

Machine Learning in Radiologic Imaging - Analysis of U-Net Performance

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Abstract - TODO: ADD ABSTRACT

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1 INTRODUCTION

Radiology, since its discovery in 1895 by Wilhelm Conrad Röntgen, that noticed how X-Rays can pass through various materials, had a long and, at the same time, fast-paced technological advancement. First radiologic imaging were performed in 1896, in order to investigate patients organs, marking the birth of Radiology in Medicine [1]. This rapid enhancement was a result of the harmful effects caused by Röntgen radiation in medical scannings, such as: increasing cases of leukemia in patients that underwent ionizing radiation procedures, severe dermatitis, eye damage and so on, that caused people to delve deeper into the radiation study and find way to make radiologic imaging safer both for patients and doctors [2]. Throughout the evolution of radiologic imaging, it became safer than it was back then, but, besides that, it also became more advanced thanks to technological development, were found other solutions for medical imaging, such as Computer Tomography (CT), Magnetic Resonance Imaging (MRI), led to higher resolution radiologic images, as well as higher number of images done during the procedure [3]. This caused an increasing load on radiologists, making them prone to errors in interpretation. For example, in a study at a tertiary care center, $\approx 18.4\%$ of the total lungs radiologic images performed had diagnostic errors [4]. A modern solution to assisting radiologists in their field is implementing Machine Learning algorithms, that involves computer-aided assistance in interpretation of radiologic images, using Image Segmentation techniques, which can greatly reduce routine work, shift current "algorithmic" approach to a personalized patient care and increase the accuracy in conclusions [5]. This paper reviews the state-of-the-art of Machine Learning and Radiology, focusing the attention on proposed solutions that involves advanced Deep Learning models, such as Convolutional Neural Networks and, less sophisticated Distance-based models, for example, K-Means Clustering, for the task of Image Segmentation.

2 RESEARCH METHODOLOGY

The aim of this paper is to delve into how Machine Learning algorithms can impact medical field, specifically Radiology, and analyze existing studies about bridging Convolutional Neural Network models and Radiologic Imaging. For this research paper, were retrieved studies published from academic search engines, including "PubMed", "Researchgate", "RSNA", "Arxiv", "Medium" and "ScienceDirect", that included information about examples of implementations of Image Segmentation in imaging, as well as the state of art of these fields, separately and together.

Besides analysis of existing research papers, were analyzed existing implementations that has shown promising results in testing environment. "GitHub" hosts several Jupyter Notebooks that show processes of processing existing datasets,

preparing them to feed to CNN models, as well as training and testing those models on cleaned data. Thus, an example of implementation was tried to produce in the frames of this paper, as well as showing the results in the future sections.

3 LITERATURE REVIEW

Machine Learning, as it was mentioned in the introduction, is a field of Artificial Intelligence that involves using computational power in order to produce output predictions by learning from input data using various algorithms without being explicitly programmed. In other words, ML is linked to the development of models, training them on datasets and making predictions based on the learned patterns during the training process. This subfield can be divided into two types:

1. **Supervised Machine Learning:** involves machines using labeled data (input data contains the actual true values for each training sample), that, after training, predicts outcomes for unseen data [6]. This field is subsequently divided into other two categories:
 - (a) *Classification:* a problem becomes a classification task when the output variable is a discrete, finite, or, in other words, categorical one. An example of a classification problem can serve the prediction of the presence of brain tumor. In this case, the output of the model is either 0 (absence) or 1 (presence), which becomes a binary classification problem. For example, Logistic Regression, involves fitting the Sigmoid Function to the input data, producing a binary output, Random Forest Classifier, that ensembles multiple Decision Tree Classifiers, are all examples of classification models.
 - (b) *Regression:* a problem becomes a regression task when the output variable is a continuous one, that is in an infinite range of possible values, but not mandatory bounded by any values. An example of a regression problem is the prediction of the age based on physiological input data. In this case, age can be taken from a range of values, that do not represent categories. For example, Linear Regression, which is one of the first models introduced in this field, involves fitting a line to the input data, by adjusting weights and bias of the line equation to the input data, Random Forest Regressor, that ensembles, similar as in classification case, multiple Decision Tree Regressors, are examples of regression models.
2. **Unsupervised Machine Learning:** involves machines using unlabeled data (input data does not contain actual true values for each training sample), that discover various patterns and information in the data without intervention (supervision) [7]. This can also be divided in several types:
 - (a) *Clustering:* a process of grouping unlabeled input data into clusters based on their similarities, used to identify different relationships between data points without prior knowledge about data itself. For example, K-Means is a Clustering algorithm that computes the centroids in the input data and assigns adjacent points to the nearest centroid.
 - (b) *Dimensionality Reduction:* a process of reducing the number of features in the input data while retaining as much information as possible. Principal Component Analysis is an example of a Dimensionality Reduction algorithm, that captures the most important features in the dataset using eigenvectors and eigenvalues.

As time passed, Deep Learning emerged as a subset of Machine Learning with the development of Multilayered Artificial Neural Networks, that simulates the decision-making ability of the human brain. Compared to classical ML models, such as the ones mentioned above, ANNs are similar to them, but consists of multiple levels of algorithms, called layers, which makes them multilayered [8].

Artificial Neural Networks are formed of several components [9]:

- Artificial Neuron:** a basic unit of a neural network, that receives several inputs, either directly from input data or from other neurons, processes them through a set of weights and an activation function, and computes an output either to output or other neurons (See fig. 1) [10].

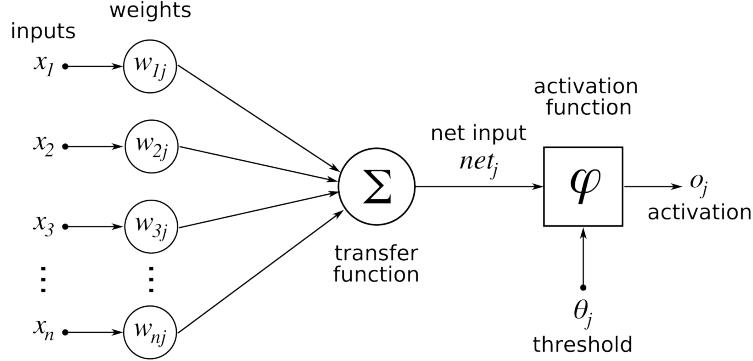


Figure 1: Artificial Neuron Structure

- Activation Function:** a mathematical function applied to the output of an Artificial Neuron, which introduces non-linearity into the model and helps it learn complex patterns in the dataset.
- Input Layer:** the first layer in an ANN, responsible for receiving raw input data, corresponds to the features in the input data and passes it to the next layers (Hidden Layers).
- Hidden Layers:** layers between Input and Output Layers in an ANN, responsible that perform most of the computations required by the network, using activation functions in order to create non-linearity. It can vary in number of layers, neurons per each level and connections between neurons.
- Output Layer:** the last layer in an ANN, that is responsible for producing the output of the model. This layer contains $n = K$ neurons, where $K \in \{class_1, class_2, \dots, class_i\}$, $i = num_{classes}$ is the number of classes, in case of classification problem, or $K = 1$ - if it used for a regression task.

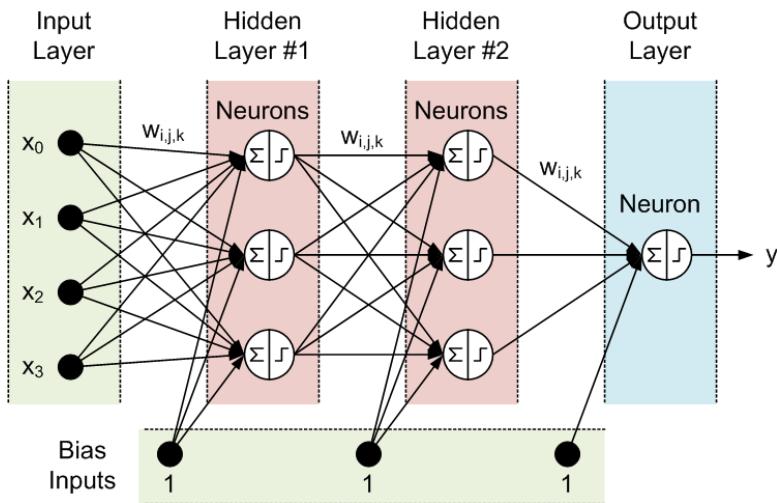


Figure 2: Artificial Neural Network Structure - Layers

Work with Radiologic Imaging involves visual analysis of the images, detection of the deviations from normality and, at the end, interpretation and conclusions. Computers do not have eyes that can perceive images and perform visual analysis.

Since images and videos can serve as valuable information and necessity of processing and analysis of above-mentioned media types, a subfield of AI - Computer Vision, has evolved largely in the last decades. Computer Vision is concerned with finding algorithms and ways that enable computers to interpret and analyze visual information from digital images and videos, similar to human sight [11]. Computer Vision is separated into several tasks [12]:

1. **Image Classification:** the task of predicting the label/class of the given image, either binary or multiclass. An example of this is predicting presence of liver metastases in the radiologic image (See fig. 3).

