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Integrating VGG-16 And CNN For Brain Tumor Detection

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Abstract—Advancements in medical technology have significantly altered the landscape of healthcare, especially in diagnostic capabilities. This project focuses on leveraging Convolutional Neural Network (CNN) technology, specifically the VGG16 architecture, for the detection of brain cancer. CNNs are renowned for their prowess in analyzing visual data, making them ideal for scrutinizing Brain Magnetic Resonance Imaging (MRI) datasets to identify tumors accurately. Brain tumor segmentation, a challenging task in medical image processing, is further complicated by the potential for errors in manual analysis. To overcome this hurdle, we propose an automated solution that combines VGG16 for feature extraction with a custom CNN tailored specifically for brain tumor detection. The objective is to minimize reliance on manual classification while maximizing prediction accuracy. The project utilizes 2D MRI images to extract brain tumors, acknowledging the vast variability in tumor appearance and the nuanced differences between tumor and normal tissues. By integrating VGG16 and a custom CNN in a two-step process, the approach ensures robust extraction of features and precise classification. To validate the efficacy of our method, experiments are conducted using a diverse dataset containing tumors of varying sizes, locations, shapes, and image intensities. The results underscore the potential of our developed model to deliver reliable and automated brain tumor detection, addressing a critical requirement in the medical domain.

Keywords: CNN, Medical Imaging Analysis, segmentation, VGG-16 Model

I. INTRODUCTION

Scientific imaging methods allow for non-invasive examination of the body, while medical photography employs diverse techniques to capture images for diagnostic and treatment purposes, significantly impacting healthcare. Picture segmentation, a crucial step in image processing, is particularly vital in medical imaging. It aids in identifying tumors or lesions, improves computer-assisted diagnostic systems, and enhances the accuracy of subsequent analysis by increasing sensitivity and specificity.

As cited in [3], brain and other nervous system cancers rank as the tenth leading cause of death globally. The six-year survival rates for individuals with brain cancer stand at 33% for men and 37% for women. Additionally, the World Health Organization (WHO) reports that approximately 400,000

individuals worldwide are grappling with brain tumors, resulting in 120,000 deaths in recent years [4]. Moreover, an estimated 86,970 new cases of primary malignant and nonmalignant brain and other central nervous system (CNS) tumors are projected to be diagnosed in United States in 2019.

A brain tumor develops as a result of aberrant cell proliferation in the brain. Generally speaking, these tumors can be categorized as benign or malignant. Because they begin in brain tissue, malignant tumors develop quickly and have an invasive nature that can affect neighboring tissues and spread to other parts of the brain. Malignant brain tumors can be classified into two basic types: primary tumors, which originate inside the brain, and secondary tumors, also called brain metastasis tumors, which spread from other parts of the body. In contrast, benign brain tumors are made up of a mass of cells within the brain and grow slowly.

One of the biggest obstacles to medical image processing is handling large amounts of data. Furthermore, tumors might have Therefore, in terms of treatment options and survival rates, early identification of brain tumors offers significant advantages. Nevertheless, segmenting tumors or lesions by hand is a tedious and takes more time because of the large amount of MRI images generated in clinical practice. The most frequent method for finding brain tumors or lesions is magnetic resonance imaging, or MRI. It becomes very difficult to appropriately segment brain tumors using MRI scans because brain tumor segmentation usually comprises poorly defined soft tissue borders.

II. LITERATURE REVIEW

Medical image processing, particularly when it comes to brain tumor identification, is hampered by the need to handle massive amounts of data. Treatment choices and survival rates for brain tumors are significantly improved by early detection. Nevertheless, the tedious and intricate process of manually segmenting tumors or lesions from these several MRI images produced in clinical practice takes time. A typical method for identifying brain tumors or lesions is

magnetic resonance imaging, or MRI. It is difficult to precisely define the boundaries of soft tissues when segmenting brain tumors using MRI data. The goal of precise segmentation research is shared by researchers worldwide; neural network-based techniques are gaining traction and demonstrating promising outcomes.

