



# Deep Multiresolution Cellular Communities for Semantic Segmentation of Multi-Gigapixel Histology Images

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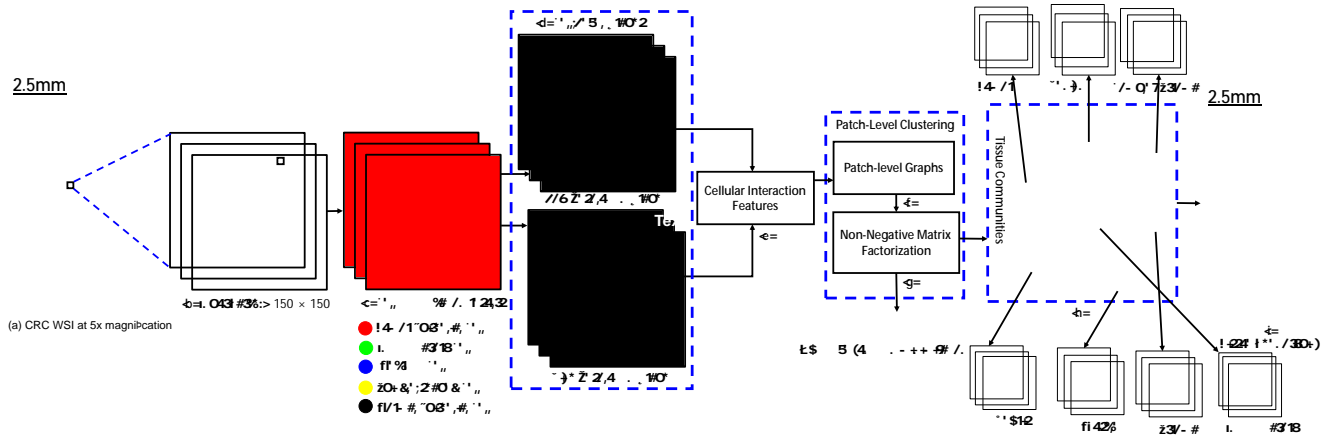


Figure 1: Schematic illustration of the semantic segmentation (or tissue phenotyping) problem in computational pathology and an overview of our proposed deep multiresolution cellular community detection for tissue phenotyping. (a) the input multi-gigapixel whole slide image (WSI) of ColoRectal Cancer (CRC) from our local university hospital; (b) Shows an input patch of size  $150 \times 150$  captured at  $20\times$ ; (c) results of cell detection and classification using spatially constrained deep neural network [26], where red, green, blue, yellow, and black colors represent tumor epithelial cell, inflammatory cell, debris or necrotic cell, spindle-shaped cell, and normal epithelial cell, respectively; (d) low- and high-resolution cell-level graphs – these graphs are constructed using cell-level coarse and fine =convolutional features of the deep neural network; (e)-(f) computation of cellular interaction features and the construction of low- and high-resolution patch-level graphs; (g) our proposed novel objective function minimized using a non-negative matrix factorization algorithm for clustering patch-level graphs into meaningful tissue components including tumor, stroma, muscle, inflammatory, debris or necrotic, benign, and complex stroma shown in (h); (i) results of the different tissue components overlaid on input CRC WSI (a). This problem is similar to the semantic segmentation problem for natural scene analysis in the computer vision community.

## Abstract

Tissue phenotyping in cancer histology images is a fundamental step in computational pathology. Automatic tools for tissue phenotyping assist pathologists for digital profiling of the tumor microenvironment. Recently, deep learning and classical machine learning methods have been proposed for tissue phenotyping. However, these methods do not integrate the cellular community interaction features which present biological significance in tissue phenotyping context. In this paper, we propose to exploit deep multiresolution cellular communities for tissue phenotyping from multi-level cell graphs and show that such communities offer better performance compared to the deep learning and

texture-based methods. We propose to use deep features extracted from two distinct layers of a deep neural network at the cell-level, in order to construct cellular graphs encoding cellular interactions at multiple scales. From these graphs, we extract cellular interaction-based features, which are then employed to construct patch-level graphs. Multiresolution communities are detected by considering the patch-level graphs as layers of multi-level graphs, and also by proposing novel objective function based on non-negative matrix factorization. We report results of our experiments on two datasets for colon cancer tissue phenotyping and demonstrate excellent performance of the proposed algorithm as compared to current state-of-the-art methods.



















