

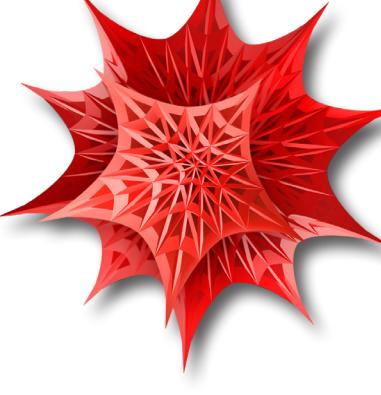
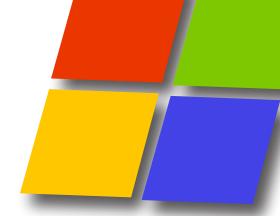
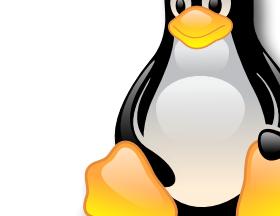
Dynamic modeling for the masses: the MASS Toolbox

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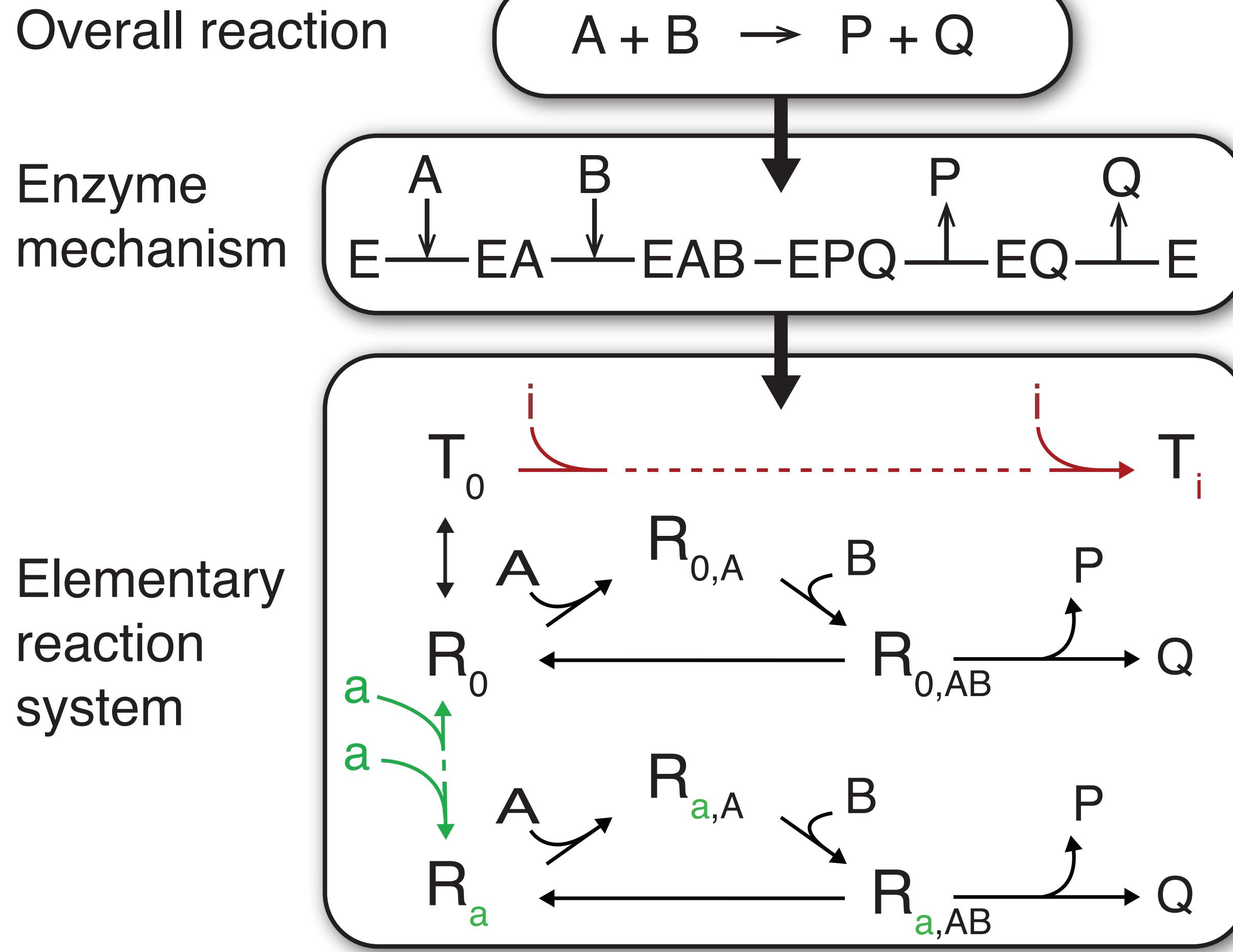
1. Overview