Using the spatial FCM algorithm and mathematical morphological procedures, Devkota et al. [2] created a comprehensive segmentation approach that reduces computing time. Nevertheless, despite the fact that the recommended treatment has not been tested, the findings indicate an 86.6% classifier accuracy and a 92% cancer detection rate. Histogram-based segmentation was employed by Yantao et al. [6]. The brain tumor segmentation task involved three categories: tumor with necrosis, tumor with edema, and normal-class categorization (which tissue). There were problems in two of the modalities, FLAIR and T1. The region-based active contour model of the FLAIR modality was used to identify aberrant regions. On the basis of contrast-enhanced T1 modalities, edema and tumor tissues were identified within the aberrant regions using the OK- method methodology, giving a Dice coefficient of 73.6% and sensitivity of 90.3%.

Badran et al. [5] used adaptive thresholding in conjunction with the Canny edge detection model to extract the Region of Interest (ROI) from a collection of 102 photos using region identification techniques. After preprocessing the photos, two neural network sets were applied, one using Canny edgedetection and the other using adaptive thresholding. After the photos were divided, level numbers were assigned, and the Harris method was used to extract features. The neural network was then applied to two tasks: distinguishing between several types of malignancies and identifying regions that were either healthy or harbored tumors. When the outcomes of these two models were compared, the Canny edge detection method showed more accuracy. Pei and associates.[4] proposed an improved texture-based tumor segmentation technique in longitudinal MRI by utilizing tumor development patterns as new features. After extracting textures and intensity data, label maps were used to forecast cellular density and help with modeling tumor progression. The Dice Similarity Coefficient (DSC) with tumor cellular density was used to evaluate the model's performance, and the result was a score of 0.819302.

A model that combines learning vector quantization with a probabilistic neural network model was described by Dina et al. [1]. A dataset of 64 MRI pictures was used to evaluate the model's performance, of which 18 were used for validation and the remaining images for training. After the images were smoothed using Gaussian filtering, the updated PNN approach was able to reduce processing time by 79%. Principal Component Analysis (PCA) was used by Othman et al. in their probabilistic neural network-based segmentation technique for feature extraction and

dimensionality reduction [2]. This method involved first converting MRI pictures into matrices, then classifying the data using a probabilistic neural network. Performance analysis was then carried out with a test dataset of 15 subjects and a training dataset of 20 subjects. The accuracy was calculated using the spread value, which ranged from 73% to 100%. By applying deformable models and fuzzy clustering to target regions, Sara et al. [3] used an improved probabilistic fuzzy C-means model with extra morphological operations and obtained 95.3% and 82.1%, respectively, in terms of ASM and Jaccard index. LinkNet network was utilized by Zahra et al. [4] for tumor segmentation. At first, they used one LinkNet network for segmentation, applying it to all seven datasets. They presented a technique for CNN to automatically segregate the most frequent forms of brain tumors, removing the requirement for preprocessing stages and doing so without taking the viewing angle of the pictures into account. A Dice score of 0.79 was attained for several structures, compared to 0.73 for a single network.

III. PROPOSED METHODOLOGY

The proposed system integrates machine and deep learning algorithms to enhance brain tumor detection accuracy. Leveraging K-Nearest Neighbors (KNN), Random Forest, and Decision Tree, alongside ensemble techniques such as Voting Classifier, we aim to establish a robust foundation for traditional machine learning analysis. Furthermore, the system incorporates Convolutional Neural Networks (CNN) and VGG16, renowned for their proficiency in extracting intricate features from medical images. By integrating these algorithms, we seek to address the limitations of conventional diagnostic methods and improve the precision and efficiency of brain tumor detection. The system will analyze diverse datasets, considering the variability in tumor characteristics, to ensure comprehensive coverage and adaptability. Through rigorous testing and validation, we anticipate achieving superior diagnostic accuracy, enabling timely interventions and improving patient outcomes. This proposed system represents a holistic approach to brain tumor detection, harnessing the power of both traditional machine learning and deep learning methodologies to advance medical image analysis in clinical settings. Using Conventional Classifiers for Tumor Segmentation and Classification: A Proposed Methodology

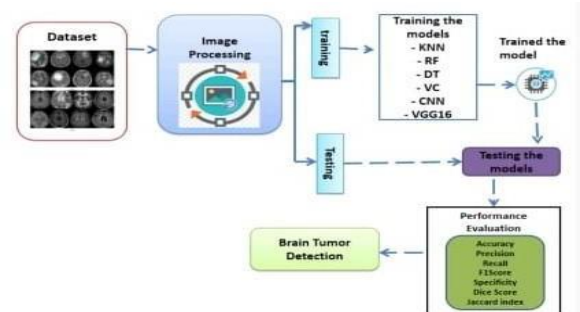


Fig. 1: Proposed Methodology - The

Architecture

The suggested technique for classification using traditional classifiers is explained below:

1) **Skull Stripping:** Since the MRI picture's background usually contains no useful information and greatly increases processing time, skull removal is an essential stage in medical image processing. In this study, we used a three- step procedure to remove the skull component from MRI pictures.

