Integration of high-throughput datasets in microbiology through dynamical modeling of regulatory networks

Hidde de Jong
INRIA Grenoble - Rhône-Alpes
Projet IBIS

Understanding the cellular processes that shape the response of microbial cells to changes in their environment requires the study of the interactions between gene expression and metabolism. In recent years high-throughput datasets comprising simultaneous measurements of metabolism (fluxes, metabolite concentrations) and gene expression (protein and mRNA concentrations) have become available. These datasets provide a rich store of information for modeling the dynamics of the networks of biochemical reactions underlying cellular processes. In my presentation I will review some of these approaches and identify a number of open problems.