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The cancer digital slide archive (CDSA): A web based resource linking pathology, radiology and genomics

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The Cancer Genome Atlas (TCGA) is an NCI funded project integrating clinical, histopathological, molecular (mRNA/miRNA, protein, copy number, etc) and metadata for over 25 different cancer types. The overall goal is to harness large data sets to discover insights in cancer progression. Several recent TCGA studies have illustrated important relationships between morphology observed in whole-slide images, clinical data and genetic events and therefore the ability to link these data sources over hundreds of patients could potentially lead to a greater insight in cancer progression. However, the integration and visualization is a common challenge in biomedical informatics and better tools are needed to combine the vast and disparate data types. Our group has developed a number of web-based tools to support the federation, visualization and analysis of both pathology and radiology imaging data. The CDSA houses over 25000 digital pathology images as well as integrated tools to view related metadata, as well as for image markup and data analysis. A brief overview of some of the capabilities and data available in this public resource will be discussed. In addition, we will review some of the open-source tools used to power this archive. Finally, some of the science that this technology has enabled will be reviewed.

Biography

David A Gutman has received his MD/PhD from Emory University and then completed a Psychiatry Residency. He has published over 75 papers and has a broad range of interests in the digital imaging (radiology and pathology) and clinical informatics. He is currently an Assistant Professor of Neurology, Psychiatry & Biomedical Informatics and is also a Staff Physician at the Atlanta VA.

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