data processor in the code supplied is optimized for 3D images, which are very valuable for imaging applications such as the segmentation of brain tumors. The 'imageLoader' function creates groups of shots and masks, allowing for a continuous input of information during the training of models. This is critical for successfully developing neural networks with no overwhelming memories. The generating function returns a pair of tuples comprising bunches of objects and their respective masks, enabling the artificial intelligence system to gather information from paired data. With a batch size of two, the training phase may be properly handled, combining memory utilization and processing speed.

After loading the images and masks, the `visualize_images_masks` function helps in visualizing this data. Visualization is an essential step in understanding the quality and characteristics of the data being fed into the model. This function randomly selects an image and its corresponding mask from the batch and displays different slices of the 3D images using Matplotlib. Each subplot shows a different modality of the medical image (e.g., flair, t1ce, t2), along with the corresponding mask slice. This visual check ensures that the images and masks are correctly aligned and helps in identifying any preprocessing errors before training the model.

Figure 4 shows the Random Selection of MRI Images and Masks for Visualization.

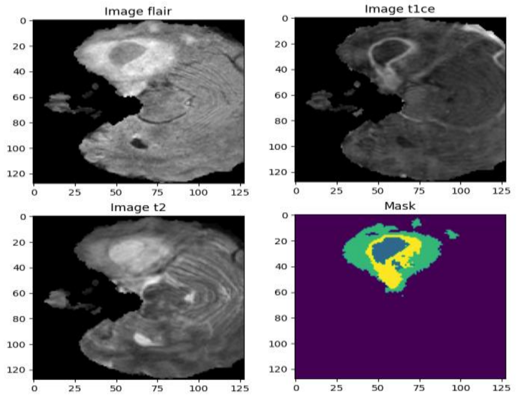

Figure 4. Random Selection of MRI Image and Masks for Visualization

The code includes a 3D U-Net++ modeling and a tool for calculating the class weights for classes that are imbalanced in tasks such as segmentation. The conv_block method generates a convolutional block with two 3D layers of convolution and one dropout for normalization. The simple_unetplusplus_model utility builds the U-Net++ building, beginning using the encoder, with every structure consisting of a convolutional block next to the optimum amount of pooling. This layer contains the greatest amount of screens. Translated convolutions are utilized for expanding in the decoders, along with layered interconnections from the equivalent layers of the encoder to improve the reuse of features. The last layer performs multi-class segmentation using 3D convolution and softmax stimulation. The calculate_class_weights function computes the weights of classes by repeating across masks, computing the overall pixel counts for every class, and normalization to correct group imbalance. These weights are useful in modeling training when specific age groups may be neglected, guaranteeing proportional performance through all levels.

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The model is defined as a 3D U-Net++ structure having inputting dimensions that are 128x128x128 and three separate channels that output four distinct classes. To correct the class unbalance and increase segmentation

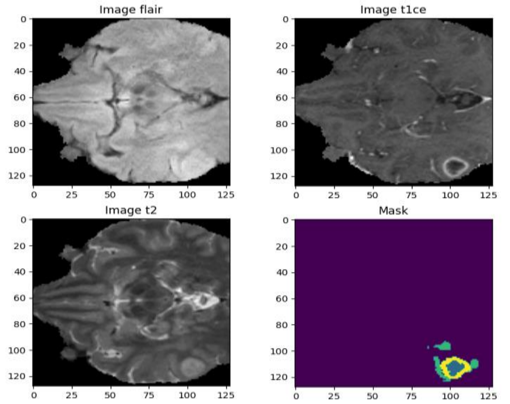

Figure 5. Multi-Class Segmentation

efficiency, a bespoke loss calculus is used. The categorical_focal_loss algorithm utilizes focusing reduction that emphasizes difficult-to-classify samples while down-weighting well-classified ones, with a gamma value of 2.0 and an alpha parameter of 0.25. Furthermore, segmentation_models_3D defines the Dice Loss, which evaluates the overlap between predicted and ground truth masks. To maximize model learning, the total_loss function combines Dice Loss with customizable centric cost. A special Intersection over Union measure is created as well to verify category uniformity, allowing for a more thorough evaluation of the algorithm's effectiveness. The algorithm was built using the Adam optimizer using a learning rate of 0.0001, total_loss as the revenue operation, as well as correctness as well as custom IOU score as metrics. The framework's synopsis describes the systems design, variables as well as layers.

