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An Automatic Detection of Brain Tumor using CNN & VGG19

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Abstract— According to the 2019 cancer statistics by WHO, brain tumors are considered the main cause of mortality related to cancer throughout the world and are known as one of the most common forms of cancer both in children as well as adults. Among the most common brain tumors, we have those that begin and tend to remain in the brain, which as meningioma with 34% of presence, another type of tumor is called glioma, arising from the surrounding tissue in the brain, it is part of 30% of all tumors in the brain, however, this glioma represents 80% of malignant tumors, making it the most common tumor common that causes death. However, this scheme depicts how convolutional neural networks using VGG19 model can provide an effective mechanism to detect brain tumors at an early stage using MRI images and can save the lives of mankind. Consequently, this research classified glioma brain tumor images using VGG-19 with HE preprocessing data. The model was tested to get a comparison of accuracy, precision, recall, and f1-score of the two test data, namely the original data and HE data. Based on the results of model testing, we can see in table2 that the original data produced the highest values of accuracy, precision, recall, and F1-score, with values of 97% accuracy, 100% precision, 97% recall, and 98% f1 score. While data using HE preprocessing has an accuracy value of 92%, precision of 100%, recall of 92%, and f1 score of 96%t..

Keywords- Cancer Detection, Deep Learning, Neural Network, Convolutional Neural Network, Histogram Equalization

I. INTRODUCTION

The identification of brain pathologies is a topic that can be summed up in “life or death”. The reality in India places us at an average of 1 radiologist per 100,000 inhabitants, according to what is indicated by [1] and the health services do not have an efficient system for the delivery of imaging test results. Image translation is the process that is having long waiting times to obtain the radiological report. Unfortunately, this does not help when there are patients who, without knowing it, are "against the clock" and, being concrete, a timely preliminary diagnosis could make the difference between timely treatments or a fatal outcome.

Considering this context, the present work shows a computer solution for the automation of the recognition of pathologies in clinical images. Although it would not be a definitive diagnosis as it is not signed by a doctor, it would allow mitigating the time associated with the process, helping to discriminate cases that could be of greater risk to the patient and thus allowing prioritization of a professional evaluation. To achieve the above, we have seen deep learning, like other authors, as an effective tool for the prediction and detection of various conditions in humans. For example, [2] explored brain imaging classification for cancer tumor identification using ELM-LRF, and in a related area, [3] worked on the recognition of breast cancer in ultrasound images via deep learning.

Currently, the most popular method in the category of computer vision including image classification is deep learning [19]. For image classification, CNN has been proven very powerful and is successfully applied in various fields such as galaxy morphology prediction [20], self-development driving on cars [21], and face detection [22] and many CAD systems implement CNN for disease diagnosis [23].

Related research that forms the basis for the application of deep learning with the modified CNN method for classifying brain tumors is like research conducted by [19] classifying brain tumor types into three, namely meningioma, glioma, and pituitary and also classifying the grade of glioma tumors. into three classes namely grade II, grade III, and grade IV with respective accuracy of 96.13% and 98.7%. Subsequent research was carried out by [24], by classifying brain tumor MRI using 4 VGG architectures, namely VGG-11, VGG-13, VGG-16, and VGG-19. In this study brain cancer. The results showed that VGG-16 had the best performance, with an accuracy of 96% for brain cancer classification.

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Further related research is by [25]. This study classifies 3 types of brain tumors using the VGG16 architecture and also uses the GLCM (Gray Level Co-occurrence Matrix) feature extraction and obtains an accuracy of 96.5%. Furthermore, research conducted by [26] uses a modified CNN architecture and has 6 weight layers consisting of 4 convolution layers and 2 fully-connected layers. The research uses Histogram Equalization (HE) preprocessing and compares the accuracy between images using Histogram Equalization (HE) and not using Histogram Equalization (HE). The results of this study concluded that using Histogram Equalization (HE) on images resulted in better performance from 98.83% to 99.8%.

