CHEMICAL ENGINEERING
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CHEMICAL ENGINEERING 290 SEMINAR SERIES PRESENTS

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Optimization driven reconstruction, analysis and redesign of metabolism.

4pm - Thursday, January 14th 2016 in ENGR II rm 1519

Metabolism is defined as the full complement of chemical transformations in living systems. Systems biology techniques are increasingly being used to elucidate and quantify the full range of molecules and processes at work. In this talk, we will discuss how we can speed up the process of building and correcting organism-specific metabolic models using the recently developed MetRxn knowledgebase of standardized metabolite and reaction information (http://www.metrxn.che.psu.edu/). MetRxn is a standardized, non-redundant, searchable collection of published metabolic models and databases from a wide variety of organisms including atom mapping information across all reactions and enhanced integration with other databases. We will describe how this resource can impact genome-scale metabolic model reconstruction by providing curated reaction and metabolite content. This content is also leveraged for identifying thermodynamically feasible, carbon and energy efficient, overall stoichiometries from a substrate to a target product by globally assessing all co-reactant/products combinations. In addition, we will discuss how reaction atom mapping information in MetRxn can be used to perform metabolic flux elucidation at a genome-scale revealing how the assumptions implied by core metabolic models propagate in the inference of internal metabolic fluxes. Finally, we will present computational tools for strain optimization leading to the microbial overproduction of target biomolecules using both stoichiometric and large-scale kinetic models. Experimental results for a number of collaborative projects will be highlighted and the integration of kinetic information will be detailed.

Costas D. Maranas (b. 1967), Donald B. Broughton Professor, Department of Chemical Engineering, The Pennsylvania State University, BS, Chemical Engineering, Aristotle University, Greece, (1990); MA, Chemical Engineering, Princeton University (1992); Ph.D. in Chemical Engineering, Princeton University (1995); Allan P. Colburn Award for Excellence in Publications by a Young Member of AIChE (2002), Outstanding Young Investigator Award of the Computing and Systems Technology AIChE Division (2006), S.V. Sotirchos Lectureship at 6th Panhellenic Chemical Engineering Conference (2007), Penn State Engineering Alumni Society (PSEAS) Outstanding Research Award (2012); Editorial Boards for Biophysical Journal, PLoS Computational Biology, BMC Systems Biology, Biotechnology Journal and Metabolic Engineering; Fellow of the American Institute of Medical and Biological Engineering (AIMBE); Reviewer for NSF, NIH and DOE; Research interests: Computational protein, enzyme and antibody design; reconstruction, curation and analysis of metabolic networks; microbial strain optimization; design of biological circuits and synthetic biology; signaling networks and multi-scale modeling in cancer biology, network science, optimization theory and algorithms.

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