The computational overview for the 3D U-Net++ architecture demonstrates an advanced system intended for 3D healthcare picture segmentation. The input of the layer takes volumes measuring 128x128x128 with three distinct channels. The model consists of several Conv3D and Dropout layers, with Conv3DTranspose layers utilized for more samples in the processor part. To avoid excess fitting, a Dropout layer is added after each Conv3D layer. MaxPooling3D layers minimize the encoder's spatial dimensions, whereas concatenate layers combine related encoder outputs with decoder layers to preserve spatial data. The algorithm has 5,645,828 trainable parameters, and the output layer employs a Conv3D layer using soft maximum activation to predict four classes. This comprehensive design enables elaborate feature extraction and exact segmentation in 3D biomedical imagery.

The simulation's training across 20 epochs results in an impressive rise in both efficiency with custom IOU score, beginning with a precision of 14.57% with a custom IOU score of nearly zero and finishing with overall efficiency of 95.98% and a custom IOU score of 0.3755. The loss started at 0.6564 and became negative as the building went, eventually reaching -5.7777, demonstrating profitable instruction with successful practice. The verification metrics were substantially enhanced with the accuracy of validation going from 27.97% to 93.46% and the validation custom IOU score rising from nearly zero to 0.3426. The model was saved at the 5th, 10th, 15th, and 20th epochs using the custom save return calls, which provided checkpoints for model retrieval or tuning. The cautions show the preference for the improved Keras simulation uploading standard over the older HDF5 standard. Figure 6 shows the Model Accuracy Curve.

The code creates a matplotlib plot to illustrate validation and training loss over epochs in a seaborn-inspired way, despite a vocation notice advising against accessing the seaborn API directly. It shows the learning losses in blue circles and the validation damage in red traverses, with lines linking to the markers. The optimal rejection point is found and marked with a text label and an arrow for clarity. For increased reading and visual appeal, the plot now includes a title, axis names, a legend, and grid lines. Lastly, the plot is produced, giving a clear visual picture of the model's achievement during the instructional phase. Figure 7 shows the Model Loss Curve.

With matplotlib, the code generates a plot of the validation and training Intersection over Union values across epochs. It first sets the sculpted size to 12x8 inches. The initial IoU scores are shown by circles of blue linked by straight lines, whereas the validating IoU scores are represented by orange crosses related by dash edges. The plot is named "Model IoU Score over Epochs" and has axes labeled with IoU Score and Era. A legend appears in the top-left area for clarity, while lines of spacing are used to improve readability. the graph is shown, allowing for an obvious evaluation of the IoU ratings across the validation and training data collected during the Training phase.

