Katedry fyzikálnej a teoretickej chémie, biochémie a genetiky PriF UK
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Vás pozývajú na 97. prednášku v rámci Kuželových seminárov:

prof. Igor Jurišica

Princess Margaret Cancer Centre, Toronto

Precision medicine through integrative computational biology

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Igor Jurišica, PhD is a Senior Scientist at University Health Network and a Professor at the Departments of Medical Biophysics and Computer Science at the University of Toronto, an Adjunct Professor at the School of Computing and Pathology and Molecular Medicine at Queen's University, and Department of Computer Science at York University, and an Honorary Professor, Shanghai Jiao Tong University. He is also a Faculty Member of the Centre for Math Medicine at the Fields Institute and a Visiting Scientist at the IBM Centre for Advanced Studies, and an Informatics and Communications Technology Scientific Co-Lead at the TECHNA Institute for the Advancement of Technology for Health.

Dr. Jurisica has won numerous awards, including a Tier I Canada Research Chair in Integrative Cancer Informatics, the IBM Faculty Partnership Award, and IBM Shared University Research Award. He has also recently been included in Thomson Reuters' 2014 list of Highly Cited Researchers, documenting the world's most influential researchers spanning 21 fields of sciences and social sciences. Each researcher included in this list has had multiple Highly Cited Papers that represent the top 1% of their respective fields. His research focuses on integrative cancer informatics and the representation, analysis and visualization of high-dimensional data to identify prognostic/predictive signatures, drug mechanism of action and *in silico* re-positioning of drugs. Interests include comparative analysis for mining different integrated data sets (e.g., protein-protein interactions, high-dimensional cancer data, and high-throughput screens for protein crystallization). Two example "big data" projects that systematically and comprehensively explore protein crystallization screens and clinically-relevant cancer biomarkers.

Tézy prednášky: Biomedical researchers use models of biological systems to integrate diverse types of information. This ranges from multiple high-throughput datasets, functional annotations and orthology data to expert knowledge about biochemical reactions and biological pathways. Such integrative systems are used to develop new hypotheses and answer complex questions such as what factors cause disease; which patients are at high risk; will patients respond to a given treatment; how to rationally select a combination therapy to individual patient, etc.

Precision medicine needs to be data driven and corresponding analyses comprehensive and systematic. We will not find new treatments if only testing known targets and studying characterized pathways. Thousands of potentially important proteins remain poorly characterized. Computational biology methods can help fill this gap with accurate predictions, making disease modeling more comprehensive. Intertwining computational prediction and modeling with biological experiments will lead to more useful findings faster and more economically.

The rapidly growing amount of data and knowledge in scientific articles and in public datasets is increasing the complexity of these models daily, making the work of maintaining them up-to-date ever more challenging and highlighting the pressing need to develop computational techniques to help with the associated tasks. Among these methods, diverse semantic web technologies, from linked data to ontologies, are increasingly becoming core components of a wide range of tools that are central to systems biology. These integrative tools enable scientists to combine quantitative and qualitative biological data and knowledge represented as formal concepts and rules to generate hypotheses as well as to test if they are sound and consistent. They are also instrumental to answer complex queries and perform advanced tasks, such as combining individual reactions into potential new pathways.

Semantic biological pathway modelling, in particular, has been studied for some time, but it is still at an early stage of development. Specifically, we discuss challenges and experiences in the design and construction of pathway representation models, as well as tools and strategies for using these models for visualization, data integration, and hypotheses generation. These computational predictions improved human interactome coverage relevant to both basic and cancer biology, and importantly, helped us to identify, validate and characterize prognostic signatures. Combined, these results may lead to unraveling mechanism of action for therapeutics, re-positioning existing drugs for novel use and prioritizing multiple candidates based on predicted toxicity, identifying groups of patients that may benefit from treatment and those where a given drug would be ineffective.

Recent Publications

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