



Analysis of Efficient Net Model Using Binary Segmentation Results from Magnetic Resonance Imaging (MRI) T1 Weighted Contrast Images in Classifying Brain Tumors Types

Muhammad Alifian Ihtisyamuddin*, M.Choiroel Anwar, Rasyid, Yeti Kartikasari, Leny Latifah, Gatot Murti Wibowo

Politeknik Kesehatan Kementerian Kesehatan Semarang, Indonesia

Email: alifianimuhammad@gmail.com, choirul1960@gmail.com, rasyid.lihawa@gmail.com, yeti.kartikasari@gmail.com, leny003@brin.go.id, gatotmurtiw@gmail.com

| KEYWORDS | ABSTRACT |
|---|---|
| MRI Brain, Brain Tumor, Binary Segmentation, EfficientNet | Brain tumors consist of abnormal tissues resulting from uncontrolled cell proliferation and have no physiological function in the brain. The application of binary image segmentation is important because it is widely used in medical imaging to assist in brain tumor diagnosis. There has been prior work on MRI image classification for brain tumor types, such as using EfficientNet. This study aims to investigate the application of binary segmentation results from T1-weighted contrast MRI images in the EfficientNet model. The study employed a Research and Development (R&D) methodology. The dataset comprised 1,400 images, including 700 glioma and 700 meningioma cases. MRI images and tumor masks were combined using a binary masking segmentation method. Subsequently, the segmented images were input into the EfficientNet model and evaluated using a confusion matrix. The model testing yielded an accuracy of 0.6, precision of 0.627, recall of 0.492, and an F1 score of 0.551. However, the loss value was relatively high at 0.678. These results suggest that binary segmentation images from T1-weighted contrast MRI scans of brain tumor cases can be applied effectively to the EfficientNet model. |

Corresponding Author: Muhammad Alifian Ihtisyamuddin

Email: alifianimuhammad@gmail.com

INTRODUCTION

Brain tumors are abnormally developing tissues caused by unregulated cell proliferation that have no physiological function in the brain. Brain tumors exhibit different characteristics compared to tumors in other organs; although often histologically benign, they have the potential to become malignant due to their location within confined intracranial structures (Jiang et al., 2017). Glioma is the most prevalent primary brain tumor, accounting for 81% of all central nervous system malignancies. Gliomas arise from glial or progenitor cells. According to the World Health Organization (WHO), gliomas are classified into four grades: Grade 1 and Grade 2 correspond to low-grade gliomas, while Grade 3 and Grade 4 are categorized as high-grade gliomas (Xu et al., 2020).

Meningioma is a central nervous system tumor originating from arachnoid cap cells. Meningiomas represent approximately 30% of all primary intracranial tumors in adults but are rare in children and adolescents (0.4–4.6%) (Zhao et al., 2020). Although most meningiomas are benign, about 20% of cases are high-grade tumors requiring aggressive clinical intervention (Hanna et al., 2023). WHO classifies meningiomas into three grades: Grade I (80.5% of cases) with benign histology, Grade II (17.7%) and Grade III (1.7%) with atypical to malignant histology associated with a more aggressive clinical course (Ogasawara et al., 2021).

Magnetic resonance imaging (MRI) represents the most advanced neuroimaging modality, providing detailed images of brain anatomy. MRI uses magnetic fields and radiofrequency (RF)

pulses instead of ionizing radiation, making it safer than X-ray-based diagnostic techniques such as computed tomography (CT) scans (Lefevre et al., 2016). CT scans have limited sensitivity for soft tissue differentiation in brain tumors, whereas MRI offers superior contrast resolution, enabling clear visualization of both soft and hard brain tissues (Suta et al., 2019). Due to its non-invasive nature and high-resolution imaging capabilities, MRI is widely employed for the early diagnosis and characterization of brain tumors (Naser & Deen, 2020).

Manual diagnosis of brain tumors often relies on biopsy and direct observation. Histopathological examination of biopsy samples typically requires 10–15 days, during which diagnostic errors may occur (Andre et al., 2021). Moreover, biopsy carries risks, with cerebral hemorrhage being a common complication that may lead to neurological deficits, whether symptomatic or asymptomatic (Li et al., 2022). Given these limitations, low-risk, non-invasive diagnostic methods are needed to assist clinicians. Image segmentation analysis offers an alternative approach for tumor assessment.

