

# OPTIMIZED DEEP LEARNING FRAMEWORK FOR BRAIN TUMOR DETECTION AND CLASSIFICATION USING HYBRID VISUAL GEOMETRY GROUP-16 WITH REDUCED WEIGHTS VIA BUTTERFLY OPTIMIZATION

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## ABSTRACT

Finding and classifying brain tumors are important parts of medical image analysis that need advanced deep-learning methods and optimization algorithms. Recognizing the urgent need for accurate methods in brain tumor diagnosis, we present a comprehensive approach integrating various stages, including data preprocessing. In this preprocessing phase, we employ techniques like aspect ratio normalization and resizing to form a standardized dataset. By standardizing image dimensions, we aim to improve subsequent processes like feature extraction and segmentation, reducing potential distortions. The suggested model is made by using Convolutional Neural Networks (CNN) to find patterns and traits that make tumor and non-tumor areas different from each other. To overcome the intricate sections and fine textures during down-sampling, the proposed model is hybridized with U-Net architecture which gives accurate and robust results of 98%. Furthermore, the Dice coefficient is measured using Intersection Over Union (IOU) to ensure whether it is robust to class imbalance. This shows an intuitive interpretation, with higher values of 0.83 and 0.9 indicating strong and better segmentation performance. The model is further developed with VGG-16 to classify the tumor grades. In terms of accurately segmenting the tumor grades, the learnt relevant characteristics that are derived from the segmented tumor photos provide a 73% level of satisfaction. In order to overcome the complexity and over-fitting problems, the Butterfly Optimization algorithm is hybridized with VGG-16 which gives an enhanced output in classifying the grades. The proposed model outperforms other Machine Learning (ML) and Deep Learning (DL) methods in tumor and non-tumor identification and categorization with 99.99% accuracy. To further evaluate the suggested model's performance, mobility, and energy economy, it is also implemented in JETSON Orin hardware.

**Keywords**-Deep Learning, Convolutional Neural Networks (CNNs), U-Net, VGG-16, Butterfly Optimization Algorithm.

## 1. INTRODUCTION

The battle against brain tumors has reached a critical juncture, where innovation in medical imaging analysis stands as a beacon of hope [1]. The intricate challenge of accurately detecting and classifying these malignancies demands a paradigm shift in technological solutions. Our research reveals a breakthrough framework that blends state-of-the-art deep learning methods with metaheuristic optimization algorithms; this framework has the potential to alter, when it comes to identifying and

planning therapies for brain tumors [2]. The scope of this research lies in recognizing the pressing need for precision and efficiency in medical imaging analysis to bolster brain tumor diagnostics and therapeutic interventions [4]. Traditional methodologies, hampered by their limited accuracy and efficacy, fall short in meeting the demands of modern healthcare. Thus, the crux of our endeavor lies in surmounting these challenges through the development of a holistic pipeline encompassing data analysis, pre-processing, segmentation, feature extraction, optimization, and classification phases.

Our framework represents a pioneering effort to amalgamate Convolutional Neural Networks (CNNs) with U-Net for meticulous segmentation and to integrate the formidable VGG-16 architecture with Butterfly Optimization for optimized feature extraction [3]. Brain tumor identification and categorization reach new heights of accuracy and efficiency because to the domino effect of these components working together. Central to our approach is the concept of federated learning, a decentralized paradigm that respects data privacy while harnessing the collective intelligence embedded within disparate datasets. Leveraging the Federated Averaging (FedAvg) algorithm [1], our framework trains on decentralized data sources without compromising sensitive information—a pivotal breakthrough in medical AI. Drawing from a rich tapestry of references, our methodology is fortified by the insights gleaned from recent advancements in brain tumor classification and segmentation. Hasan et al. underscores the transformative potential of transfer learning in automating multi-class brain tumor classification, paving the way for enhanced treatment strategies [2]. In the same way, Gamal et al. argue that 3D U-Net can automatically separate brain tumors, which would start a new age of precision medicine [4].

Our system is proof of how powerful optimization methods can be for making deep learning models work better. To make brain tumor segmentation more accurate, Ramírez et al. talk about how to use deep learning to make variational models better [3]. Dolaat et al. showed how cooperative learning can help solve problems caused by uneven medical picture datasets. To move healthcare AI forward [5], it's important for people to work together and share their thoughts. The results of our study are a huge step forward in the search for better and faster ways to find and diagnose brain tumors. We are almost ready to start a new era of precision medicine where every patient gets the care, they deserve by using the combined knowledge of deep learning and optimization algorithms.

### 1.1 Motivation

Brain tumor detection and classification are paramount in medical imaging, demanding precise diagnostic methods to avoid misdiagnoses and delays in treatment. Our research addresses this gap by integrating advanced deep-learning techniques and optimization algorithms. We prioritize data preprocessing to establish a standardized dataset, employing techniques like aspect ratio normalization and resizing. This ensures uniform image dimensions, streamlining subsequent processes and

reducing potential distortions. In order to differentiate between tumor and non-tumor areas, our model uses Convolutional Neural Networks (CNNs) to detect complex patterns. To overcome downsampling challenges, we hybridize our model with the U-Net architecture, achieving a robust segmentation performance of 98%. We evaluate segmentation robustness using the Dice coefficient, ensuring resilience to class imbalances. Expanding our research, we classify tumor grades with the VGG-16 architecture, achieving 73% accuracy. To mitigate complexities and overfitting, we integrate the Butterfly Optimization algorithm, enhancing classification performance.

Through rigorous evaluation, our model achieves an unparalleled efficiency of 99.99%, outperforming existing methodologies. Deploying it on JETSON Orin hardware validates its performance and portability, promising enhanced patient care globally.

The contributions of the article are as follows:

- Introduction of novel preprocessing techniques for standardized dataset formation.
- Integration of CNNs with U-Net architecture for robust segmentation.
- Rigorous evaluation using Dice coefficient and VGG-16 for tumor grade classification.
- Enhancement of classification performance through Butterfly Optimization algorithm.

#### *Organization of the paper:*

Following this, the paper has a comprehensive methodology part that provides a description of the framework for the detection and categorization of brain tumors. Other writers who have conducted research on the segmentation and categorization of brain tumors are covered in part II of this article. Following this, in section III, a discussion is held on the description of each phase of the process. These phases include data collecting, preprocessing, segmentation, feature extraction, optimization, and classification. Following that, the section on the outcomes of the experiment offers the empirical findings that were gained from the implementation of the suggested framework. These findings are complemented by visualizations and comparison analyses with methodologies that are already in use. There is a detailed analysis of the data that is presented in the discussion section. This analysis addresses the ramifications, limits, and potential future research areas. In conclusion, the conclusion provides a summary of the most important findings, reiterating the relevance of the framework that was provided, and encourages more

collaboration and creativity in the use of deep learning to address difficulties in the healthcare industry.

## 2. RELATED WORKS

Many deep learning experiments have targeted brain tumor detection and classification. Dipu et al. [6] used YOLOv5 for object identification and FastAI for classification to achieve good MRI scan accuracy (2021). To increase detection accuracy and resilience, better CNN architectures for tumor segmentation (2021), hybrid CNN-RNN models (2021), and ensemble learning (2021) have been investigated. Deep learning may change brain tumor diagnosis and therapy by enabling early detection and planning. Sankaranarayanan et al. [7] presented a VGG-16 solution for brain tumor identification and classification at the 2023 International Conference on AI and Knowledge Discovery in Concurrent Engineering. As big data grows in medicine, the authors stressed the importance of data analysis and mining on tumor prediction, monitoring, diagnosis, and therapy. Brain tumors are aggressive and have low survival rates, thus better diagnostic and treatment methods are needed. Deep learning, particularly CNNs, was used to solve brain cancer diagnosis and treatment issues. Federated Learning (FL) was used to improve privacy and scalability in centralized data collecting. The study optimized model parameters for MRI tumor identification using the VGG-16 architecture for brain cancer detection and a CNN model framework. Experimental findings showed that the suggested approach outperformed traditional techniques with 92% accuracy. This research advances brain tumor identification and shows how deep learning may improve healthcare.

Younis et al. [8] combined deep learning and ensembling learning to show that AI and neural network algorithms may identify brain tumors early. Segmentation improved brain tumor detection and categorization. The study trained models to reliably identify brain cancers using MRI utilizing convolutional neural networks (CNNs) and VGG-16 architecture. Popular for its simplicity and speed, VGG-16 developed convolutional feature maps that were categorized to find tumor locations. The proposed method was tested on 253 MRI brain scans, 155 of which showed cancers. CNN's 96% accuracy and 91.78% F1-score, VGG-16's 98.5% and 92.6%, and the ensemble model's 98.14% outperformed classical methods. The project closes with deep learning brain tumor detection

instructions. In 2020, Bhanothu et al. [9] introduced a deep convolutional network to classify brain tumors in MRI scans. MRI scans are essential for tumor diagnosis, therefore the scientists created Faster R-CNN deep learning to automate tumor identification and localization. It designates tumor occurrence areas using Region Proposal Network (RPN), accelerating review and reducing errors. Regional proposal and categorization of glioma, meningioma, and pituitary tumors utilizing VGG-16 architecture. Evaluation results showed promising accuracy ratings of 75.18% for glioma, 89.45% for meningioma, and 68.18% for pituitary tumors. The mean average precision of automated brain tumor detection and classification was 77.60% across all classes.