Classification: liver metastases

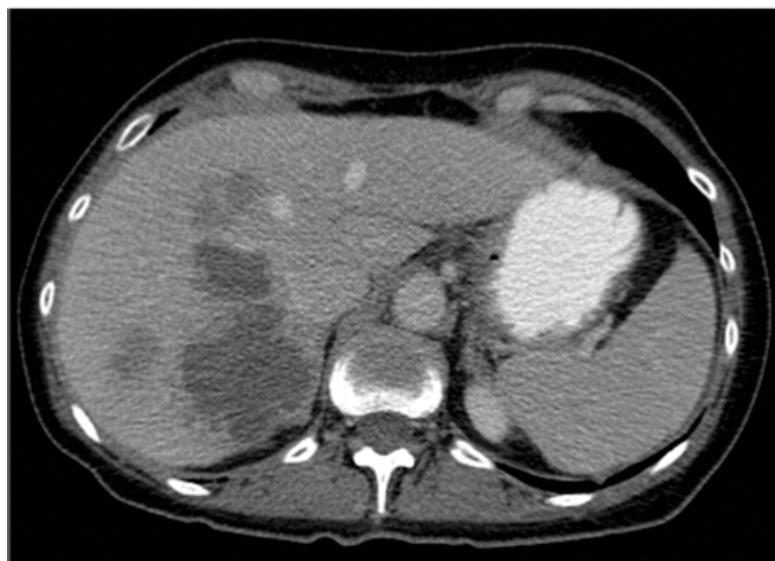


Figure 3: Image Classification Task

2. **Object Detection:** the task of identification and localization of examples of a specific class on an image. Typically for this problem, algorithms specifies the location and spatial extension of the objects that are detected in the given image by plotting a bounding box around the object. For example, in the same image of liver metastases may be noticed boxes around several metastases in the liver, as well as other classes in the image, such as: aorta, stomach and other organs (See fig. 4).

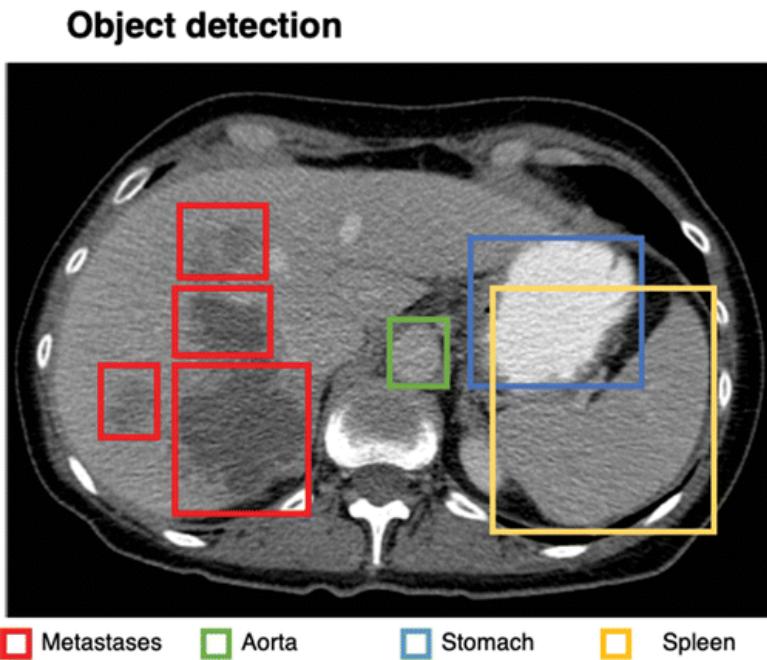


Figure 4: Object Detection Task

3. **Semantic Segmentation:** the task of assigning to each pixel of the given image a specific label/class, that results in binary masks (for each possible target variable), where 0 shows that $pixel_i \notin class_j$, where $class_j$ is the class that is being the target for the binary mask, and 1 characterizes $pixel_i \in class_j$, meaning that specific $pixel_i$ is assigned $class_j$. In the previous image, after semantic segmentation, every liver metastasis is colored red, without specifics about instances (See fig. 5).

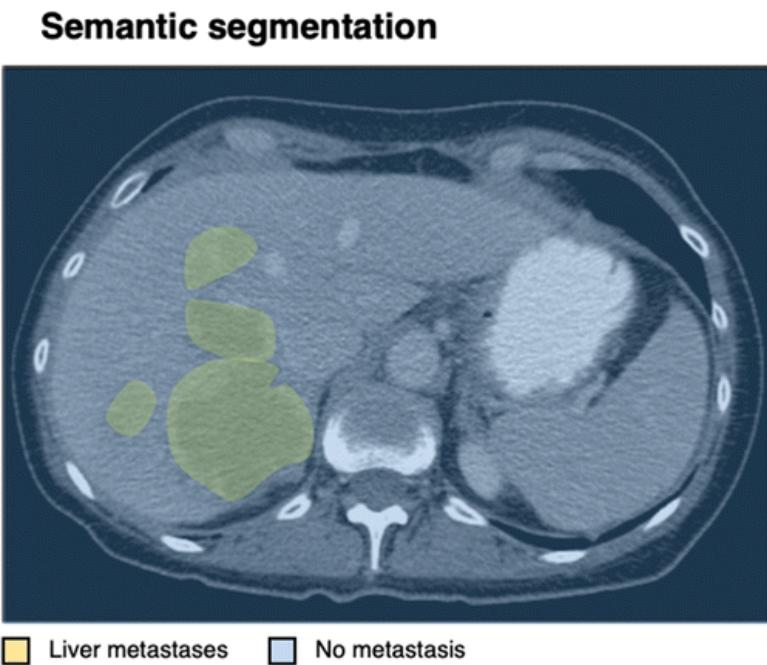


Figure 5: Semantic Segmentation Task

4. **Instance Segmentation:** the task similar to Semantic Segmentation, but focused on delineation of the objects within the same class instance-wise. In this case, each liver metastasis is colored differently, marking each object of the class of metastases (See fig. 6).

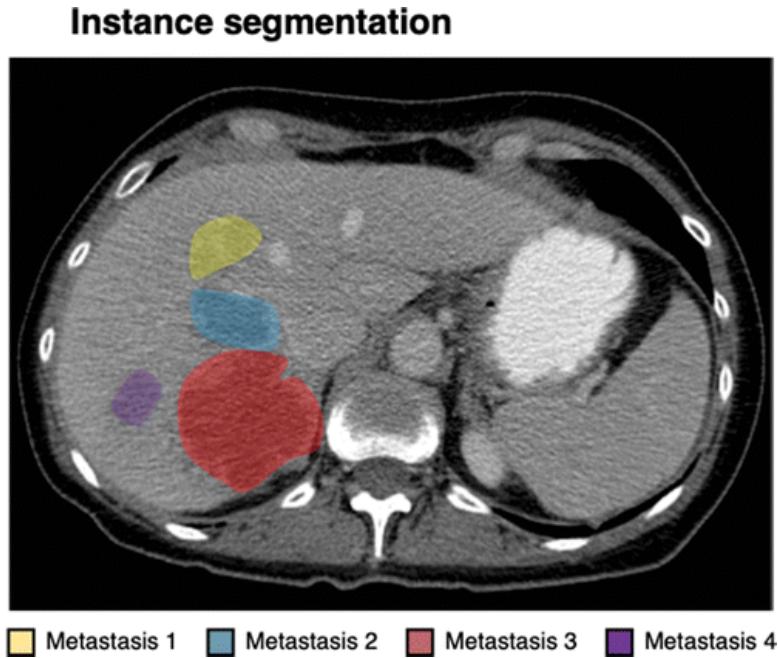


Figure 6: Instance Segmentation Task

As a result, radiologists may benefit a lot from Computer Vision in general. The main focus of this paper is Image Segmentation, that has the potency to specifically and accurately predict the position, shape and size of the abnormalities in the images [13]. Depending on the point of interest of the radiologists, they may be interested in general interpretation, which can be done using Semantic Segmentation, or, in case of particularities and separate instances of the analyzed class - using Instance Segmentation.

For the task of Image Analysis, the most appropriate type of ANNs is Convolutional Neural Network. This type of ANN was first introduced in the 1960s. Due to its promising performance results in Computer Vision, it quickly became one of the most commonly used ANNs in this field [14] [15]. CNNs are formed of 4 layers:

1. **Convolutional Layer:** a layer that uses a kernel filter that slides across the input image step by step and, called convolution operation, calculates the dot product between the weights of the filter and pixel values of the image at each step and produces a new matrix, called 2D activation map. This operation can be expressed as it follows in Eq. 3.1 (See fig. 7):

$$\text{Activation map} = \text{Input} * \text{Filter} = \sum_{y=0}^{\text{columns}} \left(\sum_{x=0}^{\text{rows}} \text{Input}(x-p, y-q) \text{Filter}(x, y) \right) \quad (3.1)$$

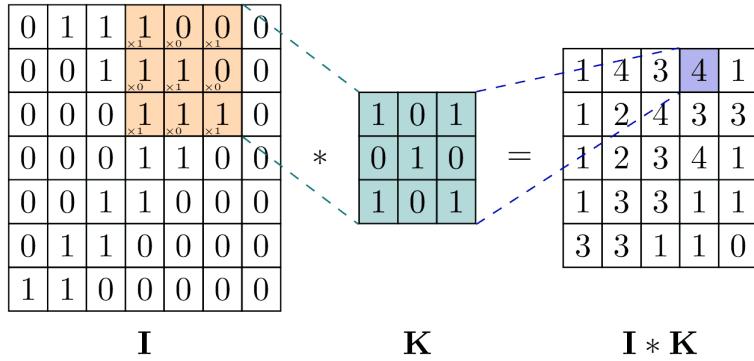


Figure 7: Convolution Operation

2. **Pooling Layer:** a layer that reduces the spatial dimensions (down-sampling) of the feature maps while retaining the most significant and valuable information, by the same mechanism of sliding a filter across the input map. One of the most common types of pooling layer is Max-Pooling layer, that selects highest value pixel and retains it (See fig. 8).

