Primaa
The power of AI for pathologists

An Automated Tumour Infiltrating Lymphocytes (TILs) Scoring Tool

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Introduction

TILs score has been identified by specialists to hold high predictive and prognostic value for Her2 positive and Triple Negative breast cancer [1]. While accurate protocols have been developed for its evaluation, pathologists demonstrate significant inter- and intra-observer variability attributed to **cognitive biases** [2]. The guidelines go as follows:

- identify the Invasive Ductal Carcinoma (IDC) bench
- identify tumour-associated stroma within it
- calculate percentage of stroma occupied by TILs

These guidelines served as a basis for developing our automated scoring tool as described on Fig. 1. A **comprehensive interface** (Fig. 3) was built to display results, **providing explicability** and mitigating cognitive biases.

Material and Method

- A patch-classification network with an EfficientNet B1 architecture was trained using cycleGAN stain augmentation for generalisation [4]
- A U-Net like deep learning network with a ResNet backbone followed by a double deconvolution head for stroma and lymphocytes semantic segmentations.
- The publicly available Tiger Dataset is used [3]:
  - WSIROIS (195 slides, 1879 ROIs): all ROIs and their labels are used for training and testing the segmentation model.
  - WSITILS (82 slides): slides were used for testing the final scores. For reliability, the annotation was performed internally by 3 experienced pathologists. The ground truth is the average score.

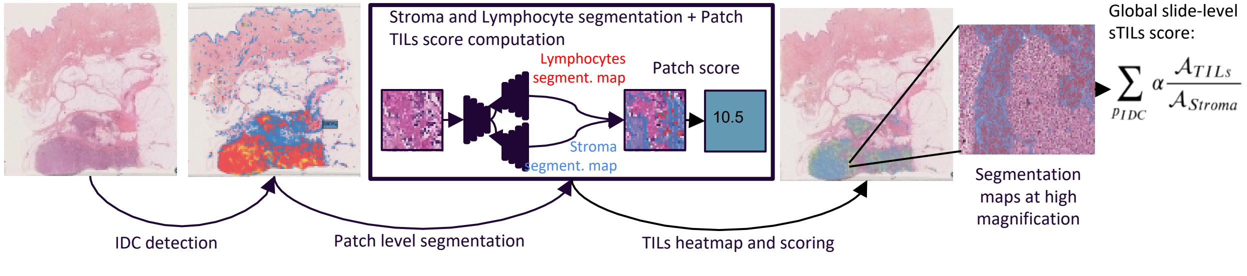


Fig. 1 - WSI processing pipeline for sTILs score

Results and Discussion

- We demonstrate a **high correlation** (Pearson's coefficient: 0.86) between the computed TILs score and the ground truth (Fig. 2)
- Raw scores computed by the algorithm are consistently below those provided by pathologists: it seems that through eye-balling, practicians tend to overestimate the surface ratio between lymphocytes and stroma. To compensate for this shift, a corrective coefficient α ≈ 4.6 is applied to obtain the final TILs score.

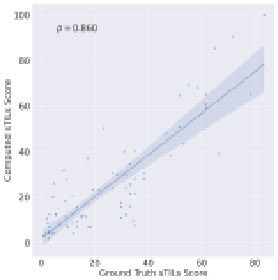
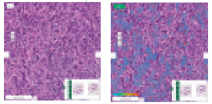


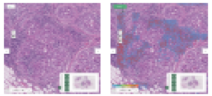
Fig. 2 - sTILs scores correlation

Errors analysis - Main sources of error:

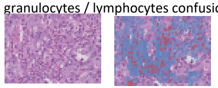
- stroma and epithelium are intertwined



- DCIS mimics the IDC

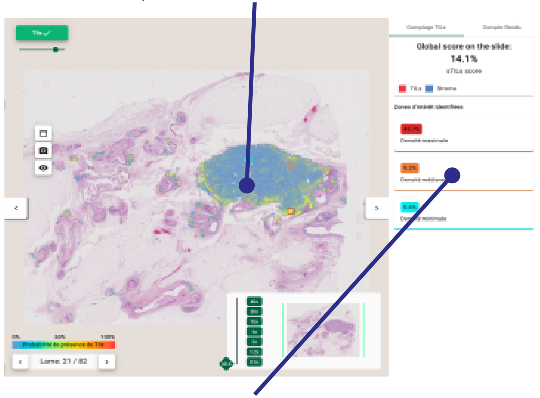


- granulocytes / lymphocytes confusion



The proposed interface

The heatmap helps pathologists not to focus on hotspots and give score more representative of the true distribution of sTILs density.



In order to show a variation of TILs density, 3 ROIs are displayed (the highest, lowest and median density ROIs) with their local sTILs score. Within these ROIs, segmentation maps are displayed for explainability.

Fig. 3 - A comprehensive interface

Conclusions

- The proposed sTILs scoring processing pipeline is **highly accurate**
- The proposed tool for Computer-Aided TILs assessment, using TILs heatmap and ROI proposal:
  - helps **preventing biases**
  - displays **characteristic regions proposal**
  - provides **explainability**
- Some difficult cases are still to be tackled (DCIS-like IDC, granulocytes vs lymphocytes, intertwined stroma and epithelium)

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