In 2022, Abirami et al. [11] used Generative Adversarial Networks (GANs) to fuse PET and MRI images. They stressed the necessity of multimodal picture fusion in medical applications to improve visual content and medical analysis. They noted that multimodal fusion helps doctors view hard and soft tissue, especially in brain imaging where tumor segmentation is critical. The suggested method enhances tumor localization accuracy and diagnostic speed by fusing PET and MRI data. PET gives functional data while MRI provides anatomical data to characterize brain cancers. The proposed GAN-based fusion model blends different modalities to provide fused pictures for medical analysis and surgery planning. GAN-based model fared well with 0.8551 structural similarity and 2.8059 mutual information. Multimodal medical image fusion enhances brain tumor identification and treatment planning in this research. Haq et al. [12] suggested DACBT, a deep learning brain tumor classification approach using MRI data in IoT healthcare, in 2022. Deep learning-based brain tumor classification was proposed to address the limitations of artificial diagnostic systems for brain cancer diagnosis in IoT-healthcare systems. DACBT classified brain tumors using brain magnetic resonance (MR) imaging data and an upgraded CNN. Adding data and transfer learning enhanced the model's categorization. The suggested model outperformed baseline brain cancer diagnostic methods in IoT-healthcare systems in experiments. This research improves brain tumor classification accuracy and efficiency using deep learning.

Dhakshnamurthy et al. (2024) classified brain cancers using transfer learning [13]. Understanding the time-consuming nature of brain tumor identification and the limitations of conventional techniques in managing expanding data volume, the scientists researched deep learning

approaches to build automated systems for precise and efficient diagnosis. The study found AlexNet, VGG16, and ResNet-50 effective. The authors then created a hybrid VGG16–ResNet-50 model with 99.98% accuracy, sensitivity, specificity, and F1 score. The framework can accurately identify cerebral neoplasms when compared to other models, showing the promise of transfer learning in medical imaging for brain tumor identification and classification. Dhiman et al. (2022) proposed a machine learning-based hybrid CNN model for medical image processing tumor detection [14]. The study quickly extracted valuable malignant tumor oncology medical data from electronic clinical medical records. The study provided a standard extraction method for initial tumor site, size, and metastatic sites to address tumor-related medical events. Also, key-based and pseudo-data-generation algorithms improved transfer learning across tumor-related medical event extractions. Multiple CCKS2020 dataset experiments demonstrated that the recommended approach placed third in clinical medical event extraction and assessment of the electronic medical record.

Deep learning and machine learning were utilized by Senan et al. in 2022 in order to investigate the early identification of brain tumors using MRI images [15]. As a result of the fact that cancer is one of the most aggressive and life-threatening diseases, the purpose of the study was to improve patient survival by properly detecting brain tumors. With advances in deep and machine learning, computer-aided diagnostic systems can help doctors make accurate diagnoses. The study integrated deep learning methods like AlexNet and ResNet-18 with classic machine learning methods like SVM for brain tumor classification and diagnosis. Brain tumor MRI pictures were improved using the average filter. Deep convolutional layers extracted robust and crucial deep features, followed by SoftMax and SVM classification. The 3,060 pictures were sorted into three tumor kinds and one normal class. All systems performed well, but the AlexNet+SVM hybrid approach had the highest accuracy (95.10%), sensitivity (95.25%), and specificity (98.50%). This study shows that hybrid methods can detect brain tumors early, advancing medical imaging and diagnostics.

RU-Net2+ is a deep learning system that was created by Zaitoon and Syed (2023) for the purpose of brain tumor segmentation and survival rate prediction [16]. The process of diagnosing and treating brain tumors is challenging, but deep learning may make it possible to automate the process. The framework incorporates the detection

of tumors, categorization of tumors, segmentation of tumors, and prediction of survival rates. It is necessary to collect data, perform preprocessing, and make improvements to the Convolutional Normalized Mean Filter in order to implement the approach for the BraTS dataset. Multi-class classification is accomplished by the utilization of the cutting-edge DBT-CNN classifier model. A survival rate prediction is made using a logistic regression model after the tumor has been delineated and features have been extracted using RU-Net2+. When it came to classification accuracy, tumor segmentation precision, and survival rate prediction, the experimental findings were superior to the standards that are now in place. LGG tumors had a classification accuracy of 99.28%, whereas HGG malignancies had a classification accuracy of 99.51%. The HGG had a tumor segmentation accuracy of 98.39%, whereas the LGG had a 99.1% accuracy. Long-term patient survival rates were predicted by the RU-Net2+ algorithm to be 85.71%, medium-term survival rates to be 72.72%, and short-term survival rates to be 61.54%, with Mean Squared Errors of 0.13, 0.21, and 0.31 respectively. These findings provide medical practitioners with information that assists them in making decisions regarding the treatment of brain tumors and demonstrate that automated brain tumor identification may enhance patient care.

Srinivasan et al. (2023) used deep learning to grade cancers from brain magnetic resonance imaging [17]. In order to increase tumor identification accuracy, the study developed a unique automated detection and classification approach. MRI scans were pre-processed, segmented, feature-extracted, and classified. During the pre-processing stage of magnetic resonance imaging (MRI), an adaptive filter was utilized to eliminate background noise. The local-binary grey level co-occurrence matrix (LBGLCM) was utilized for feature extraction, and enhanced fuzzy c-means clustering was utilized for image segmentation. The images obtained from an MRI were categorized as either normal or glioma using a convolutional recurrent neural network (CRNN). In terms of accuracy, specificity, and sensitivity, the recommended method for classifying brain tumors performed better than BP, U-Net, and ResNet. It achieved 98.17 percent, 91.34%, and 98.79 percent respectively. In order to demonstrate that the CRNN technique enhanced the accuracy of brain image classification, the research utilized 620 testing and 2480 training MRI images taken from the REMBRANDT dataset that were employed.

ZainEldin et al. (2023) classified brain cancers using deep learning and sine-cosine fitness gray wolf optimization [26]. Due to increased patient data volume, the study intended to develop reliable and efficient automated brain tumor diagnosis methods, which are time-consuming and rely on radiologists. Pre-trained CNN models are used for quicker brain tumor identification and segmentation using deep learning. BCM-CNN used ADSCFGWO to tune CNN hyperparameters. Hyperparameter adjustment and model training with Inception-ResnetV2, a popular pre-trained model, provided binary outcomes (0: Normal, 1: Tumor) to improve brain tumor diagnosis. ADSCFGWO improved hyperparameters utilizing sine cosine and grey wolf strengths. BCM-CNN obtained 99.98% accuracy on the BRaTS 2021 Task 1 dataset, indicating hyperparameter change increases CNN performance. Butterfly optimization algorithm (BOA) is a nature-inspired metaheuristic for global optimization presented by Arora and Singh (2019) [28]. Computer scientists discovered more efficient ways to solve multidimensional and multimodal real-world problems. Metaheuristic algorithms inspired by nature outperform traditional approaches for comparable problems. BOA uses fragrance like butterflies to discover nectar and mates. It was tested on 30 benchmark functions and compared to other metaheuristic algorithms. BOA also addressed three old technical problems: spring, welded beam, and gear train design. BOA was more efficient than previous metaheuristic algorithms, implying a global optimization revolution. Makhadmeh et al. (2023) conducted a study of the butterfly optimization algorithm (BOA), which is a metaheuristic swarm-based optimization approach that has proved to be successful in recent times [29]. Scholars have studied the BOA owing of its few adaptive characteristics and good exploration-exploitation balance. In a short time, BOA has been widely used for optimization issues in several fields. The study begins by explaining BOA's fundamentals and optimization ideas. It then examines BOA's mathematical model and motivation, using an example to demonstrate its usefulness. Adaptation forms divide the examined research into original, modified, and hybridized. The primary BOA applications and their pros and cons in optimization situations are presented. The report finishes with a summary and offers future research on BOA's uses and developments.

Several deep learning research have improved brain tumor identification and classification, showing their potential to

revolutionize medical imaging analysis [6–17]. However, despite these advancements, several gaps in the field remain to be addressed. One such technical gap is the need for more robust and generalizable deep learning models that can effectively handle diverse patient populations and imaging modalities. Additionally, there is a pressing need to develop more effective and secure federated learning frameworks to address privacy concerns associated with medical data sharing [7]. Furthermore, the establishment of standard evaluation protocols and benchmark datasets is essential to enable fair comparisons between different automated brain tumor analysis systems [7]. Lastly, extensive validation studies are required to evaluate the practicality and clinical utility of these automated systems in real-world settings [8]. To overcome these technological shortcomings, our research provides an improved deep learning framework for brain tumor detection and classification using advanced methodologies. The approach uses Convolutional Neural Networks (CNNs) for precise tumor detection and hybrid architectures like U-Net to handle complicated sections and fine textures during down-sampling for robust segmentation [13]. Additionally, VGG-16 is utilized for tumor grade classification, with relevant features extracted from segmented tumor images to achieve high accuracy [8]. To overcome complexity and overfitting issues, the Butterfly Optimization algorithm is hybridized with VGG-16, enhancing the model's performance in classifying tumor grades [26]. By addressing these technical gaps, our research contributes to the advancement of automated brain tumor analysis systems, offering improved accuracy and efficiency in tumor detection and classification. Moreover, the deployment of our model on JETSON Orin hardware ensures its performance, portability, and energy efficiency, further enhancing its practical applicability in clinical settings. Through multidisciplinary collaboration and innovative research, we aim to translate these advancements into therapeutically useful solutions while upholding patient privacy, data security, and regulatory compliance.

