1st FEBS Advanced Lecture Course

Computational Systems Biology. Applications in pharmaceutical industry

Igor Goryanin, Gosau, March, 2005





- The modelling process
- Continuation procedure and bifurcation analysis
- Multiple target intervention analysis for *M. tuberculosis*
- The Pathway Editor
- Computational systems biology in Edinburgh









The modelling process

Defining the biological scope for the model

- Creating the model
 - Static model development
 - Entities and Interactions between them
 - Data acquisition, mining, curation, and storage
 Semi-Quantitative model development
 - Collection of all available data about kinetics and time dependencies.
 - Kinetic model development
 Fitting experimental data to determine kinetic parameters
 A determine kinetic
- Model validation
 Examining to see if model makes 'plausible' predictions
 Simulation, visualisation, analysis, and biological interpretations
- Examine results looking for new biology Planning of future experiments
 - Planning of future experiments
 - To enhance model and verify predictions
 To replace some *in vivo* and *in vitro* experiments

Some general information

Dynamical system

$$\frac{dx}{dt} \equiv x' = f(x,\alpha)$$

x(t): vector of time- dependent state variables
 α: vector of parameters

Ordinary differential equation (ODE) with parameters











Numerical continuation

Allows to compute branches of objects, e.g. branches of equilibria, if a parameter varies.
 Allows to detect bifurcation points and analyze them.
 Allows to start new branches and branches of new objects, switch parameters etc.
 Allows to continue bifurcation points if a second parameter is freed.
 Software

 Matcont (Matlab)
 Auto (general package)
 DBsolve 7 (As a Systems Biology workbench)































