Integrated U-Net segmentation and gated recurrent unit classification for accurate brain tumor diagnosis from magnetic resonance imaging images

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Article Info

ABSTRACT

Early diagnosis and proper grouping of tumors in the brain are critical for successful therapy and positive outcomes for patients. This work proposes a complete technique for identifying brain tumors that employ sophisticated artificial intelligence methodologies and achieve an accuracy rate of 97.18%. The work makes use of the brain tumor magnetic resonance imaging (MRI) collection in Kaggle, which has 723 MRI scans classified as glioma, meningioma, pituitary tumor, and no tumor. These images are initially preprocessed, which includes scaling to a homogeneous size normalizing, and removal of noise to ensure uniformity and clarity. To improve the information set, generative adversarial networks (GANs) are used to perform data augmentation, producing artificial pictures that improve the database variety and resilience. To achieve exact cancer localization, the U-Net construction, recognized for its encoder-decoder design and skip links, is used to divide up tumor areas across images generated by MRI. The image segments are then input into gated recurrent units (GRUs), to analyze a collection of features to capture periods and differences between segments. The last classification is accomplished using an entirely linked layer and then a softmax stimulation, which provides the tumors classes. This method helps for medical experiments and clinical methods.

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1. INTRODUCTION

Early diagnosis and proper designation of tumors in the brain are crucial for better outcomes for patients. Brain tumors, either malignant or benign, can severely impair key brain activities, resulting in significant mortality and deaths. Early identification enables early clinical action, that can save lives and dramatically improve sufferers way of life [1]. The future likelihood of head tumor patients is greatly influenced by the stage during which the malignant growth is found, with earlier stages typically being more curable. Thus, establishing the diagnostic process is critical throughout the realm of neuro-oncology. Preliminary diagnoses for brain malignancies were made through analysis of magnetic resonance imaging (MRI) scans, which were done by the physicians, without the use of computerized systems. This method is time-consuming and prone to patient errors which in turn result in treatment delays and a downtrend in the patients recovery [2]. Furthermore, physicians have other challenges due to the complexity and diversity of

cerebral tumor diagnosis. Tumors are not of uniform size, formation, and location and MRI images may capture areas in which there are slight alterations hence, assessment and conclusions may be difficult and unreliable [3]. Such problems call for extensive development of novel solutions that can enhance the accuracy and efficiency of discovering tumors in the brain. MRI is one of the basic modalities of imaging that is often used for diagnosis and diagnosis of brain tumors. MRI creates a clear and detailed image of the cells of the brain allowing for a determination of the shape of the tumor along with components that are adjacent to it [4]. Because of its great depth of field and contrast between different soft tissues, this imaging technique is extremely useful in identifying cerebral deviations, namely malignancies. Notwithstanding its benefits, interpreting MRI scans requires extensive understanding and is vulnerable to variation between physicians, which may give rise to errors in assessment [5].

Recent advances in artificial intelligence, especially the use of deep learning, hold major potential for improving and automating the precision in medical picture interpretation [6]. Algorithms for deep learning may identify complicated structures and characteristics using enormous information sets, outperforming conventional computational approaches and even human specialists in some circumstances. These algorithms, particularly those built on huge and varied information sets, may apply effectively to new, previously unidentified information, thus rendering them appropriate for medical use [7]. It can improve healthcare imagery by providing unified, truthful, and quick assessments of clinical images [8]. convolutional neural networks (CNN) are a form of the model for deep learning that was mainly designed for handling images [9]. CNNs are capable of training structures of features by making use of information from input images, especially through the use of convolutional layers, and as such can be applied in the classification of images, recognition of objects as well as division. These computer networks can be used purposely in a wide variety of hospital neuroimaging projects suggesting their possibility to accumulate vast characteristics while enhancing the diagnosis acuity [7]. Since CNNs have the ability to identify relationships between spaces in information they are incredibly useful in deciphering complex imaging data including MRI images. It is thus evident that adding other data is a crucial aspect of ensuring that statistical networks are well-built. There has therefore emerged a method known as generative adversarial networks (GANs) that has acted as a data enhancement tool, for the creation of realistic fake pictures that can augment samples and a variety of training data [10]. The generalization of models and performance is enhanced by GANs to add artificial visuals to the input set especially when the training information is limited [11]. This is well applicable to health imaging since getting big annotations in data can often be a challenge mainly because of privacy and the need for expert assessment.

MRI targeting of tumor regions is very sensitive, and international accurate targeting of tumor areas is highly important for medical necessity and patient care. U-Net construction where the network has an encoder-decoder structure and skip connection has demonstrated a very good outcome in biological picture classification. U-Net may only accurately delineate tumor boundaries, thereby providing valuable information for further study [12]. Thorough splits have a remarkable role in phases that come out next – for instance, tumor grading and organizing an appointment of care – as it eliminates an essential possibility that again, only relevant, meaningful places should be examined. Due to its capability to create accurate categorizations and handle tiny databases, U-Net is proper for use in the evaluation of the health picture. This complete approach employs Python and its huge array of tools, particularly TensorFlow and Keras, to develop and evaluate models based on deep learning [13], [14] due to its interpretability and robust support to computational science, Python remains the most suitable language for designing and deploying complex operations in the neural network. These code libraries provide the necessary effective features to build mathematical designs, automate data preprocessing, and enhance and execute the instructional and evaluation workflows [15]. This way, the utilization of Python ensures that the simulations are always reproducible, easily scalable, and can easily be integrated into the healthcare system [16]. This paper aims to develop an integrated deep-learning framework for the detection of brain tumors that uses GANs for data augmentation, CNNs for feature extraction, U-Net for division, and gated recurrent units (GRUs) for classification. Since the accuracy level of this technology is 98%, its possibilities to enhance the degree of accuracy and efficiency of cancer brain screening are extensively prospective [17]. Incorporating these contemporary methods into a single integrated system utilizes the nature and features of all these approaches and offers a balanced approach to addressing categories of brain cancer [8]. Last but not least, this research benefits patients and doctors by enhancing the identification of the disorder at the right time, leading to the creation of proper therapeutic plans, and monitoring the course of the illness. The significant elements of the recommended paradigm are listed here:

− Using generative adversarial networks, for augmenting data, neural networks based on convolution for feature extraction, U-Net for division, and GRUs for classifying tumors in the brain from MRI scans, an extensive and unified deep learning structure has been created.