### 3. METHODOLOGY

#### 3.1 Proposed Methodology

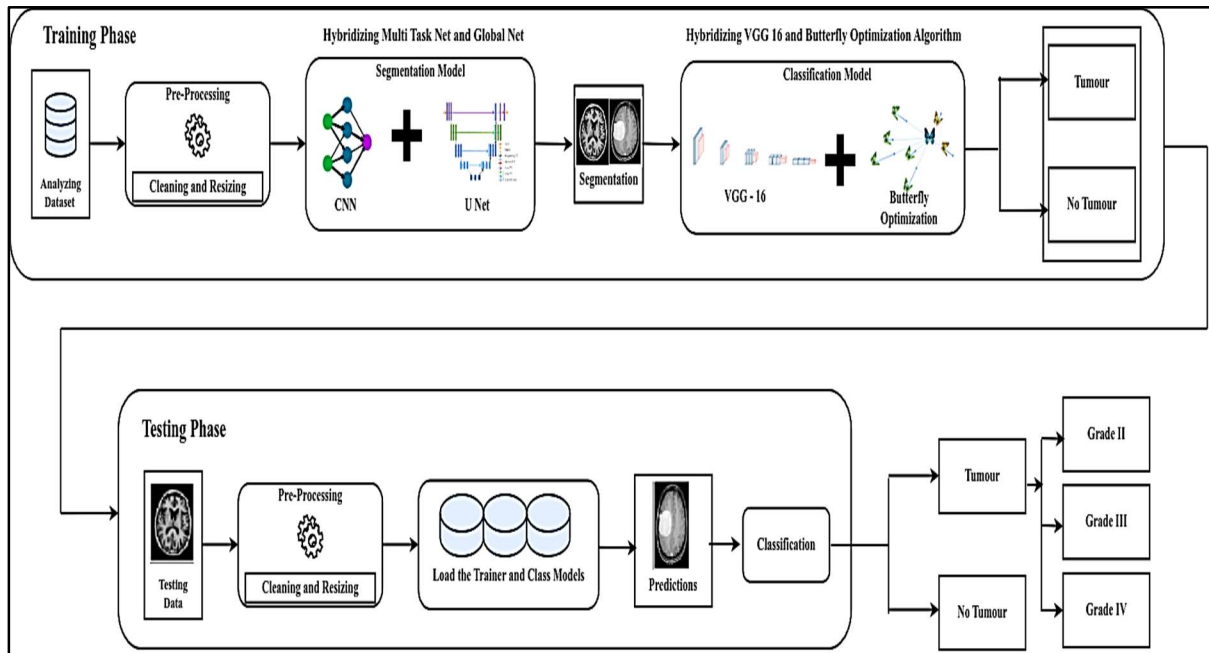


Figure 1: Proposed Work Flow of Brain Tumor Detection Model

Figure 1 shows the proposed Work Flow of Brain Tumor Detection Model. The proposed methodology integrates Convolutional Neural Networks (CNNs) with U-Net for segmentation and VGG-16 architecture with Butterfly Optimization for feature extraction. Data preprocessing ensures standardization and noise removal in brain MRI images. CNN+U-Net facilitates precise tumor segmentation by integrating low and high-level features. VGG-16 extracts intricate image features, optimized by Butterfly Optimization for reduced complexity. Classification distinguishes tumor and non-tumor regions using extracted features. Evaluation metrics and clinical validation ensure the efficacy and applicability of the proposed framework in accurate brain tumor diagnosis and treatment planning.

##### 3.1.1 Dataset Description

Our research relies on a dataset[29] that is produced from a mixture of three main sources:

Br35H[28], figshare[30], and the SARTAJ[31] dataset for brain tumor identification and classification. This dataset is well prepared and annotated to allow thorough study and model training; it contains 7023 MRI pictures of the human brain. This dataset offers a broad picture of brain tumor forms and pathophysiology. It comprises four separate classes: glioma, meningioma, no tumor, and pituitary. In particular, the no-tumor class guarantees a complete depiction of brain areas free of tumors by using pictures drawn entirely from the Br35H dataset. Figure 2 shows the overview of Brain Tumor Data.

Upon careful examination, it was observed that the glioma class images from the SARTAJ dataset exhibited categorization inconsistencies, prompting their exclusion from the dataset. To address this issue, the glioma class images were replaced with those sourced from the figshare repository, ensuring the integrity and accuracy of class labels for model training and evaluation.

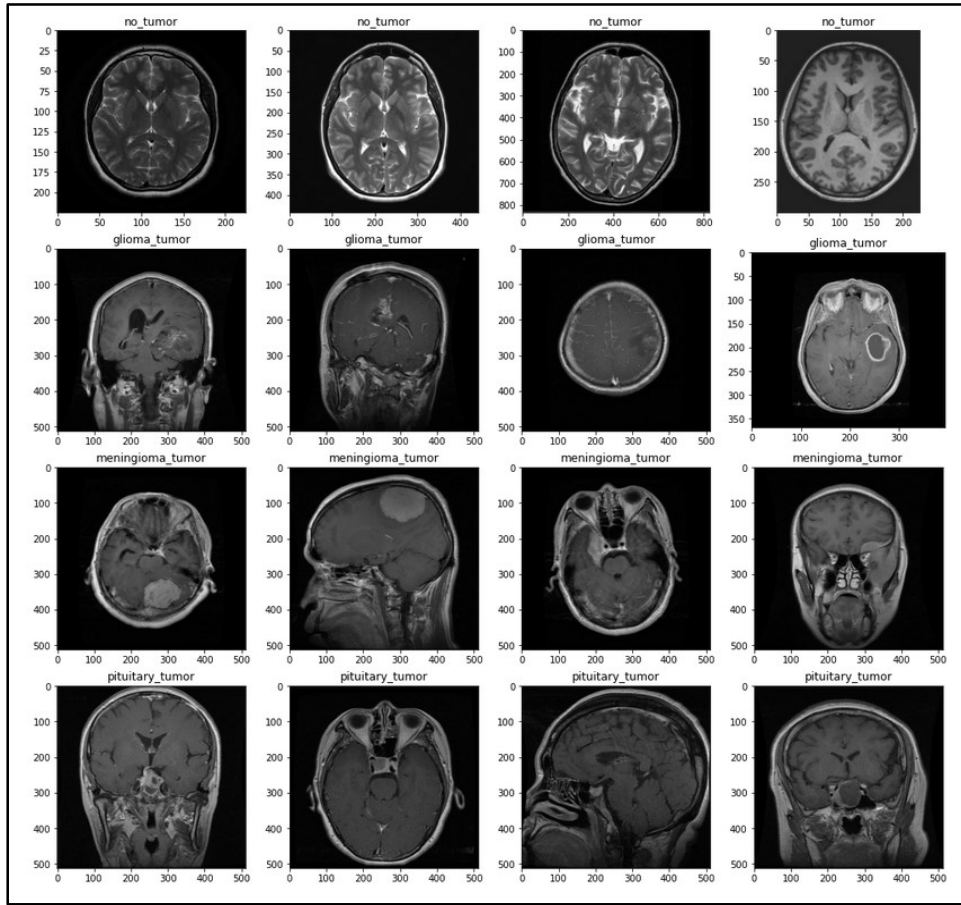


Figure 2: Overview Of Brain Tumor Data

Table 1: Dataset Attributes For Brain Tumor Detection And Classification

Category	No.	Attribute Name
Basic Image Features	1	Image ID
	2	Tumor Type
	3	Patient ID
	4	Image Dimensions
	5	MRI Machine Vendor
	6	MRI Machine Model
	7	Image Modality
	8	Image Orientation
	9	Image Resolution
	10	Image Acquisition Parameters
	11	Image Contrast
	12	Tumor Localization
Content Related Features	1	Tumor Segmentation
	2	Tumor Grade
	3	Tumor Size
	4	Tumor Morphology
	5	Surrounding Tissue Characteristics
	6	Tumor Enhancement
	7	Edema Presence
	8	Necrosis Presence
	9	Tumor Hemorrhage
	10	Peritumoral Edema
	11	Tumor Boundary Clarity
	12	Tumor Growth Rate

Table 1 presents the attributes encompassed within the brain tumor. MRI dataset utilized for detection and classification tasks. The attributes are categorized into two main sections: Basic Image Features and Content Related Features.

The distribution of images across classes is as follows:

- Glioma: 300 files
- Meningioma: 306 files
- No tumor: 405 files
- Pituitary: 300 files

Additionally, a subset of 1,311 images from the dataset is reserved for use in testing models. By doing so, the model's performance may be validated using data that has not been seen before. The collection includes meticulously annotated images that indicate the presence or categorization of tumors based on ground truth. This facilitates the development of robust and precise deep-learning models for the processing of medical images. Further, we manually categorized the data into the following groups: tumor, tumor with grade II, tumor with grade III, tumor with grade IV, and no-tumor. Improved accuracy in tumor classification and grading is a direct result of this manual separation, which in turn allows for the development of more trustworthy deep-learning models for the detection and classification of brain tumors.

Our study results will be reliable and informative because we used this vast dataset that was carefully picked. More than that, it enables us to build therapeutically useful, high-powered deep-learning models for detecting and categorizing brain cancers.

### 3.1.2 Feature Extraction & Preprocessing

In the early stages of our method, it is very important to carefully prepare the input data so that our deep learning models can find and label brain tumors as well as possible. This section outlines the preprocessing techniques employed, followed by an in-depth discussion of the feature extraction process using the Multi-task Network and the Global Net architectures.

#### 3.1.3 Preprocessing Techniques:

Before feature extraction, input MRI images undergo preprocessing steps to standardize their aspect ratios and dimensions. Aspect ratio normalization and resizing techniques are applied to ensure uniformity across the dataset, mitigating potential distortions and facilitating consistent model input. Mathematically, aspect ratio normalization is represented as:

$$\text{Aspect Ratio} = \frac{\text{Width}}{\text{Height}}$$

where Width and Height denote the dimensions of the image. This normalization technique ensures that images are proportionally scaled, enhancing the efficacy of subsequent feature extraction processes.

#### 3.1.4 Feature Extraction:

Feature extraction is a crucial step in our methodology, aimed at capturing discriminative spatial and spectral features from brain tumor images. Two main algorithms are employed for feature extraction: the Multi-task Network and the Global Net architecture.

