AI-powered 3D tumor evaluation platform for breast cancer

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Abstract

Analysis of the environment around tumor cells, which is the so-called tumor microenvironment (TME), helps deduce several features that can be used to sort patients into different categories. However, the reality of any tissue structure is determined by its three-dimensional (3D) space, while the conventional two-dimensional (2D) histopathology using hematoxylin and eosin (H&E) and immunohistochemistry (IHC) images are unable to reveal comprehensive information. As a result, 3D tissue imaging with cellular resolution is an important approach to reveal spatial TME information in support of clinical cancer diagnostic and new drug discovery. Since a 3D tissue image usually contains hundred folds of conventional 2D histopathology data, it is difficult to review all information manually within short time. A versatile pre-screening platform is essential for collecting the most significant information from the 3D tissue image during pathologist reviewing.

In this study, an artificial intelligence (AI)-powered 3D tumor evaluation platform for breast cancer tissues was established to accelerate the 3D image analysis process. This platform was trained by annotating fluorescent human breast cancer images equivalent to 30,000 sets of 128 by 128 pixel images, and testing on 6,400 sets of 128 by 128 pixel images. The inference result showed 92% pixel-based segmentation accuracy as compared to conventional pathologist diagnosis. The acceleration performance of this AI-powered platform is evaluated *via* 10 sets of 3D image stacks containing 150 fluorescent 2D images of human breast cancer at 1.4-μm z-axis intervals. These 3D images, which are ~2*2*0.2 mm in size were generated through a process including fluorescence staining, optical tissue clearing and confocal microscopic imaging. The images were recognized and separated into tumor/non-tumor region layer by layer with the AI-powered platform, and reconstructed into their 3D structure, and the planes of maximum and minimum tumor expression were specified and collected from the 3D images for further analysis by the pathologists. The total time consumed by the 3D recognition process was below 10 min, indeed saving plenty of time in 3D tissue image analysis, which in turn would contribute to the future application of the 3D pathological tissue image.