BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Network Science Seminar

October 6 (Friday), 2017, 11am @ 5th floor conference room

Vrushali Fangal

Associate Computational Biologist
Broad Institute of MIT and Harvard

MIDAS - automatic translation of MechanIstic rules to DynAmic logic ruleS

Abstract - Gene regulatory network cascades dictate various functions involved in cell fate such as apoptosis, cell differentiation, angiogenesis and growth in response to an external stimulus. This ability of cellular networks to predict cell fate makes it engaging for researchers to simulate networks. In spite of high-throughput technologies giving rise to an astronomical amount of interaction data in publicly available databases, a qualitative interpretation of heterogeneous pathways involved in diseases still remains an obstacle. Discrete dynamic models such as Logic models provide a good way of integrating partial information of regulatory interactions into predictive mathematical models that describe system evolution without the requirement of additional kinetic parameters. In this talk, we focus on automatic translation of mechanistic models from literature and publicly available databases to logic models and also provide a guideline for standardizing rule translation from mechanistic rules to logic rules. From a Systems Biology perspective, scientists are interested in inspecting the crosstalk between different pathways involved in a disease. It is a hard task to amalgamate polymorphous pathways into a succinct master pathway manually. Our algorithm provides an automatic and fast way of concisely integrating individual pathways into a panoramic pathway by transforming atomic interactions/reactions into a logic predicate, thereby bridging the gap between mechanistic models and rule-based models. This work was done under the supervision of Dr. Amitabh Sharma at the Channing Division of Network Medicine, Harvard Medical School.

Bio: Ms. Vrushali Fangal is Associate Computational Biologist at the Broad Institute of MIT and Harvard. She is interested in studying the Dynamical systems of networks in biology to detect novel drug discovery targets and therapies. She completed her B.Tech at IIT (ISM) Dhanbad, India majoring in Computer Science and Engineering. She has gained her experience in Computational biology through her research experience at leading companies like Novartis(May, 2013-May, 2014) and Roche Diagnostics (May, 2015-Aug, 2015). She worked as a Research assistant at Carnegie Mellon University (Aug, 2014-May, 2016) in the Computational biology department at the School of Computer Science. In addition to this, she has gained international scholarships to participate in Summer Research programs in Bioinformatics at University of Queensland, Australia (Dec, 2011 - Feb, 2012); NASA Astrobiology Institute through Virginia Tech (June, 2012 - Aug, 2012).

Hosted by Yang-Yu Liu