

Establishing Qualitative Image Analysis Methods for Tumor Microenvironment Research

Caner Ercan, Luigi Terracciano

Institute of Pathology and Medical Genetics, University Hospital Basel, Basel, Switzerland

I. Introduction

Tumour microenvironment (TME) evaluation requires combination of many cellular and spatial information. Hepatocellular carcinoma (HCC) is the most common primary liver tumour however the correlation between TME features and prognosis remains still unclear. With implementing computational pathology workflow, we aim to define morphological, immunological characteristics of HCC TME as well as their relationship with clinicopathological features.

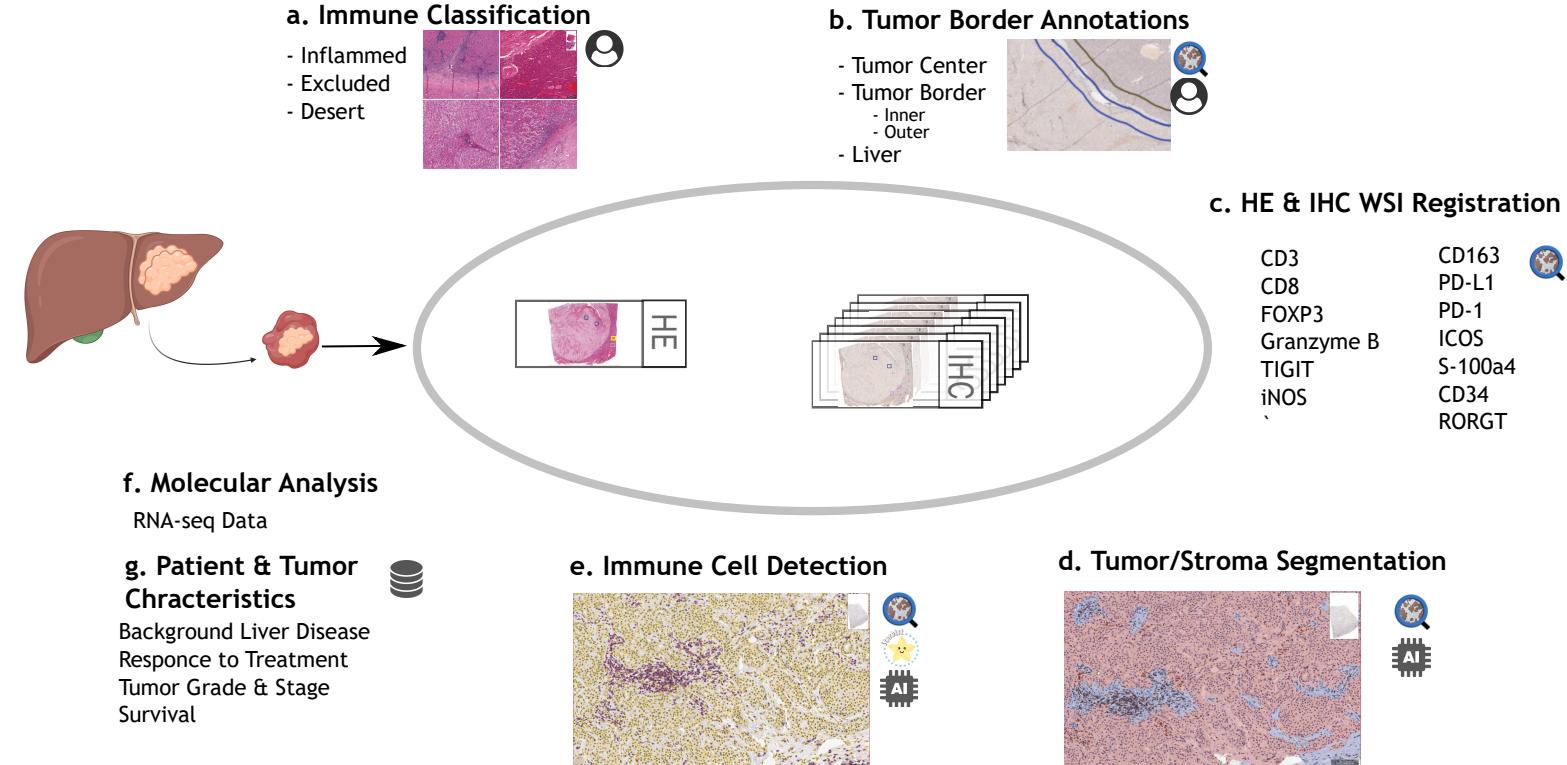
II. Materials and Methods

0. Sample Collection

HCC resection materials were collected from archive of Institute of Pathology University Hospital Basel (n=95). The patient characteristics, such as background liver disease, response to treatment, tumor stage, survival, were collected from hospital database. Tumor slides reviewed by a pathologist and tumor stage, special morphological variants, growth pattern were evaluated for each tumor.

a. Immune Classification

Tumors were evaluated by pathologist for morphological features and classified according to their immune nature. **Inflamed tumors** are those with prominent intratumoral lymphocytic infiltrate and lymphocytes. **Immune-excluded tumors** present lymphocytes only at tumor edges or in the tumor stroma in the immediate vicinity of the tumor cells. **Immune-desert tumors** are those with minimal lymphocytes near the tumor tissue.



III. Outlook & Expected Outcome

Although, the AI models have promising accuracy, there is still need to improve them. Following the fully development of Tumor/Stroma segmentation and Immune cell detection models.

After obtaining the results, immune phenotype class and immune cellular composition will be compared with clinicopathological and molecular characteristics with HCC to reveal the correlations between specific features/groups of HCC with its immune microenvironment. The findings will be confirmed and validated on large publicly available datasets.

IV. Conclusion

We present a pipeline which implements effectively open-source solutions for research and enhances the collected data effectively. The semi-automated computational pathology workflow is able to discover tumour specific spatial TME features.

References

- Chen DS, Mellman I. Elements of cancer immunity and the cancer-immune set point. *Nature* 2017;541:321–30.
- Di Blasi D et al. Unique T-Cell Populations Define Immune-Inflamed Hepatocellular Carcinoma. *Cell Mol Gastroenterol Hepatol* 2020;9:195–218.
- Uwe Schmidt, et al. QuPath: Open source software for digital pathology image analysis. *Sci Rep* 2017;7:16878.
- Uwe Schmidt, et al. Cell Detection with Star-convex Polygons. International Conference on Medical Image Computing and Computer-Assisted Intervention (MICCAI), Granada, Spain, September 2018.

caner.ercan@usb.ch
 caner_ercan
 caner-ercan