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HistomicsTK: Developing an open-sourced platform for integrated histopathology analysis

Lee Cooper[1,2]
[1]Emory University School of Medicine, USA
[2]Georgia Institute of Technology, USA

Open-sourced software is an important resource for research communities, providing transparency, reproducibility and enabling broad engagement among researchers to understand and build upon the communities' work. While mature open-sourced image analysis tools are commonplace in the radiology domain, the digital pathology domain has relatively few open source tools for histopathology image analysis. This talk will discuss ongoing efforts by Emory and Kitware, Inc. to develop HistomicsTK, an open source platform for histopathology image analysis. HistomicsTK enables users to analyze large collections of whole-slide images, providing algorithms for common image analysis tasks including segmentation, feature extraction and classification. It provides infrastructure for the parallel execution of image analysis pipelines and enables algorithm/pipeline portability and easy deployment using containerization technology and network-based access to computational capabilities through REST interfaces. Case studies using HistomicsTK and its precursor tools will be presented including systems for interactive classification, nuclear morphometrics and immunohistochemical quantification. Using data from The Cancer Genome Atlas we will demonstrate how HistomicsTK can used to analyze multifaceted datasets containing digital pathology images and comprehensive genomic and clinical characterizations of cancers to explore prognostic imaging biomarkers and to investigate fundamental disease processes like angiogenesis and lymphocytic infiltration.

Biography

Lee Cooper is an Assistant Professor with joint appointments in Biomedical Informatics and Biomedical Engineering at Emory University and Georgia Tech. He has received his PhD degree in Electrical Engineering from Ohio State University in 2009 and then joined Emory University; where he currently leads the Cancer Data Science lab. His research investigates computational methods for the analysis and integration of digital pathology, genomic and clinical data with the goals of improving prognostic accuracy and disease classification.

lee.cooper@emory.edu

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