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BRAIN TUMOR CLASSIFICATION BASED ON 3D AUTO ENCODING TECHNIQUE

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ABSTRACT

The brain is an essential part of the entire nervous system because it can control and regulate body parts. The International Agency for Research on Cancer (IARC) estimates that 76% of deaths from brain tumors are cancer related. Abnormal cells in the brain cause brain tumors and make life dangerous if untreated at the early stages. A significant portion of the Image is extracted using image processing techniques during tumor image classification. The 3D shape is a complex structure in the 3D space; because of this reason, there would be a minimal of 3D shapes for feature learning. To cope with those challenges, research paper transform 3D shapes into 2D space and use automatic encoders to learn features from 2D images. The proposed 3D based Spatial Auto Encoder (3D-SpAE) approach is automated by learning a state representation directly from camera images and the state-space constructions. Once the autoencoder is trained, the coefficients acquired for reconstructing an image based on prototypes which are utilized as a feature for 3D shape matching and retrieval. The autoencoder can achieve high performance for image retrieval because it can learn feature adaptively from training data. 3D-SpAE classified the brain tumor data into Whole-Tumor, Tumor Core, and Enhancing Tumor. The results showed that the suggested method obtained better values of the accuracy of 99.4% when compared to the existing Nonparametric Localization Enhancement Methods with U-Net, 3 D Context Deep Supervised U-Net, Deep Elman Neural network with adaptive fuzzy clustering, NSGA, Convolutional Neural Network, and Kernel-based SVM.

Keywords: *Brain Tumor, Complex Structure, Classification, Feature Points, 3D Based Spatial Autoencoder*

1. INTRODUCTION

The brain is an essential part of the whole nervous system as it can control and coordinate body parts [1]. Abnormal cells are referred to as brain tumors that threaten the life of a person if not treated [2]. Thus, the tumors are classified in two types: primary and secondary tumors [3]. The malignant tumor primarily starts to grow inside the brain, yet the secondary malignant tumor initiates into other organs that could propagate to the brain by metastasis [4]. The human body has a brain tumor, and a malignant tumor is very daunting if left untreated [5]. Segmentation of brain tumor is essential to diagnosis and helps to plan for cancer treatment. That detects the stages of the tumor, such as Low-grade (LGG) and High-Grade Gliomas (HGG). The specialists can use Computed Tomography (CT), Ultrasound, and Magnetic Resonance Imaging (MRI) for screening the patients [5].

The MRI Image is an impressive technology that shows various modalities as it is non-invasive in nature and obtains a better representation of internal tumor information. Yet, the manual classification of brain tumors shows vulnerability concerning the formidable task, time consumption, and error [7]. Therefore, deep learning models are used, which classify the brain tumor based on MR data [8]. The model operated fast and obtained higher accuracy, showing treatment better for the patients [9]. The MRI segmentation is done based on the learning strategies and recognizes the patterns successfully for analyzing the brain images [10]. The density-based function is used for selecting the operations as it considers the parametric model [11].

Currently, both the medical and technical communities are paying close attention to the field of research in brain tumor analysis. Existing models such as Convolutional Neural Networks (CNN) [6], Fully Convolutional Neural Networks (FCNN), Cascaded Neural Networks, DeconvNets, and 3D-

CNN were used for the detection of brain tumors based on MR image analysis. However, most of these methodologies are either sensitive to irrelevant data or the decease similarities may not be clear. Therefore to have a proper understanding of the brain images even in low resolution channels, techniques need to be developed. So that better reorganization accuracy of the decease can be minimized. Therefore, this research introduced 3D based Spatial Auto Encoder (3D-SpAE) approach to overcome the above-stated issues. The major contributions of this research are mentioned as follows:

- In the present research work, the proposed semantic segmentation is deepened the spatial information which present in the feature map to minimizes the time.
- The spatial information is lost; thus, the system acquires a collection of feature points that describe the positions of tumors using a deep spatial auto encoder and then learns from these feature points.

The paper and structure are arranged as shown in the following sections: Section 2 explains the existing models under the literature review section. Section 3 is the proposed method section that consists of various steps involved. Section 4 describes the results and discussion of the proposed method. Section 5 is the conclusion and the future work of the proposed method.