These three actions are as follows:

- a) **Otsu Thresholding:** The threshold used in this method is selected to minimize the intra-class variance, which is expressed as a weighted sum of the variances between the two classes.
- b) **Connected Component Analysis:** To exclude the skull component, we used region analysis to separate the brain region alone after our skull stripping procedure.

2) Filtering and Enhancement:

Improving MRI picture quality while lowering noise is crucial for better segmentation accuracy. In this work, we used Gaussian blurring with filtering to improve segmentation performance by lowering Gaussian noise that is frequently seen in brain MRI images.

3) Fuzzy C-Means clustering method segmentation:

We used this technique to divide up the data such that each piece of information may be assigned to two or more clusters. We now have a fuzz clustered segmented image, which guarantees better segmentation quality.

4) Morphological Operation:

Rather than concentrating on the skull section, we targeted the brain component in order to isolate the tumor. Thereafter, dilation was used.

5) **Tumor Contouring:** An intensity-based method called thresholding is now used to extract tumor clusters. With a dark background, the tumor site is emphasized in the final photograph.

6) **Features Extraction:** Two feature sets were extracted in order to aid in categorization. Texture-based characteristics were extracted from segmented MRI images, including dissimilarity, homogeneity, energy, correlation, and ASM. It was also possible to retrieve statistically based features such as centroid, implied entropy, skewness, kurtosis, and trending deviation.

7) **Traditional Classifiers:** KNN, Logistic Regression, Multilayer Perceptron, Naive Bayes, Random Forest, and Support Vector Machine are the six classic machine learning classifiers that we used to assess the accuracy of

our suggested model in tumor identification.

A. **Assessment Phase:** Our model successfully isolates the Region of Interest (ROI) and separates the tumor component by utilizing several region-based segmentation methods and comparing them with our suggested segmentation strategy. An example that is representative of the full procedure is shown in Figure 5. We used six classification techniques after tumor segmentation and feature extraction. Notably, with an accuracy of 92.42%, VGG16 produced the best results.

B. Proposed Approach using CNNs

In medical image processing, CNN are frequently used as researchers attempt to create models for more accurate tumor identification.. We choose CNN for our model despite the fact that a fully-connected neural network would also be able to detect cancers because of its benefits in parameter sharing and connection sparsity.

We present and implement a tumor detection system based on a five-layer convolutional neural network. The most noteworthy result in tumor detection is produced by this composite model, which consists of seven phases including hidden layers. The suggested methodology is provided below with a brief explanation.

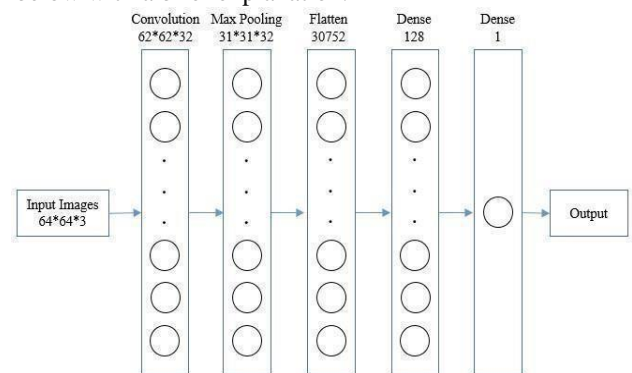


Fig. 2: 5-Layer Convolutional Neural Network-Based Tumor Detection Methodology

We build an input shape of 64643 for the MRI scans, starting with a convolutional layer, to provide consistent dimensions throughout all images. The 32 convolutional filters, each with a size of 3*3, are then integrated across 3-channel tensors to generate a convolutional kernel, which is then applied to the input layer. ReLU is used as the activation function to guarantee that it has no effect on the output.