- Biochemical network modeling package with a focus on mass-action kinetic and constraint-based models
- Developed in *Mathematica*® 
- Platform independent   
- Import models from different sources, e.g. SBML, COBRA Toolbox, Biomodels.net etc.
- Literate modeling enabled through Mathematica's notebook interface 
- Merge and compare models
- High-level plotting functions
- Open source & BSD license



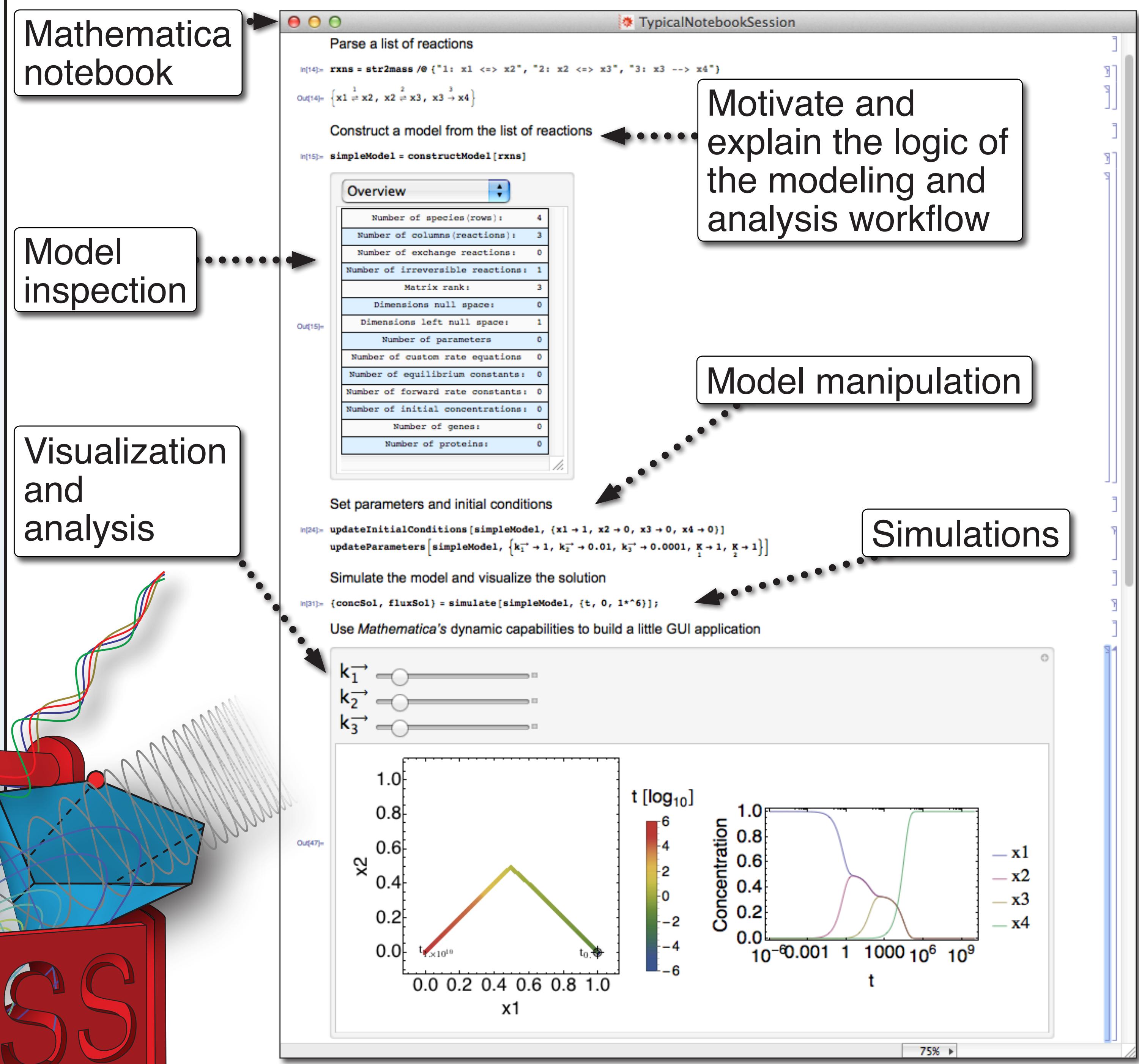
3. Enzyme kinetics

- Compile elementary reaction systems from Cleland's notation



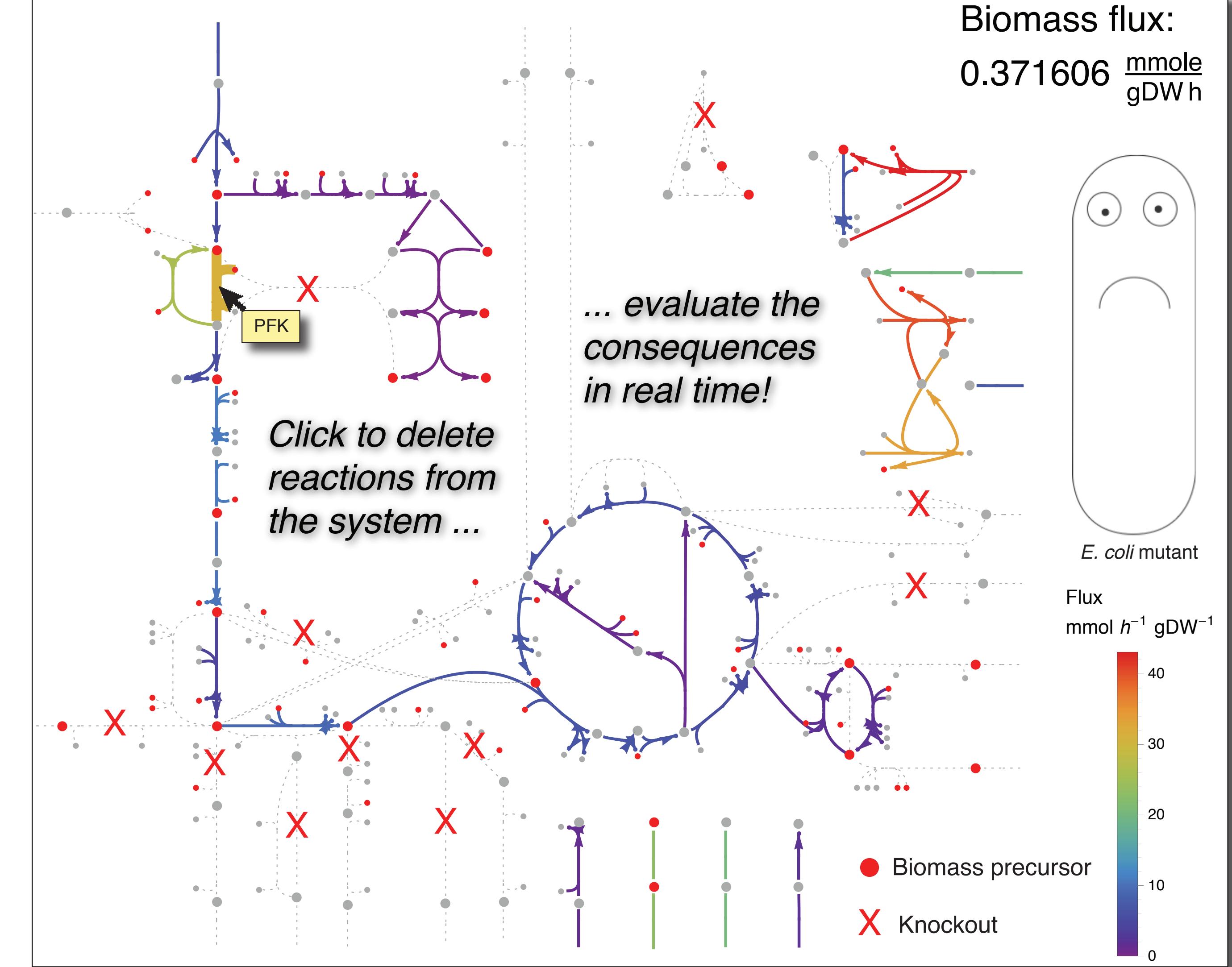
- Solve steady-state equations symbolically and apply other simplifications transparently

2. Literate modeling



4. Dynamic & interactive visualizations

- Create *ad hoc* GUIs to explore, for example, parameter dependencies, gene knockouts, etc.
- Please, ask for a demonstration!



5. References

- Sonnenschein N., Zielinski, D.C., de Bree, J., Palsson, S., Thomas, A., Bordbar, A., Jamshidi, N., Palsson, B.Ø. The MASS Toolbox: Accessible dynamic modeling. *Submitted*
- Jamshidi, N. & Palsson, B. Ø. Mass Action Stoichiometric Simulation Models: Incorporating Kinetics and Regulation into Stoichiometric Models. *Biophys J* 98, 175–185 (2010).
- Jamshidi, N. & Palsson, B. Ø. Formulating genome-scale kinetic models in the post-genome era. *Mol Syst Biol* 4, 171 (2008).



Get more information at sbrg.github.io/MASS-Toolbox

Documentation • Downloads •
Support • Github repository •
Issue tracker • Course materials •
How to's ... and a lot more!