Based on the related research above, this research will conduct future work experiments conducted by [25] by applying the Convolutional Neural Network (CNN) method using the VGG19 architecture on MRI images of brain tumors. The study said that brain tumors can be classified based on the grade or severity of the tumor. Determining the grade of a brain tumor is very important because it plays a role in analyzing the development of the tumor, and determines the stage of treatment and recovery of brain tumor patients. In this study, brain tumors that will be classified based on grade are glioma brain tumors measuring 224 x 224. Glioma MRI is classified into 3 classes, namely Grade II, Grade III, and Grade IV and this study added Histogram Equalization (HE) to the preprocessing because of the research conducted by [27], using a preprocessing method for images such as Histogram Equalization (HE) can improve the accuracy of the CNN model because the model can recognize images better and reduce image recognition errors caused by changes in lighting conditions. The first step is preprocessing using Histogram Equalization (HE), then the results of the preprocessing are entered into the VGG19 architecture with the first step the feature space is formed using several 3×3 convolution filters and then reduced by pooling layers in one block. This operation is repeated with a different number of convolution filters in the next block. Subsequent to the amount of blocks has been determined, the fully connected layer is used with the activation method to categorize the specified input.

II. RELATED WORK

- ***Deep Learning in Radiology***

In medicine and, more specifically, in radiology, a great need has arisen to include new techniques, not only to relieve the workload of the health professional but also to improve patient follow-up seeking an early diagnosis based on prognosis and response to treatment. In addition, given the advances in medical technologies used today in daily clinical practice, there is currently a multitude of parameters and variables obtained directly and indirectly from the patient, which are, in most cases, wasted due to the non-existence of a suitable algorithm for the exploitation of this type of information.

Machine learning techniques arise in this context, in which deep learning is the current state of the art. Machine learning is a branch of the so-called Artificial Intelligence (AI), which includes a multitude of techniques that allow a computer system or algorithm to learn from its environment, adapt to changes in it, and provide solutions to a given problem.

Therefore, machine learning can be defined as the optimization process of a performance criterion using data or experience, to finally obtain a model to be used to solve the problem for which it was designed [4]. Most machine learning algorithms require a previous feature extraction phase with which to feed the model to be designed. This fact makes the models extremely dependent on this phase, which is why good previous processing of the data is necessary. Similarly, there is a type of method that does not require this previous stage, which is called learning by representation, where the algorithm uses the best features to classify the data provided [5].

In this way, deep learning is nothing more than a specialization of the so-called learning by representation, mainly composed of the use of neural networks designed with a multitude of layers together with a series of convolutional filters with free parameters [6]. Thus, the algorithm can learn the set of features that reproduce a hierarchy of composition in the records that allow multifaceted demonstration to be expressed through straightforward illustration. As can be seen in figure 1, the Convolutional Neural Networks (CNN) designed for a certain classification task are capable of extracting simple characteristics from the most superficial layers, such as intensities or edges, and finally recognizing more complex shapes and objects in its deepest layers[7].

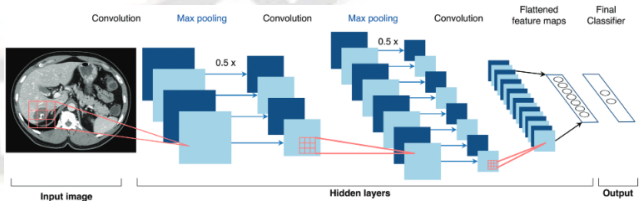

Fig.1 Classification task by CNN [6]

- ***Convolutional Networks***

Convolutional networks were introduced by[8] and refer to a type of neural network designed to work with grid-structured inputs, which have a strong spatial dependence on the local region of the grid [9]. An example of this type of input is two-dimensional images. Concerning their layers, convolutional networks generally have 3 types of layers: Convolution layer, pooling layer, and dense layer [10]. The convolution layer, as

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indicated in [11], generates a new matrix from the one obtained by the input, by applying a filter with which it calculates the values for each quadrant. The filter can have different values depending on what process you want to perform on the input, but this filter will always create a single characteristic mapping regardless of depth. The result reached the output is that of the dot products between the input and the filter. An example (summary) of a convolution between a 7x7x1 input and a 3x3x1 filter with a stride of 1 is presented in Figure 2.