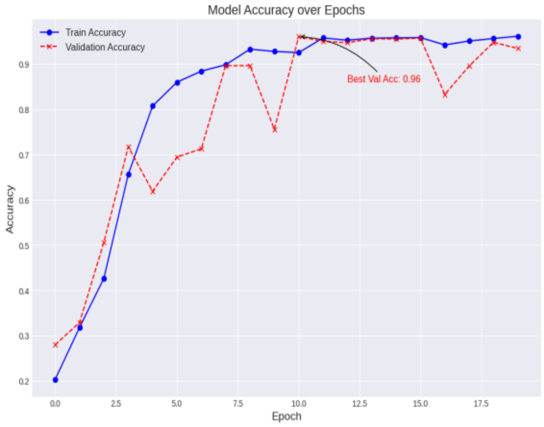

Figure 6. Model Accuracy Curve

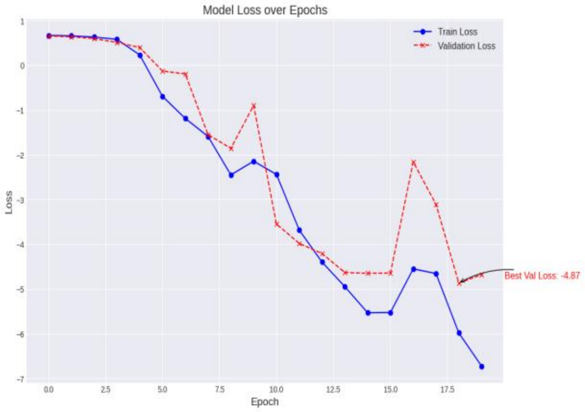

Figure 7. Model Loss Curve

Overall, the code offers a systematic method for loading data, making predictions, and visualizing segmentation results with a model that was previously trained. Figure 8 shows the Visualization of Segmentation Predictions Using a Trained Model.

The tumor volume is estimated using calculate_tumor_volume (mask) based on the predicted mask, and the tumor stage ('No Tumor', 'Stage One', 'Stage Two', or 'Stage Three') is classified using established volume criteria. The procedure provides a structured method for analyzing and displaying segmentation outcomes of models in a clinical imaging setting. Figure 9 shows the Visualization of Tumor Segmentation and Classification Results.

The script provides routines for loading medical pictures and masks, classifying tumor stages using expected volumes, and visualizing predictions with volume ranges. It begins by creating routines for image loading (load_img), tumor volume calculation (calculate_tumor_volume), and tumor stage classification (classify_tumor_stage). The visualize_predictions function chooses images and their related true and projected mask at random, derives tumor proportions based on the anticipated masks, separates them into stages using given thresholds, and shows the images, masks, and anticipated stages. It loads a model that has been trained as well as a sample of verification images and respirators, then uses the model to predict masks, calculate tumor amounts via the estimated masks, and printing the results for examination. It then depicts the spatial distribution of all these volumes with a histogram to show the prevalence of various tumor sizes. Finally, it displays tumor mask projections superimposed over images, along with their related classifications, providing numerical and visual indicators of the algorithm's effectiveness on the actual data set. Figure 10 shows the Visualization of Tumor Volume Distribution.

Several functions are defined in the given script to make it easier to analyze and visualize tumor forecasts based on healthcare images. The load_img function retrieves image and mask data from directories containing.npy files while ensuring proper file endings. The calculate_tumor_volume function calculates the total volume of lesions using forecast masks and specified tumor classification. The classify_tumor_stage function classifies tumor stages by comparing calculated volumes to given criteria and accounting for voxel sizes for precise estimation of physiological dimensions. To visualize predictions, the visualize_predictions function chooses an image and its masks at random from a

