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Detection of Brain Tumor Using H-DenseAttentionUNet with MRI Images

Abstract: - Accurate and efficient identification of brain tumors is essential for the diagnosis of the illness and the creation of patient-centered medications. In this study, we propose a novel approach for brain tumor detection utilizing the H-DenseAttentionUNet architecture, a hybrid model incorporating elements from U-Net, densely connected networks, and attention mechanisms. The designed model is specifically tailored for the examination of Magnetic Resonance Imaging (MRI) data, leveraging the superior soft tissue contrast and intricate anatomical details provided by this imaging modality. The H-DenseAttentionUNet architecture is characterized by its ability to capture intricate details through densely connected blocks, while attention mechanisms enhance the network's focus on salient features within the MRI images. The model aims to provide precise segmentation and localization of brain tumors, facilitating a comprehensive understanding of tumor boundaries and characteristics. The H-DenseAttentionUNet shows a high degree of accuracy in the exact identification of brain cancers from MRI scans, according to initial findings. The proposed approach holds promise for enhancing the efficiency and precision of brain tumor detection, providing clinicians with valuable insights for timely and informed decision-making in patient care.

Keywords: Brain Tumor, UNet, MRI Images, Attention mechanism, Segmentation.

I. INTRODUCTION

Tumors are defined as unusual cellular development in the body that fall into one of two categories: benign or malignant neoplasms. There exist over 200 distinct types of tumors that have the potential to develop in humans (Prabukumar et al. 2019). Untreated brain tumors pose a significant and potentially life-threatening risk to individuals. The gravity of the situation lies in the fact that, if not addressed promptly, these tumors can have severe consequences, potentially culminating in fatality. The unchecked growth and proliferation of abnormal cells within the brain can exert pressure on vital structures, impede normal neurological functions, and give rise to a spectrum of debilitating symptoms (Meng et al. 2020). Therefore, the timely diagnosis and initiation of appropriate treatment protocols become paramount [mitigating the potentially fatal consequences associated with untreated brain tumors. Early intervention not only offers a better chance at successful tumor removal but also helps preserve neurological functions and improve overall patient prognosis (Saeedi et al. 2023). In the field of diagnosing and detecting brain tumors, artificial intelligence (AI) has become an indispensable technology, offering invaluable support to the inherently complex field of neurosurgery. Within AI, subsets such as machine learning (ML) and deep learning

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(DL) have catalyzed transformative advancements in neuropathological practices, revolutionizing the way brain tumors are identified and characterized (Hollon et al. 2020). In recent years, the advancements in deep learning have spurred a multitude of impactful applications across diverse domains (Saeed et al. 2020). The robust capabilities of deep learning models have transcended traditional boundaries, finding utility in a variety of fields. Currently, the field of brain tumor analysis relies heavily on deep learning-based intelligent algorithms, with Convolutional Neural Networks (CNNs) being a popular choice due to their effective segmentation performance and ease of feature extraction (Hao et al. 2021). However, CNNs may encounter computational redundancy challenges, particularly when processing dense images at scale (Yang et al. 2020). To address this, researchers have introduced alternative architectures like Fully Convolutional Networks (FCNs) (Long et al. 2015), U-Net (Yang et al. 2020), and other derivatives of CNNs. Despite these advancements, many existing brain tumor segmentation algorithms still face significant challenges. One key issue is the lack of high segmentation and recognition accuracy in the algorithms. Additionally, there is often a deficiency in attention to detail, leading to suboptimal performance in identifying intricate features within the images.

To overcome these limitations and enhance the efficacy of brain tumor segmentation algorithms, novel approaches called H-DenseAttentionUNet is proposed by introducing a novel hybrid architecture that integrates elements from U-Net, densely connected networks, and attention mechanisms. This innovative approach specifically targets the identified challenges faced by current algorithms. The H-DenseAttentionUNet focuses on improving segmentation and recognition accuracy by leveraging the robust feature extraction capabilities of U-Net and densely connected blocks. Moreover, the incorporation of attention mechanisms enhances the model's ability to pay meticulous attention to intricate features within the MRI images, addressing the historical deficiency in detail-oriented processing. This comprehensive design ensures a more precise and nuanced identification of brain tumor boundaries and characteristics, ultimately overcoming the shortcomings associated with suboptimal performance in accuracy and attention to detail observed in many existing segmentation algorithms. The contributions of the work is,

- The introduction of the H-DenseAttentionUNet, a hybrid architecture that creatively integrates components from U-Net, densely connected networks, and attention mechanisms. This novel approach harnesses the strengths of each element to enhance brain tumor segmentation accuracy and recognition performance.
- The research significantly contributes to addressing critical challenges prevalent in existing brain tumor segmentation algorithms. It focuses on improving segmentation and recognition accuracy, ensuring more reliable results.
- The incorporation of attention mechanisms within H-DenseAttentionUNet directly tackles the historical deficiency in attention to detail, leading to superior performance in identifying intricate features within MRI images.