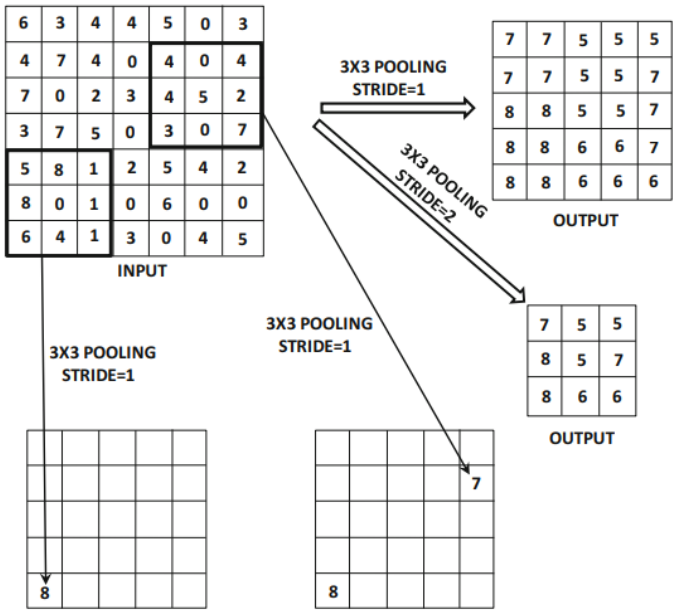

Fig.2 Convolutional Example by [111]

The pooling layer [10] performs down sampling of the character mapping of the previous layer, producing a new mapping with a condensed resolution, abruptly reducing the spatial dimension of the input. Its purposes are to reduce the number of parameters or weights to decrease computational cost and control network over fitting [12] and the dense layer, also known as the fully connected layer [10].

This is the set of "last layers" (it can be one or more) that is responsible for producing the expected result and is nothing more than a fully connected neural network. It takes the result obtained from the pooling layer as input and, through processes called forward propagation and backward propagation, adjusts the weights to achieve a correct prediction. In classification problems, the activation function of the last layer is generally a softmax that tells us the likelihood of belonging to one of the study classes. Other layers can use another type of activation function, among which ReLu stands out since it better reflects the biological functioning of a neuron and achieves better performance compared to the hyperbolic and sigmoid activation functions. Despite not being differentiable at zero and not being completely linear, ReLu also allows the creation of "sparse" representations that favor training when the number of data is scarce [13].

- ***Transfer Learning***

Traditionally, learning algorithms are designed to tackle problems independently. Depending on the requirements of the case and the information available, an algorithm is applied to train the model for that task. However, the process called “Transfer Learning” takes learning a step further and “closes” it to the way humans use information through tasks. In simple terms, the process consists of reusing an existing and already trained model for a related task, and extending or adapting it for a new task [14].

For his part, [15] defines it as "the enhancement of learning in a novel task throughout the transfer of knowledge from a related undertaking that has previously been learned", so we can infer that rapid progress is obtained in this way and high performance. Additionally, this technique is widely used due to its diverse approach and in [16] it is defined that Transfer learning is "the idea of breaking the paradigm of solving an isolated problem and using the knowledge acquired to focus it on a task Similarly". To simplify the comparison, Figure 3 shows the dissimilarity involving “traditional” Machine Learning and Transfer Learning.

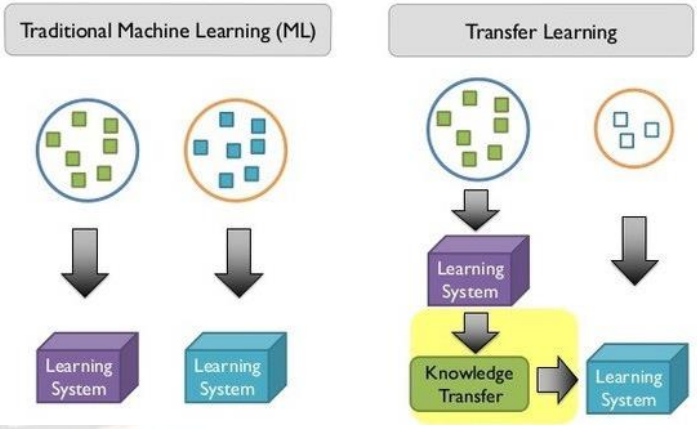

Fig.3 Machine Learning and Transfer Learning Process [17]

- ***VGG19 Model***

VGG19 Architecture [18] was developed under the convolutional neural network, Oxford Visual Geometry Group (VGG19). As can be seen in figure 4, this architecture is made up of 16 convolutional layers. each group is followed by a layer of max pooling. These are followed by 3 fully connected layers and 5 max-pool layers and 1softmax layer. This red is characterized by having several parameters to train, which can make your workout last longer than the rest of the nets. It also has the advantage of having pre-trained weights available from

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the Images dataset. The input of the network is of sizes 224, 224, and 3. Then, in each convolution block, a convolution, a ReLU activation function, and a dimensionality reduction via the pooling layer. Finally, the softmax activation function is used as the output of the network to determine which of the 1000 categories the input belongs to the respective image.