2. LITERATURE REVIEW

The existing methodologies involved in brain tumor classification are as follows:

Champakamala Sundar Rao and K. Karunakara [12] developed a Kernel based SVM model (KSVM) with Social Ski Driver (SSD) for the detection of brain tumor. An efficient brain tumor detection is vital by using an algorithm that uses a binomial thresholding approach for segmentation. From the segmented region, the features were fused and were undergone for feature selection using Harris Hawk's Optimization. The proposed KSVM-SSD performed an effective and accurate results classification that classified as benign or malignant and the SSD Optimization further helped to find the tumor as high, medium, or low. Yet, the optimization algorithm was sensitive to the irrelevant data features due to feature occurrences.

Muhammad Irfan Sharif et al. [13] developed an improved framework to detect the brain tumors using MRI based on CNN and YOLOv2 models. The features were extracted from the inceptionV3 model for pre-training the informative segments. From the extracted features, the non-dominated sorted genetic algorithm (NSGA) was used to select features. The features were optimized by forwarding to the classifier at the depth concatenation mixed four layers, which are then supplied to YOLOv2. However, the disease severity levels were not identified at the segmentation stage.

K. Sakthidasan Sankaran et al. [14] developed a fuzzy clustering approach adaptively with a deep Elman Neural Network to perform segmentation and clustering for identifying the brain tumor grade. The regions from the tumor are segmented by using an adaptive Fuzzy Tsallis Entropy clustering with Cuckoo Search Optimization. Initially, the Images were pre-processed using the anisotropic diffusion and non-parametric region model for the removal of noise and skull. The deep Elman neural network (DENN) was used to categorize the brain tumor that was developed classified as a brain tumor. This model improves the accuracy of the medical images in large databases by using multiple classifiers.

Mingquan Lin et al. [15] developed a Fully Automated Segmentation with 3D Context Deep Supervised U-Net model for the segmentation of brain tumor. The multiple parametric from the brain tumor images are evaluated using the 3D context deep supervised U-Net model [18]. The developed approach enlarged the receptive field effectively using the CNN model. With this, accuracy can be improved for the segmentation of brain tumor regions. However, the 3D-CNN network required GPU for processing large Images, which took a long time for network training.

Ahmet Ilhan et al. [16] developed a U-Net-based model for classifying brain tumor images based on non-parametric localization. The developed model used an efficient approach for segmenting brain tumors based on tumor localization using deep learning architecture. The histogram-based non-parametric tumor localization approach is applied to modify the localized regions and indistinctly increase the virtual appearance of low-contrast tumors. The tumorous regions show better performances for the deep learning models that effectively segmented the trained and untrained datasets without any requirement for augmented data.

3. PROPOSED METHODOLOGY

The block diagram for the proposed research is shown in Figure 1. The block diagram consists of the dataset, pre-processing of the dataset, segmentation, and lastly, classification. The classified results are WT, TC, and ET of brain tumor images.

This method addresses the challenges of the earlier methods such as necessity for GPU, sensitivity of data, irrelevant data features, decease severity levels can also be efficiently managed by using the proposed method.

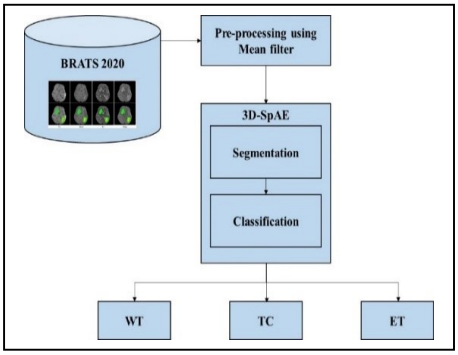

Figure 1: Resultant Graph of the Proposed System

3.1 Data Collection

The BraTS Dataset mainly focuses on the evaluation state based on the state of art techniques. The segmentation of brain tumors is performed for the multi-modal MRI scans. The BraTS 2020 utilizes a multi-institutional consisting of pre-operative scans from the MRI that focus on segmentation of heterogeneous data, which pinpoints the relevance based on the segmentation task; the BraTS 20 focuses on patient's survival prediction overall. The distinction between the pseudo-progression and recurrence of an actual tumor through integrative analysis is performed based on the random features. There are a total of 335 images from the BRATS 2020 dataset. Among the total dataset images, 76 are from Low-Grade Glioma (LGG), and the leftover 259 are from the High-Grade Glioma (HGG) type of Image. The MRI scans focus mainly on three primary tasks: segmentation, intrinsic heterogeneous Image based on shape and appearance, and prediction for the survival of a patient [17] using histology images.