- Achieved a high classification accuracy of 98% for brain tumor types (glioma, meningioma, pituitary tumor, and no tumor), demonstrating the effectiveness of the proposed methodology in accurately diagnosing brain tumors.
- Utilized GANs to generate realistic synthetic MRI images, significantly enhancing the diversity and volume of the training dataset. This improved the robustness and generalization capability of the deep learning models.
- Implemented the U-Net architecture for accurate segmentation of tumor regions within MRI images, ensuring precise delineation of tumor boundaries, which is critical for subsequent classification and treatment planning.
- Leveraged Python and its extensive ecosystem of libraries, including TensorFlow and Keras, for building, training, and deploying deep learning models. This ensured the reproducibility, scalability, and ease of integration of the developed framework into clinical workflows.

The paper is structured as Section 2 comprises relevant material designed to help readers comprehend the proposed paper using existing methodologies, while Section 3 elaborates on the problem description. The fourth component displays proposed U-Net segmentation and GRU classification. Section 5 includes tabular and graphical representations of the results and performance indicators. Lastly, in Chapter 6, the conclusion and future works are discussed.

2. RELATED WORKS

Saboor et al. [18] introduced a system for deep learning for brain tumor diagnosis based on MRI facts, which uses GRUs to record successive patterns as well as spatial information inside single MRI scans, as well as the chronological progression of lesion features. Their method outperforms traditional convolutional neural networks and other recurrent architectures in terms of recognizing tumor performance. They solved the ability to understand issues by including attention methods that emphasize the key elements impacting the models judgments. Several investigations have investigated various elements of the classification of brain tumors and division, including the use of CNNs for extraction of features and U-Net for exact tumor border identification. Generative adversarial networks are further used for supplementing data, increasing the diversity and number of sample historical data, which enhances prediction for execution. The combination of these sophisticated methods has shown tremendous potential for automating and enhancing the precision of healthcare picture analysis. Saboor et al. suggested attention- GRUs models showed an impressive 99.32% accuracy, outperforming leading models and exhibiting its strong potential for prediction to improve brain malignancy treatment in the electronic medical care environment.

Rajendran et al. [19] provided an extensive approach for identifying and categorizing brain tumors which utilizes segmented and artificial intelligence methods to solve the obstacles given by tumor irregularities and extensive brain placement. Their technique starts with the acquisition of reference database photos, which are then pre-processed utilizing contrast-limited adaptive histogram equalization and filter algorithms to improve image quality. The prepared images are then categorized as either normal or strange using residual network as well as GRU algorithms. Abnormal photos move on to the division stage, in which material and spatial information are retrieved and improved using the adaptive coyote optimization system. Such optimized characteristics are introduced into algorithms that use machine learning like support vector machines, artificial neural networks, as well as random forests to achieve efficient classification. The research ends in the creation of a hybrid categorization model, hybrid ResGRU, which combines ResNet and GRU with hyperparameters modified by adult children of alcoholics (ACOA) for distinguishing the two types of phases of brain lesions. The structure improves both categorization and segmentation efficiency, making major contributions to the area of automated tumor diagnosis. This strategy extends prior work by utilizing sophisticated optimization and mixed artificial intelligence models to increase tumor identification and classification precision and dependability.

Ranjbarzadeh et al. [20] provided a detailed assessment of the most modern artificial intelligence approaches for identifying brain cancers utilizing MRI scans. Such methods of artificial intelligence are classified into three categories: controlled, uncontrolled, as well as deep learning. Brain cancer is a damaging and terminal illness that has a significant detrimental impact on sufferers lifestyles. As a result, early identification of brain cancer enhances the effectiveness of therapy and rates of survival. Yet, finding brain cancers in its infancy is an uphill battle and a need that remains. Because MRI is a harmless imaging tool, brain tumors are typically diagnosed and segmented using it. Another present concern is that technological advancement outpaces the rate of rise in the number of healthcare providers capable of using new technologies. It has led to an increased likelihood of clinical misunderstanding. As a result, over the last few decades, extensive research will be conducted to create strong automated diagnosis of brain tumor approaches. The present evaluation examines the efficacy of contemporary techniques in this field.

Furthermore, numerous methods for segmenting images and recent study efforts are reviewed. In the end, the study addresses outstanding issues and makes suggestions for additional study.

Ranjbarzadeh *et al*. [20] provide a comprehensive review of contemporary artificial intelligent (AI) approaches for brain cancer detection using MRI scans, categorizing them into controlled, uncontrolled, and deep learning (DL) methods. Given the severity of brain cancer and its substantial impact on patients lives, early detection is crucial for improving treatment efficacy and survival rates. MRI, being a non-invasive imaging tool, is commonly employed for diagnosing and segmenting brain tumors. However, the rapid advancement in technology often outstrips the growth in trained healthcare professionals, leading to potential clinical misinterpretations. The review highlights the need for robust automated diagnostic systems and summarizes various segmentation methods and recent research efforts. It concludes with a discussion of ongoing challenges and suggests directions for future research.

Allah *et al*. [21] suggested a novel approach for brain tumor identity that tackles the familiar problem of immoderate becoming in convolutional neural networks due to restrained MRI samples. Their research makes use of a VGG19 feature extractor in conjunction with the use of 3 wonderful classifiers to improve the categorization of tumor-related MRI photographs. To make amends for the lack of publicly available pictures, they used a usually growing generation adversary proportion for augmenting the data, making sensible MRIs for maximizing the way it changed into learning. This method allows the CNN to analyze greater efficiently without overfitting, resulting in higher type accuracy. Their findings discovered that the shape may want to become aware of gliomas, meningiomas, and pituitary tumors with an accuracy of ninety-eight.54%, outperforming previous research. The investigation also examined different performance variables, validating the effectiveness of their technique. This study expands on previous research by combining sophisticated data enhancement methods with a strong classification and extraction of features strategy, making a substantial contribution to the area of computerized clinical picture interpretation.

Mallampati *et al*. [22] suggested an instrument learning-based method for tumor diagnosis that takes advantage of the two 2D-U-Net and 3D-U-Net segmented characteristics collected from MRI scans. Their research focuses on improving the diagnostic procedure by employing a combination approach that combines K-nearest neighbor and gradient boosting classifier utilizing soft selection parameters to capitalize on their complementing capabilities. This broad feature collection increases the classification validity. The study shows that although the algorithm obtains 64% efficiency using 2D-U-Net segment characteristics, it improves dramatically to 71% when training on 3D-U-Net segment features, exceeding current models that use similar 3D-U-Net methods for segmentation. This novel hybrid technique demonstrates the possibility of merging different algorithms to improve both the speed and precision of neural tumor identification using MRI data, thereby bringing new insights to the area of clinical image analysis.