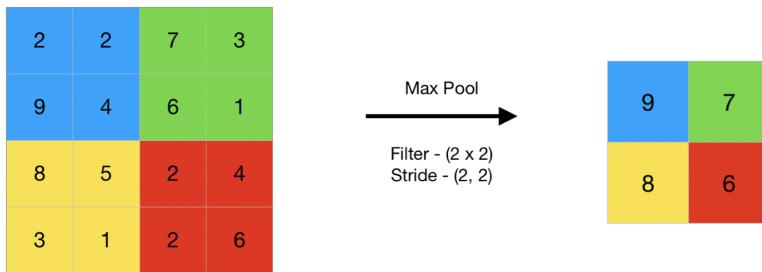


Figure 8: Max-Pooling Layer

3. **Activation Function Layer:** each convolutional layer employs an activation function that is applied to the output map, derived after convolution, in order to add non-linearity for complex patterns and ensure consistency in pixel values. One of the most popular activation functions is ReLU (Rectified Linear Unit Function) as in Eq. 3.2, however other functions, such as: Sigmoid Function, can also be used.

$$f(x) = \begin{cases} x, & \text{for } x > 0 \\ 0, & \text{for } x \leq 0 \end{cases} \quad (3.2)$$

4. **Fully-Connected Layer:** a layer that receives, after last pooling or convolutional layer, the output of the maps, that is flattened, and that acts as input features. This layer is responsible for the final prediction.

Classical CNN architecture solves the problem of Image Classification, but Image Segmentation takes a step further, by employing inside of CNN an Encoder and Decoder, transforming it into a Fully Convolutional Neural Network. The following structure is based on the original research paper by Shelhamer et. al. (See fig. 9).

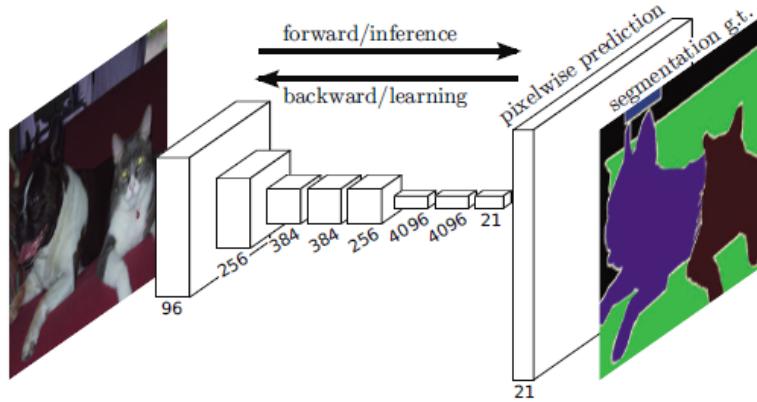


Figure 9: Fully Convolutional Neural Network Structure [16]

1. **Encoder:** a part responsible for down-sampling, similar as in description above, using sequences of Convolutional and Pooling layers. Basically, this is the exactly above-mentioned CNN structure, but without the fully-connected layer
2. **Decoder:** a single layer that is responsible for up-sampling the output from the Encoder in order to restore the original size of the image and reconstruct spatial details that may have been lost during the down-sampling process. This is done by transposed convolution operations (See fig. 10).

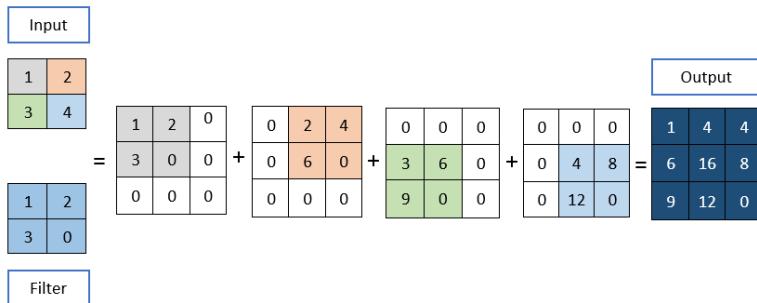


Figure 10: Transposed Convolution Operation [17]

One of the most used Image Segmentation models that was researched for the task of Semantic Segmentation in Medical Imaging is U-Net, due to its accuracy in segmentation of small targets, scalable architecture and requirement of high computational efficiency algorithms, backed up by the necessity of making fast decisions in critical situations, common in medical and healthcare institutions [18].

U-Net is a Fully Convolutional Neural Network, but instead of using a single up-sampling layer in Decoder, it implements multiple steps of up-sampling. This increases the resolution of the output image. At the same time, U-Net adds so-called skip connections, that are derived from the concept of ResNet (Residual Networks) (See fig. 11). These connections are shortcuts from earlier steps in Encoder to Decoder corresponding step. This ensures that small details of the output feature maps at each step, that may be lost during down-sampling, are kept across the algorithm. In other words, these connections pass context to upper layers in Encoder [19].

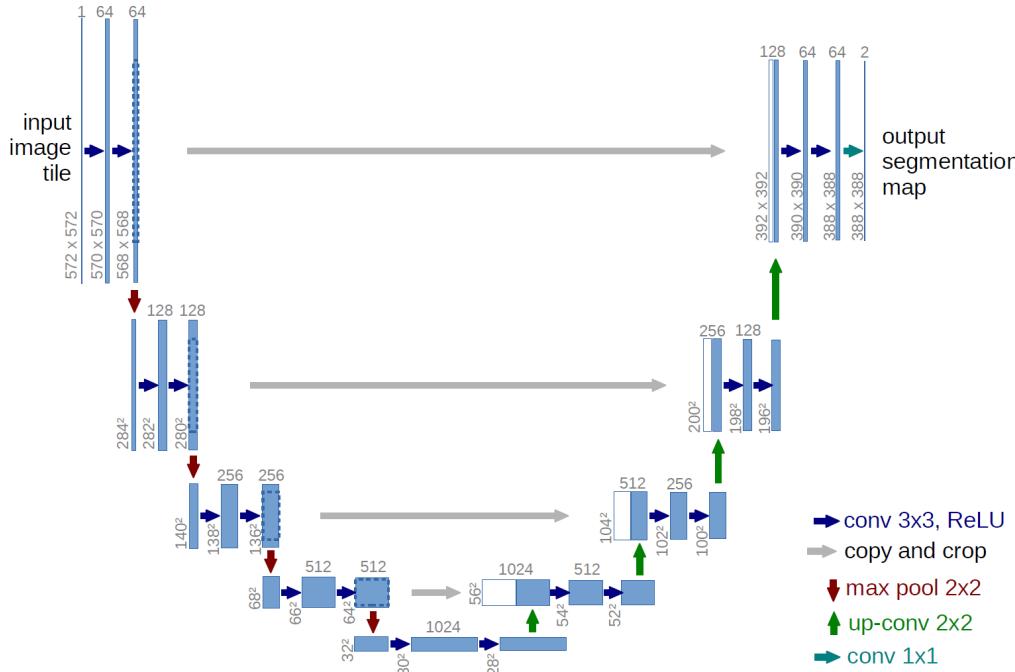


Figure 11: U-Net Architecture

All these additions makes U-Net better at reconstruction of the original image spatial characteristics, as well as overlapping binary maps onto the image, creating the segments around predicted as positive class pixels (See fig. 12).

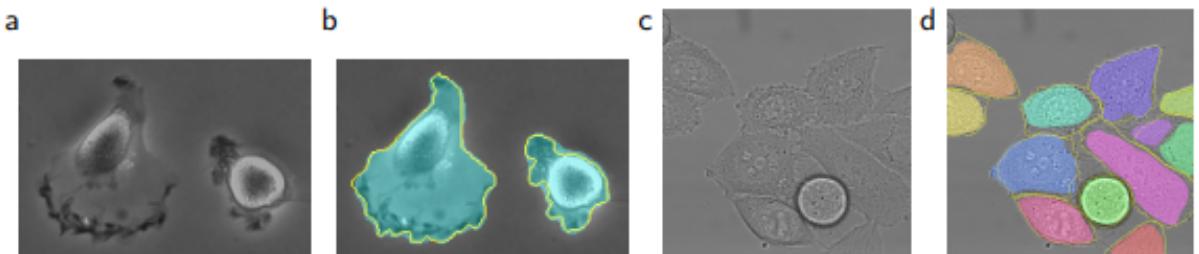


Figure 12: Example of Image Segmentation using U-Net - Result on the ISBI cell tracking challenge. (a) part of an input image of the “PhC-US373” data set. (b) Segmentation result (cyan mask) with manual ground truth (yellow border) (c) input image of the “DIC-HeLa” data set. (d) Segmentation result (random colored masks) with manual ground truth (yellow border) [17]

Medical Images contain many structures, both normal, such as organs, bones, muscles, fat and others, and abnormal ones - tumors, lesions, absence, duplication or changes in normal structures, etc. Segmentation, in this context, covers the process of identification of both types of structures in radiologic images. Since human body is not the same for all people, some differences in particularities of their anatomical characteristics, radiologic images can differ from one patient to another, especially in abnormalities of the human body [20]. This increases the complexity in training Image Segmentation models.