3.2 Preprocessing

The experimentation is conducted based on the input available in the dataset. The first step in this process is to enhance the Image, for which, in this article, a mean filter is considered. In general, a mean filter is a 3X3 grid containing pixels. This 3X3 grid is run on the input image from the top left corner by using the process of convolution and replacing the so obtained values against the pixel. The process is repeated for the entire Image.

3.3 Segmentation and Classification using Spatial Autoencoders

After image enhancement, the spatial auto encoding technique [19] is considered for effective segmentation. In this encoding process, a 3D shape model 'S' performs a Deep Belief Network (DBN) [20] by initiating the autoencoder; the shape of the image regions is extracted based on the shape code. The step-by-step process of auto encoding is presented below:

- In the first phase, each input image under consideration is normalized to be free from translation and scaling.
- In the second phase, the shape of the images is represented in 3D using a set of depth buffer images.
- In the final phase, all the projections from the depth buffer are considered for training the autoencoder, and from this process, the 3D shapes of the images are retrieved.
- In the ultimate phase, the dotted projections from the depth buffer considered the features are taken, and the features are extracted based on these dotted lines.
- The following process is to collect the 2D projection set of 'S' from the 3D projected planes using fundamental transformations, including scaling, translation, and normalization.

This projection is represented in the form of the following equation:

$$P(S) = \{V_1, V_2, V_3, \ldots. V_{NP}\} \quad (1)$$

Where $V_1, V_2, V_3, \ldots, V_{NP}$ represent the number of projections present in each input image. For the experiment, we have considered T1, T2, T1 contrast, and Flair (Fluid-attenuated Inversion recovery) images. The series of projections in different view elevation angles are presented in the following Figure 2 of the article. This figure depicts all the multi-model scans that are manually

segmented with a mask. It also highlights the segmented regions obtained by non-enhancing tumor core, peritumoral edema, and GD-enhancing tumor.

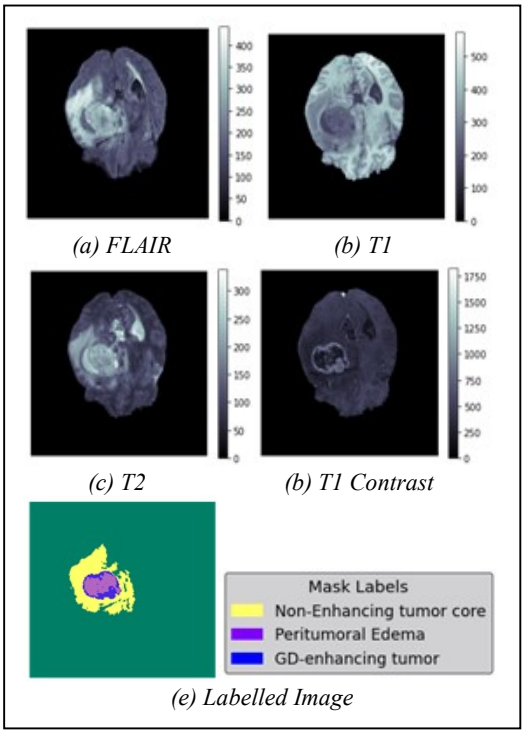

Figure 2: Multi-modal Scans which are manually segmented with the mask are targeted

3.4 Proposed 3D-based Deep Spatial Autoencoders

In the auto encoding process, the features are acquired by mapping the input to self-imposing constraints to trivial solutions like the self-identity function. In this process, the steps may include sparsity together with a low-dimensional bottleneck. In the auto encoding process, all the information considered in the input image is passed using this bottleneck, considered a spatial feature. For effective feature identification, low dimensional dense vectors are generally more suited; hence, these vectors are considered for feature representation. In this article, we try to encode the features using the bottlenecks rather than considering feature vectors. This process enhances the standard procedures and ensures effective image reconstruction.