Segmentation is the process of partitioning an image into multiple regions to extract Regions of Interest (ROIs), such as tumor masses, enabling more accurate localization and characterization (Michael et al., 2021). Binary segmentation specifically divides image data into two categories—typically, tumor versus non-tumor regions—based on selected features or criteria. This technique is extensively used in medical image analysis for object detection and classification tasks. Tumor segmentation plays a crucial role in clinical practice by supporting diagnosis, prognosis, tumor growth prediction, density monitoring, and treatment planning (Aggarwal et al., 2023).

EfficientNet is a family of convolutional neural networks designed by scaling a baseline network in terms of width, depth, and resolution using a compound scaling method (Lin et al., 2023; Oza et al., 2022; Tan & Le, 2019). This approach balances these dimensions to improve model accuracy effectively (Tan & Le, 2019). EfficientNet-B0 is the simplest variant with the fewest parameters, yet it maintains strong image classification performance with computational efficiency (Fajrina et al., 2024).

In recent years, the importance of MRI for brain tumor diagnosis and management has been widely acknowledged. Lefevre et al. (2016) emphasized that MRI outperforms CT scans by providing superior anatomical detail of brain tissues. Despite MRI's diagnostic utility, manual interpretation and invasive biopsy procedures present challenges such as procedural risks and diagnostic delays, highlighting the need for safer, automated methods. Li et al. (2022) further pointed out cerebral hemorrhage as a significant biopsy-related risk, underscoring the need for alternative low-risk diagnostic strategies. These findings drive the advancement of segmentation technologies as supportive tools in tumor diagnosis.

Binary segmentation methods have demonstrated value in extracting ROIs from MRI scans for medical decision-making (Michael et al., 2021). Applied to brain tumors, such techniques can improve tumor characterization, growth monitoring, and therapeutic planning. However, conventional segmentation methods face limitations in accuracy and computational speed, creating an opportunity to integrate modern artificial intelligence models for automation and enhanced performance.

Therefore, this study aims to apply binary segmentation results from T1-weighted contrast-enhanced MRI images of brain tumors to the EfficientNet model and evaluate its performance using metrics such as accuracy, precision, recall, and F1 score. The outcomes of this research could contribute to more accurate early diagnosis and optimized treatment planning for patients with brain tumors.

METHOD

The study method used is Research and Development (RnD) that aim to create a brain tumor classification model by entering binary segmentation image results into EfficientNet. This study used images from MRI scans of brain tumors that acquired from figshare with the name “Brain Tumor Dataset” by Jun Cheng (Cheng, 2024). The images contain 3064 T1 weighted contrast consisting of 708 meningioma images, 1426 glioma images and 930 pituitary tumor images. However, the images used were 1400 images consisting of 700 glioma images and 700 meningioma images.

The data still in MAT format. Each MAT file consists of a tumor type label (1: Meningioma, 2: Glioma, 3: Pituitary), patient ID, original tumor MRI image, tumor border, and tumor mask. This study only used original tumor MRI images and tumor masks. MRI images and masking images are combined in the MATLAB application with the binary masking segmentation method. Then the results of the binary masking segmentation are entered into the EfficientNet B0 architecture. The results of testing the model using a confusion matrix assessment consisting of accuracy, precision, recall and F1 score.

RESULT AND DISCUSSION

Brain Tumor Image Segmentation Process

This study aims to determine the results of binary segmentation of brain tumors can be tested using the EfficientNet model along with the accuracy results obtained. This study uses data acquired from the internet that include 3064 T1 weighted contrast images consisting of 708 meningioma images, 1426 glioma images and 930 pituitary tumor images. This study uses data of 1400 images consisting of 700 glioma images and 700 meningioma images. The images are divided using a ratio of 80:20, 80% for data training and 20% for data testing, resulting in 1,120 data training images and 280 data testing images. The binary masking segmentation process using MATLAB software. The results of binary masking processing are shown in Figure 1.