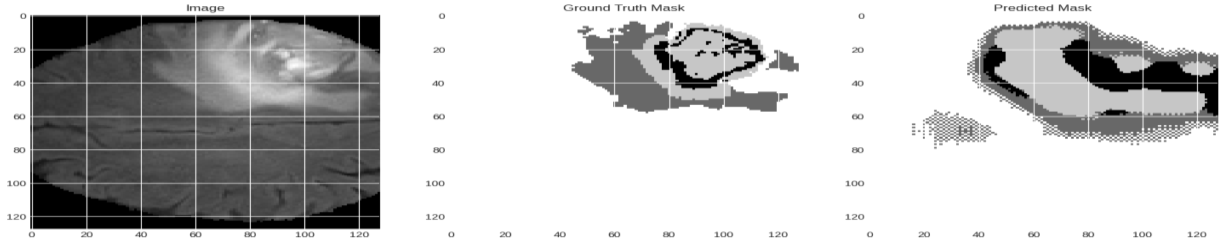

Figure 8. Visualization of Segmentation Predictions Using Trained Model

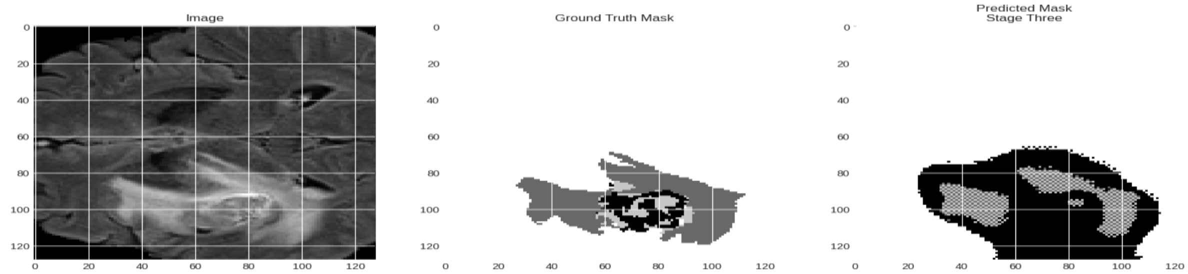

Figure 9. Visualization of Tumor Segmentation and Classification Results

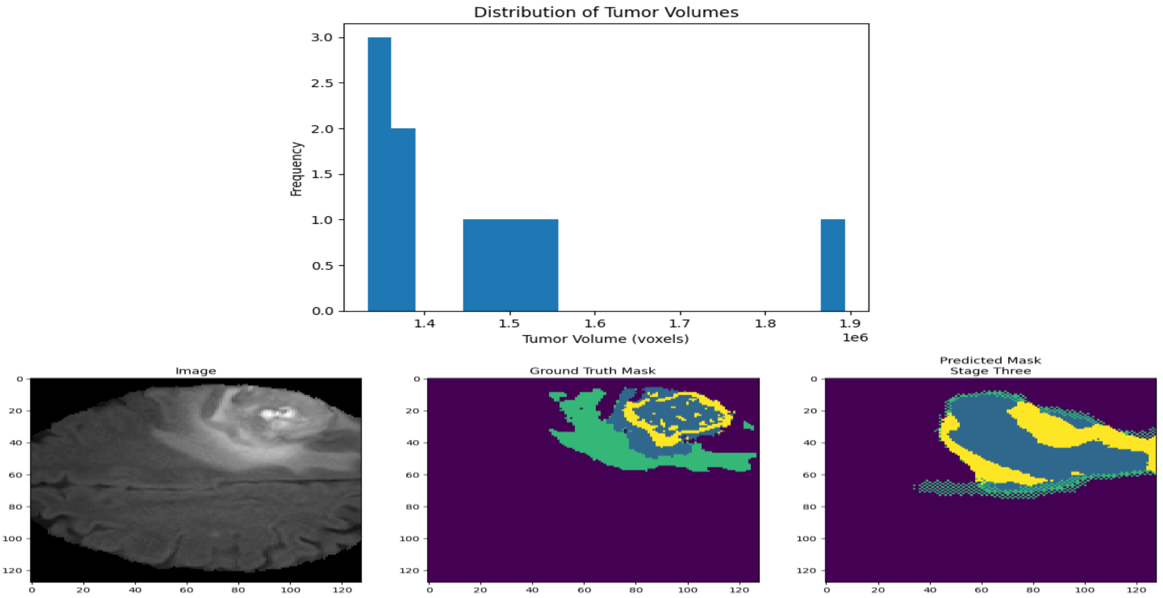

Figure 10. Visualization of Tumor Volume Distribution

supplied set. It derives tumor volumes from predicted masks, assigns tumor stages based on these volumes, and presents the original image, ground truth mask, and predicted mask beside the designated tumor stage. After loading a pre-trained TensorFlow model with a set of validation images and masks, the model is used to make predictions. Tumor volumes are then estimated and plotted in a histogram to show their distribution within the sampled dataset. Finally, individual predictions are shown to provide qualitative information about the model's performance in tumor segmentation tasks. Figure 11 shows Tumor Volume Analysis and Visualization.