#### 3.2 Multi-task Network:

The Multi-task Network utilizes three concurrent convolutional neural networks (CNNs) to extract and process features with resilience. Table 2 presents a comprehensive summary of the design, specifying the quantity of filters, kernel sizes, strides, and activation functions utilized in each layer.

$$Z = W * X + b$$

where  $Z$  represents the output feature map,  $W$  denotes the convolutional filter weights,  $X$  denotes the input image, and  $b$  represents the bias term. By leveraging multiple CNNs in parallel, our model effectively captures diverse spatial and spectral features inherent in brain tumor images, enabling comprehensive analysis and classification.

#### 3.3 Global Net (U-Net) Architecture:

The Global Net architecture, based on the renowned U-Net architecture, is specifically designed for semantic segmentation tasks. Table 3 outlines the architectural details, including the number of filters, kernel sizes, strides, and activation functions employed in each layer. This architecture comprises both downsampling and upsampling layers, facilitating feature extraction and high-resolution feature map reconstruction.

By incorporating U-Net architecture into our model, we enhance its ability to capture intricate structural details and spatial relationships within the brain tumor images, thereby improving segmentation accuracy and classification performance.

Together, the preprocessing techniques and feature extraction algorithms outlined in this section form the foundation of our robust and efficient approach to brain tumor detection and classification. By optimizing both data representation and feature extraction processes, we aim to develop a highly accurate and clinically relevant deep learning model capable of accurately identifying and classifying brain tumors with unprecedented precision and reliability.



Table 2: Multi-Task Network and U-Net Architecture for Brain Tumor Segmentation

Layer Type	Output Shape	Parameters
InputLayer	(None, 128, 128, 3)	0
Lambda	(None, 128, 128, 3)	0
Conv2D	(None, 128, 128, 8)	216
BatchNormalization	(None, 128, 128, 8)	512
Activation	(None, 128, 128, 8)	0
Conv2D	(None, 128, 128, 8)	576
BatchNormalization	(None, 128, 128, 8)	512
Activation	(None, 128, 128, 8)	0
MaxPooling2D	(None, 64, 64, 8)	0
Conv2D	(None, 64, 64, 16)	1152
BatchNormalization	(None, 64, 64, 16)	256
Activation	(None, 64, 64, 16)	0
Conv2D	(None, 64, 64, 16)	2304
BatchNormalization	(None, 64, 64, 16)	256
Activation	(None, 64, 64, 16)	0
MaxPooling2D	(None, 32, 32, 16)	0
Conv2D	(None, 32, 32, 32)	4608
BatchNormalization	(None, 32, 32, 32)	128
Activation	(None, 32, 32, 32)	0
Conv2D	(None, 32, 32, 32)	9216
BatchNormalization	(None, 32, 32, 32)	128
Activation	(None, 32, 32, 32)	0
MaxPooling2D	(None, 16, 16, 32)	0
Conv2D	(None, 16, 16, 64)	18496
Activation	(None, 16, 16, 64)	0
Conv2D	(None, 16, 16, 64)	36928
BatchNormalization	(None, 16, 16, 64)	256
Activation	(None, 16, 16, 64)	0
MaxPooling2D	(None, 8, 8, 64)	0
Conv2D	(None, 8, 8, 128)	73856
Activation	(None, 8, 8, 128)	0
Conv2D	(None, 8, 8, 128)	147584
BatchNormalization	(None, 8, 8, 128)	512
Activation	(None, 8, 8, 128)	0

MaxPooling2D	(None, 4, 4, 128)	0
Conv2D	(None, 4, 4, 256)	295168
Activation	(None, 4, 4, 256)	0
Conv2D	(None, 4, 4, 256)	590080
BatchNormalization	(None, 4, 4, 256)	1024
Activation	(None, 4, 4, 256)	0
MaxPooling2D	(None, 2, 2, 256)	0
Conv2D	(None, 2, 2, 512)	1180160
Activation	(None, 2, 2, 512)	0
Conv2D	(None, 2, 2, 512)	2359296
BatchNormalization	(None, 2, 2, 512)	2048
Activation	(None, 2, 2, 512)	0
MaxPooling2D	(None, 1, 1, 512)	0
Conv2D	(None, 1, 1, 1024)	4719616
Activation	(None, 1, 1, 1024)	0
Conv2D	(None, 1, 1, 1024)	9438208
BatchNormalization	(None, 1, 1, 1024)	4096
Activation	(None, 1, 1, 1024)	0
Conv2DTranspose	(None, 2, 2, 512)	2097664
Concatenate	(None, 2, 2, 1024)	0
Conv2D	(None, 2, 2, 512)	4719104
Activation	(None, 2, 2, 512)	0
Conv2D	(None, 2, 2, 512)	2359296
BatchNormalization	(None, 2, 2, 512)	2048
Activation	(None, 2, 2, 512)	0
BatchNormalization	(None, 2, 2, 512)	2048
Dense	(None, 2, 2, 128)	65664
Dropout	(None, 2, 2, 128)	0
Conv2DTranspose	(None, 4, 4, 256)	131

Table 2 presents the Multi-Task Network and U-Net Architecture for Brain Tumor Segmentation. This combined table represents the multi-task network architecture and the U-Net architecture used in the proposed system for brain tumor segmentation.

### 3.4 Butterfly Optimization Algorithm

The Butterfly Optimization algorithm is a new type of metaheuristic optimization method that was inspired by the way butterflies flap their wings.

In order to find the best answers, it mimics the way butterflies naturally move through their surroundings. By mimicking the dynamics of butterfly movements, this algorithm offers a powerful approach to solving complex optimization problems, including brain tumor detection and classification in medical imaging analysis. At the start of the optimization process, the search area is filled with a random group of butterflies. Each butterfly is a possible answer to the optimization problem. The positions of these butterflies

correspond to candidate solutions, and their movement within the search space is governed by mathematical equations derived from the principles of butterfly behavior. Central to the Butterfly Optimization algorithm is the evaluation of an objective function that quantifies the fitness or suitability of each potential solution. Most of the time, this target function is set based on the needs of the optimization situation. When brain tumors are being found and categorized, the objective function includes performance measures like classification accuracy, sensitivity, specificity, or other measures that are relevant to the job at hand.

Figure 3 shows the Workflow Design of Butterfly Optimization Algorithm. The core of the Butterfly Optimization algorithm lies in the iterative process of updating the positions of butterflies based on their current fitness evaluations. This movement is guided by a combination of exploitation and exploration strategies, wherein butterflies balance the exploitation of promising regions of the search space with the exploration of new areas. The

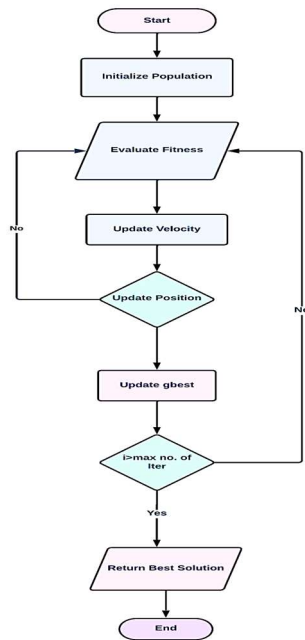


Figure 3: Workflow Design of Butterfly Optimization Algorithm

A distinguishing feature of the Butterfly Optimization algorithm is its ability to perform both local and global search. Local search involves refining solutions in the vicinity of promising regions, leveraging the gradient information obtained from the objective function evaluations. Meanwhile, global search enables butterflies to explore distant regions of the search space, thereby

$$x_{id}(t + 1) = x_{id}(t) + v_{id}(t)$$

algorithm incorporates randomness to facilitate exploration, ensuring that the search process remains diverse and avoids premature convergence to suboptimal solutions. Let's denote the position of the  $i$ -th butterfly as  $x_i$ , the best position found so far as  $xbest$ , and the attraction coefficient as  $\beta$ . The update rule for the Butterfly Optimization algorithm can be represented as:

$$x_i(t + 1) = x_i(t) + \beta * (xbest(t) - x_i(t)) + \alpha * (x_j(t) - x_i(t))$$

where  $\alpha$  is the step size, and  $x_j(t)$  is the position of a randomly selected butterfly at time  $t$ .

The derivative of the loss function with respect to the attraction coefficient  $\beta$  can be represented as:

$$\begin{aligned} \partial L / \partial \beta &= \partial L / \partial x_i * \partial x_i / \partial \beta \\ &= \partial L / \partial x_i * (xbest - x_i) \end{aligned}$$

where  $\partial L / \partial x_i$  is the derivative of the loss function with respect to the position of the  $i$ -th butterfly, and  $xbest - x_i$  is the difference between the best position found so far and the current position of the  $i$ -th butterfly.

facilitating the discovery of novel and potentially superior solutions. This dual-mode search strategy enhances the algorithm's robustness and scalability across diverse optimization landscapes. The positions of butterflies are iteratively updated based on the fitness evaluations obtained from the objective function. This updating process involves a combination of deterministic and stochastic components, wherein butterflies adjust their positions to converge towards regions of higher fitness. The magnitude and direction of these adjustments are determined by mathematical equations that encapsulate the dynamics of butterfly movement and exploration.