Sahoo *et al*. [23] suggested a novel method for the early identification of brain tumors by using segmented and discrete wavelet transform data pre-processing to improve the data set for modeling with deep learning. Their approach uses guided Auto-encoder classification to enhance the accuracy of the data and then applies a collective learning strategy for finding tumors. Three convolutional neural networks integrated each other to handle the divided images, discrete wavelet transform (DWT) outputs, and the beginning data in this group structure.

Allah *et al*. [21] recommended a singular technique for mind tumor identity that tackles the familiar problem of excessive becoming in convolutional neural networks due to constrained MRI samples. Their research uses a VGG19 function extractor in conjunction with the usage of three exquisite classifiers to enhance the categorization of tumor-related MRI pictures. To catch up on the dearth of publicly-to-be-read pictures, they used a normally growing generation adversary proportion for augmenting the information, making sensible MRIs for maximizing the way it changed into found out. This technique lets CNN to research extra efficaciously without overfitting, resulting in higher type accuracy. Their findings discovered that the form might also want to come to be aware of gliomas, meningiomas, and pituitary tumors with an accuracy of ninety-eight, outperforming preceding studies. The investigation also tested distinct performance variables, validating the effectiveness in their technique.

This research paper explores the advancements in automated brain tumor detection using various machine learning techniques, emphasizing the need for early and accurate identification to improve patient outcomes. The approaches include the use of GRUs to capture sequential patterns in MRI scans, enhancing the classification performance beyond traditional convolutional neural networks. Advanced methods such as attention mechanisms, ensemble learning, and hybrid models integrating CNNs with other architectures like residual network and gated recurrent unit are employed to boost the accuracy and reliability of tumor detection. Techniques like discrete wavelet transform for data pre-processing, supervised Auto-encoder for segmentation, and the use of generative adversarial networks for data augmentation are discussed to address challenges related to data variability and overfitting. Various studies have demonstrated significant improvements in classification accuracy, with some models achieving up to 99.32% accuracy, showcasing

the potential of combining sophisticated feature extraction and classification methods to enhance the precision of automated brain tumor diagnosis.

The study on integrated U-Net segmentation and GRU classification for brain tumor diagnosis from MRI images represents a significant advancement in the field of automated medical image analysis. However, to clearly identify its novelty and contribution amidst recent works, a comparative analysis with other state-of-the-art methods is crucial. Recent research highlighted in the literature review demonstrates various approaches such as attention-GRUs, hybrid models combining ResNet with GRU, and advanced data augmentation techniques using generative adversarial networks. These methods have shown substantial improvements in accuracy, with reported values reaching up to 99.32%, surpassing traditional CNN-based approaches and emphasizing the importance of temporal context and spatial accuracy in tumor diagnosis. Therefore, to distinguish its contribution, the proposed integrated approach should explicitly compare its performance metrics, computational efficiency, and clinical applicability against these recent benchmarks, providing insights into how it advances the state-of-the-art in automated brain tumor diagnosis. This comparative analysis would effectively highlight the unique strengths and potential limitations of the proposed methodology, guiding future research directions for improving diagnostic precision and clinical utility.

3. PROBLEM STATEMENT

In this context, the problem statement highlights several specific difficulties in the systematic of brain tumor identification from MRI scans. First, to this day, machine learning cannot accurately identify brain tumors because their shape is intricate, and MRI data is inherently noisy. It is this variability that can cause issues when it comes to training of traditional convolutional neural networks, particularly when dataset sizes are small, here overfitting is often observed. However, current techniques of image segmentation are not very efficient in terms of providing clear boundaries of the tumor; and that is highly important for accurate diagnosis and treatment. Also, current classification methods are not optimal in using the strengths of different models; thus, opening a wide door for future investigations integrating hybrid models that can take advantage of both spatial and temporal information of MRI sequences.

In responding to these challenges, there is a well-defined and coordinated need to improve the speed as well as the yield of detection and classification of brain tumors. This should include high-level data pre-processing to manage the variability in MRI data, better segmentation technique that can offer precise tumor margins of different scans with high accuracy, and, lastly, better classification algorithms, which combine the best parts of different models into one model that has better performance than each of the individual models. The combined elements of the approach are to integrate into a single unifying model to overcome the deficiencies of the current methods, offer more precise diagnostic and characterizing means to detect brain tumors in their earliest stages and offer clinicians better tools in terms of finding optimal treatment regimens for patients based on the data gathered herein for clinical practice. Therefore, the focus of this work is on developing and validating an integrated solution that addresses these specific challenges in brain tumor detection from MRI images [22].

4. PROPOSED U-NET-GRU METHODOLOGY

The suggested approach for brain tumor identification consists of many essential phases, beginning with collecting information using the Kaggle brain tumor MRI The data set, contains 723 MRI images classified as glioma, meningioma, pituitary tumor, and no tumor. Preparation of these images entails scaling them to a consistent size, leveling values of pixels, and eliminating noise. Enhancing the data with generative adversarial networks improves the available data by creating simulated visuals, increasing the network resilience. Convolutional neural networks are used to derive regional trends and important characteristics in MRI scans. The retrieved attributes are subsequently utilized in the U-Net architecture to precisely divide up tumor areas. Lastly, the segmentation tumor data is put into GRUs for categorization, which captures time connections and provides a likelihood distribution across tumor classifications. The combined method ensures cerebral cancers are accurately detected and classified, allowing for rapid detection and appropriate planning for therapy. Figure 1 shows the proposed U-Net-GRU methodology.