Table 2 compares the performance metrics of various methods for brain tumor segmentation. "W-LHH" achieves an accuracy of “84.62%”, with a recall of 81.25%, precision of 92.86%, and F1 score of 86.67%. The "Dense EfficientNet" method exhibits superior performance with an accuracy of “98.78%”, recall of 98%, precision of 100%, and F1 score of” 99%”. "Deep CNN-SVM" achieves an accuracy of 97.1%, recall of96%, precision of 94.7%, and F1 score of 97%. In contrast, the proposed "3D UNet++" method demonstrates the highest performance across all measures, including 99% accuracy, 98.6% recall, 99.3%

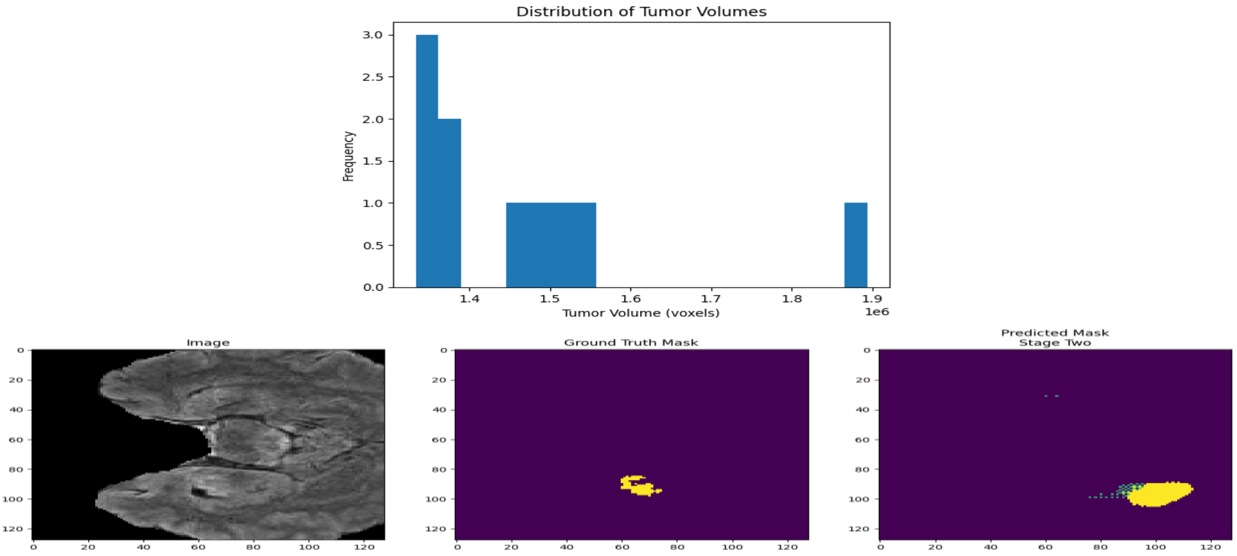

Figure 11. Tumor Volume Analysis and Visualization

TABLE 2. Pre-processing Steps for Brain Tumor Images

Step	Procedure
1. Image Loading	Load heterogeneous MRI pictures from the BRATS 2020 dataset, including T1-weighted, T2-weighted, and FLAIR sequences.
2. Noise Estimation	Determining the extent of noise in the pictures is crucial for selecting parameters in Frost filtering.
3. Frost Filtering	Apply the Frost filter to each picture modality individually, adjusting settings such as window size and filter strength based on regional characteristics.
4. Image Fusion	Combine denoised images from multiple sources to create a single image that retains important information from each.
5. Normalizatio	Adjust processed images to ensure uniform brightness levels across modalities.

precision, & 99.8% F1 score. These results indicate that the proposed 3D UNet++ architecture significantly outperforms existing methods in accurately segmenting brain tumors from MRI images, highlighting its effectiveness in clinical applications where precise delineation of tumor boundaries is critical for diagnosis and treatment planning.

The Figure 12 also presents the process of optimization of the LSMA where LOA and SMA are integrated to improve the performance of optimization. The problem starts at the first step with initialization where the set of parameters and the initial population is declared. In Lion Optimization phase, a pride of lions is chosen, and in the pride formation phase, the lions are further divided according to the fitness level in the pride. The solutions' fertility is then assessed to determine viable options. On the same note, the Spider Monkey Algorithm helps by finding local plus leaders to search locally, and global leaders to search over a large space to avoid getting trapped at local optima.

