



Current Position: Assistant Professor in the Department of Pharmacology and Systems Therapeutics at Mount Sinai School of Medicine in New York, NY

Education: Ph.D. in Biomedical Sciences (2006) from Mount Sinai School of Medicine of New York University

Non-scientific Interests: Distance running, and cooking

After graduating with B.S. and M.S. degrees in Computer Science and working as a software engineer for five years, I entered the Ph.D. program in Biomedical Sciences at Mount Sinai School of Medicine in New York in 2002 without much biological background. For my thesis, I looked for a project that would combine my computer science background with the rigorous molecular and cell biology program (with which I struggled during the first two years). I noticed that many biochemistry papers describe molecular interactions between proteins typically in the following format: “A” activates or inhibits “B” as well as “A” phosphorylates or dephosphorylates and/or binds to “B.” There were thousands of these papers and a lot of confusion about how to organize and integrate the data. It was clear to me that combining regulatory relations between proteins from those papers into a directed graph format is possible and might be useful.

I joined the laboratory of Professor Ravi Iyengar, where we constructed and analyzed a large-scale neuronal signaling network from functional studies. With the help of other lab members, we extracted all the interactions in this network manually, which was a lot of hard work. When I had a large-scale directed mammalian cell signaling network in my hands, I looked for ways to analyze its topology. This required opening some old computer science and math books on graph theory, and learning from similar work that others have done. This minireview describes applications of graph theory to understand the topology of biological intracellular networks. It also describes ways graph theory is used for integrating background knowledge about properties of genes and proteins for the purpose of building more informed hypotheses when analyzing high-throughput data.

Read Dr. Ma'ayan's article entitled: Insights into the Organization of Biochemical Regulatory Networks Using Graph Theory Analyses

<http://www.jbc.org/cgi/content/full/284/9/5451>