



Biomedical Image Computing and Informatics Seminar

“Radiomics of Cancer in the Post-genomic Era”

Robert Gillies, PhD

Vice Chair of Radiology
Director of Molecular and Functional Imaging
Department of Cancer Physiology
H Lee Moffitt Cancer Center

Smilow Rubenstein Auditorium & Commons

3400 Civic Center Blvd.

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****Pizza lunch at 12:45pm***

Abstract

Although cancer is often referred to as “a disease of the genes”, it is indisputable that the genetic and epigenetic properties of individual cancer cells are highly variable, even within the same tumor. These heritable genomic differences can impart distinct phenotypic properties on cells, such as pre-existing resistance to targeted therapy. Hence, upon therapy, pre-existing resistant clones will emerge and proliferate following therapeutic selection that targets sensitive clones. Quantitative image analytics, known as “radiomics,” can be used to quantify and characterize this heterogeneity prior to and during the course of therapy. The goal of the radiomics enterprise is to provide informed decision support for the practice of Precision Oncology. This may be clinically important, as virtually every cancer patient is imaged radiologically during the course of their care. Radiomics is predicated on the beliefs that these images reflect underlying pathophysiologies, and that they can be converted into mineable data for improved diagnosis, prognosis, prediction, and therapy monitoring. In the last decade, radiomics of cancer has grown from a few labs to now a worldwide enterprise. During this growth, radiomics has established a convention, wherein a large set (1-2,000) of annotated image features are extracted from segmented regions of interest and used to build classifier models to separate individual patients into their appropriate class (e.g., indolent vs. aggressive disease). Conventional radiomics requires user defined VOI segmentation and feature sets. In contrast, an extension of conventional radiomics called “habitat imaging” foregoes the need for operator-define VOIs in favor of identifying tumor sub-regions with clustering algorithms. These sub-regions have common physiologies and are spatially distinct and hence are known as “habitats”, which can be explicitly linked to underlying local bio-chemistries and pathophysiologies. A further extension foregoes the need for user-defined features, in favor of those defined by “Deep Learning” algorithms, wherein, e.g. convolutional neural networks can be used to detect the most informative regions and features without human intervention. While this has been very successful at classifying at the pixel level (auto-detect and auto-segment), its potential to classify at the patient level cannot be reached with the small size of our current data sets. Data sharing via distributed learning is one possible solution to this limitation.

Bio

Dr. Robert J. Gillies is the Martin Silbiger endowed chair of the Department of Cancer Physiology and Vice-chair in the Department of Radiology for research at the H. Lee Moffitt Cancer Center and Research Institute in Tampa, Florida. He received his PhD in Zoology from UC Davis in 1979 under David. W. Deamer and subsequently pursued a post-doctoral fellowship in in-vivo Magnetic Resonance Spectroscopy at Yale University with Robert G. Shulman. He joined the faculty at Colorado State University as an Assistant Professor of Biochemistry in 1982. He moved to the University of Arizona as an associate professor with tenure in 1988 to establish a research program in biomedical Molecular Imaging. While at Arizona, he was founding directors of the Cancer Imaging program and the Advanced Research Institute for Biomedical Imaging, ARIBI. He relocated to Moffitt in 2008 as part of a major investment in radiology and imaging research.

Dr. Gillies’ research is guided by the general principle that cancers are complex and dynamic systems fundamentally governed by the often non-linear forces of ecology and evolution. Throughout his career, Dr. Gillies has had an unwavering interest in characterizing the causes and consequences of tumor metabolic heterogeneity. His research into this issue is a continuum from “wet” cell & molecular bench science to “dry” lab of computational imaging analytics (“radiomics”).