U-Net, due to its approach at preserving context across the steps of the algorithm, its authors, in their original paper, mentioned its efficiency in medical image segmentation applications. Further will be described a study case of U-Net

Image Segmentation of tumors in brain radiologic images. Some papers cover the problem of data acquisition, since medical images comes in various formats, for example, "Digital Imaging and Communications in Medicine" (*DICOM*) and "Neuroimaging Informatics Technology Initiative" (*NIFTI*), that represent 3-dimensional data, that can be thought as stacked sliced 2-dimensional images in all 3 plans - Axial, Coronal and Sagittal (See fig. 13) [21].

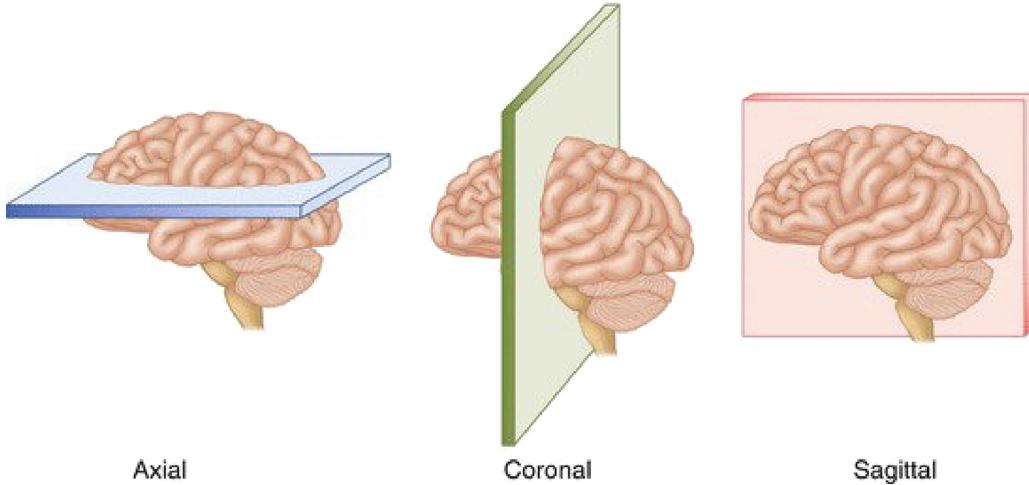


Figure 13: The three perspective planes used in medical imaging - Axial/Transversal, Coronal and Saggital

Several datasets are available on web, including the one used in the study case of Brain Tumor Segmentation using enhanced versions of U-Net with EfficientNet-B4 Encoder, pretrained on ImageNet resources, which means that the only part of the network that requires training, is Decoder. This reduces training time and enables features extraction using pretrained weights, resulting in higher accuracy in extracting hierarchical features, such as edges, shapes, patterns and so on. The proposed workflow of the model is displayed below (See fig. 14):

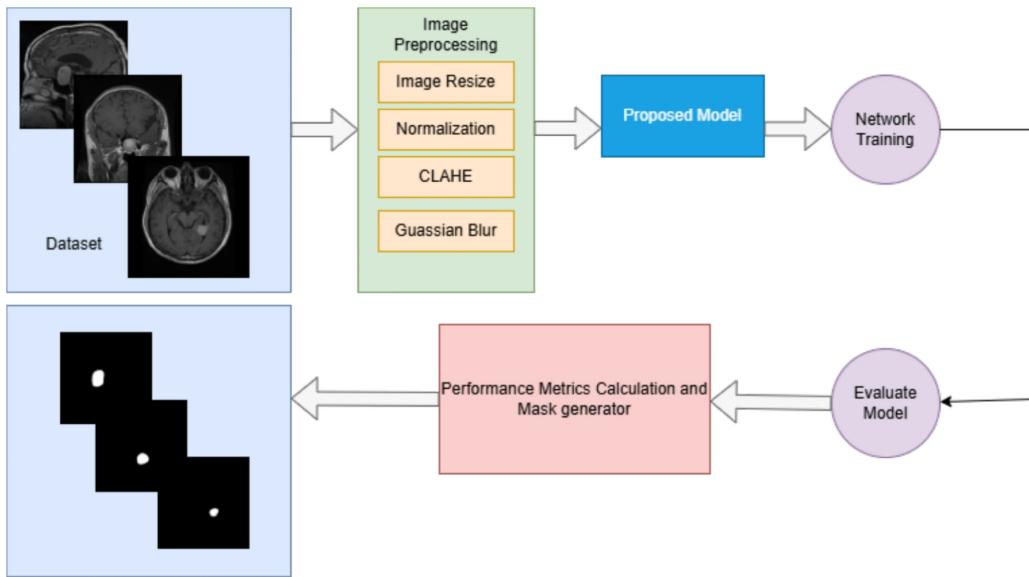


Figure 14: The three perspective planes used in medical imaging - Axial/Transversal, Coronal and Saggital

First step of the workflow focuses on the image preprocessing. ImageNet brain tumor dataset, used in the referenced paper, is available on ImageNet and contains 3064 T1-weighted contrast-enhanced images from 233 patients with three kinds of brain tumor: meningioma, glioma and pituitary tumor, alongside with true label of each sample, and tumor border

in format of a vector storing the coordinates of tumor border in the format $[x_1, y_1, x_2, y_2, \dots, x_i, y_i]$. All the data is stored in .mat file. As addition to the dataset, original authors provided a snippet to convert images to .jpg image format. With additional implementation of extracting binary mask, that represents ground truth segmentation, the code looks as it follows:

```

1 input_folder = 'your input path';
2 output_folder = 'your output path';
3 file_list = dir(fullfile(input_folder, '*.mat'));
4 disp(file_list);
5 for i = 1:numel(file_list)
6     file_name = file_list(i).name;
7     file_path = fullfile(input_folder, file_name);
8
9     mat_data = load(file_path);
10    cjdata = mat_data.cjdata;
11
12    im1 = double(cjdata.image);
13    min1 = min(im1(:));
14    max1 = max(im1(:));
15    im = uint8(255/(max1-min1)*(im1-min1));
16
17    im1_mask = double(cjdata.tumorMask);
18    min1_mask = min(im1_mask(:));
19    max1_mask = max(im1_mask(:));
20    im_mask = uint8(255/(max1_mask-min1_mask)*(im1_mask-min1_mask));
21
22    label = cjdata.label;
23
24    tumorBorder = cjdata.tumorBorder;
25
26    disp(tumorBorder);
27
28    label_folder = fullfile(output_folder, num2str(label));
29    if ~exist(label_folder, 'dir')
30        mkdir(label_folder);
31    end
32
33    [~, file_name_base, ~] = fileparts(file_name);
34    output_file_path = fullfile(label_folder, strcat(file_name_base, '.jpg'));
35    output_file_path_mask = fullfile(label_folder, strcat(file_name_base, '_mask', '.jpg'));
36
37    imwrite(im, output_file_path);
38    imwrite(im_mask, output_file_path_mask);
39 end

```

As a result, an example of input images is provided below (See fig. 15). On the left side, can be seen the original image of the brain and on the right side the corresponding binary mask that represents the surrounded brain tumor border with white color.

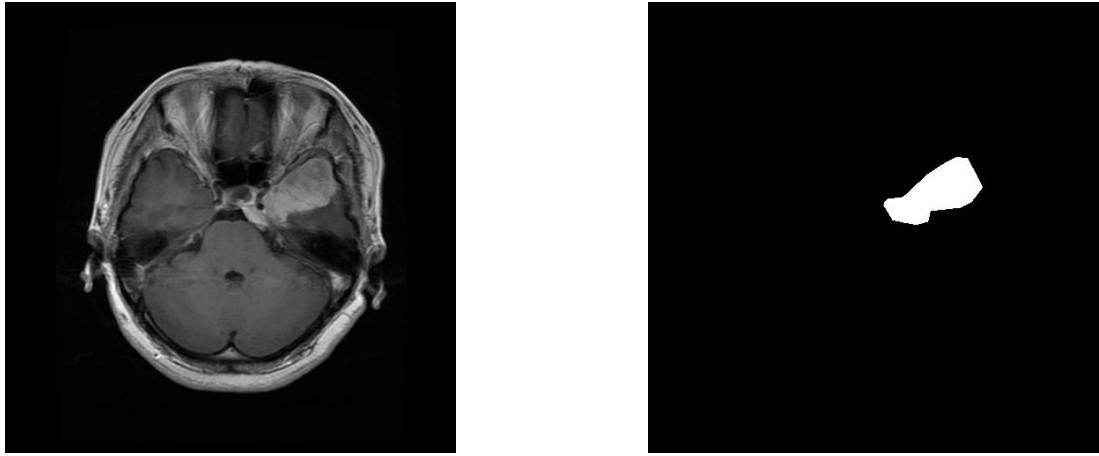


Figure 15: First Sample of the Brain Tumor Dataset

However, images are converted to *RGB* color map, which, taken in consideration the importance of image preprocessing, can be an obstacle in this process. One of the outlined preprocessing steps is CLAHE (Contrast Limited Adaptive Histogram Equalization), which is used to improve the contrast of images, but, instead of changing the contrast of the entire image, it divides images in smaller parts and adjusts their contrast separately, avoiding getting the image too bright or too dark [22]. An example of advantage of this approach can be seen in the following example (See fig. 16):

