Master Thesis proposal

Investigating Perturbed Metabolic Networks through Flux Balance Analysis

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This proposal is for a Master thesis in in the field of **Systems Biology.**

An organism-wide metabolic network consists of approx. a thousands of metabolic reaction involving a thousand of metabolites. In databases such as BIGG (http://bigg.ucsd.edu), reconstructed metabolic networks are available for many organisms, from simple bacteria to humans. A popular way to study these metabolic networks is through constrained-based methods such as Flux Balance Analysis [2, 1], which consists in treating the network as a constrained optimization problem. The basic idea is that since the biochemical reactions that form these networks have short time constants, they equilibrate fast in response to perturbations. Hence steady state analysis is often times enough to characterize their behavior. Among all admissible flux distributions that can occur at steady state, the one maximizing a certain cost function (for example the growth rate in bacteria) can then be selected as most plausible stationary flux distribution.

The objective of the thesis is to do a computational study of the response of the metabolic network of the bacterium *E.coli* to perturbations such as knock-out of some of its enzymes or changes of the growth substrates.

The ideal candidate for the thesis will have a curriculum in Engineering or Computer Science or Bioinformatics. Given that the nature of the work is essentially computational, a background in Biology is not strictly necessary, although willingness to acquire some basic notions is a prerequisite.

References

[1] N. Jamshidi and B. Palsson. Formulating genome-scale kinetic models in the post-genome era. *Mol. Syst. Biol.*, 4:171, 2008.

[2] A. Varma and B. Ø. Palsson. Metabolic flux balancing: Basic concepts, scientific and practical use. *Nat. Biotech.*, 12(10):994–998, 1994.