

Quantification of immune cell infiltration in immunohistochemical whole-slide images

Visual inspection of tissue sections is an important part of pathological histology. Different stains can provide additional pathological information. Using different staining techniques can preferentially stain specific components of a tissue section to observe various tissue properties. In recent years, there has been a rapid growth in staining techniques with the development of histology and histopathology [1]. In addition to some conventional staining procedures, many new staining methods, such as Immunohistochemistry (IHC) is constantly proposed.

H&E stain is the most frequently used combination for general staining that consists of two histopathology stains, namely hematoxylin, and eosin. With the H&E staining, pathologists could distinguish between tissue types through the size and shape of cells and nuclei. However, in the interposed connective tissue (“tumor stroma”), there are typically many immune cells that cannot be discriminated solely based on their morphology, thus requiring immunohistochemistry (IHC). IHC staining utilizes antibodies to detect antigens in cells or tissues, which visualize the specific target in tissue samples while maintaining the spatial context and tissue structure. For instance, an antibody that binds to CD8 can be added to the tissue to visualize CD8 through a color reaction (usually brown). The CD8 molecule is a marker for the cytotoxic T cell population with particular immune system features

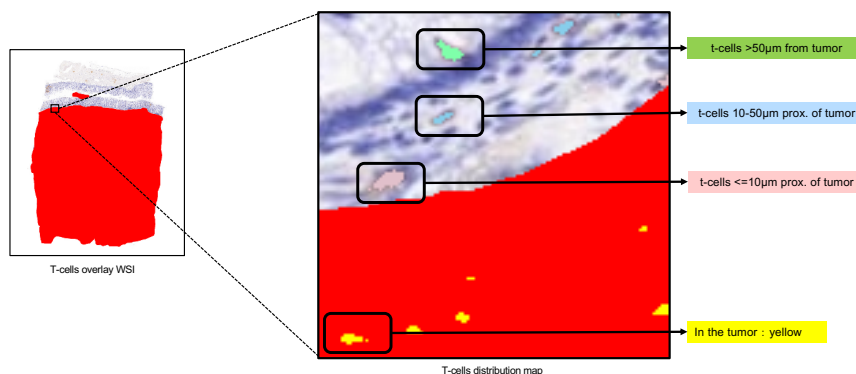


Figure 1: A T-cell distribution map indicates T-cells in and around the tumor.

Many studies show that patients with too much CD8 in the tumor have a much better prognosis [2, 3]. According to the results obtained from these studies, the degree of infiltration of CD8 cells into cancer plays a vital role in the predictive value of the disease.

In this study, a previously developed deep neural network-based method will be improved by leveraging graph network [4] as well as extending the dataset.

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