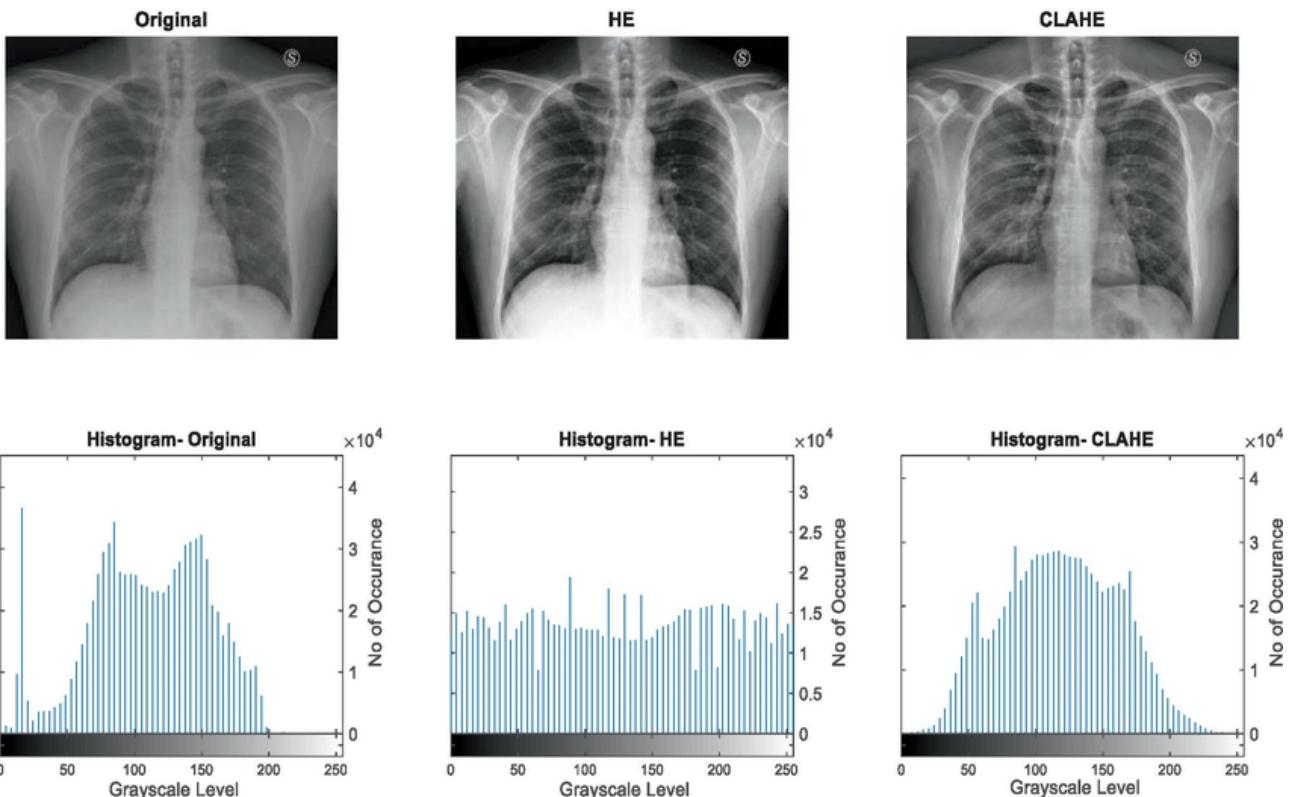


Figure 16: Comparison between original, HE, and CLAHE equalized X-ray images with corresponding histograms

As it may be seen, CLAHE provides a better histogram equalization than in traditional HE method. As it was mentioned,

converted images are in *RGB* color space, but CLAHE, applied on this color map, impacts the coloring of the images, since it modifies at least one of the three color channels, that are highly-correlated, thus producing new artifact colors [23], which can make ML Models capture new unwanted data as patterns. Besides that, in imaging, an important aspect is device-dependency. *RGB* is device-dependent, meaning images in *RGB* are interpreted differently depending on the device it is viewed. Thus, a need of a consistent and device-independent color map has appeared. This need was full-filled in 1976 when *CIELAB* color map was developed. *CIELAB* is a color map that is formed of 3 components: L - Perceptual Lightness ($L \in [0, 100]$, where $0 = \text{Black}$ and $100 = \text{White}$), a^* - first color component ($a^* \in [-127, 127]$, where $-127 = \text{Green}$ and $127 = \text{Red}$) and b^* - second color component ($b^* \in [-127, 127]$, where $-127 = \text{Yellow}$ and $100 = 127$), which can represent the gamut of human color perception, thus making it the most appropriate for accurate color interpretation in images, especially in restoring details CNN output [24]. For example, *RGB* can represent a small portion of the range of possible color nuances (See fig. 17).

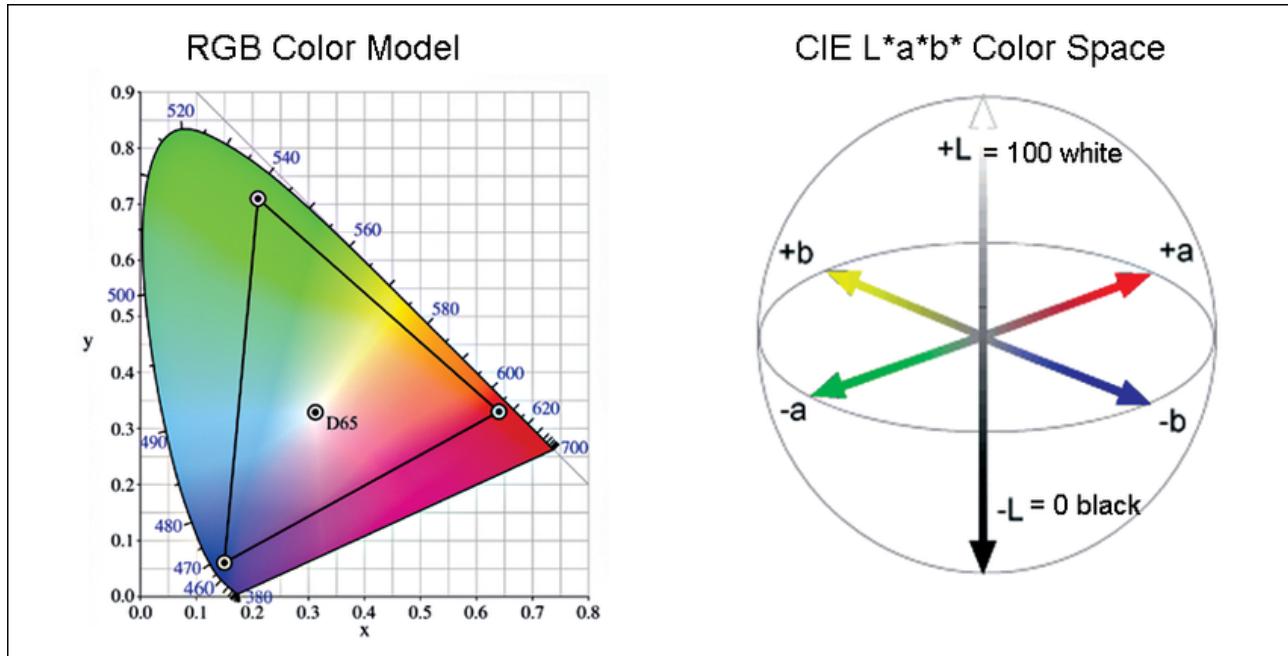


Figure 17: Comparison between *RGB* and *CIELAB* color spaces

As it may be seen, the triangle on the left side represents how *RGB* captures color nuances, being a subset of the possible colors represented in *CIELAB* color space. Since *CIELAB* contains a separate channel for Lightness, it can be used for CLAHE algorithm, thus leaving color channels untouched, that will not produce color artifacts, making it appropriate for application in Medical Imaging.

