P11 *Exploring the gap between dynamic and steady-state models of metabolism*

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Integration of different kinds of biological networks, is within the holistic approach of Systems Biology. However, looking at metabolic networks only, one already finds a separation between dynamic [2] and steady-state [3] models of metabolism. This work reviews the differences between both modeling approaches and explores the gap between them. Common properties of both kind of models are studied in detail, using as case study the central carbon metabolism of E. coli. Steady-state models are underdetermined and define a space of possible solutions, the so-called flux cone [4]. On the other hand, the kinetic properties of dynamic models define a specific flux distribution inside this space of solutions. We explore how this particular solution changes in function of initial conditions and the different kinetic parameters. Due to changes in experimental conditions and experimental measurement error, these parameters can vary in a wide range, changing the flux distribution around its original value within a kinetically feasible solution space. We perform Monte Carlo sampling [5] to analyze the solution space of both the dynamic and steady-state models. We estimate the volume of the kinetically feasible solution space under different restrictions and find it to be considerably smaller than the volume of the steady-state flux cone. Therefore, it is possible to cope with the lack and uncertainty in experimental data by defining refined solution spaces that can be used in constraint-based methods [1] such as Flux Balance Analysis.

References

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