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Nathan Price is an Associate Professor at the Institute for Systems Biology. He is also an Affiliate Associate Professor in the Departments of Bioengineering and Computer Science & Engineering at the University of Washington, where he advises graduate students as a member of the Graduate College. Prior to moving to ISB, he was an Assistant Professor at the University of Illinois at Urbana-Champaign from 2007-2011, where he continues to hold adjunct appointments in the Department of Chemical and Biomolecular Engineering and the Institute for Genomic Biology. In December 2006, Dr. Price was named one of the inaugural "Tomorrow's PIs" as a "rising young investigator" in systems biology by *Genome Technology*, and in 2008 was the recipient of the Howard Temin Pathway to Independence Award in Cancer Research from the National Institutes of Health. In 2009, he received the NSF CAREER Award to use system biology approaches to guide genome-scale synthetic biology efforts. In 2010, he received the Young Investigator Award from the Roy J. Carver Charitable Trust for his work to build genome-scale biomolecular network models of human glioblastoma (brain cancer). In 2011, he was one of 13 chemical scientists in the country to be named a Camille-Dreyfus Teacher-Scholar by the Dreyfus Foundation. Dr. Price served on the steering committee of the Illinois-Mayo Clinic Alliance for Personalized Medicine from 2010-2011, and currently serves on the National Academies-Institute of Medicine committee to review omics based tests to predict clinical outcome in clinical trials. Dr. Price is an associate editor of *BMC Systems Biology* and *Biotechnology Journal,* and a Deputy Editor-in-Chief of *PLoS Computational Biology*. Dr. Price also serves on the scientific advisory board of TetraVitae Bioscience, and is a member of the Board of Directors and Scientific Advisory Board of the P4 Medicine Institute.

Title: Systems analysis of genome-scale metabolic and regulatory networks

Abstract: The rise of genomics and associated technologies has given us a powerful new lens to study the biological world – providing a torrent of data that requires deep network contexts to interpret deeply. To harness the power of genomics, it is thus essential to link genotype to phenotype through the construction of quantitative systems models — and to integrate unified models across a diversity of biological network types. I will discuss approaches for the creation of such quantitative models that can simulate a variety of cellular functions, and show examples of a number of such models we have built in my lab. I will focus particularly on automated methods for integrating metabolic and regulatory networks such as our newly developed approach, Probabilistic Regulation of Metabolism (PROM) (Chandrasekaran and Price, PNAS, 2010). PROM is notable in that it represents the successful integration of a top-down reconstructed, statistically inferred regulatory network with a bottom-up reconstructed, biochemically detailed metabolic network, bridging two important classes of systems biology modelsthat are rarely combined quantitatively. In addition, I will also briefly address some of the implications for biochemical reaction networks from emerging single-cell enzyme copy number data (e.g. Kim, P.J, and Price, N.D., Physical Review Letters, 2010).