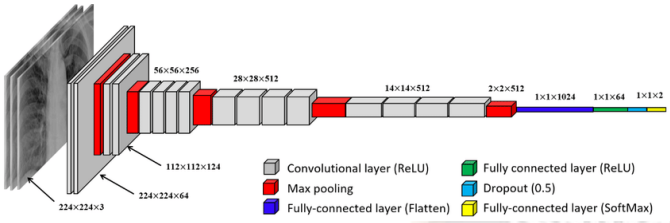

Fig.4 VGG19 Model [18]

III. PROPOSED MODEL

The steps taken to classify MRI Grade Glioma images consist of 5 main stages, namely data collection, data preprocessing, data sharing, CNN architecture, and conclusion as shown in Figure 5.

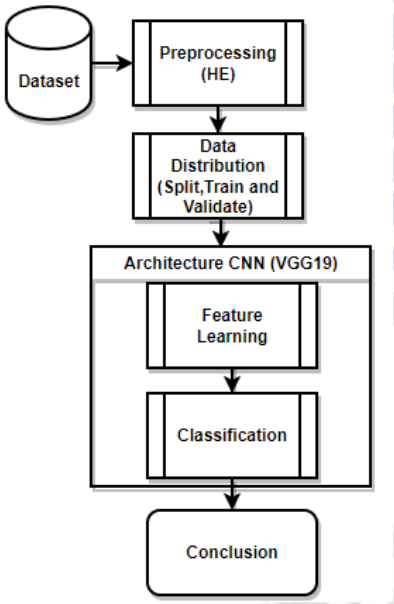

Fig.5 Stages of Research Methodology [self]

- ***Data Collection***

The stages of data collection in this study were searching for MRI glioma tumor data obtained from the TCIA and REMBRANDT [24]. The data obtained is in the form of data in DCIM format, then the data is converted so that the format becomes jpg. The data contains 110,020 images from 130 patients, then the data is sorted by grade, namely grade II, grade III, and grade IV [25]. The image grade of the brain tumor contained in the data is 224 x 224 pixels. The data used is an image on the axial part of the brain and produces a total of 3206 images from 73 patients with a total of 1258 images for grade II, 1022 images for grade III, and 926 images for grade IV.

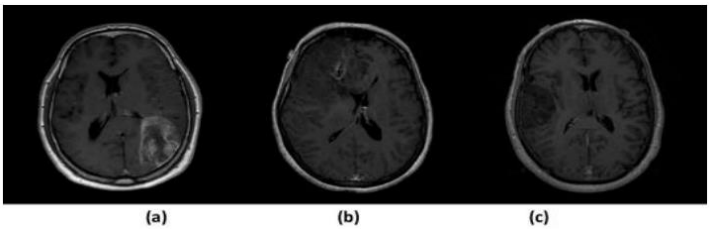

Fig.6. (a) Grade IV Glioma Dataset, (b) Grade III, and (c) Grade II [self]

- ***Pre-Processing***

The method used for the pre-processing stage is the HE method. HE is used to improving the quality of an image that has low contrast. The HE (Histogram Equalization) method aims to avoid excessive contrast enhancement [28]. Figure 7. shows an example of an image resulting from the HE pre-processing process on MRI Glioma grade II, III, and IV images.

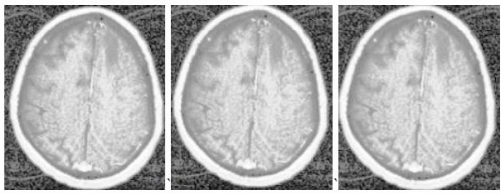

Fig.7 Glioma MRI image using HE [self]

- ***Data Sharing***

The distribution of data in this study uses the split validation technique. This Split validation technique divides the data into two parts based on the desired data comparison. Two parts of the data consisting of training data and testing data were selected randomly. In this study, the distribution of the data tested was 30% testing 70% training, 20% testing 80% training, and 10% testing 90% training.