In general, in any encoding process, the input is first encoded into a series of vectors, and these vectors are given as input to identify the depth. In the decoding process, reverse technology, i.e., the decoder, is considered to decode the vectors such that the output image in 3D can be derived. The main advantage of encoding using auto encoders is that it eliminates the necessity of methodologies based on traditional methods like PCA [22]. To effectively encode, the process is divided into stages, wherein a three-layer CNN [6] with ReLu is considered and which is of the form:

$$a_{cij} \max(0, z_{cij})$$
$$\text{for every channel c and pixel (i,j)} \quad (2)$$

The spatial features are computed from the convolution layer using the technique of soft-arg max. This output helps identify the image pixels in each channel of the convolution network. All the points so formulated from the spatial features and help the autoencoder to identify the object plane. The following equation (3) represents the response of the spatial softmax in the convolution network:

$$s_{cij} = \frac{e^{a_{cij}/\alpha}}{\sum_{i'j'} e^{a_{ci'j'}/\alpha}} \quad (3)$$

Where 'α' is a parameter representing the intensity of the pixel. To compute the 2D position of each pixel that uses a probability distribution represented by:

$$f_C = (\Sigma_i\, i \times S_{cij},\ \Sigma_j\, j \times S_{cij}) \quad (4)$$

The probability density function output helps identify the maximal densities of each activation channel in a convolution network. The decoder is considered for decoding the sequence of the encoded densities using the down-sampling process. The main advantage in this process is that the considered autoencoder helps compress the sum of the pixels, which are not necessary to identify the image depth. During this process of compression, the background information is eliminated, and the corresponding equations for the elimination process are given by:

$$\| (f_{t+1} - f_t) - (f_t - f_{t-1}) \| \quad (5)$$

Where f is a feature point.

Use the equation above to encourage the feature points to change velocity slowly. As a result, the overall auto encoder goal is to encode the feature points of the t^{th} image in the k^{th} sequence using the input image I. The proposed technique regarding dice and Jaccard Coefficients were evaluated for the WT, TC, and ET.

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4. RESULTS AND DISCUSSION

The results obtained by the proposed method were obtained by conducting it in an Intel Core i7 processor with 2 GHz CPU utilization time working with 48 GB of RAM.

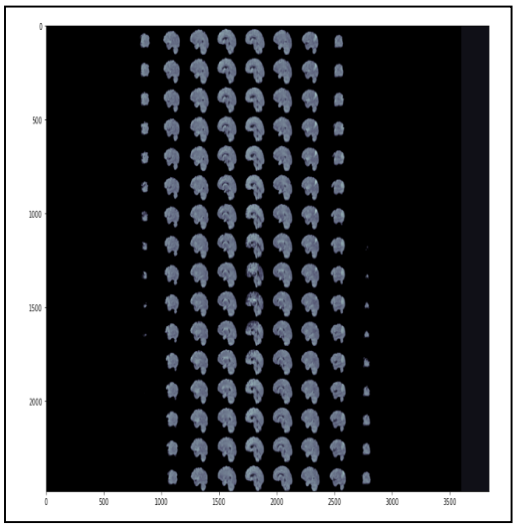

Figure 3: The segmented input brain images using the proposed method

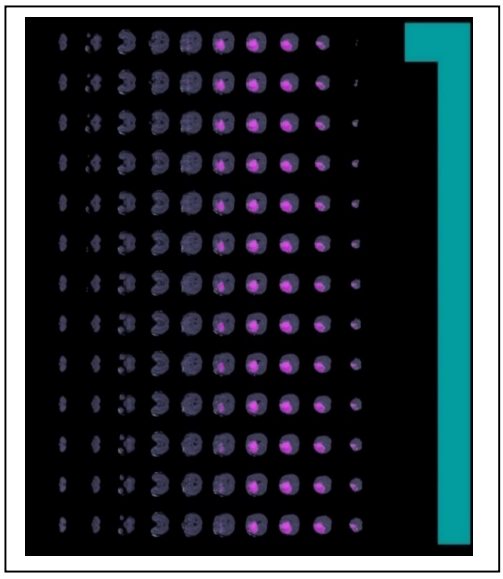

Figure 4: Results obtained by the proposed method

4.1 Performance Metrics

The present research feeds the training data to the classifier that evaluates the testing data. Accuracy, precision, recall, and F1-measure are used to assess the performances.

