UR-15

Analyzing Breast Cancer Histopathology Images Using Deep Neural Network Models

Abstract

Our project aims to explore human tissue cells digitized by whole slide scanners for a better understanding of complex tumor microenvironments in breast cancer histopathology images, using various deep neural network models. First, we experimented with 70% percentages of tumor cells on image classification using ResNet50, VGG16, and Inception-ResNet. Second, we performed instance image segmentation using Mask-RCNN. Third, we applied two well-known explainable artificial intelligence (AI) techniques including Gradient-weighted Class Activation Mapping (Grad-CAM) and Shapley Additive Explanations (SHAP) to determine the effectiveness of the models.

Introduction

Advances in tissue slide imaging techniques have enabled physicians to identify human tissue cells for patients' care using digitized slide images. Analyzing the digitized slide images, however, requires a lot of time for physicians and even causes inter-intra-observer variation, thereby, having a significantly negative impact on patients' outcomes. Many research articles agree that deep learning algorithms are suitable for identifying complex diseases on histopathological images. Our research focuses on exploring human tissue cells and determining the effectiveness of the various deep neural network models through three different computational techniques: image classification, instance image segmentation, and explainable artificial intelligence.

Research Question(s)

1. Can start-of-the-art deep learning models effectively identify cancer image regions by using 70% percentages of tumor cells?
2. Can an instance image segmentation model be used for detecting single cell images?
3. Can explainable AI models be effectively used visualizing the cancer image regions?

Materials and Methods

The one of objectives of our research project is to determine if training images with 70% percentages of tumors would affect the performance of image classification. We randomly collected 100 breast cancer histopathology images and then labeled them with two classes: tumor and non-tumor. Three deep neural network models (ResNet50, VGG16, and Inception-ResNet) were used for the evaluation of the image classification performance. We then visualize the results using two explainable AIs: Grad-CAM and SHAP to explain the deep neural networks. In addition to the image classification, we performed an instance image segmentation using Mask-RCNN for identifying cancerous regions in breast cancer histopathology images.

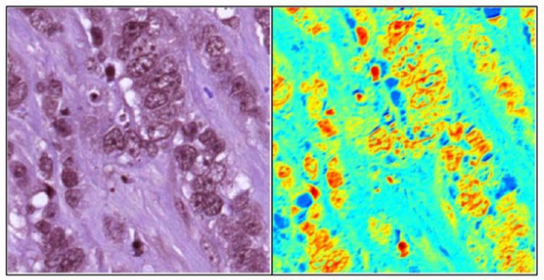

Fig.1 Grad-CAM visualization on tumor regions (Original Hematoxylin & Eosin Image: left, Grad-CAM generated heatmap: right)

Results

Dataset

Two datasets, the Breast Cancer Semantic Segmentation (BCSS) dataset and the Nucleus Classification, Localization, and Segmentation in Breast Cancer (NuCLS) dataset, were used to accomplish our objectives. BCSS dataset consists of 151 large-sized images extracted from whole slide images openly available on the Genomic Data Commons Data Portal, annotated by senior and junior residents and even medical pathology students. The NuCLS dataset is a collection of over 200,000 nuclei annotations of breast cancer tissue. Each slide contains high-resolution pictures with over 10,000 regions and over 500,000 nuclei.

Baselines and Metrics

Three deep neural network models, ResNet50, VGG16, and Inception-ResNet, were used for the image classification tasks, and two explainable AIs, Grad-CAM, and SHAP, were applied to visualize the results. The performance of the models was evaluated using metrics: Precision, Recall, Accuracy, and F1-Score. A confusion matrix was created to compute the evaluation matrix; Precision = TP(TP+FP), Recall=TP/(TP+FN), Accuracy=(TP+TN)/(Positive+Negative), and F1-Score=2xPrecisonxRecall/(Precision+Recall), where TP represents True Positive, FP represents False Positive, and FN represents False Negative.

The results of the image classification using the breast cancer histopathology images are shown in Table 1. Our experiment shows that VGG-16 provides the best results on image classification with 70% of cancer regions. The visualization of the Grad-CAM and SHAP are shown in Figure 1 and Figure 2. The results of signal cell image detection using MaskRCNN in shown in Figure 3.

Table 1. Performance metrics for each model of 70%

Models	F1 Score	Accuracy	Recall	Precision
ResNet-50	0.8205	0.8250	0.800	0.8421
VGG-16	**0.8571**	**0.8650**	**0.8200**	0.9055
Incep.ResNet	0.8519	**0.8650**	0.7800	**0.9396**

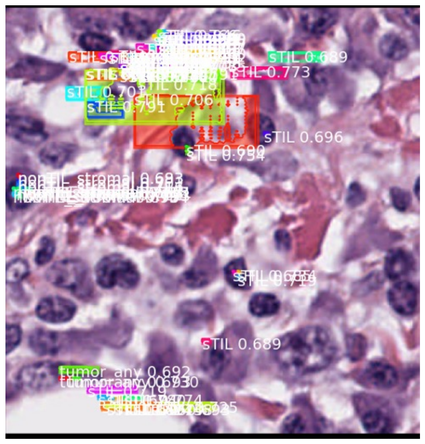

Fig.2 Results of single cell image detection using MaskRCNN

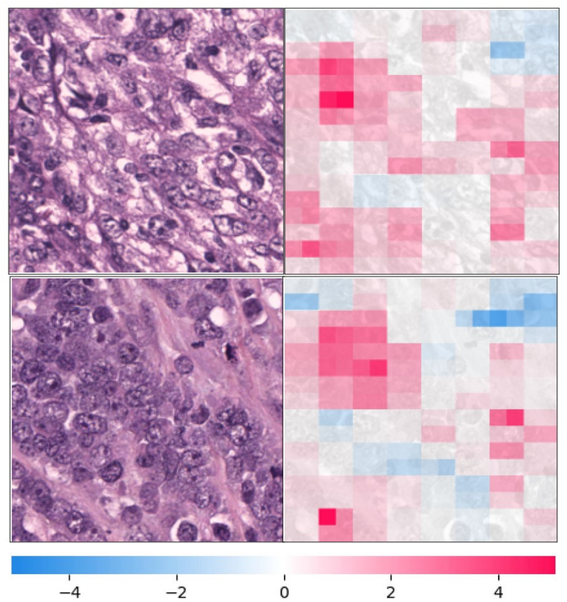

Fig.3 SHAP visualization on tumor regions (Original Hematoxylin & Eosin Image: left, SHAP generated heatmap: right)

Conclusions

We showed the start-of-the-art deep learning models for image classification can be effectively used for identifying cancer image regions by using 70% percentages of tumor cells. In addition to the experiments, we performed the image interpretation on cancerous regions and conducted the visualization using Grad-CAM and SHAP. Moreover, we used MaskRCNN to detect the single cell images and showed the example of the results. In the future, we plan to work on the identification of other types of cancer cell imagers with different percentage.

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References

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