In order to lower the number of parameters and the network's processing time, we progressively reduce the spatial dimension of the representation in our ConvNet design. In the model, we use MaxPooling2D to handle spatial data that corresponds to our input image. The dimensions of this convolutional layer are 31*31*32. The input photographs are downscaled in both spatial dimensions, as specified by a tuple of two values for vertical

and horizontal scaling, because the pool size is 2,2

After the pooling layer, a map of pooled features is generated. This is where flattening becomes important since we need to convert the whole matrix containing the input photos into a single column vector in order to process the data further. After that, the data is kept in the neural network to be processed further. Dense1 and Dense-2, two nearly related layers, were used to symbolize the dense layers. The produced vector is used as the input for this layer of the neural network processing process in Keras, where the dense feature is implemented. 128 nodes make up the buried layer. In order to achieve optimal performance, we chose a comparatively small number of nodes, taking into account the computational resources required by our model. Thus, we get the optimum result

with 128 nodes. The goal of this choice is to improve execution time by using less processing power. Although the sigmoid function may hinder learning in deep networks, we reduce this danger by scaling the sigmoid function and lowering the node count to make this deep network's maintenance easier.

To put it briefly

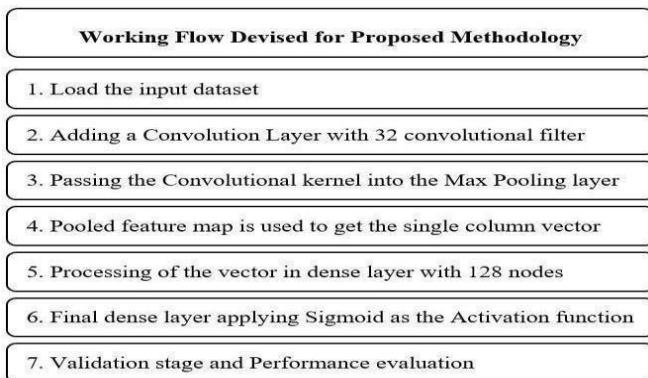


Fig 3: Shows how suggested CNN – VGG16 functions

Algorithm 1: Evaluation process of CNN model

```

1 loadImage();
2 dataAugmentation();
3 splitData();
4 loadModel();
5 for each epoch in epochNumber do
6     for each batch in batchSize do
7         ŷ = model(features);
8         loss = crossEntropy(y, ŷ);
9         optimization(loss);
10        accuracy();
11        bestAccuracy = max(bestAccuracy, accuracy);
12 return
    
```

Fig 4: Algorithm of performance evaluation

We Constructed the model and used the Adam optimizer Binary cross-entropy as the loss function to assess the model's tumor recognition capability. The algorithm used to evaluate the model's performance is shown in Diagram 4. TableI contains a complete list of all hyperparameter

values. A precision of almost 97.87% was reached.

Stage	Hyper-parameter	Value
Intialization	Bias	Zero
	Weights	uniform
Training	Learning rate	0.001
	Decay	0
	Epsilon	None
	Epoch	10
	Batch size	32
	Steps per epoch	30