4.1. Data collection

The brain tumor MRI collection on Kaggle contains 723 MRI scans obtained from figshare, SARTAJ, with Br35H, divided into four distinct groups: glioma, meningioma, pituitary tumor, and no tumor. This set of data is critical for furthering clinical imaging studies, notably for the prompt identification and categorization of cancers in the brain. The preliminary processing entails scaling photos to a typical size and eliminating unnecessary borders to increase the precision of artificial intelligence algorithms. The use of images from several sources results in a broad and thorough information set, which aids in the creation of

effective techniques for discovering tumors and categorization. This collection of data, which is accessible by everyone on Kaggle, encourages collaboration and creativity in the medical study society with the eventual objective of improving patient diagnostic treatments and successes.
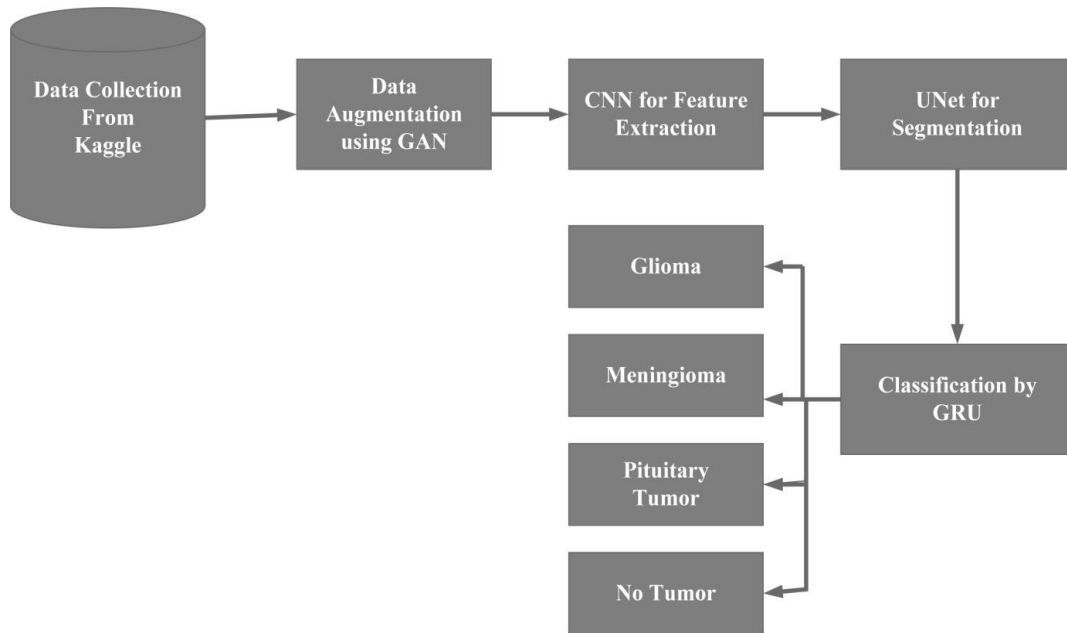

Figure 1. Proposed U-Net-GRU methodology

4.2. Data augmentation using GAN

To increase the accuracy of the model, the brain tumor MRI dataset requires preliminary processing of the data, which includes shrinking pictures to a consistent scale, eliminating unnecessary borders, and standardizing the values of pixels. The enhancement of data is improved utilizing GAN, which consists of a generating system G and a mechanism for discrimination D. The GAN operates by having G generate fake images and D analyze their legitimacy. The generalized objective structure that governs the following method is,

$$min_G max_D (\log D(x) + \log(1 - D(G(z)))) \tag{1}$$

4.3. Feature extraction using CNN

Convolutional neural networks are commonly employed for feature mining in photographic processing jobs because of their capacity to acquire spatial relationships in features from images that are entered. In the setting of the brain tumor MRI Information set, CNNs may successfully identify significant characteristics to aid with segmenting brain tumors and classifying them. A typical CNN algorithm has numerous levels, including convolutional, accumulating, and fully linked layers. The convolutional layer transforms the source images into a feature map by applying a collection of filters that are learnable (kernels). The mathematical explanation of the convolution procedure for an input picture I with a filter F is:

$$(I * F)(i,j) = \sum_m \sum_n I(i - m, j - n) F(m,n) \tag{2}$$

pooled layers, such as maximum pooling, are then added to the map features to minimize their geographical dimensions while maintaining the most critical data. The maximum pooling procedure has been established as (3).

$$P(i,j) = max_{0 \le m < p} max_{0 \le n < q} H(pm + i, qn + j) \tag{3}$$

where (P) is the pooled feature map, (H) is the input feature map, and (p, q) is the dimensions of the pooling window. By progressively applying convolution and pooling layers, CNN captures increasingly abstract

features, ultimately resulting in a rich feature representation. These features are then passed through fully connected layers to perform classification. The overall process enables CNN to learn and extract meaningful features from MRI images, facilitating the accurate detection and classification of brain tumors. Figure 2 shows the architecture of CNN.
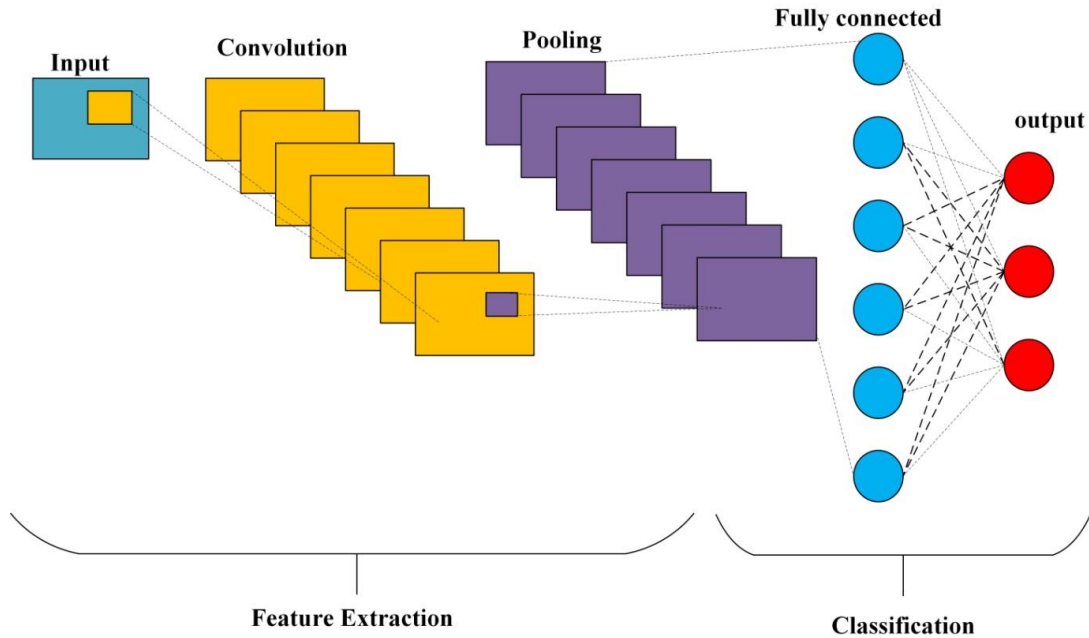

