Performance Evaluation of Deep Learning-based Tumor-Infiltrating Lymphocyte Cell Detection Algorithms for Histopathology Whole Slide Images

Abstract

- Tumor-infiltrating lymphocytes (TILs) are promising prognostic biomarkers for HER2+ and triple-negative breast cancer patients.
- Automated TILs detection using deep learning models holds clinical potential, but standardized assessment methods are lacking.
- In this study, we developed and evaluated two TILs detection models (a YOLOv10 and an EfficientNetB0-U-Net) using data from a public challenge (TiGER)^{1.}
- The TiGER dataset was divided into patient-level subsets for model development and testing, with the development set further split into five folds at the ROI level.
- Using development ROIs, the models were trained five times, using four folds for training and one for tuning.
- We used a bagging ensemble method (majority voting) to combine the five finetuned models' outputs.
- Using these finetuned models, we evaluated their performance on the hold-out test data for the cell detection task.
- We calculated several performance metrics at the patient-level. Using bootstrapped samples, we obtained confidence intervals for the selected metrics at the operating points determined during model's finetuning.

Purpose

- Cell detection by an AI model is commonly used in whole slide image (WSI)-based software as a medical device (SaMD). A standardized framework for evaluating these models can help streamline the premarket assessment of such SaMDs and facilitate their translation into clinical use.
- The overall purpose of our project is to develop assessment methods for cell detection algorithms that are commonly used in many pathology devices, with the detection of Tumorinfiltrating lymphocytes (TILs) as a use case.

Pipeline Overview



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Development and T	Sesting Data Split	Strategy
TiGER data are from th	ree sources:	
TCGA: 151 Slides, Cell le	vel annotations derived f	rom BCSS and NuCLS c
JB: 26 Slides, Cell level a	nnotations made by a pa	nel of board-certified bre
C: 18 Slidess Cell level a	annotations made by a pa	anel of board-certified bro
Number of slides from TCGA, TC, and JB	TCGA 151 Slides 1640 ROIs 18950 TILs	TC 26 Slides 81 ROIs 4720 TILs
Randomly splitting slides into "Development" and "Testing" sets	DevelopmentTesting113 Slides38 Slides1285 ROIs362 ROIs14361 TILs4920 TILs	Development 20 Slides 63 ROIs 4031 TILs Testing 6 Slides 18 ROIs 689 TILs
Model Training and YOLO model: An en	Tuning d-to-end detection model	odel leveraging the Y(
II-Net model: A sem	antic segmentation m	odel based on the LL
using a lightweight F	-fficientNet-B0 as the	backbone
Development Tuning ROIs ROIs	Training ROIs	Bound Patches Labels
Development ROIs TCGA 1285 ROIs 14361 TILs	Training ROIs V Pold S F Pold S F Pold S	Bound Patches Labels

Model Testing

JB

39 ROIs

4043 TIL

For each of the ROIs in the test set, we used the sliding window technique (strides of 64 pixels) to obtain patches of size 128×128 pixels. Models' outputs were obtained at the patch level and stitched together to obtain model's predictions at the ROI level. We used non-max suppression to obtain individual TILs locations and used a bagging ensemble method (majority voting) to combine predictions obtained from the five models trained using different training/tuning folds.

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References:

1. <u>https://tiger.grand-challenge.org/</u>

2. Arab A. et al. Assessment of machine learning algorithms for TILs scoring using whole slide images: comparison with pathologists, Proc SPIE Medical Imaging 2024: Digital and Computational Pathology 12933, 285-289.

5-fold Training and Tuning Splits at ROI Level

rotating over the five folds

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Data & Methods

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OLOv10 architecture e version).

Net architecture,



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FDA

YOLO models in this task using the TiGER datasets.