Returning back to the discussed research paper on U-Net application in Radiology Imaging, one important step in dataset preprocessing is conversion from *RGB* color space to *CIELAB*.

```

1 # Using OpenCV, read radiologic images.
2 img_rgb = cv2.imread(os.path.join(dataset_directory, filename))
3 # By default, OpenCV library reads images in BGR color space, therefore, for the
   conversion to LAB, images should be in RGB color space.
4 img_rgb = cv2.cvtColor(img_rgb, cv2.COLOR_BGR2RGB)
5 # OpenCV supports LAB color space and offers functions to operate with LAB format.
6 img_lab = cv2.cvtColor(img_rgb, cv2.COLOR_RGB2LAB)

```

After conversion to *CIELAB* color space, CLAHE algorithm is safely applied on the L channel. Thus, the contrast of the

images are enhanced.

```

1 # Initialize CLAHE object using default arguments
2 clahe = cv2.createCLAHE(clipLimit=2.0, tileSize=(8, 8))
3 # Split the image by channels (L, a*, b*)
4 l, a, b = cv2.split(img_lab)
5 # Apply CLAHE Transformation on L channel
6 l_clahe = clahe.apply(l)
7 # Restore back the image by combining all 3 channels
8 img_lab_clahe = cv2.merge([l_clahe, a, b])
9 # Convert back to RGB for visualization (alternatively, save in .tiff format, because
   supports float pixel values)
10 img_lab_rgb = cv2.cvtColor(img_lab, cv2.COLOR_LAB2RGB)
11 img_lab_clahe_rgb = cv2.cvtColor(img_lab_clahe, cv2.COLOR_LAB2RGB)

```

Next step of preprocessing in the paper is applying Gaussian Filter in order to reduce the noise and smooth the image, increasing the overall quality of the image.

```

1 # Apply Gaussian Filter with kernel size 5x5 and standard deviation on X-axis 0
2 img_lab_clahe_gauss = cv2.GaussianBlur(img_lab_clahe, (5, 5), 0)
3 # Convert LAB image to RGB for visualization
4 img_lab_clahe_gauss_rgb = cv2.cvtColor(img_lab_clahe_gauss, cv2.COLOR_LAB2RGB)

```

After that, all the resulting images are resized to 256×256 to imply consistency in images and adhere to U-Net architecture input dimensions, and normalized. All of the masks were also resized to the same dimension, normalized and reshaped to include a single channel.

As an example of the preprocessing, below is provided, step-by-step, modifications of the images alongside with ground-truth segmentation from the training examples (See fig. 18).

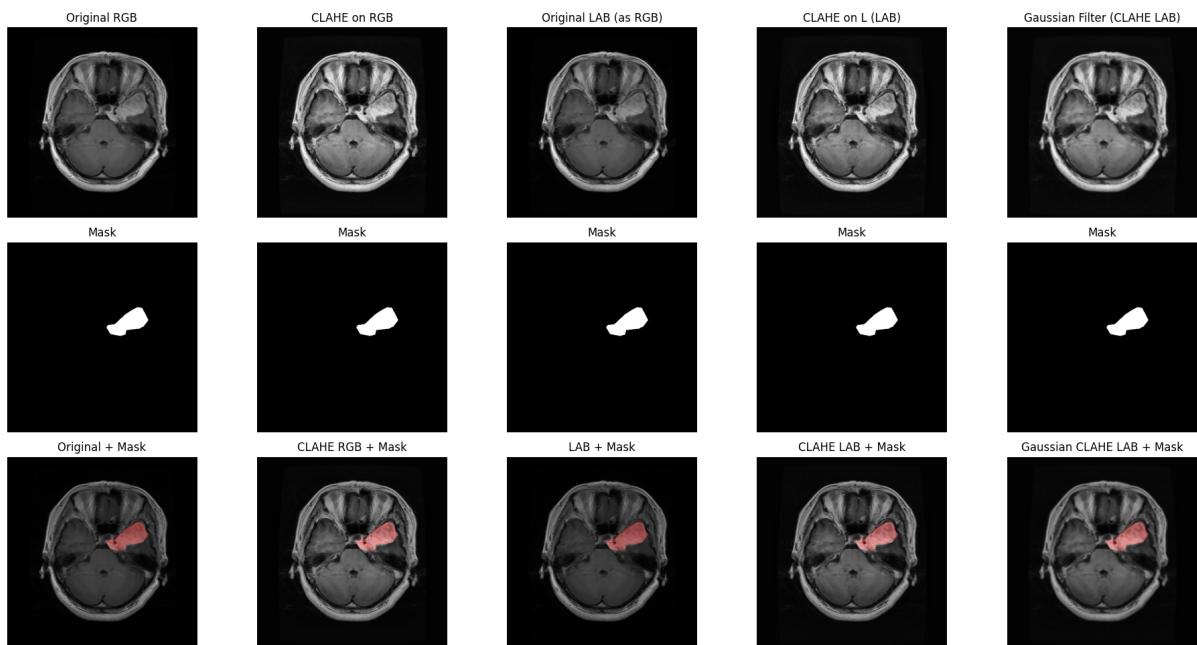


Figure 18: Original and Applied *LAB* conversion and CLAHE algorithm - Original dimension

The proposed model in the reviewed paper is Multi-Scale Attention U-Net with EfficientNet-B4 Encoder. As it was mentioned, U-Net is formed of two components - Encoder and Decoder.

1. **Encoder:** EfficientNet-B4 encoder that is pretrained of ImageNet dataset, provides very high performance results, responsible for hierarchical feature extraction and captures low-level and high-level features useful for brain tumor segmentation. Besides classical convolution layer, it uses the concept of Mobile Inverted Bottleneck Convolution (MBConv) layers (See fig. 19).

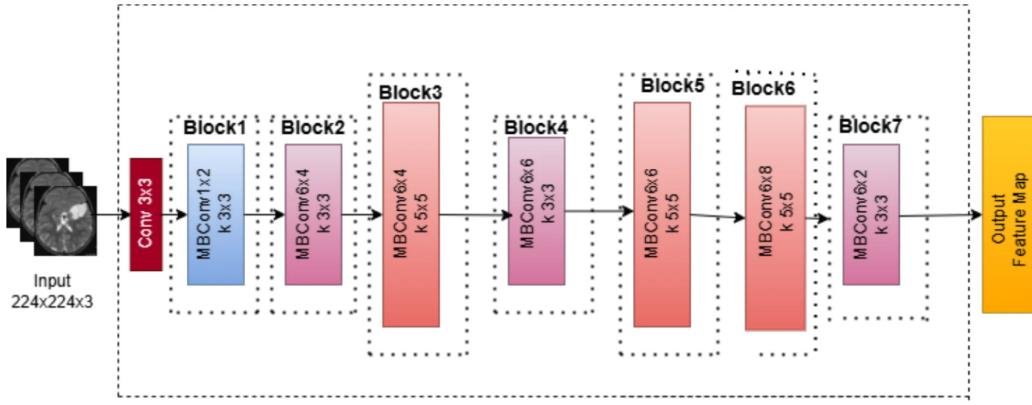


Figure 19: EfficientNet-B4 Architecture

First step is to pass input image through simple convolution layer, while the rest of the blocks are MBConv layers, that comprises multiple convolution operations. Initially, 1×1 convolution block expands the number of input channels, then depth-wise 3×3 convolution block is applied over produced channels. After that, the output is sent through a skip connection to the end of the layer and, at the same time, to the Squeeze-and-Excitation block, that reduces the map, applies non-linear activation function and restores the spatial dimensions, where first the map is squeezed and then expanded back to original shape. This allows model to perceive important feature better, since their "weights" are higher than for non-important features, and this type of layer can perceive them better (See fig. 20).

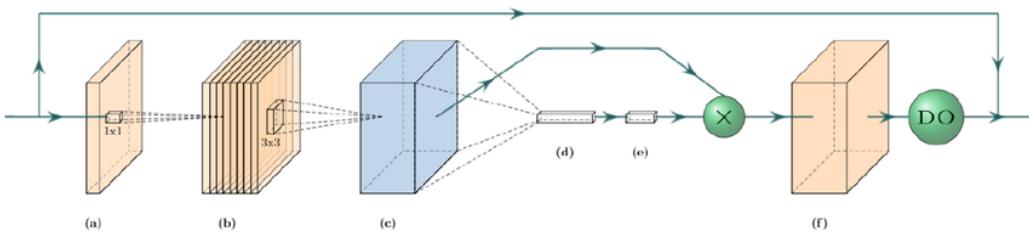


Figure 20: MBConv Architecture

2. **Decoder:** Multi-Scale Attention architecture is embedded inside of the Decoder and focuses on spatial position of important features in the encoder feature maps by applying additional residual attention blocks and combining them with features from the encoder using skip connections, improving model segmentation on relevant features. Each decoder block acts as a Residual Attention Block, which combines skip connections with multi-scale attention techniques. First, as in original U-Net, feature map is up-sampled using transposed convolution, increasing spatial dimensions of the maps. "Multi-Scale", in this context, uses convolutions with different kernel sizes, in order to obtain contextual information at different scales. After that, using simple convolution, all the generated maps are merged into a single one. An attention mask is produced by passing multiscale features through another convolution and activation layer, that is later applied through element-wise multiplication to the feature map (See fig. 21).

