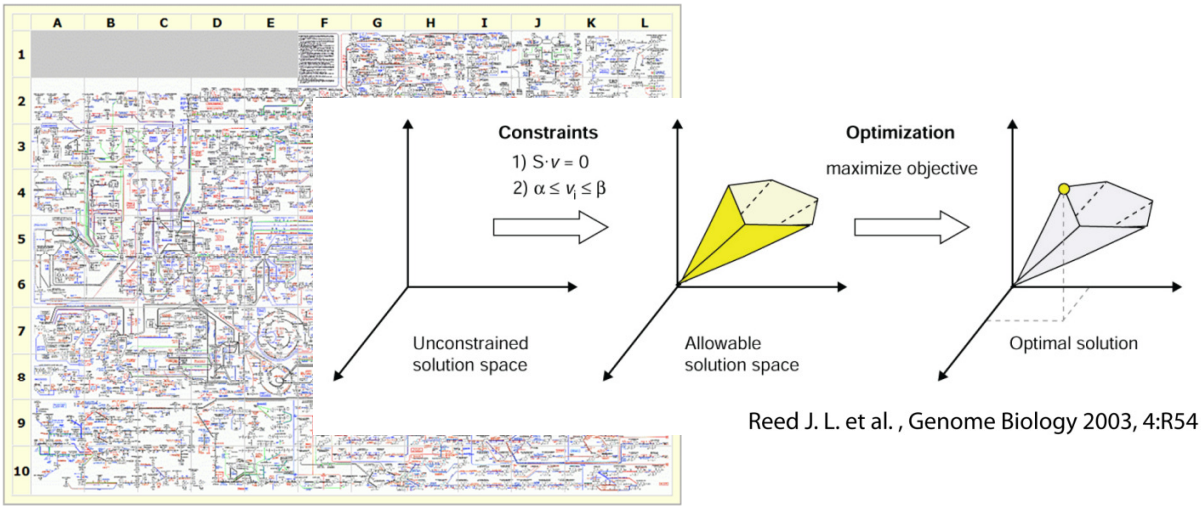
Understanding the metabolism of cancer cells: A computational approach

Background

At low glucose uptake rates, the yeast *Saccharomyces cerevisiae* respires, while it ferments at a high uptake rates. Also other cell types including mammalian cells show these uptake rate dependent phenotypes. This phenomenon is known since nearly a century, but the underlying reasons are yet not understood. Since this phenomenon is spread across evolutionary distant species, we hypothesized that it must be due to universal physicochemical constraints, e.g. arising from the laws of thermodynamics.

Project description

The goal of this project is to continue the development of a model describing the metabolic stoichiometry and biochemical thermodynamics of a mammalian cell. Evolutionary principles are used to predict the physiological behavior of mammalian cells with the aid of numerical optimization. The analysis of these predictions gives then a detailed understanding of the mechanistic principles behind these uptake rate dependent changes in the metabolic mode.



Reed J. L. et al. , Genome Biology 2003, 4:R54

Requirements

- Project ideally suited for students from engineering, computer sciences or with another quantitative background.
- Experience in numerical optimization is beneficial but not required
- Knowledge in biology is not required

Techniques

- Stoichiometric metabolic modeling
- Biochemical thermodynamics
- Numerical optimization
- Statistical data analysis