Title: Data-efficient and multimodal computational pathology

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LECTURE ABSTRACT

Abstract: Advances in digital pathology and artificial intelligence have presented the potential to build assistive tools for objective diagnosis, prognosis and therapeutic-response and resistance prediction. In this talk we will discuss: 1) Data-efficient methods for weakly-supervised whole slide classification with examples in cancer diagnosis and subtyping, allograft rejection etc. (Nature Biomedical Engineering, 2021). 2) Harnessing weakly-supervised, fast and data-efficient WSI classification for identifying origins for cancers of unknown primary (Nature, 2021). 3) Discovering integrative histology-genomic prognostic markers via interpretable multimodal deep learning (IEEE TMI, 2020). 4) Deploying weakly supervised models in low resource settings without slide scanners, network connections, computational resources and expensive microscopes. 5) Bias and fairness in computational pathology algorithms.

SPEAKER BIOSKETCH

Dr. Mahmood is an Assistant Professor of Pathology at Harvard Medical School and the Division of Computational Pathology at the Brigham and Women's Hospital. He received his Ph.D. in Biomedical Imaging from the Okinawa Institute of Science and Technology, Japan and was a postdoctoral fellow at the department of biomedical engineering at Johns Hopkins University. His research interests include pathology image analysis, morphological feature, and biomarker discovery using data fusion and multimodal analysis. Dr. Mahmood is a full member of the Dana-Farber Cancer Institute / Harvard Cancer Center ; an Associate Member of the Broad Institute of Harvard and MIT, and a member of the Harvard Bioinformatics and Integrative Genomics (BIG) faculty.