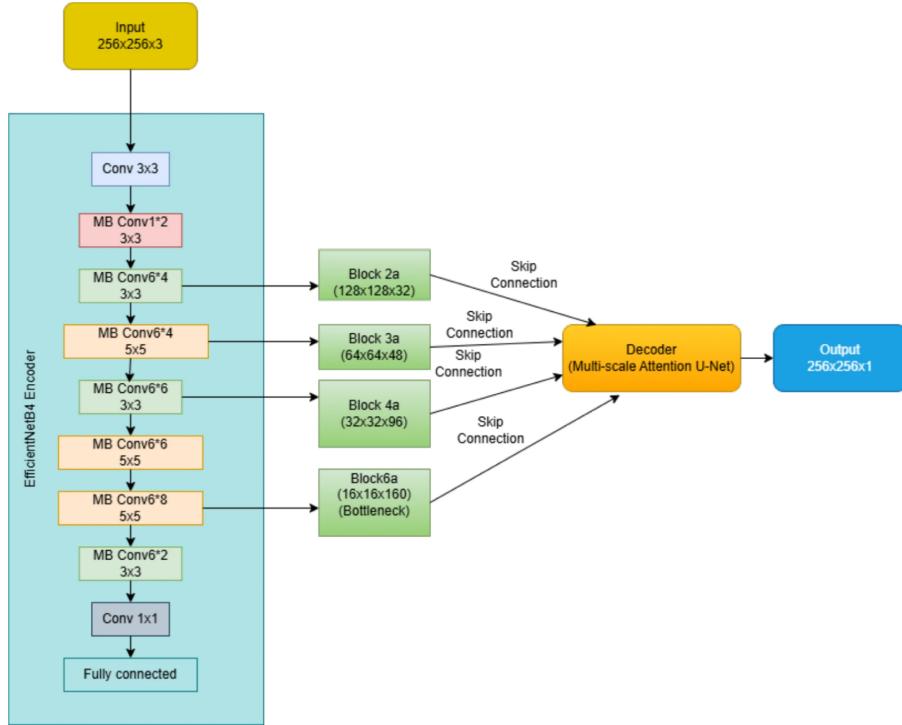


Figure 21: Multi-Scale Attention Decoder

In the paper, researchers focused on several metrics:

1. **Dice similarity coefficient (DSC)**: measures the overlap between Predicted Segmentation and Ground Truth Segmentation. Higher values of DSC coefficient indicate accurate tumor localization.

$$DSC = \frac{2|P \cap G|}{|P| + |G|}$$

P - Predicted Segmentation

G - Ground Truth Segmentation

$|P|$ - total number of pixels in predicted segmentation

$|G|$ - total number of pixels in ground truth segmentation

$|P \cap G|$ - total number of overlapping pixels in between predicted and ground truth segmentation

2. **Intersection over union (IoU)**: known as Jaccard Index, measures the ratio between the intersection and union between Predicted Segmentation and Ground Truth Segmentation. Compared to DSC, IoU penalizes more under-and over-segmentation. However, those two metrics are pretty similar and offer relatively similar values. One of the most used metrics is DSC, due to the fact that, using DSC, can be computed Dice Loss $DiceLoss = 1 - DSC$,

that is differentiable, while IoU is not.

$$IoU = \frac{|P \cap G|}{|P \cup G|} = \frac{|P \cap G|}{|P| + |G| - |P \cap G|}$$

P - Predicted Segmentation

G - Ground Truth Segmentation

$|P|$ - total number of pixels in predicted segmentation

$|G|$ - total number of pixels in ground truth segmentation

$|P \cap G|$ - total number of overlapping pixels in between predicted and ground truth segmentation

$|P \cup G|$ - total number of distinct pixels either in predicted or ground truth segmentation

3. **Mean intersection over union (mean IoU):** measures the average intersection between the predicted and ground-truth segmentation across all classes in order to give a general interpretation of models performance.

$$IoU_{mean} = \frac{1}{C} \sum_{c=1}^C \frac{|P_c \cap G_c|}{|P_c \cup G_c|} = \frac{1}{C} \sum_{c=1}^C \frac{|P_c \cap G_c|}{|P_c| + |G_c| - |P_c \cap G_c|}$$

C - total number of classes

P_c - Predicted Segmentation for class c

G_c - Ground Truth Segmentation for class c

$|P_c|$ - total number of pixels in predicted segmentation for class c

$|G_c|$ - total number of pixels in ground truth segmentation for class c

$|P_c \cap G_c|$ - total number of overlapping pixels in between predicted and ground truth segmentation for class c

$|P_c \cup G_c|$ - total number of distinct pixels either in predicted or ground truth segmentation for class c

4. **Precision:** measures the ratio of correctly identified tumor pixels of the total number of pixels that were classified as tumors.

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

TP - total number of correctly classified pixels as tumors

FP - total number of incorrectly classified non-tumor pixels as tumors

5. **Recall:** measures the ratio of correctly classified tumor pixels and the total number of actual tumor pixels.

$$Recall = \frac{TP}{TP + FN}$$

TP - total number of correctly classified pixels as tumors

FN - total number of incorrectly classified tumor pixels as non-tumors

6. **Specificity:** measures the ratio between correctly identified non-tumor pixels and the total number of actual non-tumor pixels.

$$Sensitivity = \frac{TN}{TN + FP}$$

TN - total number of correctly classified pixels as non-tumors

FP - total number of incorrectly classified non-tumor pixels as tumors

7. **Accuracy:** measures the ratio of correctly predicted pixels to the total number of pixels. This metric, taken alone, may be misleading, because it does not take into consideration cases of imbalanced datasets (ratio of one class to another class is very high, e.g. Brain Tumor Classification Problems). For example, if a model was trained on an imbalanced dataset, it might learn to predict the majority class to all samples, and since there is a very high number of samples of majority class, this metric will show high accuracy, but the model is still performing badly, since it misclassifies all of the minority class.

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

TP - total number of correctly classified pixels as tumors

TN - total number of correctly classified pixels as non-tumors

FP - total number of incorrectly classified non-tumor pixels as tumors

FN - total number of incorrectly classified tumor pixels as non-tumors

As a result, their proposed enhanced U-Net performed very well. Specifically, they performed a comparative analysis between different types of EfficientNet-B family of Encoders. With EfficientNet-B4 Encoder, their model obtained highest DSC, IoU and Recall, that resulted in the best segmentation of tumor pixels. Besides that, since medicine is a field where mistakes may have heavy consequences, it is a practice to sacrifice Precision in order to obtain higher Recall, which means that it is better to misclassify some radiologic images that exhibit non-tumor patients rather than to misclassify some patients that actually have a tumor or multiple ones as being non-tumor patients. Besides that, EfficientNet-B4 Encoder manifested lower consumption of computational power compared to EfficientNet-B6, that had similar results in performance metrics.

Table 1: Comparison of EfficientNet-B Encoder Family variants performance

Model	DSC	IoU	Precision	Recall	Specificity
<i>EfficientNet-B0</i>	0.9127	0.8476	0.9756	0.8683	0.9998
<i>EfficientNet-B1</i>	0.9026	0.8419	0.9738	0.8645	0.9997
<i>EfficientNet-B2</i>	0.9289	0.8725	0.9705	0.8983	0.9997
<i>EfficientNet-B3</i>	0.8986	0.8222	0.9864	0.8327	0.9999
<i>EfficientNet-B4</i>	0.9339	0.8795	0.9657	0.9103	0.9996
<i>EfficientNet-B5</i>	0.8806	0.8212	0.9647	0.8498	0.9996
<i>EfficientNet-B6</i>	0.9327	0.8778	0.9671	0.9063	0.9997
<i>EfficientNet-B7</i>	0.9171	0.8120	0.9817	0.8664	0.9998

As a result of testing the model with those encoder, they obtained the following plot (See fig. 22). It may be noticed that EfficientNet-B4 obtained the closest segmentation to the original ground-truth one.

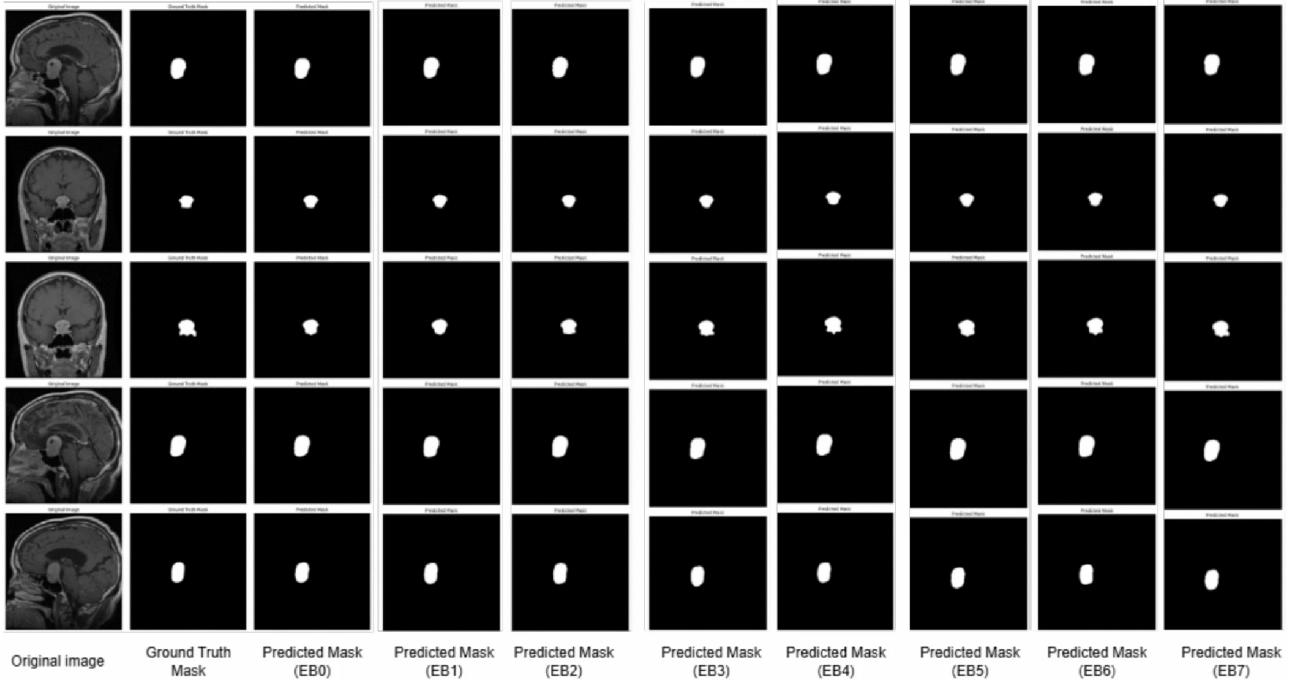


Figure 22: Predicted Binary Masks by Multi-Scale Attention U-Net with each Encoder of EfficientNet-B Family alongside with Ground-Truth Mask and original Image.