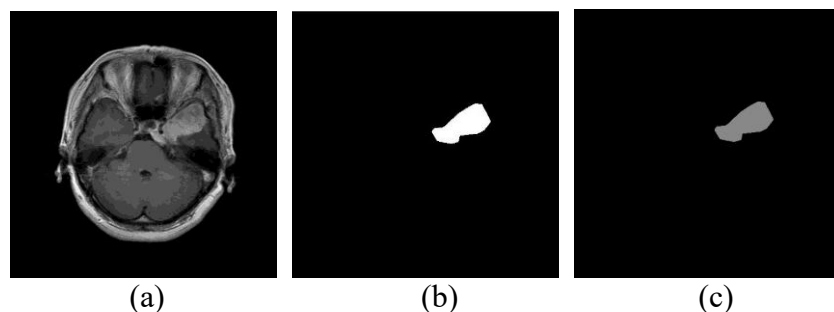


Figure 1. (a) Original image (b) Masking image (c) New binary segmentation image

Model Testing Using EfficientNet

The uploaded data is entered into the tumor dataset folder. The folder consists of a testing folder (data testing) and a training folder (data training). Each folder also contains 2 folders according to the type of brain tumor. After the tumor dataset is available, the EfficientNet model is tested with Google Colab. For the Google Colab system using RAM (random access memory) system of 12.7 GB, a GPU (Graphics Processing Unit) RAM of 15 GB, and a storage of 235.7 GB.

Before testing the model, the first step is install libraries like TensorFlow, Keras, and Google Drive library. This procedure to ensure that the EfficientNet model is controlled and runs properly according to the installation. After the library has been installed, the next step is to authenticate to gain access to the dataset in Google Drive, so that can be entered in the EfficientNet model.

Data preprocessing parameters are set like size and normalization to prepare the model into EfficientNet. For EfficientNet B0, a target size of 224 x 224 is used, a batch size of 32, and a

“binary” class mode. The target size aims to ensure that all images have the same dimensions during the training process. The choice of the “binary” class mode because only uses 2 tumor categories, namely glioma and meningioma. The batch size used is 32 due to memory efficiency. A large batch size can increase training speed because more computation is made. However, large batch size can consume more GPU memory. (Hastomo et al., 2024).

```
class_names = ['glioma', 'meningioma'] # Ganti dengan nama folder Anda

from tensorflow.keras.preprocessing.image import ImageDataGenerator

train_datagen = ImageDataGenerator(
    rescale=1./255,
    shear_range=0.2,
    zoom_range=0.2,
    horizontal_flip=True
)

train_generator = train_datagen.flow_from_directory(
    path_to_your_dataset + '/training',
    target_size=(224, 224),
    batch_size=32,
    class_mode='binary',
    classes=class_names
)

Found 1120 images belonging to 2 classes.
```

Figure 2. EfficientNet model pre-processing settings

After the data pre-processing setup, the next step is to build the EfficientNet B0 model and train the model with 10 epochs. The number of epochs indicates how much of the whole dataset is sent into the model (Hastomo et al., 2024). The higher the epoch, the greater the accuracy but the longer the time required. Therefore, this study uses an epoch of 10 so that the time required is not too long, which is around 1 hour 3 minutes. The results of the data training can be seen in Table 1, which shows that the higher the accuracy value of the training data, the lower the loss value given.

Table 1. Results of the data training process

| Epoch | Time | Loss Value | Accuracy Value |
|-------|-------|------------|----------------|
| 1 | 420 s | 0.6941 | 0.6009 |
| 2 | 381 s | 0.6739 | 0.6071 |
| 3 | 378 s | 0.5949 | 0.6848 |
| 4 | 378 s | 0.5762 | 0.7071 |
| 5 | 381 s | 0.5535 | 0.7188 |
| 6 | 387 s | 0.5332 | 0.7304 |
| 7 | 377 s | 0.4998 | 0.7500 |
| 8 | 378 s | 0.5136 | 0.7616 |
| 9 | 377 s | 0.4705 | 0.7670 |
| 10 | 376 s | 0.4696 | 0.7741 |

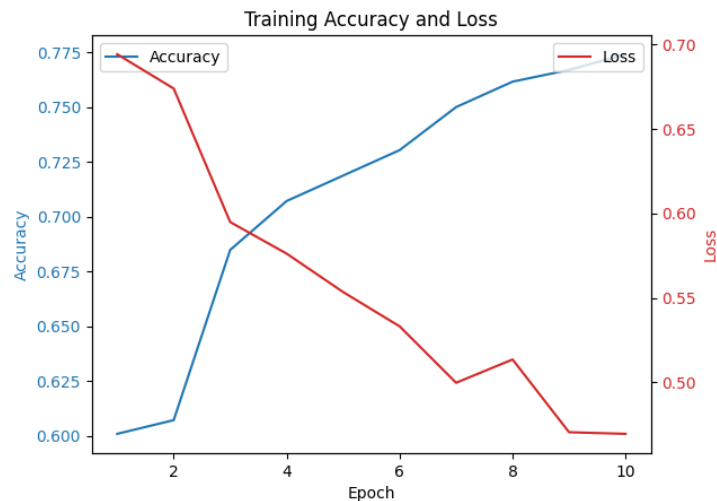


Figure 3. Comparison graph between accuracy value and loss value on training data

