

# Colorectal Cancer Histology Classification with EfficientNetB5

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## Abstract

This project explores the application of EfficientNetB5 in automating histological tissue classification for colorectal cancer diagnosis. Leveraging the "NCT-CRC-HE-100K" dataset, containing 100,000 image patches across nine tissue types, the model was trained on a local machine due to AWS limitations. Despite this challenge, the model achieved outstanding results in epoch 10, attaining a training accuracy of 90.96%, with validation and test accuracies maintaining consistency at 90.22.

## 1 Introduction

Colorectal cancer (CRC) is a pervasive and potentially life-threatening malignancy that affects millions of individuals around the world. Early detection and accurate prognosis are important in improving patient health results. In this context, the field of histological analysis provides valuable insights into the good understanding of CRC. Microscopy of histological images stained with hematoxylin and eosin (H&E) provides complex details about tissue composition and structure. However, evaluating these images manually can be time-consuming and subjective, so this project will leverage deep learning methods, especially convolutional neural networks (CNN), for automated histological analysis.

The "NCT-CRC-HE-100K" dataset(1) consists of 100,000 individual image patches obtained from histological images stained with hematoxylin and eosin (H&E) depicting human colorectal cancer (CRC) and normal tissue. Each image patch measures 224x224 pixels at 0.5 microns (MPP) per pixel and is color-normalized. These images cover a wide variety of tissue types, including lipid (ADI), background (BACK), debris (DEB), lymphocytes (LYM), mucus (MUC), smooth muscle (MUS), normal colonic mucosa (NORM), and cancer cells. Related substrates (STR) and colon adenocarcinoma epithelium (TUM)(1).

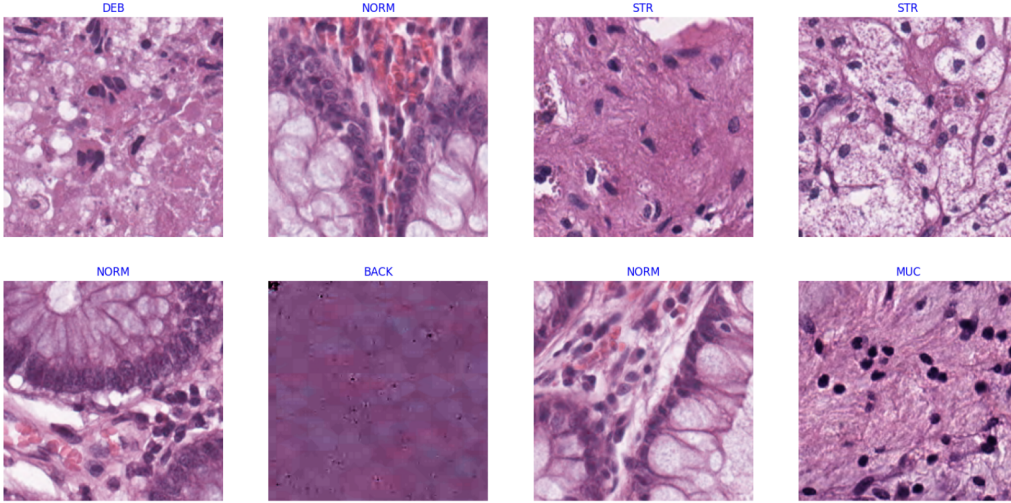


Figure 1: Sample Data

Automating histological tissue classification and increasing the accuracy of colon cancer diagnosis can play an important role. This project is critical as it can have a direct and positive impact on the health and prognosis of patients who are suffering from this condition. This project will eventually lead to faster diagnosis, more personalized treatment plans, and increased likelihood of early detection, all of which can contribute to increased survival and improved overall well-being in people affected by this wide range of malignancies(2).

## 2 Methodology

This project aims to leverage deep learning to build a predictive model for histological tissue type classification. I initially planned to utilize VGG16, but while searching for some information, EfficientNetB5(3) came up and I decided to conduct the project with this model. EfficientNet is a mobile friendly pure convolutional model (ConvNet) that proposes a new scaling method that uniformly scales all dimensions of depth/width/resolution using a simple but highly effective compound coefficient (2).

The goal of this project is to predict tissue types from histological images and classify them into nine classes that are stated in 1. b. Background of the Dataset. The architecture of the project was planned to leverage AWS cloud services (including AWS S3 for data storage and AWS SageMaker for computing performance) for efficient data processing. AWS has limits for their services, and for SageMaker, there was a strict limit for setting a jupyter notebook. I requested a limite increase, but it did not get accepted early enough to conduct this project on it. Instead, this project was conducted in a local machine.

