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PhD Program in Applied Biotechnologies

"Metabolic modeling of bacterial metabolism: biotechnological outcomes of phenotypic space exploration"

September 10, 2013 - h. 15.00

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Abstract:

Microbial physiology is largely dependent on metabolism. Indeed, living organisms possess complex metabolic networks, ranging from hundreds to thousands of chemical reactions and conferring them the capability to synthesize and/or catabolize the building blocks of their cells. The overall sum of these chemical reactions represents the core of any living organism and the coordination of these processes results in the physiology we associate with each organism, from bacteria to humans. Interestingly, bacteria continuously provide industry with novel products and processes based on the use of their metabolism. Accordingly, because of their biotechnological impact, numerous efforts are being undertaken worldwide, with an ultimate goal to deliver new usable substances of microbial origin to the marketplace, including pharmaceuticals, biofuels and bioactive compounds in general.

Powerful tools for the in silico exploration of the metabolic circuits of a given cell are represented by computational modeling approaches, often adopted by metabolic engineers to quantitatively simulate chemical reactions fluxes within the whole microbial metabolism. According to genome-scale modeling of metabolism, a cellular metabolic network is transformed into a model by defining the boundaries of the system, a biomass assembly reaction, and exchange fluxes with the environment. This constraint-based modeling framework (e.g. Flux Balance Analysis, FBA) is then used to automatically compute the resulting balance of all the chemical reactions predicted to be active in the cell and, in turn, to bridge the gap between knowledge of the metabolic network structure and observed metabolic phenotypes. Possible outcomes of this modeling include i) essential genes identification (e.g. drug targets in pathogenic strains), ii) strategies for overproducing metabolites of interest (e.g. knock-outs identification) and iii) optimization of growth conditions (i.e. optimized biomass production).
The theory behind constrained-based computational modeling of bacterial metabolism will be illustrated, together with valuable examples from real-world application of FBA and possible future implementations of such approach.

The lecture will take place in the **room A** of **Cà Vignal - Strada Le Grazie, 15 - Verona**

Local organization and contact: Prof.ssa Sandra Torriani
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For attending this seminar will be recognized 2 of 150 CFR provided for the specific activities of PhD Program in Applied Biotechnologies.