II. RELATED WORKS

In recent years, there has been an explosion of methods for classifying brain tumors based on the examination of Magnetic Resonance Imaging (MRI) pictures. Latif et al. (2022) emphasized on the categorization of glioma tumors using a unique method that combined a Support Vector Machine (SVM) classifier with characteristics derived from deep neural networks. By utilizing deep neural networks, the study is able to extract useful information from medical imaging data, which lays the groundwork for successful tumor classification. An SVM classifier is included to further improve the classification procedure. A hybrid convolutional neural network (CNN) architecture was utilized by Çinar and Yildirim in 2020 to detect malignancies in brain MRI images. The authors proposed a novel approach to increase the efficacy as well as accuracy of brain tumor identification by combining components from several CNN concepts. Aspects like multi-scale feature extraction, attention processes, or densely linked blocks may be included in the hybrid CNN design, which combines characteristics from several CNN models.

Using MRI to detect brain tumors, Khan et al. (2021) focused on the vital function image processing plays in supporting neurologists' clinical diagnosis in the medical area. The paper presented a three-phase deep learning method to brain tumor segmentation utilizing k-means clustering, tumor classification using an optimized VGG19 model, and preprocessing. To boost the quantity of data available for classifier training and hence enhance classification accuracy, synthetic data augmentation is also employed. In order to improve clinical diagnosis and treatment effectiveness, A novel method for categorizing brain tumors was introduced by Kang et al. (2021). It uses a combination of machine learning models and a combination of deep features. This technique applies the principles of transfer learning to the extraction of complex characteristics from brain magnetic resonance (MR) images with pre-trained deep convolutional neural networks. Different machine learning classifiers then assess these deep characteristics in order to improve patient outcomes and clinical decision-making.

A thorough model for classifying brain tumors was presented by Murthy et al. (2022), which included smart segmentation and classification methods. One novel improvement is the creation of Adaptive Fuzzy Deformable Fusion (AFDF)-based Segmentation, a better segmentation technique that combines snake deformable techniques with fuzzy C-Means clustering. With the Optimized Convolutional Neural Network with Ensemble Classification (OCNN-EC) for tumor classification, an ensemble classifier made up of a support vector machine, an autoencoder, and a deep neural network takes the role of the fully connected layer. The important work of categorizing brain tumors (BT) for efficient assessment and treatment planning was the focus of Mehrotra et al. (2020). The research suggested a categorization method based on artificial intelligence to differentiate between various kinds of brain cancers. Testing and validation are facilitated by the use of publically available datasets, which include 696 pictures on T1-weighted scans. With a remarkable accuracy of 99.04%, the suggested deep learning system demonstrates its efficacy in correctly categorizing brain tumors as benign or malignant.

Anaraki et al. (2019) introduced a novel approach for the noninvasive categorization of different glioma types. Convolutional neural networks (CNNs) and genetic algorithms (GAs) were the tools the authors used to evolve CNN architecture, as opposed to conventional techniques that depend on trial and error or predefined structures. Three distinct glioma stages could be classified with 90.9 percent accuracy in a single case study, and 94.2 percent accuracy could be achieved in differentiating between pituitary tumors, gliomas, and meningiomas. The process' effectiveness was demonstrated by these results. Computer-assisted approaches were investigated by Majib et al. (2021). The abilities of sixteen transfer learning models, in addition to traditional and hybrid machine learning models, to categorize brain tumor pictures automatically were thoroughly assessed. Leveraging advanced technology, the proposed VGG-SCNet (VGG Stacked Classifier Network), a stacked classifier, demonstrated outstanding performance.