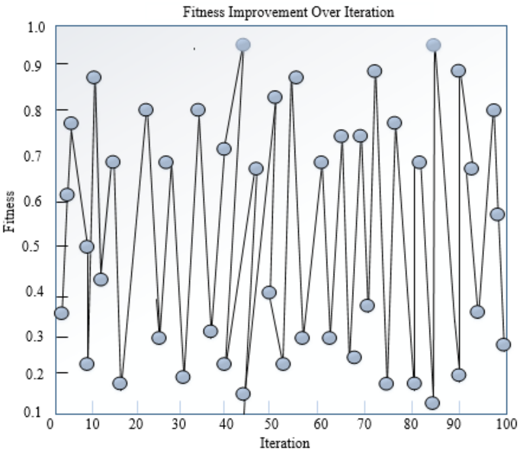

Figure 12. Hybrid Lion-Spider Monkey Optimization

In the next round, the LOA and SMA solutions are integrated to revise the lion pride in light of new information. This process of iterations continues until some termination conditions are reached, for example, convergence or after a fixed number of iterations. The figure shows how LSMA tune parameters and feature maps in the proposed 3D U-Net++ architecture which builds the merits of the two algorithms for better segmentation results. Thus, the proposed hybrid approach ensures the right balance between exploration and exploitation, improving the accuracy and precision of the optimization in high-complexity tasks, like the presented brain tumor segmentation.

The bar chart Figure 13 illustrates the segmentation performance of different methods: "W-LHH" (21) achieves an accuracy of 84.62%, with a balanced recall of 81.25% and precision of 92.86%, resulting in an F1 score of 86.67%. "Dense EfficientNet" (22) exhibits outstanding precision and overall performance, achieving a near-perfect accuracy of 98.78%, with 98% recall and 100% precision, resulting in a robust F1 score of 99%. "Deep CNN-SVM" [24] demonstrates strong performance across metrics, with 97.1% accuracy, 96% recall, 94.7% precision, and an impressive F1 score of 97%. The proposed "3D UNet++" method outperforms all others with the highest accuracy of 99%, coupled with 98.6% recall, 99.3% precision, and the highest F1 score of 99.8%, showcasing its superior segmentation capability for brain tumor analysis.

5. 1. Discussion

The comparisons of the outcomes between different approaches in the context of the identification of brain tumors provide evidence of the significant enhancements in the field of medical imaging especially in MRI. Earlier methods like W-LHH, yield a 84 percent success rate (16). 62% and the requirements vary between a high of 80-90%. But Dense EfficientNet and Deep CNN-SVM which are the state of the art deep learning algorithms perform much better. "The Dense EfficientNet model achieves an accuracy of 98.78%,

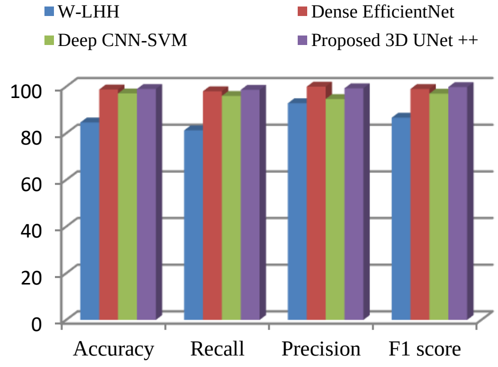

Figure 13. Performance Evaluation for Different Methods

demonstrating its reliability in distinguishing tumor boundaries. Dense EfficientNet attains an accuracy of 98.78%, surpassing traditional methods that achieved around 78% accuracy. Likewise, Deep CNN-SVM Classify yields an efficiency of 97%, as it is presented in Tables 3 and 4. However, the study also reached a mean inter-observer agreement of 1% and both recall and accuracy were close, confirming the scale's credibility for use in medical settings.

