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Breast Cancer Image Segmentation

Overview

The sequencing technique is important in learning information from tissue slides. Tissue slides provide information on a variety of disease-related topics, including cancer subtype, grade, and immune system response. The development of next-generation sequencing techniques has transformed cancer research by enabling previously unattainable insights into the genetic causes of cancer and by making big data techniques a key component of this field's core approach.

How to perform the segmentation well is a problem. Though the segmentation issue is being formulated as a regression task of the distance map, we specifically address the issue of contacting nuclei. The development of digital pathology offers us the challenging potential to automatically evaluate entire slides of sick tissue to create quantitative profiles that can be used for diagnosis and prognosis activities. Using fully convolutional networks(FCN), we introduce a novel technique in this research to automatically segregate nuclei from histopathology data stained with Haematoxylin and Eosin (H&E). We use FCN to show that our approach outperforms other approaches in terms of performance (CNN).

Background

In cancer research, the gene sequence and gene expression data were often used to predict the possibility of getting cancer, but the histopathology data is used in clinical practice for cancer diagnosis and prognosis[1]. The histopathology data includes tissue slides encompassing the tumor and the surrounding tissue which are stained with agents to highlight specific structures, such as cells, cell nuclei, or collagen.[1] The nuclei are used to be detected because they can be used to identify the mitotic index and nuclear pleomorphism, and the staining makes them distinguishable.

State-of-art Techniques

Many methods have been implemented to segment the nuclei, including mathematical morphology[2-4], pixel classification [5], level sets [6], and graph-based segmentation methods [7].

Neural networks are currently regarded as one of the most effective techniques in the field of computer vision. Deep neural networks were initially created for large-scale picture classification; nevertheless, they have quickly been applied to object detection and image segmentation. Indeed, a sliding window approach, where the window's center pixel is classified into two (object/background) or more classes, is the most direct method of applying classification networks to detection and segmentation tasks. This method has been effectively used to identify and categorize nuclei in H&E pictures and other imaging modalities. The number of processes required is relatively big because every pixel requires the classification of the corresponding image patch.

Fully convolutional neural networks directly predict binary maps from images as opposed to employing architectures designed for image classification to each pixel. As a result, these architectures are both accurate and quick for segmentation. To perform various segmentation tasks, such as cell segmentation in microscope pictures, they have also been applied to biomedical data. This paper proposes a novel CNN-based approach for segmenting nuclei. It is doing a regression task to separate nuclei that are contacting or overlapping.

Statement of Work

Datasets

Both the **annotated Stained** Hematoxylin and Eosin (H&E) **histology images** and the **slides** taken from a cohort of 11 Triple Negative Breast Cancer **(TNBC)** patients are included in the dataset[9].

For the **slides data**. All slides are taken from a cohort of TNBC patients and were scanned with Philips Ultra Fast Scanner 1.6RA. In order to represent both intra and inter-patient variability for the same cancer type. The patches are selected to meet the requirements that they consist of both low cellularity regions which can be stromal areas

or adipose tissue and high cellularity areas consisting of invasive breast carcinoma cells[1].

For the **annotated histology image data**. There is a total of 50 images and 4022 annotated cells. The annotation was done by 3 experts using ITK-SNAP: an expert pathologist and two trained research fellows.[1]

Method

We plan to compare different deep learning methods for segmenting nuclei in histopathology images, such as Fully the U-Net [10] and the Fully Convolutional Network for segmentation (FCN) [11].

The CNN has been implemented to do this. However, it does not allow for segmentation. The loss function minimized by CNNs is usually defined at the pixel level, so it is not capable of correctly handling the issue of touching objects.

In the previous work, the fully convolutional networks were highly efficient for segmenting nuclei in histopathology images[12]. It can upscale the classical CNN feature representation and thereby segment images in a single pass [11].

The U-net is invented and will be compared with FCN for superior performance.

Outcome and Performance evaluation

The classification loss and regression loss will be used, and the F1 score with the Aggregated Jaccard Index (AJI) will be used to evaluate the performance. The harmonic mean between recall and precision at the pixel level is the F1 measure, which is similar to the dice coefficient:

$$F_1 = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$$

Every ground truth component is first matched to one detected component by maximizing the global Jaccard index, which is an extension of the AJI. The ratio of the sums of the cardinals of intersection and union of these matched components, respectively, is what the AJI relates to.

$$AJI = \frac{\sum_{i=1}^{L} |G_i \cap S_k^*(i)|}{\sum_{i=1}^{L} |G_i \cup S_k^*(i)| + \sum_{l \in U} |S_l|}$$

We anticipate the U-net will have less loss than others.

Project Plan

Rough Time Table:

27/6-3/7 Start searching for project topics, review relevant papers
4/7-8/7 Write a proposal, set up the environment, and create the Github Project
9/7-17/7 Data pre-processing, and learning novel models
18/7-20/7 Progress report
21/7-24/7 Implement an existing algorithm and test it on the dataset
25/7- 31/7 Design a new algorithm
1/8-7/8 Examine our output and change some model design
8/8-12/8 Wrap up the project, and prepare for the final presentation
12/8 Final presentation
12/8-15/8 Final project report

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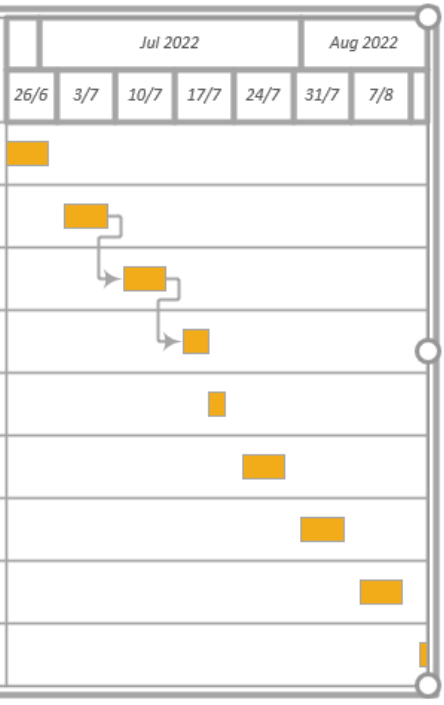
ID	Task Name	Start	Finish	Duration
1	Start searching for project topics, review relevant papers	27/06/2022	01/07/2022	5d
2	Write a proposal, set up the environment, and create the Github Project	04/07/2022	08/07/2022	5d
3	Data pre-processing, and learning novel models	11/07/2022	15/07/2022	5d
4	Progress report	18/07/2022	20/07/2022	3d
5	Implement an existing algorithm and test it on the dataset	21/07/2022	22/07/2022	2d
6	Design a new algorithm	25/07/2022	29/07/2022	5d
7	Examine our output and change some model design	01/08/2022	05/08/2022	5d
8	Wrap up the project, and prepare for the final presentation	08/08/2022	12/08/2022	5d
9	Final Report	15/08/2022	15/08/2022	1d



GitHub Project Link

https://github.com/TingyouGUO/ECE539projects

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