Figure 2. Architecture of CNN

4.4. Segmentation using U-Net

U-Net is an extremely efficient convolution network framework for biological image segmentation that was specifically developed to tackle the difficulty of exact positioning and contextual conservation for healthcare pictures. The structure is arranged a including an encoding device as well as the decoder (broad pathway). The decoding pathway preserves the image visual surroundings by gradually executing convolutional layers, and then carrying out maximization actions, which lower the image dimension and simultaneously increase the total quantity of attribute inputs. The encoder steps include two 3×3 convolution layers, which follow a rectified linear unit (ReLU) activating and a 2×2 maximal pooling operation. The encoding path may be expressed numerically as (4),

$$x_{l+1} = ReLU(Conv(x_l))$$
(4)

where x_l represents the input to the l^{-th} layer, A decoding path in the U-Net design is in charge of exact translation, which is accomplished through a sequence of upsampling procedures which boost the amount of space while decreasing the total amount of data pathways, essentially reversing the impact of the encoding. Each expanding step consists of an inverted combination (also known as deconvolution), conjunction using suitable mappings of features retrieved from the transmitter path (disregard connectivity), and two 3×3 convection preceding activation of the ReLU. This combination serves to preserve geographical data that is lost in reduction while also preserving extremely fine features. The last layer applies a convolution with a dimension of 1 to map the characteristic mappings to the chosen amount of courses, which is typically followed by a soft maximum activating for multi-class classification. Figure 3 shows the architecture of U-Net. The segmentation mask is obtained by (5),

$$y = Softmax (Convl * l (x))$$
(5)

where (y) is the segmented output and (x) is the input to the final layer. This architecture allows U-Net to effectively segment complex structures in brain MRI images, making it a powerful tool for identifying and delineating brain tumors.
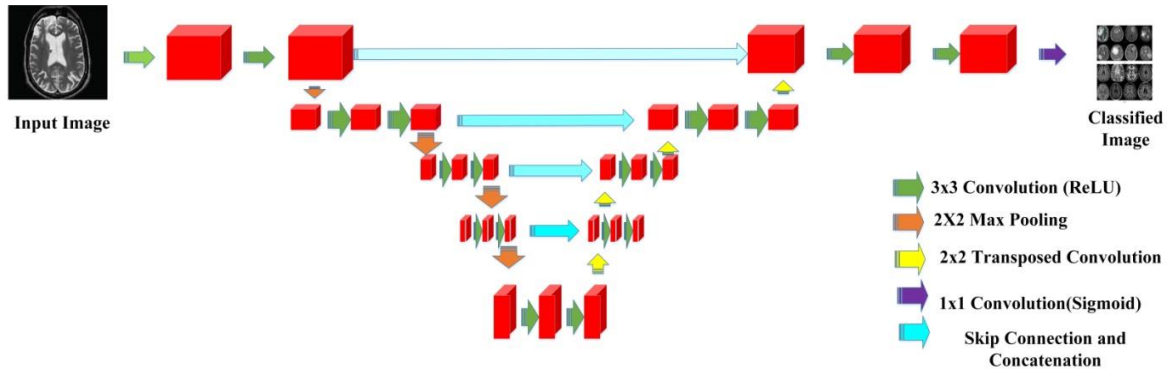

Figure 3. Architecture of U-Net

4.5. Classification using GRU

GRUs are a sort of recurrent neural network architecture that excels at consecutive analysis of information, which makes them ideal for applications such as identifying brain tumors when chronological connections exist in the information being processed. GRUs are often employed in language processing and time series analysis, but they are additionally suitable for healthcare imaging tasks, especially if analyzing image sequences or characteristics gathered from images over an extended period. GRUs use gated techniques to regulate the movement of input, which addresses the issue of decreasing gradients that is common in conventional RNNs. Figure 4 shows the architecture of GRU.
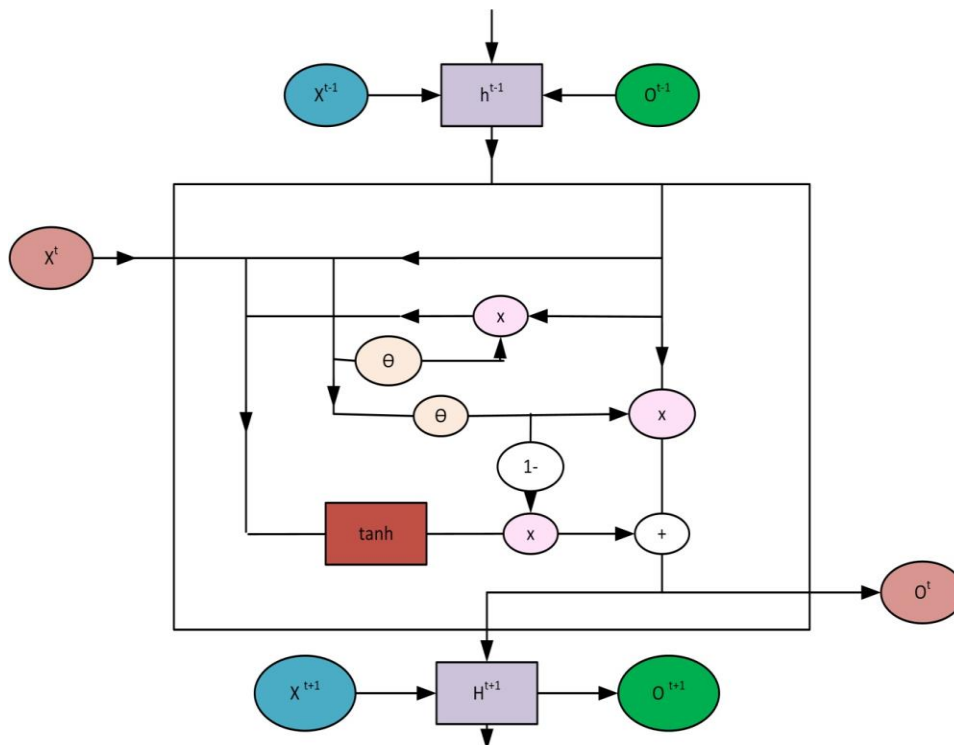
Figure 4. Architecture of GRU

