

Public Abstract

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Graduation Term:SS 2012

Department:Health Informatics

Degree:PhD

Title:Uncovering Morphoproteomic Relationships Using Probabilistic Graphical Models and Resource Description Framework Knowledgebases

The heterogeneity of individual patient responses to conventional drug therapies is one of the central problems in personalized medicine and has great impact on clinical outcomes. To address this problem a new field of morphoproteomics was recently introduced. Morphoproteomics is a new method aimed at comprehensive analysis of protein circuitries in diseased cells to design effective drug therapies for individual patient cases. However, due to the overwhelming amount of molecular information that needs to be processed, successful adoption of morphoproteomics will greatly depend on availability of a comprehensive computerized knowledgebase and intelligent retrieval technologies.

We have, therefore, initiated new research with the overall goal to develop informatics methods to support morphoproteomic studies. We integrate evidence and information extracted from Whole Slide Imaging (WSI) and Immunohistochemistry (IHC) as well as from a semantic mashup of publicly available knowledge sources to provide pathologists a comprehensive picture of morphoproteomic mechanisms. This dissertation introduces novel methods for improving IHC antibody/antigen test selection as well as uncovering morphoproteomic relationships using probabilistic graphical models and Resource Description Framework (RDF) graphs of biomedical knowledgebases. Our methods have great potential to bring a broad impact in to pathology and personalize medicine as well as to be extended to more general systems biology domain.