Table 1: Hyperparameter of CNN values

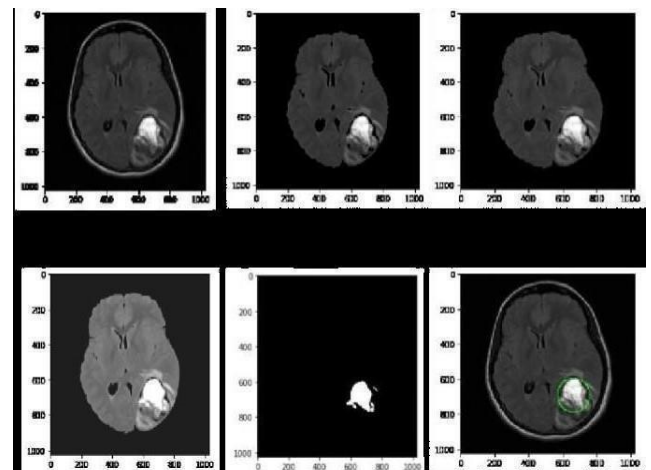


Fig 5: Outputs of Skull Stripping and Gaussian Filtering

IV. EXPERIMENTAL RESULTS

We demonstrate how to separate the tumor from 2D brain MRI and compare our proposed machine learning and deep learning classification models to bolster our proposed model. With VGG-16, we obtained 92.42% accuracy, while with CNN, we obtained 97.87% accuracy. Trial Dataset We used the BRATS dataset [6] to evaluate the efficacy of our proposed model. Class-0 and class-1 represent MRI images of tumors and non- tumors, respectively. Tumor and non-tumor categorized MRI scans are designated as class-1 and class-0, respectively. Each image is an MRI obtained using a variety of modalities, including T1, T2, and FLAIR. By dividing the dataset in training and test photos by 70:30 for basic machine learning classifiers, we achieved the best results. For CNN, the dataset is converted into both 71:29 and 81:19 ratios and compared the outputs.

C. Image processing approaches for segmentation.

We successfully segmented tumors without losing any subtle information by applying our suggested methods. Since the function of the skull differs from that of the segmented brain tumor, its removal was essential for tumor segmentation. We also measured the tumor's diameter, convex hull area, and approximate null and ambiguous areas during this procedure. We were able to classify the pictures as normal or abnormal by extrapolating these qualities from the segmented MRI. The values of several features taken from the segmented MRI are shown in Table II.

We used statistical variables extracted from the photos, such as entropy, centroid, mean, standard deviation, and kurtosis, skewness, in addition to dissimilarity, homogeneity, energy, correlation, and ASM, for classification. Six common machine learning classifiers are presented in Table-III, with

VGG-16 exhibiting the most noteworthy performance with an accuracy of 92.42%. In terms of specificity and precision, Naïve Bayes produced the greatest results; however, when compared to other performance measures, the difference with VGG-16 was small and insignificant. Successful feature extraction is indicated by additional performance indicators. We used six classifiers: VGG-16, Random Forest, Naïve Bayes, Multilayer Perceptron, Logistic Regression, and KNN. Of these, VGG-16 produced the greatest accuracy. Table-III shows the classifier performance and the confusion matrix..

Classifiers	Accuracy	Specificity	Recall	Precision	Dice Score	Jaccard Index
KNN	86.33	0.324	0.926	0.952	0.947	0.948
Logistic Regression	86.54	0.243	0.934	0.234	0.965	0.832
Multilayer Perception	87.45	0	1.650	0.687	0.856	0.234
Naïve Bayes	74.59	0.515	0.65	0.559	0.670	0.780
Random Forest	85.35	0.567	0.655	0.587	0.686	0.562
VGG - 16	97.86	0.828	0.684	0.635	0.659	0.521

Table II: Highlighted Aspects of Divided Tumor

A 2D magnetic resonance imaging (MRI) input image was chosen from the dataset. In order to properly capture the MRI features, the input image was first subjected to skull stripping (Fig. 1b) and then image enhancement (Fig. 1c). After that, noise was removed using a Gaussian filter (Fig. 1d) before the FCM segmentation method (Fig. 1e) and tumor contouring (Fig. 1f) were applied to define the Region of Interest (ROI), which is the tumor in Brain MRI. The tumor was classified using a variety of common machine learning algorithms following tumor segmentation.

D. Classification Using Machine Learning

We can differentiate between tumorous and non-tumorous MRI scans thanks to these characteristics. For classification, we used both statistical and texture-based characteristics. Precision and specificity, two texture-based metrics, differed from VGG-16 and other performance measures just slightly and insignificantly. Successful feature extraction is highlighted by additional performance indicators. Six classifiers were used in our approach: VGG-16, Random Forest, Naïve Bayes, Multilayer Perceptron, KNN, and Logistic Regression. VGG16 showed the highest accuracy. Table III provides specifics on the classifier performance and confusion matrix.