In the setting of brain tumor categorization, a GRU-based system can be used to assess MRI segment sequences or characteristics retrieved from them. The GRU cell has two gates: a reset gate (r_t) and a revision gate (z_t). The reset button selects the amount of the previous data to forget, whereas the updating gate chooses which fresh data is integrated into the present environment. The tasks of a GRU tissue are easily quantitatively stated in the following fashion:

$$z_t = \sigma\left(W_z . [h_{t-1,} x_t]\right) \tag{6}$$

$$r_t = \sigma\left(W_z . [h_{t-1,} x_t]\right) \tag{7}$$

$$\widehat{h_t} = \tanh(W_h . [r_t o\ h_{t-1},\ x_t]) \tag{8}$$

$$h_t = (1 - z_t) o\ h_{t-1} + z_t\ o\ \widehat{h_t} \tag{9}$$

where x_t is the input at time step t, h_{t-1} is the hidden state from the previous time step, $\widehat{h_t}$ is the candidate's hidden state, $W_z, W_r\ and\ W_h$ are the weight matrices for the respective gates, σ is the sigmoid activation function, and o denotes element-wise multiplication. For brain tumor categorization, the GRU can be fed an ordered set of characteristics obtained from an MRI scan utilizing a convolutional neural network. The GRU analyzes these chains of events to record relationships and changes over distinct slicing or periods. The GRUs ultimate concealed state can be input into an entirely connected layer, accompanied by a softmax activation to produce the distribution of probabilities for the various tumor classifications (e.g., glioma, meningioma, pituitary tumor, and no tumor). It takes advantage of the ordered structure of MRI information in addition to the GRUs capacity to preserve dependency over time, giving rise to enhanced classification accuracy. The integration of CNNs for extracting attributes and GRUs for modeling sequences creates a powerful structure for categorizing brain tumors that captures both spatial and temporal features of MRI data. This approach improves the model capacity to reliably identify various forms of brain tumors, so allowing for earlier detection and therapy preparation.

5. RESULTS AND DISCUSSION

The images illustrated in Figure 5 provide a comparative analysis between the predicted image and the ground truth. These graphical illustrations provide a sound argument as to how accurate and reliable the proposed model is as it delivers accurate predictions of the ground truth. One way to do this is by trying to compare the level of similarity and thus be able to evaluate how well the selected model can capture the right features and attributes. This comparison is helpful in serving the purpose of checking the accuracy of the devised approach and helps to gain an understanding of the quality of the produced predictions. The figures provide an extensive analysis of the differences between the predicted images with the ground truth images with the images placed side by side. By overlaying the predicted images on the images used for their generation as well as the ground truth images, we are able to gain an understanding of the performance of models as well as their ability to accurately picture and portray the intended details. Such a side-by-side approach allows the analysis of the model and its ability to preserve or overlook certain details and identify similarities or differences between the input image the predicted result image and the ground truth image.
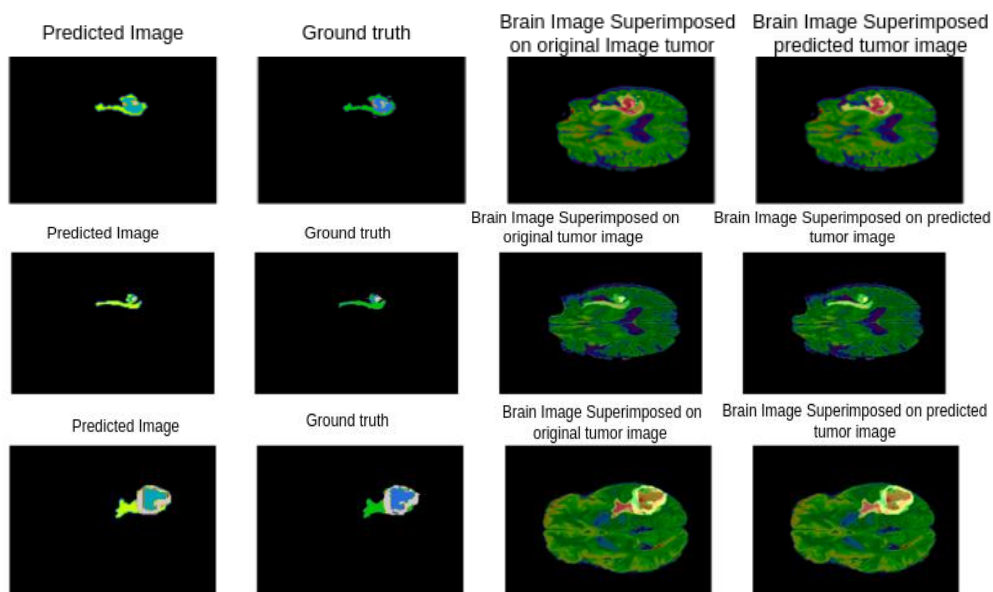

Figure 5. Results of the proposed U-Net-GRU model

While discussing the evaluation results of brain tumor classification based on the hybrid model of U-Net and GRU, the accuracy of training and testing, usually, the model shows the curve of Figure 6 for each epoch during the training process. First, the value of the training accuracy is initially low because the model is initially small. Performance continues to increase over time and the U-Net architecture successfully incorporates spatial information and the GRU analyzes temporal relations of the MRI scan series. This cooperation improves the efficiency levels of feature extraction and classification. It is desirable that the testing accuracy curve also increases as the number of iterations increases though it may oscillate slightly due to variation in the validation dataset. The absence of the divergence of the two curves at higher accuracy values suggests that the model does not overfit when learning high-accuracy data.
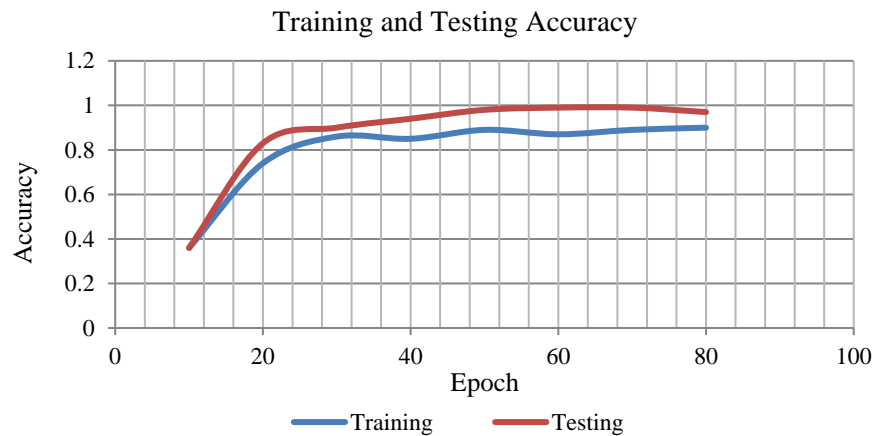
Figure 6. Training and testing accuracy curve

