Imperial College London

Centre for Process Systems Engineering
2017 Seminar Series

UCL

Using systems engineering tools to elucidate and redesign biological networks

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Abstract:

Metabolism is defined as the full complement of chemical transformations in living systems. In this talk, we will discuss how we can speed up the process of building and correcting organism-specific metabolic models (both stoichiometric and kinetic) using the recently developed MetRxn knowledgebase of curated reaction, metabolite and atom mapping content. We will describe how metabolite and reaction information can be leveraged for identifying thermodynamically feasible, carbon and energy efficient, overall conversion stoichiometries from a substrate to a target product by globally assessing all possible co-reactant/products combinations (optStoic). In addition, we will discuss how global reaction atom mapping information can be used to perform metabolic flux elucidation at a genome-scale revealing how the assumptions implied by core metabolic models may propagate in the inference of internal metabolic fluxes. Finally, we will highlight ongoing efforts that make use of multiple flux datasets of deletion mutants to robustly parameterize kinetic models that approach genome-scale for E. coli and other microbes.

Bio:

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) Premier Research Award (2016) and Outstanding Research Award in (2012). Editorial Boards for PLoS Computational Biology, BMC Systems Biology, IEEE Life Sciences, 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 design; enzyme and antibody engineering; reconstruction, curation and analysis of metabolic networks; computational strain design and synthetic biology; metabolism of photosynthetic organisms; metabolism of obligatory anaerobes; modeling of microbial communities; optimization theory and algorithms.

7 June 2017, 11am
Roberts Building 106 LT, UCL

106 LT, Roberts Building, UCL, Gower Street, WC1E 6BT, London.
Refreshments before the seminar in Room 102, Roberts Building.
This event is free and open to the public. No registration is required.

Organisers & Contacts: Dr. Gonzalo Guillen Gosalbez (g.guillen05@imperial.ac.uk), Dr. Alex Kiparissides (alex.kiparissides@ucl.ac.uk), Ms. Cristina Romano (c.romano@imperial.ac.uk)