Image-based consensus molecular subtyping (CMS) of colorectal cancer (CRC) through graph learning

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In computational pathology, reliable analysis of whole-slide images (WSIs) plays a vital role in pathological evaluation. Many studies have been done in the literature for classifying colorectal cancer (CRC) on whole slide images [1, 2]. However, many studies have focused on segmenting the tumor area but not classifying the molecular subtype of cancer.

The phenotypes observed in WSIs only help to understand the biological process of cancer. Since tumors are remarkably heterogeneous, further information, such as consensus molecular subtyping (CMS), is needed for a better cancer diagnosis. However, CMS classification has been done by gene expression profiling, such as RNA sequence analysis, which is expensive and time-consuming.

For instance, in very heterogeneous cancer types such as Colorectal cancer, the invasive CMS4 molecular subtype causing death is more difficult to detect than CMS2 due to the low density in the cancerous region. WSI analysis, which enables these analyses, which significantly affect the course of treatment, to be performed faster and more affordable, shows excellent research potential in image-based molecular subtype classification. However, when we look at the studies in the literature, it is seen that a limited number of image-based CMS analyzes have been performed [3, 4].

The aim of this study is to develop an image-based approach to predict colorectal CMS from standard HE parts using deep learning / graph network [5].

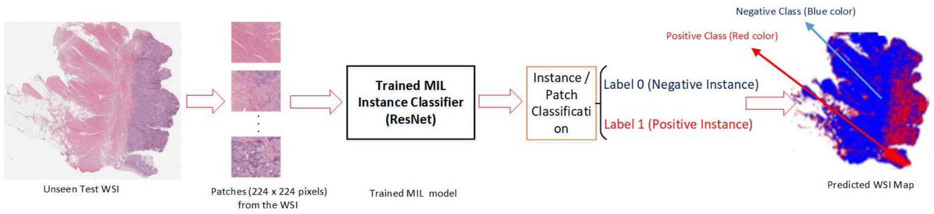

Figure 1: Inference through MIL instance classifier. Here, CMS classification is handled as a binary classification problem. Label 0 represents 'healthy' and 'CMS2' cancer, while Label 1 represents 'CMS4' class cancer.

For further information, please contact Dr. Oezdemir Cetin.

References

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