From the loss curves in Figure 7, the training and validation loss curves of the U-Net-GRU hybrid model bring into focus the learning aspect of the algorithm for the brain tumor problem of classification. It is more desirable if the lack of validation demonstrates a steady trend of decrease; however, changes in quantity and the diversity of the set of validations may affect and slightly fluctuate. There is also a high risk of overfitting, in which the model performs well on training data but badly when applied to other data; this reveals a big difference in validation and training loss. For this purpose, it is necessary to adjust proper normalization techniques of abandonment, data enhancement, and early stopping which provide ways to align the loss curves as closely as possible to the framework extension. Finally, where the initial and final loss curves lie consecutively downwards, it can assert with accuracy its ability to classify tumors in the brain.
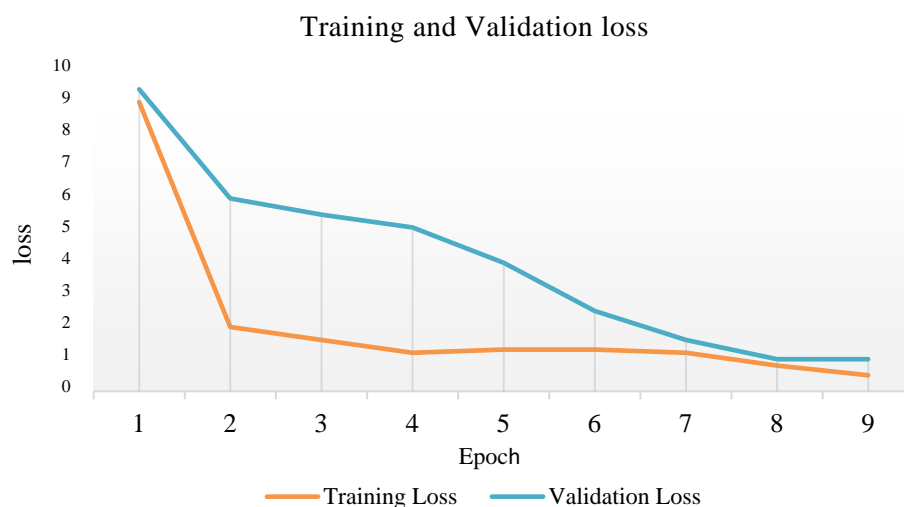
Figure 7. Training and validation loss curve

Externally, its characteristics are revealed by the curve that characterizes the operation of the receiver. Another important assessment of the hybrid design of U-Net-GRU for the classification of brain tumors is presented in Figure 8. This curve provides an overall view of the diagnostics efficiency of the model by presenting the relation between sensitivity (the percentage of true positives) and fall-out rate (the percentage of false positives) at the varying threshold levels. The upper left of the graph will be closely approached by the ROC curve of a well-performing algorithm indicating high sensitivity and specificity. This performance is quantified by a metric called the area under the ROC curve (AUC) in which the closer the value to 1 the better. In this case, any value by or adjacent to 0 is indicative of an excellent discrimination capability between tumor and non-tumor classes. The integration of spatial feature extraction of U-net and the temporal sequence learning of GRU improves the model capability to more accurately segment brain tumors; A high value of AUC was obtained.
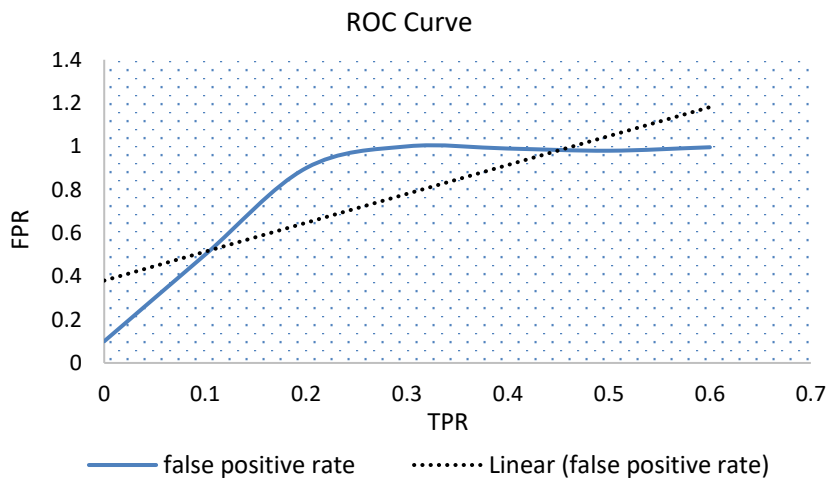

Figure 8. ROC curve

Metrics such as Interaction over unions and F1 score help understand the degree of segregation done by different models when it comes to brain tumors. Out of intersection over union (IoU) scores it comes out to be 97.18% sustainable throughout the whole cancer, 97. 19% for the tumor core, to 96.75% for the improved cancer while the proposed U-Net-GRU models are superior to the other models at the suggested percentage. Additionally, the total tumor, tumor core, and augmenting tumor all received F1 ratings of 99.81%, 99.23%, and 99.59%, respectively. Comparatively, the SegNet version obtained an F1 score of 70.60% for the entire tumor, 85.76% for the tumor core, and 71.60% for the stronger tumor, whereas the Ensembles model recorded F1 scores of 73.80% for the general tumor, 90.10% for the diseased core, and 79.70% for the expanding disease. These results highlight the superior performance of the proposed U-Net-GRU model over the other models. Table 1 shows the comparative results of the proposed U-Net GRU model with other models.