The next aspect assesses the performance – VGG- 16 yielded the most favorable outcomes

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

$$\text{Speticity} = \frac{TN}{TN+FP} \quad (2)$$

$$\text{Sensitivity(recall)} = \frac{TP}{TP+FN} \quad (3)$$

$$\text{Precision(PPV)} = \frac{TP}{TP+FP} \quad (4)$$

E. Categorization Making use of CNN

The suggested five-layer method shows a notable improvement in tumor identification. Convolution, max pooling, flattening, and two thick layers make up this CNN model. Before training the model, data augmentation was done because of CNN's translation invariance. A performance evaluation based on dataset division was carried out in two circumstances. The model's accuracy was 92.98% with a 70:30 split ratio and 99.01% during training. The accuracy in the second scenario was 97.87% and the training accuracy was 98.47% since 80% of the photos were used for training. Thus, our suggested model performs best when the split is 80:20. An overview of the suggested method's performance on CNN can be found in Table IV.

Using our five-layer CNN model, we achieved an astonishing 97.87% accuracy. In contrast to our CNN model with five layers, we explored with alternative layer configurations, but the differences in the results were not statistically significant. Batch size, steps per second, processing time, and technique complexity all rose as the number of layers increased. Furthermore, we did not fine-tune the model because the accuracy plateaued after we initially set the dropout amount at 0.2. As a result, without using dropout, this model obtained the maximum accuracy.

No	Testing Image	Training Image	Splitting Ratio	Accuracy (%)
1	64	151	71:29	92.89
2	42	175	81 : 19	97.86

TABLE III. PERFORMANCE OF THE PROPOSED CNN MODEL

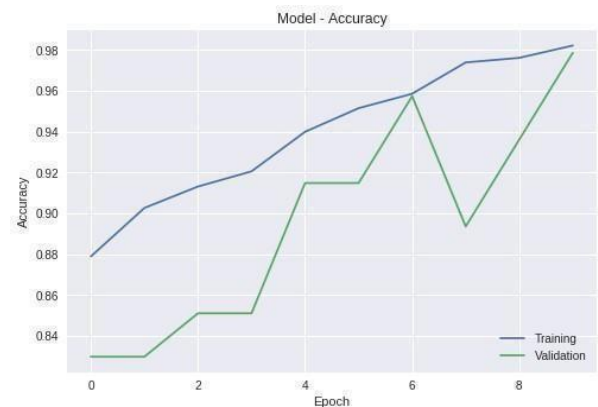


Fig. 6. Accuracy of the proposed CNN model.

Figure 6 displays the accuracy of our model during training and validation based on the Keras callback function. We evaluated the accuracy across a variety of epoch counts for both the training and validation data. It was discovered that the model had achieved its maximum accuracy in both training and validation after nine epochs.

F. Performance Comparison

At Last, we used our suggested classification algorithms to compare CNN and traditional machine learning classifiers. We also compared our findings to those of other research projects that made use of the same dataset. Saleh and colleagues (2017) reported 97.5% accuracy with CNN and 83.0% accuracy with VGG-16-based classification. Our proposed approach outperformed both CNN-based categorization and machine learning. In addition, our dice score was 96%, while the dice coefficient obtained by Mohsen et al. [8] was approximately 95%..

Methodology	Accuracy(%)
Saleh et al [7]	97.5
Proposed CNN -VGG16 Model	97.87

TABLE IV. PERFORMANCE COMPARISON

V. CONCLUSION AND FUTURE WORK

Because medical images can be very complicated, it is important to segment them when processing medical images. Our study concentrated on the use of MRI and CT scan images to segment brain tumors. Brain cancers are best classified and segmented using magnetic resonance imaging (MRI). In this work, we applied Fuzzy C-Means clustering, which has demonstrated efficacy in tumor cell prediction, to tumor segmentation. After segmentation, we classified the data using a Convolutional Neural Network in addition to conventional classifiers. The outcomes of several conventional classifiers, such as K-Nearest Neighbor, Logistic Regression, Multilayer Perceptron, Naive Bayes, Random Forest, and Support Vector Machine, were used and contrasted in the traditional classifier section. With an accuracy of 92.42%, VGG-16 outperformed the other conventional classifiers.

We used CNN to further improve our results; using an 80:20 split ratio of 217 photos, 80% were training images and 20% were test images, CNN attained an accuracy rate of 97.86%. In order to better segment brain tumors, we intend to look at 3D brain imaging in the future. Although curating a larger dataset is challenging, our objective is to create a dataset that highlights abstraction and is unique to the characteristics of our nation. We'll be able to complete our work more rapidly with this approach.

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