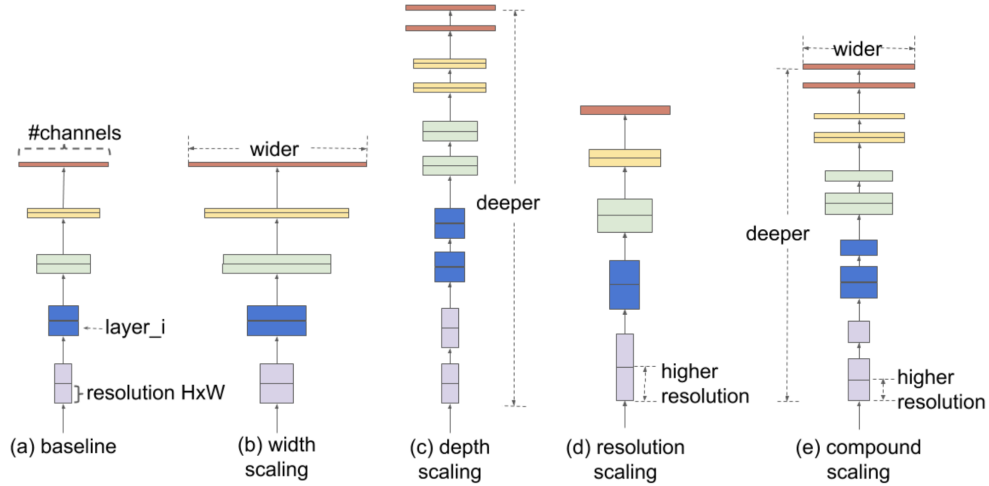


Figure 2: EfficientNetB5

### 3 Experimental Setup

The dataset is splitted into training, validation, and test sets with an 80-10-10 ratio (80000 - 10000 - 10000 images each). It is compiled with the Adamax optimizer (learning rate = 0.001), categorical cross-entropy loss, and accuracy as the evaluation metric. It is trained for 10 epochs using the training data with validation on the test data. The model implements regularization techniques, such as L2 kernel regularization, L1 activity and bias regularization, and dropout (rate = 0.45), to enhance model generalization and to prevent overfitting. The following is the model summary.

Listing 1: Model Architecture

Model: "sequential"

Layer (type)	Output Shape	Param #
efficientnetb5 (Functional)	(None, 2048)	28513527
batch_normalization (BatchNormalization)	(None, 2048)	8192
dense (Dense)	(None, 256)	524544
dropout (Dropout)	(None, 256)	0
dense_1 (Dense)	(None, 9)	2313
Total params: 29,048,576		
Trainable params: 530,953		
Non-trainable params: 28,517,623		

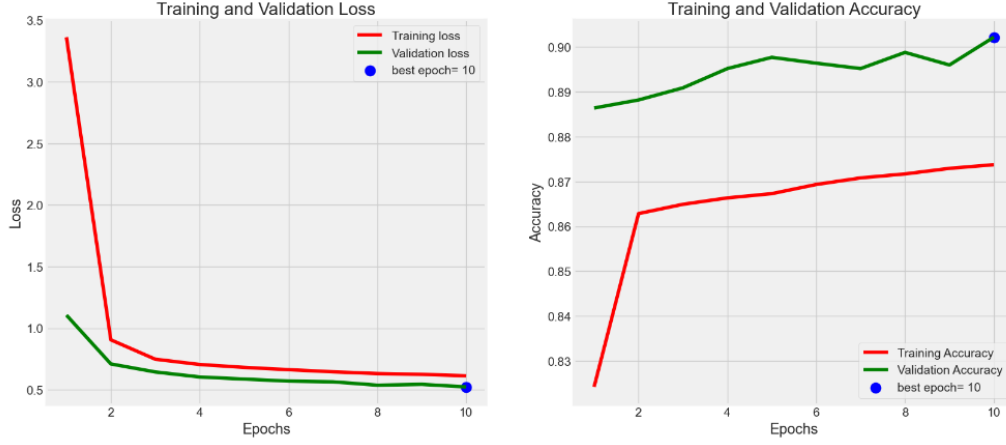


Figure 3: Result

## 4 Results

After training the model with EfficientNetB5 for colorectal cancer image classification, the results indicate that epoch 10 stands out as the most optimal iteration among the 10 epochs considered (3). The training loss reached 0.504, accompanied by an impressive training accuracy of 90.96%. The validation set showed consistent excellence with a loss of 0.522 and an accuracy of 90.22%. The model achieved a test loss of 0.523 and a test accuracy matching the validation accuracy at 90.22%.