Another study focused on implementation of Optimized Fuzzy K-Means clustering algorithm for Brain Tumor Segmentation. K-Means clustering is an iterative, centroid-based clustering Unsupervised Machine Learning algorithm that segments a dataset into similar groups based on the distance between their centroids [25]. In classical K-Means Clustering, the steps to train the model are the following:

1. Initialization of the number of Clusters K . This should be done before-hand.
2. Random selection of K points from the dataset and are assigned different labels.
3. Each point in the dataset is assigned to the closest cluster K_i by Euclidian Distance.

$$\text{Distance} = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$$

(x_1, y_1) - coordinates of K_i centroid
 (x_2, y_2) - coordinates of analyzed data point

4. After all the points are assigned, recalculate the centroids as mean of all point assigned to the cluster K_i .

$$K_i = \frac{1}{n_i} \sum_{j=1}^{n_i} \vec{x}_i$$

n_i - number of points in cluster i

K_i - new centroid of cluster i

\vec{x}_i - vector representing each data point in the cluster i

5. Repeat iteratively previous two steps until no change in clusters centroids or maximum iterations achieved.

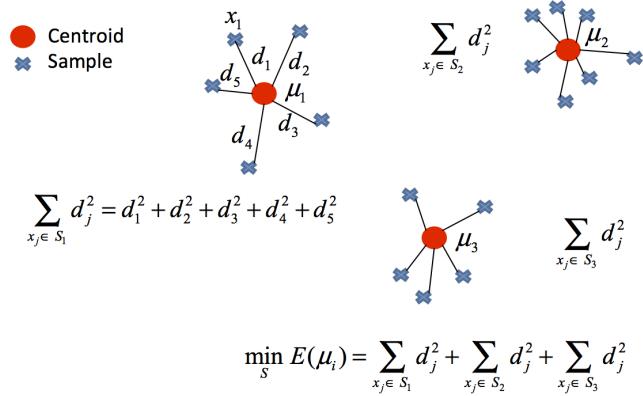


Figure 23: Example of K-Means Algorithm

Fuzzy K-Means works using Fuzzy Logic. It computes a Membership Matrix for each data point in contrast to Euclidean Distance applied in the original K-Means. This approach allows overlapping clusters and adds flexibility, since it offers soft-decision results in format of probabilities of data points cluster membership.

In the above-mentioned study, authors used Fuzzy K-Means Clustering for Brain Tumor Segmentation. As a preprocessing step of the radiologic images, they implemented Gaussian Blur and Normalization, similar to the approach from previous study case. However, no additional Contrast Enhancement techniques were applied.

As for the model, they similarly used additional implementations, such as:

1. **Centroid Initialization with K-Means++:** one centroid is selected at random and subsequent selection is done based on the probability that is proportional to the square of the Euclidean Distance between the data point and closest selected center.
2. **Use of Vectorization:** in membership update step, they used vectorized operations of matrices, and others.

As evaluation metrics, they used DSC, IoU, Precision, Recall, Accuracy and F1-Score.

As a result, they obtained the following predictions (See fig. 24). As it may be seen, Fuzzy K-Means performed close to the ground-truth binary masks segmentation. Its predictions overall visual similarities with true label masks can be seen, however False Positives and False Negatives can still be seen, but, since the approach is much less complex than CNNs, results are impressive.

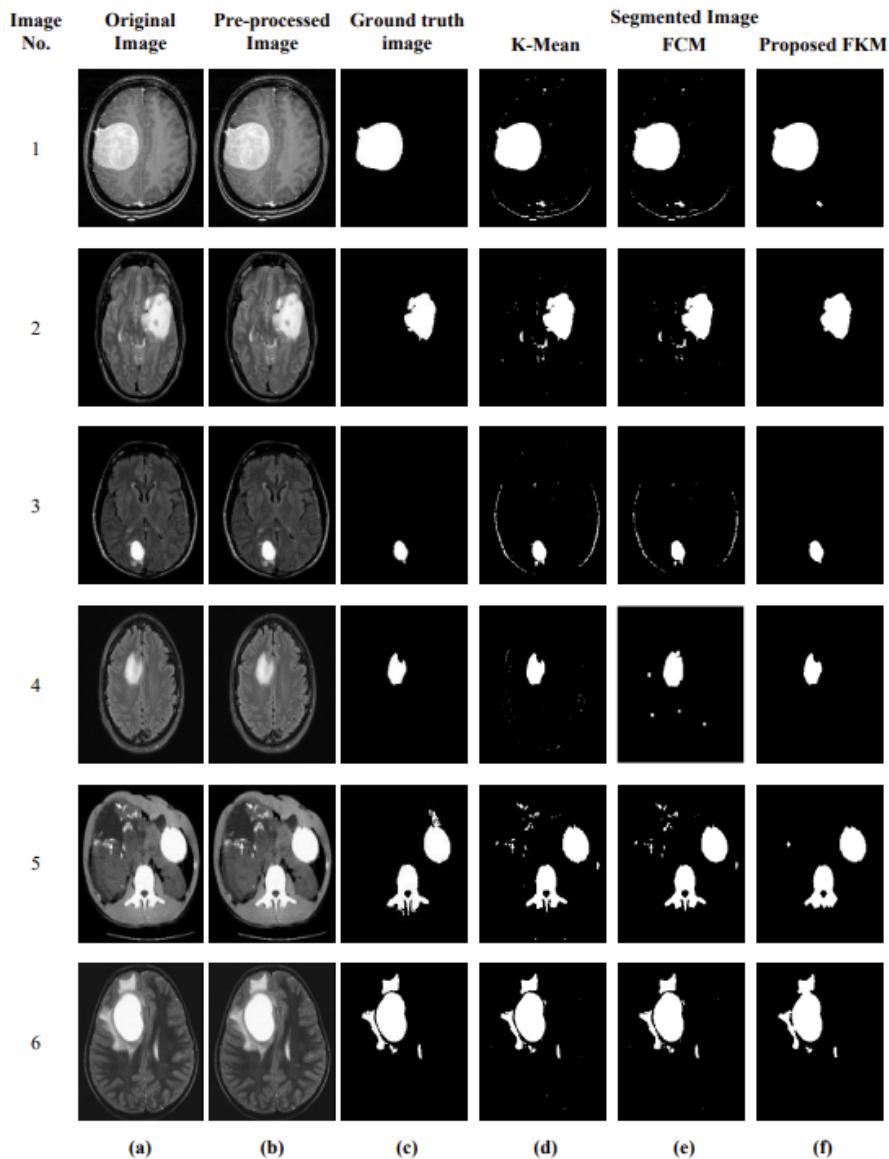


Figure 24: Segmentation Results (a) Original Image (b) Preprocessed Image, (c) Ground-Truth Binary Mask (d) K-Means Clustering, (e) FCM f Proposed Fuzzy K-Means Clustering

At the end of the paper, they offered the performance metrics of the Fuzzy K-Means Clustering in Brain Tumor Image Segmentation. The performance is very high, higher than in the previous study case with U-Net as a model. This also may be due to the differences in the dataset sizes, as well as other factors that may affect the metric performances. Besides this, not much information was provided on the algorithms and implementations in both articles, therefore no comparison between them may be done.

Table 2: Analysis of Fuzzy K-Means Clustering Performance Metrics in Brain Tumor Segmentation Task

Image No.	DSC	IoU	Precision	Recall	Accuracy	F1 Score
1	0.9776	0.9562	0.9899	0.9656	0.9960	0.9776
2	0.9724	0.9464	0.9781	0.9669	0.9972	0.9724
3	0.9721	0.9457	0.9699	0.9743	0.9994	0.9721
4	0.9707	0.9430	0.9617	0.9797	0.9988	0.9707
5	0.9145	0.8825	0.9928	0.8477	0.9862	0.9145
6	0.9861	0.9778	0.9852	0.9101	0.9912	0.9461
<i>Average</i>	0.9072	0.9419	0.9796	0.9407	0.9948	0.9589

4 RESULTS AND DISCUSSION

5 CONCLUSIONS

High performance in Image Segmentation, for example Brain Tumor Segmentation, manifested by various Machine Learning Models, especially U-Net and Fuzzy K-Means Clustering, specifically tailored for Applications in Medical Imaging, is a result of complex work of many people. As demonstrated, those models may represent a valuable assistance for radiologists in their routine work by reducing the amount of time spent per each image and assisting in image exploration and, possibly, reduce the rate of error in their practice.

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