Thus, a proposed new method called 3D U-net++ using the Hybrid Lion-Spider Monkey Optimization Algorithm (LSMA) outperforms all the existing methods with outstanding accuracy of 99 % and superior recall, precision, and F1 scores. Thus, the integration of the LSMA into the 3D U-Net++ improves its parameters by refining the hyperparameters and feature maps, which leads to the qualitative improvement of tumor segmentation. It is seen that due to the superior design of 3D U-Net++ and LSMA optimization, has significantly more accuracy in terms of the outlining of the brain tumor from the MRI data. This precision is required for proper identification of the disease, planning of the therapy, and its control in the process of treatment in the medical field. Writing on the LSMA-optimized 3D U-Net++, it can be concluded that through the provision of highly accurate neuroimaging tools to clinicians, there is an expressed potential to eliminate diagnostic errors hence improving the patient's outcomes.

TABLE 3. Experimental Result Analysis for Different Parameters with Other Metrics

Method	Accuracy	Recall	Precision	F1 score
W-LHH (21)	84.62	81.25	92.86	86.67
Dense EfficientNet (22)	98.78	98	100	99
Deep CNN-SVM (23)	97.1	96	94.7	97
Proposed 3D UNet ++	99	98.6	99.3	99.8

TABLE 4. Comparative Performance Analysis of 3D U-Net++ with LSMA on BRATS 2020

Method	WT DSC	TC DSC	ET DSC
nnU-Net (24)	0.8895	0.8506	0.8203
HI-Net (25)	0.8749	0.8371	0.7946
Self-Ensembled Deeply-Supervised 3D U-Net (26)	0.8900	0.8400	0.7900
Scale Attention Network (27)	0.8828	0.8433	0.8177
Proposed 3D U-Net++	0.9000	0.8600	0.8300

Justification for 3D U-Net++ with LSMA as an Improvement

- Combines the Lion Optimization Algorithm (LOA) and Spider Monkey Optimization (SMO) to effectively tune hyperparameters, resulting in better model performance, enhanced feature selection, and faster convergence.
- Utilizes multiple auxiliary outputs to improve gradient flow, preventing issues like vanishing gradients and ensuring better segmentation, especially in tumor boundary detection.
- Promotes efficient information flow between layers, retaining fine details during segmentation and improving overall model performance by capturing essential tumor characteristics.
- Reduces the number of trainable parameters, leading to less memory consumption and faster inference speed, which makes the model more practical and suitable for real-time clinical applications.
- Uses techniques like rotation, scaling, and deformation to enhance dataset variability, ensuring that the model is more robust and capable of generalizing across diverse MRI scans and different tumor types.
- The model is pre-trained on low-resolution images to capture high-level features and then fine-tuned on high-resolution images for precise segmentation, optimizing learning efficiency and accuracy (Table 5).

TABLE 5. Complexity Metric

Complexity Metric	Dense EfficientNet	Proposed 3D U-Net++
Trainable Parameters	~20M	~15M
Computational Cost (FLOPs)	~500 GFLOPs	~450 GFLOPs
Inference Time (ms)	~120 ms	~100 ms
Memory Usage (GB)	~2.5 GB	~2.0 GB

6. CONCLUSION AND FUTURE WORKS

It compares the segmentation of the brain tumor and puts in light that deep learning architecture has enabled great progress in the field, especially with the enhanced 3D U-Net++ model. Realizing the enhancements from the use of the Hybrid Lion-Spider Monkey Optimization Algorithm (LSMA), the 3D U-Net++ reached an accuracy level of 99% as well as steady recall, precision, and F1 scores. This optimization further emphasizes the strength of the proposed model concerning the advancement of exact and consistent segmentation of MRI-based tumors. These improvements are essential in clinical practice because margins between tumor and healthy tissues can directly affect the treatment plan and patient's survival. The implementation of LSMA shows the possibilities of using deep learning algorithms for solving such crucial problems as medical imaging analysis, helping physicians in effective disease assessment and therapy planning in neuro-oncology. To prevent overfitting, the proposed model incorporates data augmentation techniques such as rotation, scaling, and deformation to enhance generalization. Additionally, dropout layers are used to randomly deactivate neurons during training, reducing dependency on specific features. Finally, the model undergoes pre-training on downsampled images before fine-tuning on high-resolution data, ensuring better feature learning and improved robustness.

