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Department of Medicine
Channing Division of Network Medicine

Channing Methods Meeting

April 11 (Tuesday), 2023, 11AM (ET)

MCP 5th-floor large conference room

<https://us02web.zoom.us/j/579497999?pwd=cHNIWHMzWUJFUUVJTG1EeVJmY05aQT09>

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<https://scholar.harvard.edu/bgyori>

<https://indralab.github.io>

Accelerating biomedical discovery with large-scale mechanistic knowledge assembly and model generation

Computational models of biological mechanisms take substantial human effort to construct and rarely scale to the level of omics datasets, while statistical approaches often do not make use of prior knowledge about mechanisms. At the same time, scientific knowledge is rapidly evolving with about 1.4 million new publications in biomedicine per year. To address these challenges, I present INDRA, an automated knowledge assembly system that integrates multiple text-mining approaches to process scientific literature combined with human-curated databases. INDRA standardizes knowledge extracted from these sources, systematically corrects errors, resolves redundancies, infers missing information, and introduces explicit probability models and machine-learned estimators of confidence to create a coherent knowledge base, up to the scale of all available literature. Detailed simulation models, causal networks, and knowledge graphs are generated from this assembled knowledge to support further analysis. I will present applications of this technology to explaining cancer gene co-dependency data and constructing explanations for experimental observations of drug response in multiple disease areas. This opens up directions toward increasingly automating the scientific discovery cycle with the help of machines building and using models and recognizing surprising observations or proposing new hypotheses.

Bio: Benjamin M. Gyori, Ph.D. leads the Machine-assisted Modeling & Analysis group at the Laboratory of Systems Pharmacology, Harvard Medical School. Originally a computer scientist, Ben completed his Ph.D. at National University of Singapore working on probabilistic approaches to modeling uncertainty in biological systems. Ben's research at Harvard Medical School has centered around new computational frameworks for scaling up and automating scientific modeling through a combination of text mining, knowledge assembly, and causal analysis. He has also pursued research on applying these approaches to understanding disease mechanisms and drug discovery in multiple disease areas. He is currently principal investigator on three research grants and is the recent recipient of the DARPA Young Faculty Award and DARPA Director's Fellowship Award. Ben is an advocate for open science and open-source software development, having led the development of multiple research software used widely in the community.