- ***CNN Architecture***

At this stage, we will use the architecture of CNN which will be used for the Glioma MRI classification training procedure. The architecture used in this research is VGG-16. VGG generally has two kinds of layers, namely VGG-16 and VGG-19. This research will use VGG-19. VGG-19 has 16 layers and each layer consists of zero padding, a convolutional layer, a max pooling layer, an activation layer and ends with a fully connected layer. The following Figure 8 shows the VGG-19 architectural diagram.

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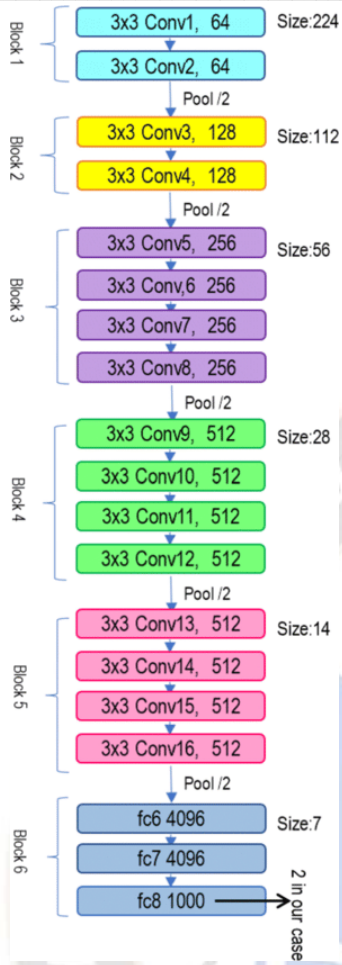

Fig.8 Architecture of VGG-19 [self]

Below is the pseudo code elaboration of VGG19 Architecture used in scheme for ready reference and perusal.

- ***Pseudo Code of VGG19***

The following are the stages VGG19 architecture in classifying images:

1. MRI data of brain tumors that have been cropped and resized in the preprocessing stage with a size of 224 x 224 pixels as input data.

2. **Stage 1**

   1. Running a convolutional process two times with a 3 x 3 filter produces 64 channels.

   2. Execute the batch normalization function.

   3. Run the activation function, namely ReLu.

   4.Then do the Max Pooling using 64 channels

3. **Stage 2**

   1. At this stage, a depth wise convolutional operation is performed two times with 3 x 3 filter producing 128 channels.

   2. Performed Batch Normalization.

   3. Then do the activation function using ReLU.

   4. Then do the Max Pooling using 128 channels.

   5. Then do the reshaping image to 112 x 112.

4. **Stage 3**

   1. At this stage, the convolutional filter operation three times with 3 x 3 filters produces 256 channels.

   2. Performed Batch Normalization.

   3. Then do the activation function using ReLU.

   4. Then do the Max Pooling using 256 channels.

   5. Then do the reshaping image to 56 x 56.

5. **Stage 4**

   1. At this stage, a convolutional operation with 3 x 3 filter is performed to produce 512 channels.

   2. Performed Batch Normalization.

   3. Then do the activation function using ReLU.

   4. Then do the Max Pooling using 512 channels.

   5. Then do the reshaping image to 28 x 28.

6. **Stage 5**

   1. At this stage, a convolutional operation with 3 x 3 filter is performed to produce 512 channels.

   2. Performed Batch Normalization.

   3. Then do the activation function using ReLU.

   4. Then do the Max Pooling using 512 channels.

   5. Then do the reshaping image to 14 x 14.

7.The output from the previous stage is continued by doing the pooling process after that in the flatten which gets the output in the form of a two-dimensional array with fully connected layer which has 4096 neurons.

8. After the flattening process, the next stage is entered into the neural network.

9. After the neural network stage is completed and the weight value is obtained and classified with softmax activation.

- ***Model Evaluation (Confusion Matrix [CM])***

Model evaluation is carried out to decide whether or not the performance of a classification model is good or bad.