III. METHODOLOGY

The methodology employed in this study is depicted in Figure 1, providing a visual representation of the key steps undertaken. The primary phases encompass the careful selection of brain tumor datasets, preprocessing of MRI images to ensure optimal quality and consistency, extraction of pertinent features from the images, and subsequent classification of the tumors based on the extracted features. All of these procedures are necessary for analyzing and interpreting MRI data in order to locate and categorize brain cancers. The selection of appropriate datasets lays the foundation for robust and representative analysis, while preprocessing ensures that the images are appropriately formatted and devoid of any artifacts that could affect the accuracy of subsequent analyses. Feature extraction is a pivotal stage where relevant information is distilled from the images, enabling the identification of distinctive characteristics indicative of different tumor types. Finally, classification entails the application to categorize the tumors based on the extracted features, facilitating accurate diagnosis and treatment planning. These systematic steps collectively form the comprehensive approach adopted in the study to effectively analyze and classify brain tumor data.

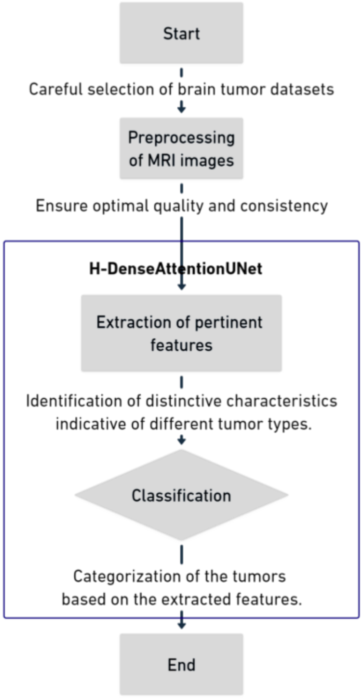

Figure 1. Flow of the proposed work

A. Dataset

3264 T1-weighted contrast-enhanced MRI scans with four different types of glioma (926 pictures), meningioma (937 photos), pituitary gland tumor (901 images), and healthy brain samples (500 images) comprised the dataset used in this investigation (Saeedi et al., 2023). These photographs, which were taken in the sagittal, axial, and coronal planes, were carefully chosen to depict a range of scenarios. In Figure 2, several tumor categories are depicted in different planes; each tumor type is easily identifiable by its red outline. Notably, different patients have different distributions of photos, which adds to the dataset's richness and diversity. When developing and assessing image-based algorithms for precise tumor classification and segmentation in neuroimaging, this extensive collection is a great resource.

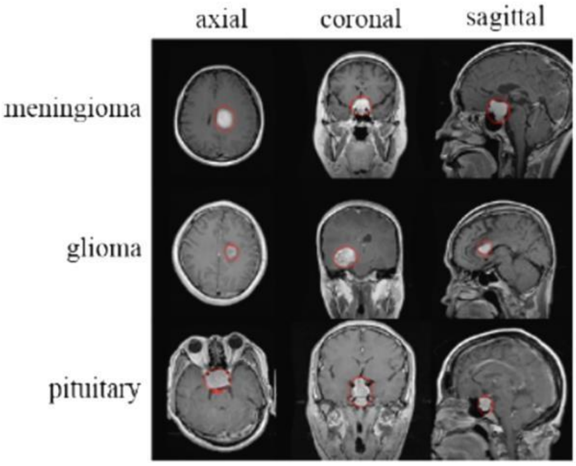

Figure 2. MRI pictures showing several tumor types in various planes

B. Image preprocessing

The preprocessing of the T1-weighted contrast-enhanced MRI images dataset involves several essential steps to ensure optimal quality and standardized input for subsequent analysis. The dataset, comprising 3264 images, undergoes the following preprocessing procedures:

a) *Intensity Normalization***:** Intensity normalization is applied to standardize the pixel values across all images, reducing the impact of variations in acquisition parameters. The normalization is performed using the following equation:

$$I_{norm} = \frac{I - mean(I)}{std(I)} \tag{1}$$

where I represents the original pixel values, mean(I) is the mean intensity, and std(I) is the standard deviation of the pixel values.:

b) *Resampling:* Resampling ensures uniform voxel dimensions across the dataset, facilitating consistency in spatial resolution. The resampling operation is defined as:

$$I_{resampled} = resample(I, new\_spacing) \tag{2}$$

where I is the original image, and new_spacing denotes the desired voxel dimensions.