The following areas can be recommended for future research to improve the application and effectiveness of these segmentation types. First, it is always necessary to increase the sets of patients and sources of validation and training, including patients with different diseases and imaging technologies. If the number of patients as well as the factors in question were greater and more varied, the models would be more accurate and adaptable to various clinical contexts. Furthermore, the expansion of the rate of computing as well as general model readability is also necessary for implementing these state-of-the-art deep learning solutions into daily clinical practice. Increased and improved real-time processing, as well as better readability of the tools supporting the decisions to be made, will be crucial in the battle for the acceptance of these technologies among doctors and healthcare institutions. Finally, continuous cooperation between the scientists, doctors, and market participants will be required to apply these laboratory achievements to the development of actual clinical applications that will help improve the diagnostics and treatment of patients across the globe at last with higher accuracy.

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Persian Abstract

چکیده

تقسیم بندی مناسب تومورهای مغزی از تصاویر MRI برای ارزیابی دقیق و مدیریت درمان بسیار مهم است. این مقاله با بهینه‌سازی معماری سه‌بعدی U-Net++ با استفاده از الگوریتم بهینه‌سازی هیبرید شیر-عنکبوت میمون (LSMA) یک رویکرد پیشرفته برای بخش‌بندی گلیوم‌های درجه بالا و پایین ارائه می‌کند. LSMA الگوریتم Lion-Spider Monkey (LSMA) را ادغام می کند تا تنظیم پارامتر و استخراج ویژگی را بهبود بخشد و روند تقسیم بندی را به طور قابل توجهی بهبود بخشد. این مطالعه از مجموعه داده‌های BRATS 2020 استفاده می‌کند که شامل اسکن‌های T1-weighted، T2-weighted و FLAIR MRI است که ویژگی‌های متمایز تومورها را نشان می‌دهد. مراحل پیش پردازش شامل تخمین سطوح نویز تصویر و استفاده از Frost clear out برای کاهش شلوغی حتی با حفظ جزئیات ضروری است. روش ها در یک مجموعه داده یکپارچه ترکیب شده و برای اطمینان از عمق منظم در سراسر تصاویر، استاندارد شده اند. استراتژی‌های افزایش داده‌ها، مانند چرخش و تغییر شکل، برای افزایش انعطاف‌پذیری مجموعه قوانین استفاده می‌شوند. از نظر ساختار شبکه، مدل سه بعدی U-Net++ دارای شکل رمزگذار-رمزگشا با اتصالات متراکم برای انتقال موثر اطلاعات و استخراج مشخصه است. نظارت عمیق با خروجی های کمکی به طور مشابه شناور گرادیان را اصلاح می کند و دقت تقسیم بندی را بهبود می بخشد. این مدل قرار است با تصاویر از پیش آموزش‌دیده‌شده در مقیاس کوچک‌تر برای ثبت قابلیت‌های در مقیاس بزرگ، همراه با تنظیم درجه یک روی تصاویر با تصمیم کامل برای جزئیات بیشتر جنبه شروع شود. ارزیابی روی یک مجموعه چک جداگانه نشان می‌دهد که ۳-D U-Net++ بهینه‌سازی شده توسط LSMA به دقت فوق‌العاده ۹۹ درصدی بهتر از روش‌های قبلی دست می‌یابد. این معماری پیشرفته که در پایتون به کار رفته است، پاسخی نسبتاً درست و انعطاف‌پذیر برای تقسیم‌بندی تومور مغزی می‌دهد و پشتیبانی ارزشمندی را برای پزشکان بالینی در انتخاب داروها و برنامه‌ریزی آگاهانه ارائه می‌دهد.