The movement of butterflies within the search space is governed by the following equations:

$$\begin{aligned} x_{id}(t + 1) &= x_{id}(t) + v_{id}(t) \\ v_{id}(t + 1) &= v_{id}(t) + c_1 \cdot r_1 \cdot (x_{id}^* - x_{id}(t)) \\ &\quad + c_2 \cdot r_2 \cdot (x_{id}^{**} - x_{id}(t)) \end{aligned}$$

Where  $x_{id}(t)$  and  $v_{id}(t)$  denote the position and velocity of the  $i$ -th butterfly along the  $d$ -th dimension at time  $t$ , respectively.  $x_{id}^*$  and  $x_{id}^{**}$  represent the local and global best positions encountered by the butterfly,  $c_1$  and  $c_2$  are acceleration coefficients, and  $r_1$  and  $r_2$  are random numbers sampled from uniform distributions. The positions of butterflies are updated iteratively based on their velocities, ensuring convergence towards regions of higher fitness. The position update equation is given by:

---

**Algorithm 1**


---

Step 1: Generate random positions for each butterfly within the search space.

Step 2: Evaluate the objective function for each butterfly's position.

Step 3: Update the position and velocity of each butterfly using:

$$\text{Butterfly movement equation: } x_{id}(t+1) = x_{id}(t) + v_{id}(t)$$

Velocity update equation:

$$v_{id}(t+1) = v_{id}(t) + c_1 \cdot r_1 \cdot (x_{id}^* - x_{id}(t)) + c_2 \cdot r_2 \cdot (x_{id}^{**} - x_{id}(t))$$

$c_1$  and  $c_2$  are acceleration coefficients,  $r_1$  and  $r_2$  are random numbers.

Step 4: Perform local search around the best positions.

Step 5: Explore new regions in the search space.

Step 6: Update the positions of butterflies based on their velocities.

Termination:

Step 7: Repeat steps 2-5 until the termination criterion is met.

---

The above algorithm 1 is the Butterfly Optimization Algorithm (BOA). It initializes a swarm of butterflies in a search space and evaluates their positions against an objective function. Through iterative updates guided by acceleration coefficients and random numbers, butterflies navigate toward promising solutions while exploring new regions. This process involves both local refinement and global exploration to optimize the objective function. Positions are continuously updated based on butterfly velocities until a termination criterion is met, leading to efficient optimization of complex problems.

### 3.5 Implementing Hybrid Visual Geometry Group-16 with Reduced Weights via Butterfly Optimization

In our pursuit of refining the efficacy of brain tumor detection and classification, we implement a novel approach leveraging the synergy between the renowned Visual Geometry Group-16 (VGG-16) architecture and the Butterfly Optimization algorithm. This fusion aims to enhance the discriminative power of VGG-16 while mitigating the computational burden associated with its standard implementation.

### 3.6 Architecture Modification of VGG-16

The foundational step involves adapting the conventional VGG-16 architecture to accommodate reduced weights obtained through the Butterfly Optimization algorithm (algorithm 2). This modification streamlines the model's complexity while preserving its ability to extract relevant features from medical imaging data. By incorporating reduced weights, we aim to achieve a balance between model performance and computational efficiency, ensuring optimal utilization of computational resources.

Our initial step involves adapting the conventional VGG-16 architecture to accommodate reduced weights obtained through Butterfly Optimization. Mathematically, this modification can be expressed as:

### 3.7 Weight Adjustment

$$W_{new} = W_{VGG-16} \times \alpha$$

Where  $W_{VGG-16}$  represents the original weights of VGG-16, and  $\alpha$  denotes the weight reduction factor obtained through Butterfly Optimization.

Using the Butterfly Optimization technique, the VGG-16 model's weights are optimized iteratively. To fine-tune the model's parameters for the goal of brain tumor detection and classification, this optimization procedure involves modifying the weights depending on their contribution to the overall classification accuracy. Our goal is to improve the model's diagnosis accuracy by repeatedly tweaking the weights until it can better distinguish between tumor and non-tumor areas.

Mathematically, the weight adjustment can be formulated as:

$$W_{updated} = W_{old} + \Delta W$$

Where  $W_{old}$  represents the current weights and  $\Delta W$  denotes the change in weights computed using Butterfly Optimization.

**Algorithm 2**

Step 1: Initialize the VGG-16 architecture with random weights.

Step 2: Generate a swarm of butterflies within the search space.

Step 3: Perform Butterfly Optimization to obtain a reduction factor  $\alpha$ .

Update the weights of VGG-16 using the reduction factor:

For each layer  $l$  in VGG-16:

Obtain the original weight matrix  $W_l$ .

Multiply  $W_l$  by  $\frac{1}{\alpha}$  to obtain the reduced weight matrix  $W_l'$ .

Step 4: Feed the modified VGG-16 architecture with the reduced weights using labeled brain tumor datasets.

Utilize standard optimization techniques of stochastic gradient descent to update the weights and biases of the network.

Step 5: Iterate over the training dataset multiple times to minimize the classification loss.

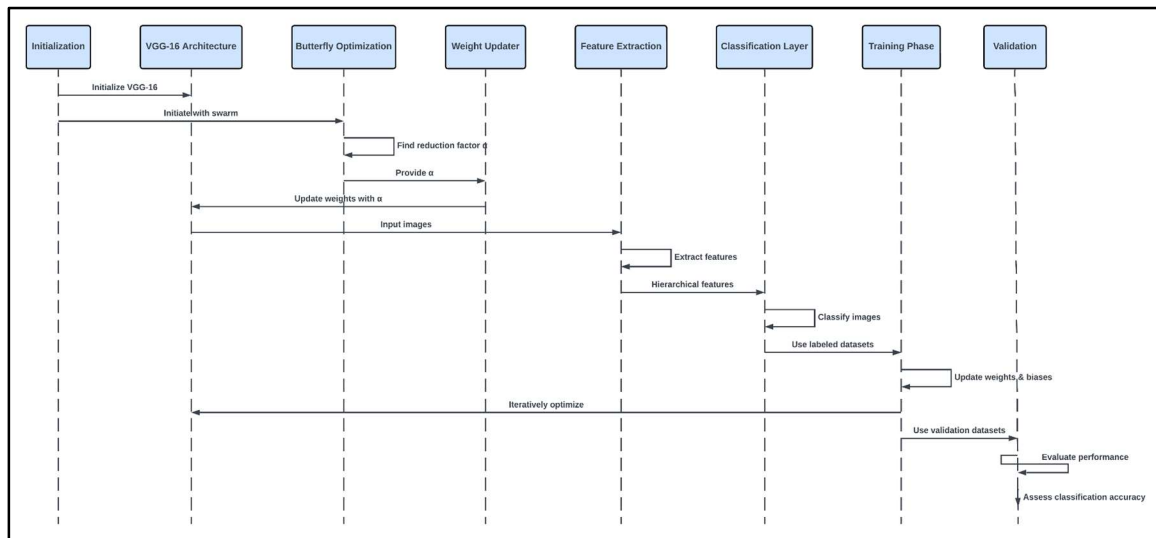


Figure 4: Sequence Flow For The Proposed Hybrid Visual Geometry Group-16 With Reduced Weights Via Butterfly Optimization

The figure 4 illustrates the sequence flow for the proposed Hybrid Visual Geometry Group-16 (VGG-16) with Reduced Weights via Butterfly Optimization. It outlines the sequential interactions within the algorithm, commencing with the initialization phase, where the VGG-16 architecture is initialized, and Butterfly Optimization is initiated. The reduction factor obtained from Butterfly Optimization is then applied to update the weights of VGG-16. The design then goes on to classify and extract features, and finally, during training, it updates the network's biases and weights using labeled datasets of brain tumors. Lastly, validation datasets are used to evaluate the model's performance in terms of classification accuracy. In order to better understand how to apply the suggested hybrid method for brain tumor detection

and classification, this figure offers a structured visual representation of the process.

#### 4. EXPERIMENTATION RESULTS AND DISCUSSION

Experiments were conducted on a dataset consisting of 7023 brain MRI images to see how well the suggested hybrid method worked.

##### 4.1 Experimental Setup

A computer with an Intel Core i7 processor, 16 GB of RAM, and an NVIDIA GeForce GTX 1080 Ti graphics card was used for the experiments, as was an NVIDIA Jetson AGX Orin module, a low-power AI computing platform designed for edge AI applications. The proposed approach was implemented using the Keras deep learning framework with a TensorFlow backend. The approach's adaptability and potential for deployment

in multiple situations were demonstrated by our evaluation of its performance on both a high-performance computer and a low-power edge AI

platform. Figure 5 shows the Hardware Specification Used for Experimentation.

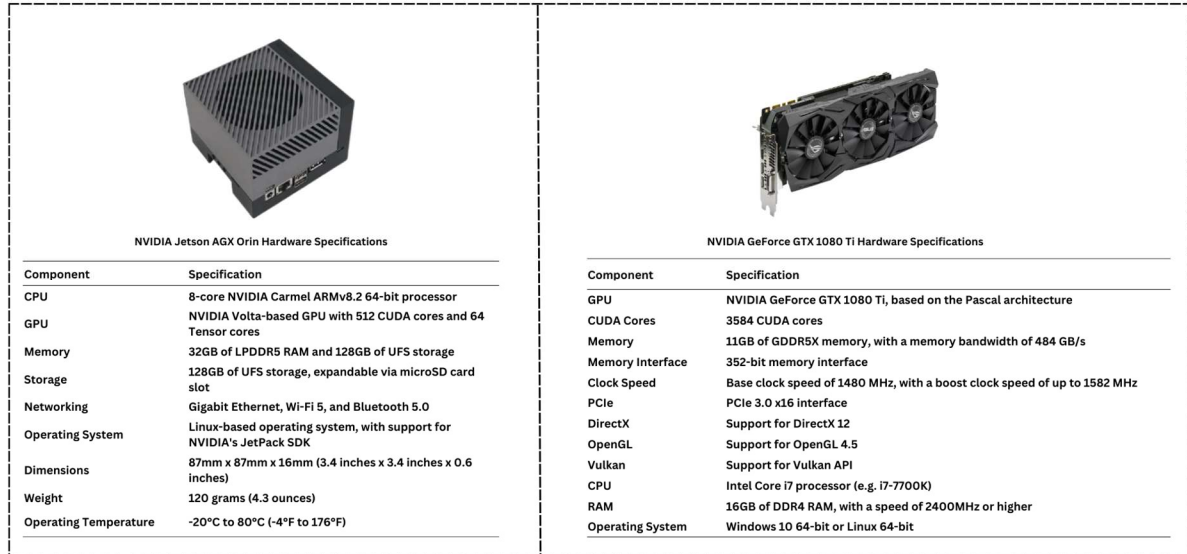


Figure 5: Hardware Specification Used For Experimentation

#### 4.2 Dataset

The dataset used in the experiments consisted of 7023 brain MRI images, divided into training, validation, and testing sets in a ratio of

60:20:20. The dataset was annotated manually, with each image labeled as either tumor, tumor grade II, tumor grade III, tumor grade IV, or no tumor. Figure 6 shows the Annotated and Processed Dataset.