Accuracy - The performance measure accuracy is the ratio of correctly predicted observations to the overall observations. The accuracy term is calculated using the below equation:

$$Accuracy = \frac{(TP + TN)}{(TP + TN + FP + FN)} \quad (6)$$

Precision - The precision is expressed as the number of total data samples that are predicted to the overall false observations concerning the actual number with false observations. The Precision term is defined as shown in the below equation:

$$Precision = \frac{TP}{TP+FP} \quad (7)$$

Recall - A recall is the actual number of traditional false observations that are considered the ratio of totally predicted false observations. The recall is expressed as shown in the below equation:

$$Recall = \frac{TP}{TP+FN} \quad (8)$$

F1-Measure - The F1 measure is known as the harmonic mean of the recall and precision, which are evaluated by using the below equation:

$$F1 - measure = \frac{2xPrecision\,xRecall}{Precision+Recall} \quad (9)$$

Jaccard Coefficient - The Jaccard similarity index, compares two sets of items to determine what is common and what is unique. This is a similarity metric for two datasets. The Jaccard Coefficient equation is as follows:

$$Jaccard\ coefficient = \frac{TP}{(FP + TP + FN)} \times 100 \quad (10)$$

Dice Coefficient - The Sorensen–Dice coefficient is a statistic used to measure the similarity between two samples. The equation for Dice Coefficient is expressed as shown in the equation:

$$Dice\ coefficient = \frac{2TP}{2TP + FP + FN} \times 100 \quad (11)$$

Where TN was stated as a true negative, FN was represented as a false negative, TP was specified as a true positive, and FP was indicated as a false positive.

4.2 Quantitative Analysis

The results from the proposed Dilated U-Net [18] based CNN model are shown in Table 1. Results are not good for training data samples when there are more feature points at each data point. Due to the high dimensionality, the KNN classifier did not work well to calculate distance. Existing RF [21] models show improved prediction accuracy, overcome complex problems that are generally inferior to gradient boosted trees, and achieve 97.07% accuracy. RF was more difficult to interpret than a decision tree that achieved 98.93% accuracy. The proposed 3D-based SpAE model can extract the edge-based features accurately during segmentation and thus obtain better results in terms of accuracy as 99.94%.

Table 1: Results obtained for the proposed method

Classifier	Accuracy (%)	Sensitivity (%)	Specificity (%)	Precision (%)
KNN	97.07	95.32	94.28	95.74
SVM	97.87	94.21	95.90	94.78
RF	98.93	95.94	96.48	95.22
Proposed 3D-based SpAE method	99.41	98.92	98.63	98.41

4.3 Comparative Analysis

Table 2 is the comparative analysis where the comparison of the existing with the proposed model is performed. The current optimization approaches were sensitive to data features as they had irrelevant features because feature occurrences obtained an accuracy of 99.15% [11]. At the segmentation stage, the severity levels of diseases were not identified, which showed an accuracy of 99% [12]. The extensive database consisting of medical images improved accuracy and thus showed 98% [13]. The developed model used more than one classifier to examine the more robust mechanisms for improving the accuracy of large databases consisting of medical images obtained 92% [14]. Also, tumorous regions showed better performance using the deep learning models, which effectively segmented the untrained and trained datasets without using augmented data requirements and obtained 99.4% accuracy [15]. The proposed Dilated-based U-Net model got better accuracy of 99.5% compared to the existing models.