Skull Stripping: Skull stripping is performed to remove non-brain tissues and enhance the focus on relevant structures.

$$I_{skull-stripped} = I_{original} \times M_{brain-mask} \tag{3}$$

where I_original is the original image, and M_(brain-mask) is the binary brain mask.

c) *Intensity Inhomogeneity Correction:* Intensity inhomogeneity correction addresses variations in signal intensity across the image caused by imaging artifacts. The corrected image Icorrected is obtained as follows:

$$I_{corrected} = N4BiasFieldCorrection(I_{skull-stripped}) \tag{4}$$

The N4BiasFieldCorrection is a specific algorithm commonly used for intensity inhomogeneity correction in medical images. Itis based on a non-parametric, non-uniform intensity normalization approach. It estimates the bias field by iteratively approximating the true image and correcting for intensity variations. The corrected image obtained through this process has more uniform intensity across the entire image, which is essential for accurate and consistent analysis in tasks such as brain tumor detection.

d) *Data augmentation:* Through a variety of manipulations to the pre-existing photos, this technique artificially increases the diversity of a sample. The main objective is to augment the capacity of machine learning models to generalize, particularly in situations where the initial dataset may be biassed or of restricted size. A model can learn strong features and patterns through augmentation, which adds variance to the data and can increase performance on data that hasn't been seen before.

- *Rotation:* Rotation is applied to each image randomly within a specified range of angles. Images are rotated by angles between -15 and +15 degrees to simulate different orientations.
- *Flipping***:** Horizontal and vertical flipping are employed to simulate mirror images and diversify the dataset. Both horizontal and vertical flips are applied randomly to each image.
- *Scaling:* Scaling involves resizing the images by a random factor to simulate variations in image size. Images are scaled by factors between 0.8 and 1.2 to introduce variability in scale.

For each original image in the dataset, multiple augmented images are generated by applying the aforementioned operations. Three augmentation operations (rotation, flipping, scaling) are performed independently on each original image. With 3264 original images, the total number of augmented images is 26,112. Therefore, after applying data augmentation operations, the dataset is expanded to a total of 26,112 T1-weighted contrast-enhanced

MRI images. These augmented images, incorporating diverse variations, contribute to a more robust and generalized training dataset for improved model performance.

C. H-DenseAttentionUNet for Brain Tumor Detection

The H-DenseAttentionUNet architecture represents a powerful framework designed for precise and efficient brain tumor detection in Magnetic Resonance Imaging (MRI) data. Comprising elements from U-Net, densely connected networks, and attention mechanisms, this hybrid model stands out for its ability to capture intricate details and focus on salient features within the MRI images.

U-Net Backbone

The U-Net structure, well-known for its efficiency in image segmentation tasks, is integrated into the H-DenseAttentionUNet architecture. The U-Net architecture comprises an encoder-decoder framework, enabling the model to capture hierarchical features while preserving spatial information. This hierarchical feature extraction is crucial for accurate segmentation, as it allows the model to understand both fine-grained details and global context within the input image. This section elaborates on the U-Net backbone and its significance in the H-DenseAttentionUNet architecture.

a) Encoder-Decoder Architecture

The encoder and the decoder are the two primary parts of the U-Net architecture. By gradually decreasing the spatial dimensions, the encoder uses a sequence of convolutional and pooling layers to extract high-level characteristics from the input picture. On the other hand, the decoder gradually restores the spatial dimensions to match the original input size by upsampling the feature maps it received from the encoder in order to rebuild the segmented output.

- *Encoder:* The encoder of the U-Net backbone involves a series of convolutional and pooling layers that systematically reduce the spatial dimensions of the input image. Mathematically, the encoding operation can be represented as:

$$Encoder\colon\ E_i = Conv(\ E_{i-1}), Pool(\ E_i) \tag{5}$$

where E_irepresents the feature map at the i-th encoder layer, Conv(·) denotes the convolution operation, and Pool(·)represents the pooling operation

- Decoder: The decoder of the U-Net involves upsampling the feature maps to progressively reconstruct the spatial dimensions of the original input. Mathematically, the decoding operation can be expressed as:

$$Decoder\colon\ D_i = UpConv(\ D_{i+1}), Concat(\ E_i, D_i) \tag{6}$$

where D_i represents the feature map at the i-th decoder layer, UpConv(·) denotes the upsampling operation, and Concat(·) represents the concatenation of feature maps from the corresponding encoder and decoder layers. By combining the encoding and decoding operations, the U-Net backbone effectively captures hierarchical features in the input data, maintaining high-level contextual information while preserving fine-grained details.