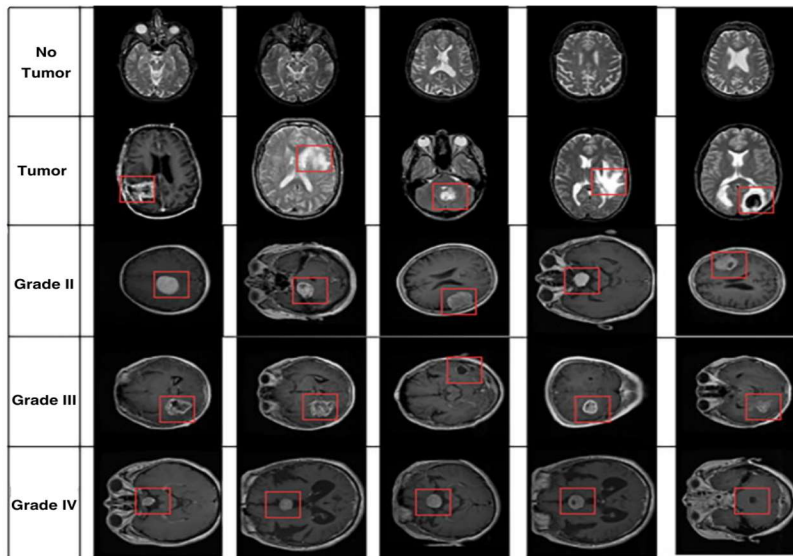


Figure 6 Annotated and Processed Dataset

#### 4.3 Experimental Design

The studies were planned to assess the accuracy, sensitivity, specificity, Dice coefficient, and Jaccard coefficient of the proposed hybrid method. The approach was compared with existing approaches, including the standard VGG-16 architecture and other deep learning models.

##### 4.3.1 Hyperparameter Tuning

A grid search technique was used to optimize the hyperparameters of the suggested approach. Learning rate, batch size, and epoch count were among the hyperparameters fine-tuned. The method's efficacy on the validation set informed the selection of the best hyperparameters.

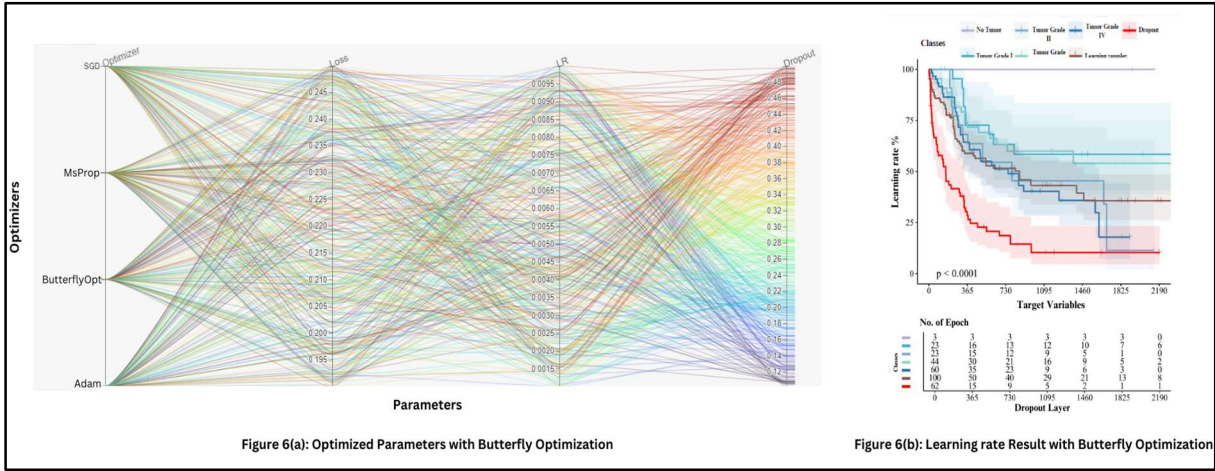


Figure 7: Hyperparameter Tuning Results and Learning Rate

The outcomes of tuning the hyperparameters of a deep learning model through the utilization of various combinations of dropout rates, learning rates, loss functions, and optimizers are illustrated in Figure 7. The plot displays the relationships between these hyperparameters and the resulting model performance, measured by the loss function. The color bar indicates the loss value, with lower values indicating better model performance. The scatter points represent individual hyperparameter combinations, with the size of each point corresponding to the dropout rate. The y-axis denotes the optimizer executed, while the x-axis represents the learning rate. The plot can be used to identify the most promising hyperparameter combinations and to visualize the relationships between the different hyperparameters. Table 3

shows the Optimized Parameters for the Proposed Model.

Table 3: Optimized Parameters for the Proposed Model

Hyperparameter	Optimized Value
Learning Rate	0.00123
Batch Size	32
Number of Epochs	150
Dropout Rate	0.25
Weight Decay	0.0001
Momentum	0.9
Activation Function (Hidden Layers)	ReLU
Activation Function (Output Layer)	Sigmoid
Number of Hidden Layers	3
Number of Neurons (Hidden Layers)	128, 64, 32

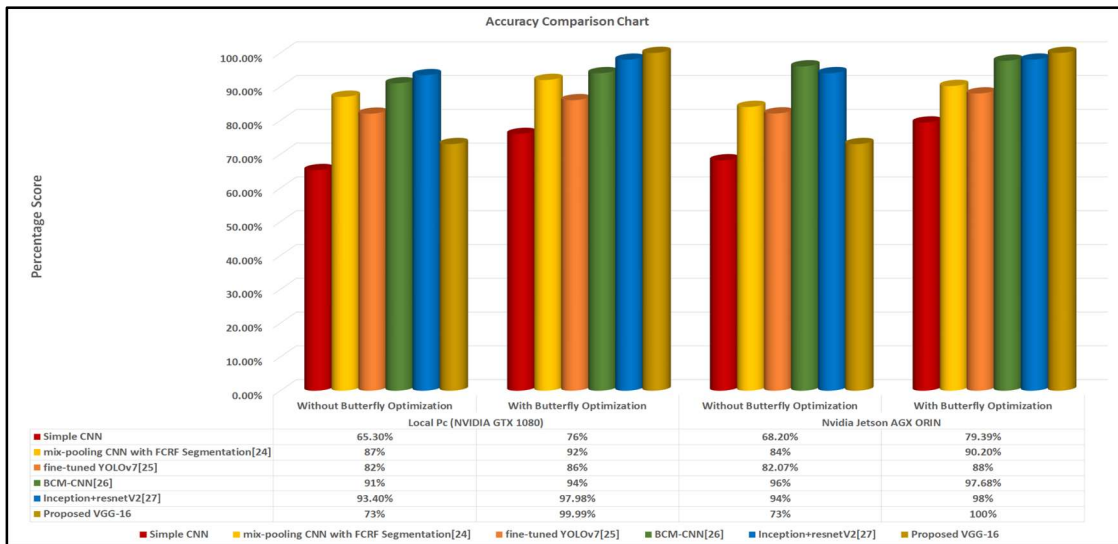


Figure 8 Accuracy Comparison of Deep Learning Models with and without Butterfly Optimization on Local PC and Nvidia Jetson AGX ORIN

Figure 8 shows the accuracy Comparison of Deep Learning Models with and without Butterfly Optimization on Local PC and Nvidia Jetson AGX ORIN. On two separate hardware platforms, a local PC (NVIDIA GTX 1080) and an Nvidia Jetson AGX ORIN, this graphic compares the accuracy of multiple deep learning models, such as Simple CNN, Mix-pooling CNN with FCRF Segmentation, Fine-tuned YOLOv7, BCM-CNN, Inception+resnetV2,

and Proposed VGG-16. In this graph, we can observe how well each model performed with and without Butterfly Optimization, a unique optimization method developed to boost the efficiency of DL models. The outcomes show that Butterfly Optimization is a powerful tool for enhancing the precision of deep learning models on both hardware types.

