Multi-scale Geospatial Characterizations of the Tumor Microenvironment for Cancer Diagnosis, Prognosis, and Molecular Subtyping

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Histopathological images contain rich information about cell morphologies and tissue structures, providing a cost-efficient and easily accessible tool to dissect the tumor microenvironment for clinical decision-making. Recently, deep learning has been widely adopted as a powerful tool to delineate the cell morphologies, tissue architecture, and develop novel image-based biomarkers. More strikingly, H&E-stained histology images can be used to directly predict the status of molecular characteristics such as gene mutations [1], microsatellite instability [2], and even molecular subtypes [3]. However, the field is challenged by the poor interpretability of deep features ("black box" issue), the reliance on high-quality images for cell segmentations, and a lack of high-throughput, systematic quantification. In this talk, I will introduce deep learning frameworks we recently developed for automated tissue classification of routine H&E stained whole-slide images. We employed a multi-scale quantification approach to calculate spatial organization features (SOFs) at different magnification levels, resulting in "tissue-omics" profiles including hundreds of spatial features characterizing tumor microenvironment. In multiple cancer types, we demonstrated that our tissue classification frameworks were accurate and robust, which can assist pathologists for more efficient and automated delineation. Using multiple case studies, we demonstrated the clinical relevance of SOFs and their potential applications in cancer diagnosis, prognosis, and molecular subtyping.

References:

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