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Foundation on the CM can be seen the performance of a representation by manipulative the level of precision, recall, F1-score, and accurateness. There are 4 conditions as a demonstration of the consequences of the categorization progression in the CM. these four terms are TruePositive(TP), TrueNegative(TN), FalsePositive(FP) and FalseNegative(FN). Here's the formula CM.

Table 1 Model Evaluation using CM

CM			
ACTUAL CLASS		POSITIVE	NEGATIVE
	POSITIVE	TP	FP
	NEGATIVE	FN	TN

$$Accuracy = \frac{TP+TN}{TP+TN+FP+TN} * 100\% \quad (1)$$

$$Precision = \frac{TP}{TP+FP} * 100\% \quad (2)$$

$$Recall = \frac{TP}{TP+FN} * 100\% \quad (3)$$

$$F1\ Score = 2 * \frac{Precision*Recall}{Precision+Recall} * 100\% \quad (4)$$

where:

TP = the number of positive data that are classified correctly

TN = the number of negative data that are classified correctly

FP = the number of positive data that are classified as incorrect

FN = the number of negative data that are classified incorrectly

III. RESULTS AND DISCUSSION

The outcome of the model testing process using training and testing data is evaluated using a confusion matrix. The CNN inculcated with VGG19 model produces precision, recall, F1-score, and accuracy values for each situation. This study classifies glimos brain tumors into 3 grades with a total of 3206 data consisting of 73 patients with a total of 1258 images for grade II, 1022 images for grade III, and 926 images for grade IV measuring 224 x 224 pixels. Split validation was used to divide the dataset with a ratio of 70% training 30% testing, 80% training 20% testing and 90 training 10% testing. The data is divided into two tests, namely using original data and data using preprocessing histogram equalization (HE). The parameters tested were the batch size consisting of 16 and 32 with an epoch of 50. Then enter the CNN implementation stage using the VGG-19 architecture and the following are the results of the tests as shown in table 2.

Table 2 Test Results

			Data Distribution in %age		Score in %age			
	Data set	Batch Size	Training	Testing	Precision	Recall	F1-Score	Accuracy
1	With HE	32	90	10	100	88	94	88
	Actual					96	98	96
2	With HE	32	80	20	100	86	92	86
	Actual					90	94	90
3	With HE	32	70	30	100	49	66	49
	Actual					59	74	59
4	With HE	16	90	10	100	92	96	92
	Actual					97	98	97
5	With HE	16	80	20	100	86	92	86
	Actual					85	92	85
6	With HE	16	70	30	100	51	67	51
	Actual					58	73	58

Based on table 2 in serial no.4, the actual data has an accuracy of 97% where the accuracy of calculating the grade prediction ratio II, III, and IV correctly from all data. The 100% precision value is the correct percentage of the glioma grade II, III, or IV from all the predicted grade data. 97% recall value means what percentage of gliomas are predicted to be grade II, III or IV compared to all grades of gliomas graded. And finally, the f1 score is 98% where the f1 score represents a balance between precision values and recalls. The original data has higher accuracy, precision, recall, and f1-score than the original data used HE preprocessing to classify the grades of glioma brain tumors. Data using HE has lower accuracy, precision, recall, and f1 scores because there is still a lot of data wrong predictions compared to the original data. So it can be concluded that in this study the use of original data has better results than the data that uses HE preprocessing.

V. CONCLUSION

This research classified glioma brain tumor images using VGG-19 with HE preprocessing data. The model was tested to get a comparison of accuracy, precision, recall, and f1-score of

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the two test data, namely the original data and HE data. Based on the results of model testing, we can see in table 3 that the original data produced the highest values of accuracy, precision, recall, and F1-score, with values of 97% accuracy, 100% precision, 97% recall, and 98% f1 score. While data using HE preprocessing has an accuracy value of 92%, precision of 100%, recall of 92%, and f1 score of 96% where there is still a lot of data that cannot be predicted correctly from the actual data. To further refine this research, it is suggested to overcome some limitations so that further research is better. The first is suggested to add the number of datasets. This is very helpful for the system to study a large number of images. Furthermore, it is recommended to try using other preprocessing methods so that the system recognizes images better such as AHE or CLAHE, and finally adding a segmentation process so that the pattern of the glioma tumor is formed in more detail so that the model can classify the grade of glioma more precisely.

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