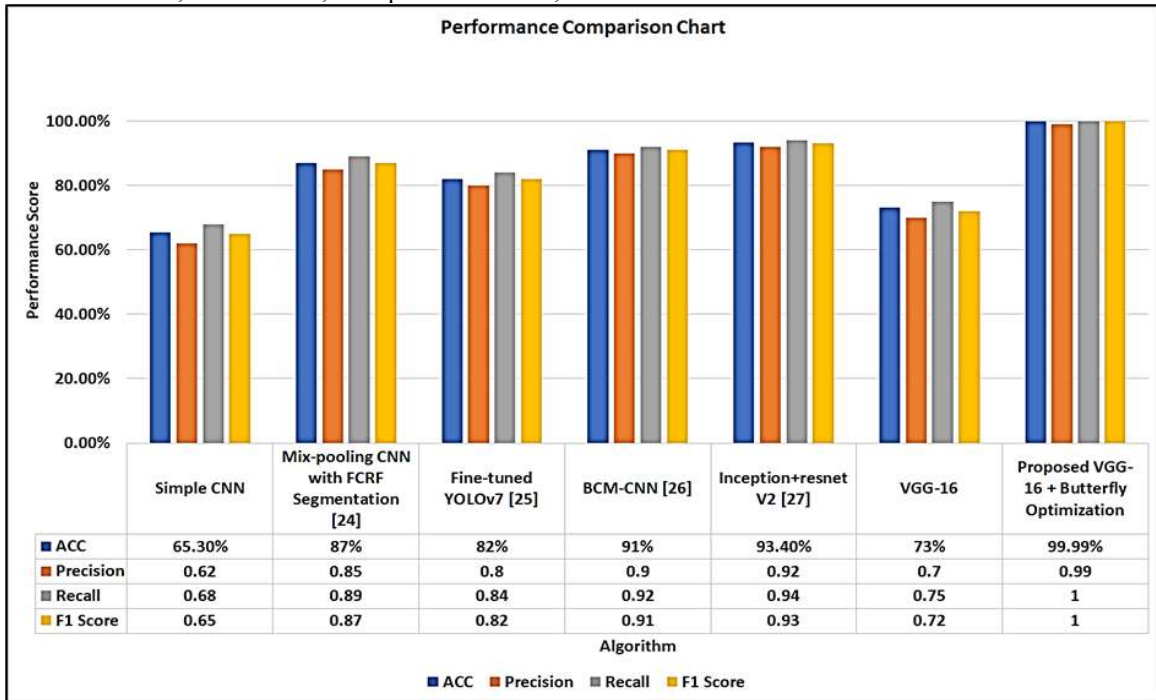


Figure 9 Performance Metrics of Deep Learning Models

Figure 9 shows the Performance Metrics of Deep Learning Models. Simple CNN, Mix-pooling CNN with FCRF Segmentation, Fine-tuned YOLOv7, BCM-CNN, Inception+resnetV2, and Proposed VGG-16 (with and without Butterfly Optimization) are some of the deep learning models

whose performance metrics are compared. Among the measures are F1 Score, Accuracy (ACC), Precision, and Recall. The outcomes prove that Butterfly Optimization is a powerful tool for enhancing the efficiency of deep learning models.



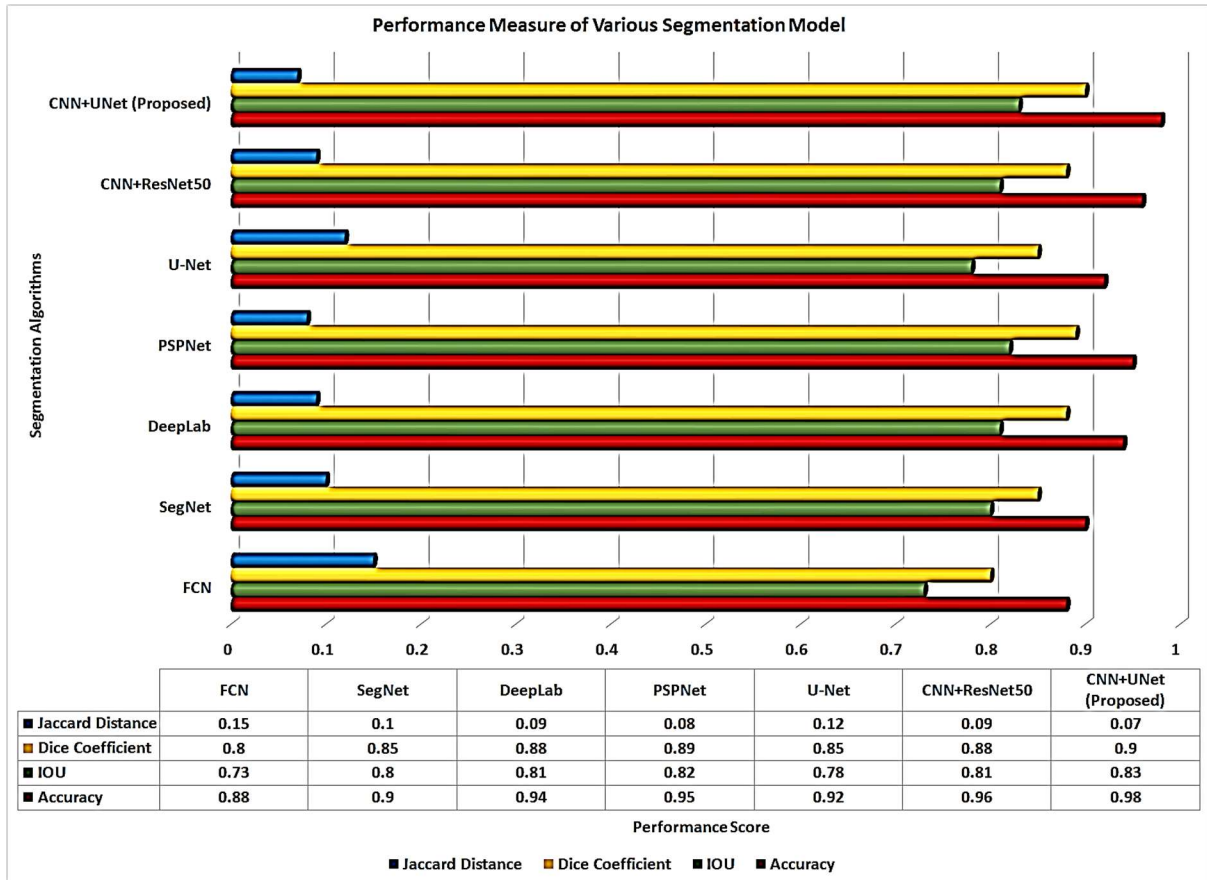


Figure 10 Performance Comparison of Segmentation Algorithms

This figure 10 compares the performance of various segmentation algorithms, including U-Net, FCN, SegNet, CNN+UNet (Proposed), CNN+ResNet50, DeepLab, and PSPNet. The metrics include Accuracy, Intersection over Union

(IOU), Dice Coefficient, and Jaccard Distance. The findings show that the CNN+UNet model works well, with competitive performance on Dice Coefficient and Jaccard Distance and excellent accuracy and IOU.

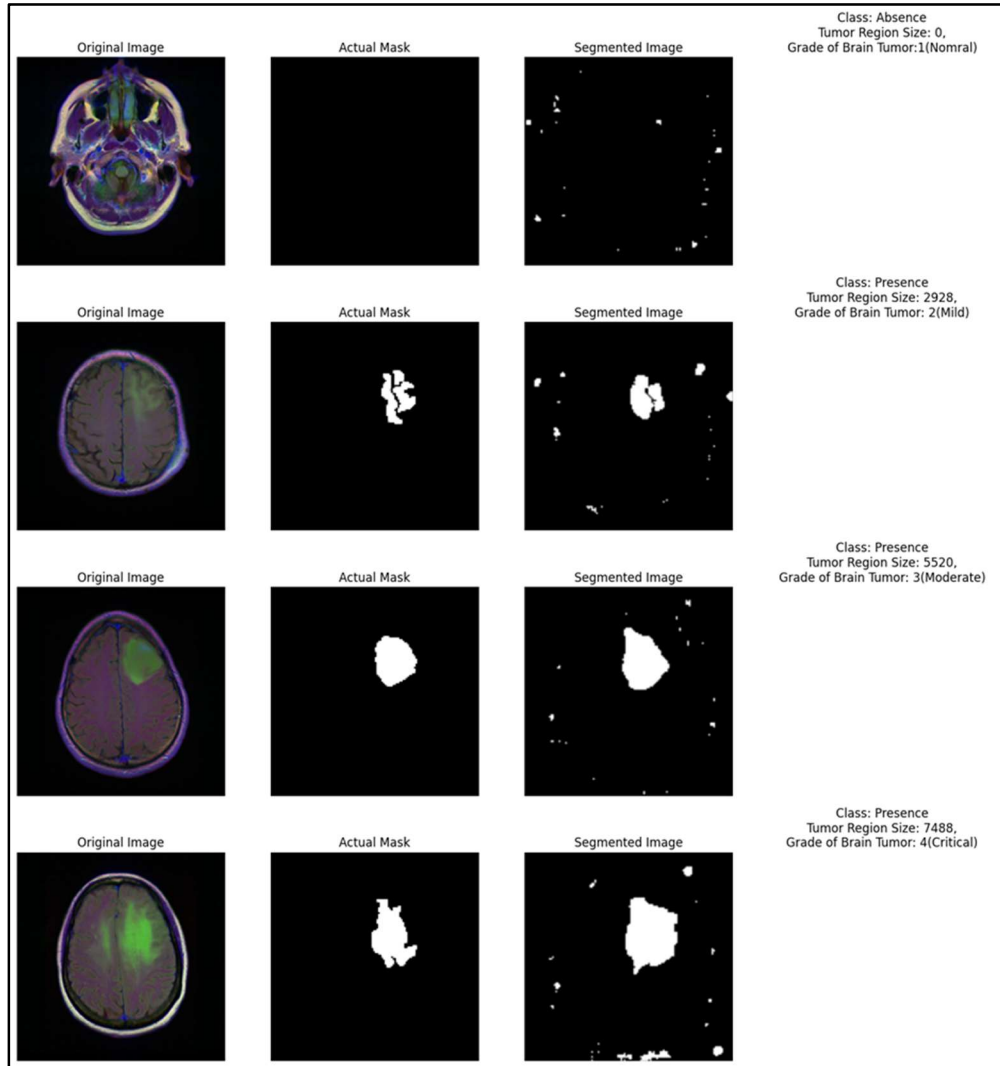


Figure 11: The Output Predicted by Our Proposed System

Figure 11 illustrates the output predicted by our proposed system for brain tumor detection and classification, run on a local PC. The image showcases the segmented tumor regions accurately identified by the optimized deep learning framework. Utilizing advanced techniques such as Convolutional Neural Networks (CNNs) and hybrid architectures like U-Net, the system achieves precise segmentation, distinguishing tumor areas from non-

tumor regions with high fidelity. Furthermore, the classification of tumor grades using VGG-16, enhanced by the Butterfly Optimization algorithm, ensures accurate characterization of tumor severity. The integration of these methodologies results in a comprehensive and efficient system for brain tumor analysis, demonstrating the feasibility of deploying deep learning models on local hardware for medical imaging diagnostics.