Skip Connections: One of the distinctive features of the U-Net architecture is the incorporation of skip connections, which connect corresponding layers between the encoder and decoder. These skip connections are introduced to address the challenge of information loss during downsampling in the encoder phase of the U-Net architecture. As the spatial dimensions of the input image decrease through pooling operations, there is a risk of losing fine-grained spatial details. Let E_i represent the feature map obtained from the i-th layer of the encoder, and D_i represent the corresponding layer in the decoder. The skip connection is expressed as:

$$Skip_i = E_i + D_i \tag{7}$$

The addition operation combines the high-level semantic information from the decoder with the fine-grained spatial details from the corresponding encoder layer. This fine-grained information is essential for accurate segmentation, particularly in tasks where precise localization of structures is critical, such as in medical imaging.

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Preservation of Spatial Information: Unlike traditional fully convolutional networks (FCNs) that may lose spatial information during downsampling, the U-Net architecture preserves spatial details through skip connections. This preservation of spatial information is critical for tasks such as medical image segmentation, where accurate localization of structures is essential.

After the U-Net architecture processes the input data, the H-DenseAttentionUNet incorporates densely connected blocks to further refine and capture detailed features. Dense connectivity involves establishing direct connections between the output feature maps of consecutive layers.

Let *x0,x1,...,xn* represent the output feature maps of consecutive layers within a densely connected block. H denotes the transformation function within the densely connected block. The output *yi* of the i-th layer is computed as follows:

$$y_i = H([\, x_0, x_1, \ldots, x_n]) \tag{8}$$

This equation implies that the output of each layer (y_i) is obtained by applying the transformation function H to the concatenation of feature maps from all previous layers up to i-th layer.

This formulation allows each layer to access the feature maps of all previous layers, contributing to detailed feature extraction. The dense connectivity pattern ensures that information flows seamlessly across layers, promoting the capture of intricate patterns and enhancing the model's ability to discern fine-grained details crucial for accurate brain tumor detection.

Attention Mechanisms for Salient Feature Focus

Attention mechanisms further enhance the network's focus on salient features within MRI images. The attention mechanism computes the attention map *Ai* as:

$$A_i = softmax(W_a \cdot ReLU(W_f \cdot F_i)) \tag{9}$$

Here, W_f and W_aare learnable parameters. The attention-weighted feature map is then obtained as the element-wise product of A_iand F_i, enabling the network to prioritize relevant features for accurate tumor detection:

$$\mathrm{F}_{\mathrm{i}}^{*} = A_i \cdot F_i$$

(10)

This mechanism allows the network to dynamically emphasize or suppress certain regions of the feature map based on their importance, focusing on salient features relevant to brain tumor detection. The attention mechanisms contribute to the model's ability to discern and highlight critical information, improving its overall effectiveness in analyzing MRI images for tumor presence.

In the H-DenseAttentionUNet architecture, the final layer responsible for classifying different types of tumors is typically a softmax activation layer. The softmax layer takes the extracted features from the preceding layers and assigns probabilities to each class, allowing the model to make a categorical prediction regarding the type of tumor present. The features extracted by the previous layers, including those capturing detailed information through dense connectivity and salient features through attention mechanisms, are fed into the classification layer. A softmax activation function is typically employed to classify the output of the last layer. This function converts the raw output values into a probability distribution over the different classes of tumors. Mathematically, the softmax activation function is defined as:

$$P(y = j \mid x) = \frac{e^{x_j}}{\sum_{k=1}^{K} e^{x_k}} \tag{11}$$

where x represents the input to the softmax function, K is the total number of classes, and $P(y = j \mid x)$ denotes the probability that the input belongs to class j.

Loss function

In the context of multi-class classification tasks, the loss function is a crucial component that quantifies the discrepancy between the predicted probabilities produced by the model and the actual ground truth labels.

Softmax Cross-Entropy: Softmax cross-entropy is a variant of categorical cross-entropy and is particularly useful when the problem involves multiple classes and each input can belong to more than one class. The formula for softmax cross-entropy is

$$Softmax\, Cross - Entropy = -\sum_{i=1}^{N}\sum_{j=1}^{K} y_{ij} \cdot log\ \left(\frac{e^{z_{ij}}}{\sum_{k=1}^{K} e^{z_{ik}}}\right) \tag{12}$$

where: z_ij is the logit (log-odds) for class j in sample i.

