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Knowledge-based image analysis algorithms for quantifying complexity in histology and MR/CT data

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Current feature-based image analysis algorithms can identify nuclei, cytoplasm, and stroma. These algorithms can also detect normal tissue versus neoplastic lesions. However, featurebased algorithms cannot detect the higher-level morphological patterns in tumors that are reminiscent of the tissue of origin. Furthermore, these algorithms cannot detect the degree of recurring sub- architectures that exist in tumors of the same type or stage (i.e. the degree of partial rosettes, the degree of subtle cellular alignments). These recurring sub- architectures in tumors can be precisely quantified by knowledge-based algorithms that capture the spatial information in normal tissues. The knowledgebased algorithms being referenced are publicly available online (ArXiv ID's: 1801.06752, 1710.06593, 1704.07571, 1704.07567, 1704.07567). Some of these algorithms are also applicable to quantifying subtilities in spatial information that are present in magnetic resonance (MR) and computed tomography (CT) images (ArXiv ID: 1801.06752), which may be useful for refining clinical classification of specimens.

Speaker Biography

David H Nguyen is a tumor biologist developing image analysis algorithms to advance digital pathology for cancer diagnostics. His algorithms quantify knowledge-based features of tissue architecture so they can be included in machine learning models that predict clinical outcome. Dave obtained his B.A. and PhD from the University of California, Berkeley. He is currently a Visiting Scholar in the Department of Radiology at Stanford University. Prior to this, he was an Affiliate Scientist in the Molecular Biophysics and Integrated Bioimaging Division at Lawrence Berkeley National Laboratory. His research interests are on Cancer Biology, Immunohistochemistry, Cancer Cell Biology, Cancer, Tumors, Image Analysis, Tumor Biology, Ionizing Radiation, Tumor Microenvironment, Digital Image Analysis, computational pathology.

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