Train Loss: 0.5040329098701477  
Train Accuracy: 0.9095625281333923  
Valid Loss: 0.5219358801841736  
Valid Accuracy: 0.9021999835968018  
Test Loss: 0.523360013961792  
Test Accuracy: 0.9021999835968018

I managed to print out a confusion matrix for this model (4). A confusion matrix is a table that is used to evaluate the performance of a classification algorithm. It is particularly useful when dealing with binary classification

problems, but the confusion matrix can also be extended to handle multi-class classification problems, where there are more than two classes. The confusion matrix provides a comprehensive view of how well a model is performing across multiple classes, helping to identify which classes may be more challenging for the model and guiding further improvements.

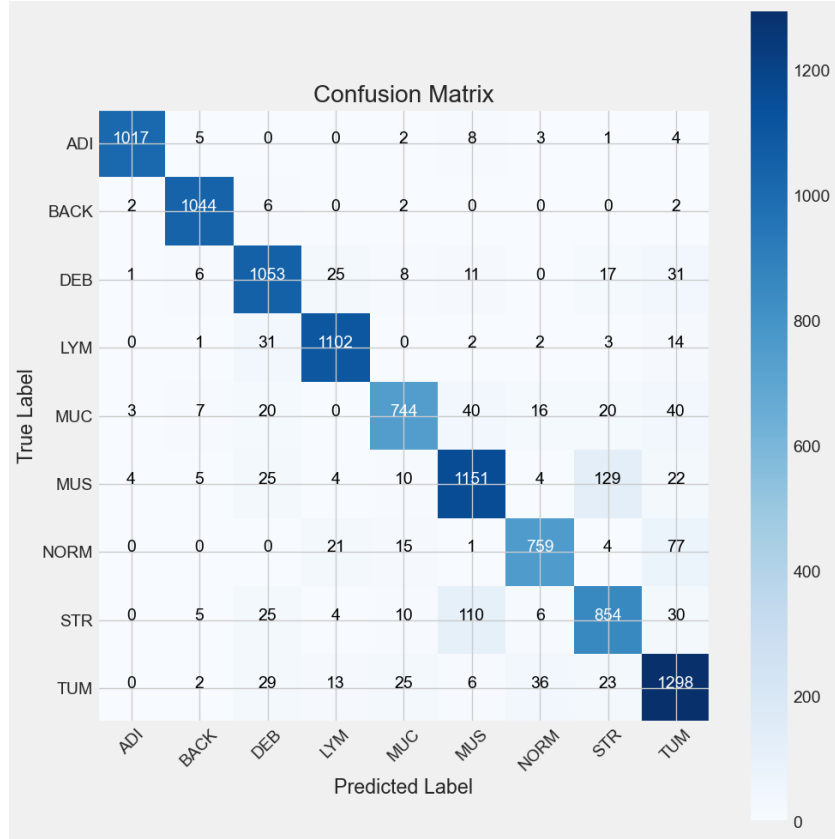


Figure 4: Confusion Matrix

## 5 Conclusion

In conclusion, this project aimed to automate histological tissue classification for colorectal cancer using deep learning, with a focus on leveraging EfficientNetB5. Despite initial challenges with AWS SageMaker limitations,

the model was successfully trained on a local machine. The architecture efficiently classified nine tissue types, demonstrating promising results.

The trained model exhibited exceptional performance in epoch 10, with a training accuracy of 90.96%, validating the effectiveness of EfficientNetB5 in capturing complex features in histological images. The validation and test accuracies remained consistently high at 90.22%. The utilization of regularization techniques, including L2 kernel regularization and dropout, contributed to enhanced generalization and prevented overfitting.

## References

- [1] J. N. Kather, N. Halama, and A. Marx, “100,000 histological images of human colorectal cancer and healthy tissue,” *Zenodo10*, vol. 5281, 2018.
- [2] J. N. Kather, J. Krisam, P. Charoentong, T. Luedde, E. Herpel, C.-A. Weis, T. Gaiser, A. Marx, N. A. Valous, D. Ferber, *et al.*, “Predicting survival from colorectal cancer histology slides using deep learning: A retrospective multicenter study,” *PLoS medicine*, vol. 16, no. 1, p. e1002730, 2019.
- [3] A. W. IBRAHIM, “Human cancer tissues classification efficientnetb5,” 2023. Accessed: 12/13/2023.