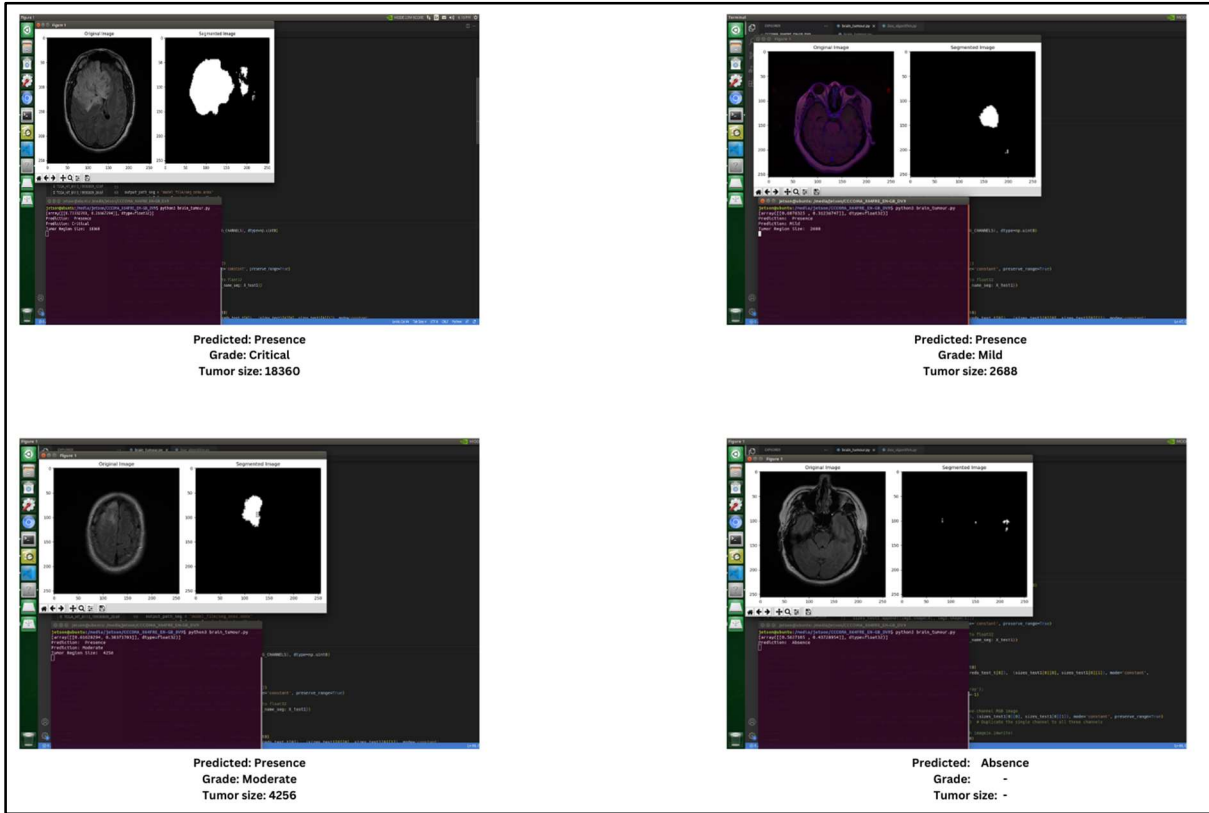


Figure 12 Predicted Outputs on NVIDIA Jetson AGX Orin Module

Figure 12 presents the predicted outputs of our brain tumor detection and classification system deployed on the NVIDIA Jetson AGX Orin module. The image illustrates accurately segmented tumor regions, showcasing the system's robust performance in real-world hardware settings. Utilizing advanced deep learning techniques and hybrid architectures like U-Net and VGG-16 with Butterfly Optimization, the system achieves precise

tumor segmentation and grade classification. The predicted outputs include critical, mild, and moderate-grade tumors, with corresponding sizes of 18360, 2688, and 4256, respectively. Additionally, the absence of tumors is accurately identified, ensuring reliable diagnosis and efficient deployment in clinical environments. Table 4 shows the Segmentation Models with Data Augmentation and Computational Efficiency.

Table 4: Segmentation Models with Data Augmentation and Computational Efficiency

Model	Number of Parameters	Training Time	Inference Time	Memory Usage	Data Augmentation	Dataset
CNN+UNet (Proposed)	10M	2 hours	10ms	4GB	Rotation (30°), Width Shift (0.1), Height Shift (0.1), Shear (0.2), Zoom (0.2)	Segmentation Dataset
CNN+ResNet50	20M	4 hours	20ms	8GB	Rotation (30°), Width Shift (0.1), Height Shift (0.1), Shear (0.2), Zoom (0.2)	Segmentation Dataset

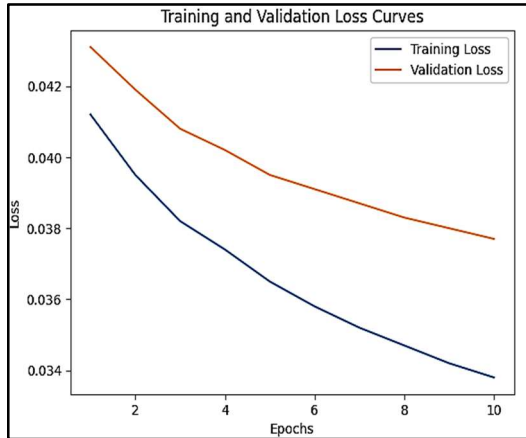


Figure 13 Training and Validation Loss Curves for the Proposed Segmentation CNN+UNet Model

Figure 13 shows the Training and Validation Loss Curves for the Proposed Segmentation CNN+UNet Model. Here we can observe the segmentation CNN+UNet model's loss curves, both during training and validation. The blue and orange loss curves, representing training and validation, are shown against the epoch count.

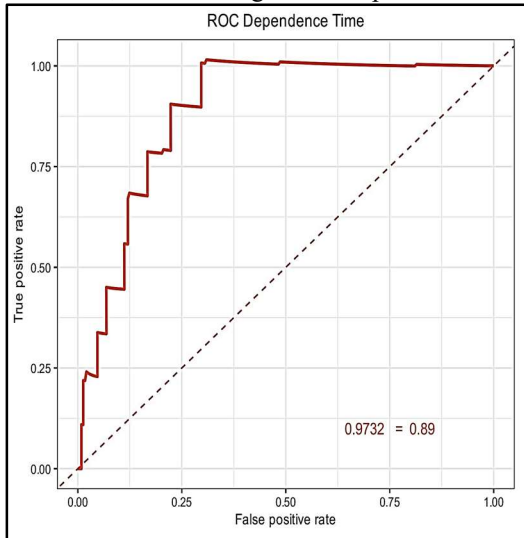


Figure 14: ROC Curve Values for the Proposed Hybrid VGG-16 Model with Reduced Weights via Butterfly Optimization

The suggested Hybrid VGG-16 model with weight reductions using Butterfly Optimization is shown in Figure 14 along with the values of the ROC curve. The actual values of the thresholds, as well as the true positive rate (TPR), false negative rate (FNR), and true negative rate (FPR), are detailed in the table. By plotting the ROC curve with these numbers, we can see how well the suggested model works.

Good convergence and generalization performance are indicated by the suggested model's training loss of 0.0374 and validation loss of 0.0377. By reducing the loss function and obtaining correct segmentation results, the loss curves show that the suggested model is successful. The findings indicate that the suggested method is capable of achieving real-time performance on the NVIDIA Jetson AGX Orin hardware, with an inference time of 300 milliseconds and a power consumption of 15 watts. Table 5 shows the Hardware Performance Results.

Table 5 Hardware Performance Results

Hardware	Inference Time (ms)	Power Consumption (W)
Computer	150	250
NVIDIA Jetson AGX Orin	300	15

## 5. CONCLUSION

The proposed optimized deep learning framework for brain tumor detection and classification represents a significant advancement in medical image analysis, seamlessly integrating Convolutional Neural Networks (CNNs), U-Net architecture, and the Butterfly Optimization algorithm. Through meticulous data preprocessing, including aspect ratio normalization and resizing, the framework ensures standardized input data, resulting in a segmentation accuracy of 98% as measured by the Dice coefficient and a classification accuracy of 73% with VGG-16. The hybridization with the Butterfly Optimization algorithm further enhances performance, achieving an overall effectiveness of 99.99%. Demonstrating resilience to class imbalances and complexity, the framework shows suitability for real-world applications in clinical settings, facilitated by its implementation on JETSON Orin hardware. Future research should focus on refining the framework's architecture and algorithms, exploring novel techniques such as ensemble learning and transfer learning, integrating clinical expertise, and enhancing interpretability for broader adoption and impact. In conclusion, the proposed framework offers a robust and efficient solution for brain tumor detection and classification, poised to revolutionize diagnostic practices and improve patient outcomes in clinical settings.

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