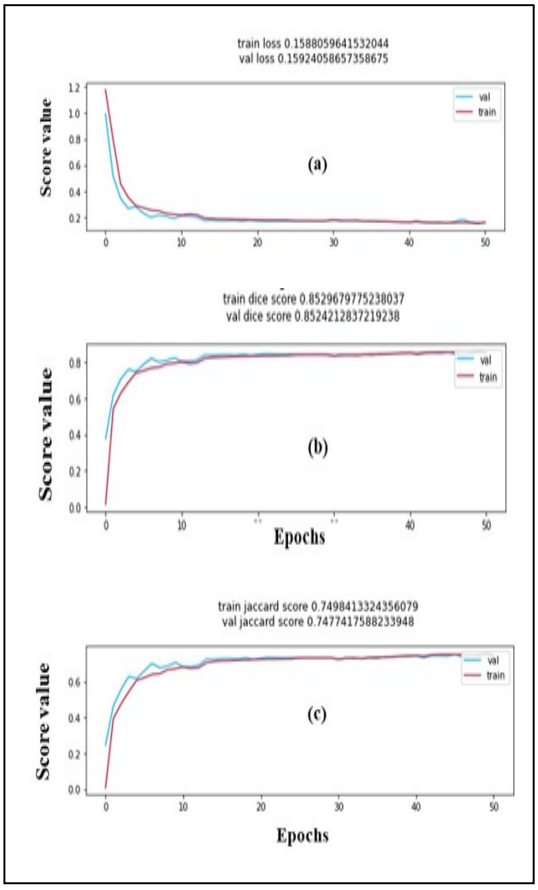

Figure 5: Graphical Representation of the proposed method (a) loss coefficients (b) Dice score (c) Jaccard Coefficient

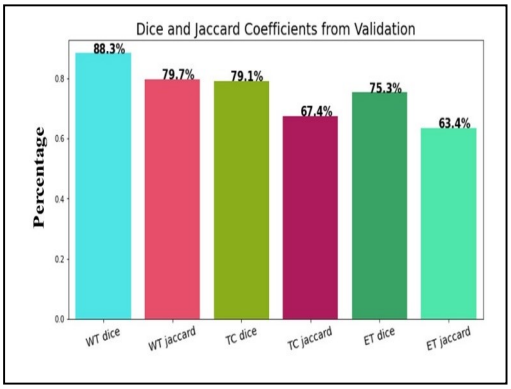

Figure 6: Graphical representation for the proposed method in terms of dice and Jaccard Coefficients

Table 2: Comparative analysis

Methods	Accuracy	Precision	Recall	Dice Coefficient	Jaccard Coefficient
A	99.15	98.99	98.5	NA	NA
B	99	99	98	97	98
C	98	96	97.2	NA	NA
D	92	NA	NA	0.923	NA
E	99.4	92.94	83.62	88	79
F	99.41	99.41	98.92	97.24	94.63

A - KSVM [11]
B - NSGA CNN [12]
C- DNN with adaptive fuzzy clustering [13]
D- 3D Context Deep Supervised U-Net [14]
E- Non-parametric Localization and Enhancement Methods with U-Net [15]
F- Proposed Dilated U-Net based CNN

5. CONCLUSIONS

In the present research work, the proposed semantic segmentation process is deepened to have spatial information in the feature map that reduces the critical time. Automated multi-modal classification is a deep learning approach to classify the brain tumors. The main aim is to extract the information of an image's edge when the convolution layer deepens and shows higher semantics. The proposed 3D based Spatial Auto Encoder (3D-SpAE) approach have a distinct advantage as they represent the data in nonlinear representations for dimensionality reduction. And also perform particularly well in feature extraction. When the spatial information is lost, the dilated convolution preserves the spatial data and showed improvement in the accuracy for segmentation prediction. The results showed that the proposed method obtained better values of the accuracy of above 99.41 %. The results are compared with that of the parameters based on Nonparametric Localization and optimization based techniques. The accuracy is also carried out using U-Net and Context Deep Supervised U-Net, Deep Elman Neural network with adaptive fuzzy clustering methods. The summarized results based on these classifiers are presented below. The methodologies based on U-Net showcased an accuracy of above 99.4%, 3D Context Deep Supervised U-Net showcased 92%, Deep Elman Neural network with adaptive fuzzy clustering resulted into 98%, NSGA Convolutional Neural Network of 99%, and Kernel-based SVM of 99.15% accuracy.

Future Scope:

Even though, in a range of visual applications, such as image classification and object recognition, deep learning has proven to be quite effective. It hasn't been utilized effectively for 3D shape identification. This is due to the fact that there aren't enough 3D forms available for feature learning and that 3D shapes have a complex structure in 3D space. In future, this research will be extended by using novel deep learning models. The objective of this research can be further extended such that it enhances the GPU activity and reduce the loss in spatial information which enhances better accuracy. Hybridization of classifiers can also be considered for identifying the deformities of the brain and classify the brain tumor types.

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