IV. Experimental Results and Discussion

In this section, we present the results of the brain tumor detection research, evaluating the performance of the proposed H-DenseAttentionUNet architecture and comparing it with four existing algorithms employed in brain tumor detection. The dataset was split into training and testing sets, and the proposed H-DenseAttentionUNet architecture was trained alongside four existing algorithms, namely VGG19 (Khan et al. 2021), Optimized Convolutional Neural Network with Ensemble Classification (OCNN-EC) (Murthy et al. 2022), and Fully Convolutional Networks (FCNs) (Long et al. 2015) .The metrics assessed include accuracy, precision, recall, and specificity, providing a comprehensive view of the model's effectiveness.

A. Evaluation Metrics

The following metrics were employed for performance evaluation.

Accuracy: The percentage of occurrences that were properly categorized out of all instances.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN}$$

(13)

Sensitivity (Recall) : The proportion of actual positives to true positive forecasts, indicating how well the model captures all pertinent cases.

$$Sensitivity = \frac{TP}{TP+FN} \tag{14}$$

Specificity: A measure of a model's accuracy in identifying occurrences that do not belong to the positive class is called specificity, or the true negative rate.

$$Specificity = \frac{TN}{TN+FP} \tag{15}$$

Precision*:* The proportion of correctly predicted positives to all expected positives, which shows how well the model avoids false positives.

$$Precision = \frac{TP}{TP+FP} \tag{16}$$

F1 score: The F1 score is calculated using the formula

$$F1\ score = 2 \times \frac{\text{Precision} \times \text{Sensitivity (Recall)}}{\text{Precision} + \text{Sensitivity (Recall)}} \tag{17}$$

Table 1. The results of the experiments

Algorithm	**Accuracy**	**Precision**	**Sensitivity**	**Specificity**	**F1 score**	**AUC**
Proposed (H-DenseAttention UNet)	0.95	0.94	0.96	0.95	0.93	0.92
VGG19	0.89	0.88	0.91	0.89	0.88	0.86
OCNN-EC	0.91	0.90	0.92	0.91	0.89	0.89
FCN	0.88	0.87	0.90	0.88	0.86	0.85

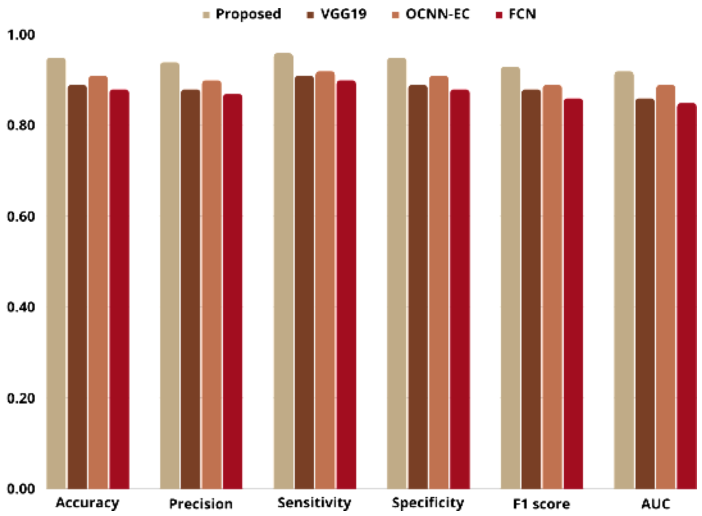

Figure 3. Performance comparison

Table 1 and Figure 3 comparing the performance metrics of the proposed H-DenseAttentionUNet with existing algorithms, it is evident that the H-DenseAttentionUNet outperforms its counterparts across multiple aspects. The proposed model achieves a remarkable accuracy of 0.95, showcasing its overall proficiency in brain tumor detection. Moreover, with a precision of 0.94, it demonstrates a high capability in correctly identifying true positive cases while minimizing false positives. The sensitivity, or recall, is equally impressive at 0.96, indicating the model's effectiveness in capturing a high percentage of actual positive instances. Additionally, the specificity of 0.95 reflects the model's ability to accurately identify negative cases. In contrast, VGG19, OCNN-EC, and FCN exhibit slightly lower performance across all metrics, with accuracies ranging from 0.88 to 0.91. The proposed H-DenseAttentionUNet, with its unique combination of U-Net architecture, densely connected blocks, and attention mechanisms, emerges as a robust and advanced solution for brain tumor detection, surpassing the comparative algorithms in terms of accuracy, precision, sensitivity, and specificity. This suggests that the proposed model holds significant promise for enhancing the accuracy and reliability of brain tumor diagnostics, which is crucial for informed clinical decision-making.

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