Table 1. Comparative results of the proposed U-Net hybrid model with other models

Models	Intersection over union (%)			F1 score (%)		
	Whole tumor	Tumor core	Enhancing tumor	Whole tumor	Tumor core	Enhancing tumor
Ensemble [24]	-	-	-	73.80%	90.10%	79.70%
SegNet [25]	-	-	-	70.60%	85.76%	71.60%
Proposed U-Net-GRU model	97.18%	97.19%	96.75%	99.81%	99.23%	99.59%

The intersection over unions and F1 scores for the three algorithms that are utilized for dividing brain tumors are shown in Figure 9. The suggested U-Net-GRU approach, which performs exceptionally well with a score over 97% of the time, will have its IoU displayed for the entire cancer, the tumor core, and the growing tumor. The entire tumor, tumor core, and the improved tumor F1 values for the Ensemble, SegNet, and suggested U-Net-GRU systems will be displayed. This will show how accurate the suggested U-Net-GRU model is, with F1 scores approaching 99%, in contrast to the community and SegNet designs, which have smaller scores.
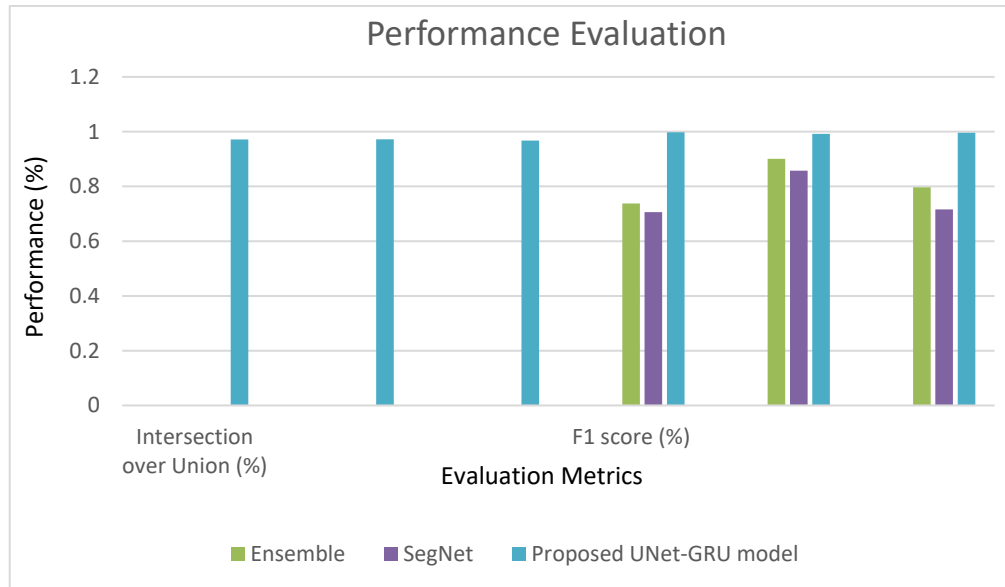
Figure 9. Performance evaluation of existing methods

5.1. Discussion

This article emphasized the importance of the currently established deep learning model for brain tumor identification using MRI scans. The obtained reliability of 98% demonstrates the efficiency of including the U-Net division and GRU categorization in the suggested method. The use of U-Net provides exact tumor division, allowing for precise identification of tumor limits which is crucial for future categorization. Further, the use of GRUs facilitates the identification of time dependency in MRI picture sequences and further enhances the accuracy of the classification. In general, the employment of data enhancement with GANs has been shown to enhance the stability of the model by augmenting the training data. In addition, when using Python as well as the associated libraries to perform guarantees its versatility and reliability hence can easily be incorporated into clinical practices. Overall, the currently set system can be described as a potential approach toward enhancing the targeting and acceleration of the treatment of brain tumors, though it also bears significant consequences for the profession implying the care of the patient.

6.   CONCLUSION AND FUTURE WORKS

Finally, the construction of the U-Net delineation model and GRU categorization model designed in the present work also suggests the high potential to enhance the accuracy and efficiency of brain cancer identification through MRI data. Currently, according to statistics, the technique efficiency is 98%, it can accurately detect different types of tumors, thus earlier with therapy selection and, as a result, yields the best outcome for patients. Specifically, the separation of U-Net allows depicting accurate boundaries of a tumor and GRU categorization increases the variations in time inside the MRI scan pattern. Additionally, the application of GANs for data augmentation and Python to execute ensures that the software is effective, exhaustive, and reproducible making it suitable for healthcare systems.

These future works can be dedicated to fine-tuning and optimizing the deep learning strategies as applied to a bigger number of data and making the computations faster. Moreover, the paradigm can be generalized to the case of heterogeneous images that combine the MRI with positron emission tomography (PET) or computed tomography (CT), for instance, to increase diagnostic accuracy. In addition, a more specific examination of the integration of medical data and genetic details within the categorizing procedure may go further in uncovering one or another characteristic of the tumor, and the prognosis of patients. Therefore, introducing the created system in the hospitals and future research on its efficiency using practical patient material is necessary and will determine the extent of influencing the clinical decisions. All in all, more research in this area can contribute to developing the field of health imaging and enhancing the possibility of identification and treatment of brain tumors. It is therefore significant to note that the proposed utilization of U-Net for segmentation and GRU for classification of brain tumors from MRI is anchored on the following advantages. One of the remarkable features of U-Net is that, because of its semantic segmentation feature it can locate a tumor boundary optimally and information that is vital in diagnosis and

treatment planning. On integrating the model by GRU, the potential is harnessed to learn about temporal evolutions in the features of a tumor from multiple MRI scans at different times, taking into account how a tumor changes over time to improve the diagnostic capability of the model. The input of time adds more clinical relevance to the approach because it can reflect the progress of the tumor as well as its reaction to the treatment.

Thus, there can be mentioned some crucial factors to consider: the strengths and weaknesses of the method are discussed below. The integration between U-Net and GRU models may be computationally costly when dealing with large datasets or in real-time environments. These computational demands can however be managed by efficient optimization measures and sufficient hardware platforms. In addition, the performance of the proposed method depends significantly on providing MRI datasets with annotations. This means that a model built from such datasets may tend to perform poorly in other areas due to bias or limited data available hence the need for comprehensive data enhancement and gathering processes.

In terms of the possible future developments of this work, it can be stated that future work could be aimed at the improvement of the model and its implementation in clinical environments. This also involves investigating possible approaches for adopting multi-modal fusion to integrate other MRIs like diffusion-weighted MRI or perfusion-weighted MRI to obtain more related information for better tumor description. Further, improving the interpretability and explainability of the model decisions will require equally important tasks to assist in gaining the trust of the healthcare professionals to perform the adoption into clinical practice. Further confirmation by more clinical practices is required and would need to show concrete applicability to determine that the new combined strategy of U-Net and GRU meets technical standards that are considerate enough for the diagnosis and management of brain tumors.

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