No. 2018-14

Mon., **23 Apr.**, 4pm

Jukhyun Bio Auditorium(RM.121)

School of Life Sciences
Seminar Series

2018
Spring
Semester

English

Automated assembly of explanatory models of biochemical mechanisms from the scientific literature

Speaker | **Benjamin Mate GYORI, Ph.D.**

Affiliation | **Harvard Medical School**

Host | **Prof. Steve K. Cho**

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Abstract

Computational models of signaling, metabolic and gene regulatory pathways have the potential to elucidate complex phenomena in healthy and diseased cells, to help understand their response to perturbations, and to explain multi-omics experimental data. However, building models has been a laborious process involving manual information gathering and model implementation by human experts. We developed INDRA (the Integrated Network and Dynamical Reasoning Assembler), a novel system for automatically assembling models of biochemical mechanisms directly from English language (including from the scientific literature) and pathway databases. INDRA interfaces with natural language processing systems to extract a large number of mechanisms from phrases such as “GRB2 binds EGFR that is phosphorylated on a tyrosine residue” and uses assembly algorithms to resolve redundant knowledge and produce models. We present applications of the INDRA system including (i) a dynamical model automatically built from an English language description which can reproduce resistance to targeted inhibition in BRAF-V600E-driven melanoma cells (ii) a dynamical model of growth-factor signaling built by machine-reading 95 thousand scientific publications, which can provide mechanistic explanations to drug perturbations in a melanoma cell line (iii) a self-updating model of RAS signaling called The RAS Machine, which reads and assembles new literature each day, as it appears and (iv) a human-machine dialogue system in which a user can gather information and build a mechanistic hypothesis to an observed phenomenon by talking with a computer partner.

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Speaker

Benjamin Mate GYORI, Ph.D.

Education/Experience

2005-2009	B.S., Computer Engineering, Budapest University of Technology and Economics
2010-2014	Ph.D., NUS Graduate School for Integrative Sciences and Engineering , National University of Singapore
2015-2017	Postdoctoral Research Fellow, Harvard Medical School
2017-present	Research Associate in Therapeutic Science, Laboratory of Systems Pharmacology, Harvard Medical School

Research Interests

As a computer scientist, I am interested in using computational methods to understand biological systems and other complex systems. My research lies at the intersection of systems biology, bioinformatics and artificial intelligence. I have been an active performer in several DARPA programs including Big Mechanism, Communicating with Computers, and World Modelers.

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