After the model training process, the next step is to evaluate the model performance using data testing. This process takes 51 seconds.

```
[ ] test_datagen = ImageDataGenerator(rescale=1./255)
test_generator = test_datagen.flow_from_directory(
    path_to_your_dataset + '/testing',
    target_size=(224, 224),
    batch_size=32,
    class_mode='binary',
    classes=class_names,
    shuffle=False # Jangan shuffle data uji
)

loss, accuracy = model.evaluate(test_generator)
print('Loss: ', loss)
print('Accuracy: ', accuracy)
```

Figure 4. EfficientNet model test setup on data testing

In the confusion matrix table, the image classification results show that 99 images were identified as glioma and 69 as meningioma. However, there was an error in calculating the confusion matrix results which caused 71 meningioma images to be classified as glioma and 41 glioma images to be classified as meningioma.

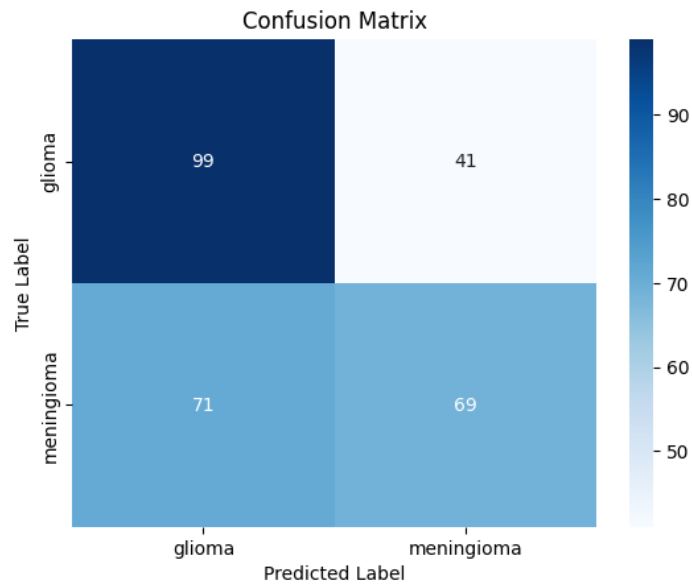


Figure 5. Confusion matrix results on data testing

For the test results, the model obtained an accuracy of 0.6, precision obtained a value of 0.627, recall obtained a value of 0.492, and the F1 score obtained a value of 0.551. But the loss value obtained was higher, which was 0.678. The cause of the loss value being higher than the accuracy value is overfitting. Overfitting is creating a model that accurately represents the training data, but fails to generalize well to new data sampled from the same distribution. (Simon & Aliferis, 2024). Overfitting can lead to high accuracy on data training, but low accuracy and high loss on data testing.

Table 2. Efficient Net model calculation results

| Data Testing Assessment Results | Accuracy | Loss | Precision | Recall | F1 score |
|---------------------------------|----------|-------|-----------|--------|----------|
| | 0,6 | 0,678 | 0,627 | 0,492 | 0,551 |

These results are still far different when compared to previous studies using original MRI images with brain tumor cases, like a research conducted by Medina and Sanchez aimed to assess the performance model of the three types of EfficientNet (B0, B3, and small) using techniques such as transfer learning, fine-tuning, and early stopping. The study used two datasets from different sources. The results show that EfficientNet B0 produces higher accuracy compared to the EfficientNet B3 and EfficientNet small types with accuracy values of 98.4% and 97.5% (Medina & Sánchez, 2023).

The limitation of this study is that if the model testing is done repeatedly, it can cause changes in the results of the test data model. This is because the computational process in Google Colab can affect the test data results produced. In addition, the accuracy of the model is still moderate so this model should be further developed.

CONCLUSION

The results of this study demonstrate that binary tumor segmentation from contrast-enhanced T1-weighted MRI images can be effectively implemented in the EfficientNet model, albeit with moderate accuracy. To enhance model performance, it is recommended to leverage variations of transfer learning techniques, including fine-tuning and early stopping, alongside expanding the dataset to include more diverse cases, such as different tumor malignancy levels and progression stages. Future research should focus on integrating larger, balanced, and clinically

representative datasets and exploring advanced EfficientNet variants or hybrid deep learning architectures. Additionally, investigating robust data augmentation strategies and model interpretability methods, like Grad-CAM, could further improve classification accuracy and clinical applicability in brain tumor diagnosis.

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