

Thomas Maiwald

DEPARTMENT OF SYSTEMS BIOLOGY,
HARVARD MEDICAL SCHOOL
e-mail: Thomas_Maiwald@hms.harvard.edu

Mathematical modeling and in silico labeling with PottersWheel

Since 2005 we are developing the MATLAB toolbox PottersWheel to apply mathematical modeling in Systems Biology [1]. The software focuses on partially observed systems which can be described by biochemical reaction networks or differential equations. It comprises advanced methods to estimate unknown parameters given experimental time-resolved measurements and to identify structural and practical parameter non-identifiabilities, where several parameters may compensate each other's effect and lead to the same observed trajectories [2]. Recently, we developed a novel approach called in silico labeling to track species in complex and potentially non-linear dynamical systems, for example to determine their half-life and the transit time within system compartments. PottersWheel is freely available for academic research at www.potterswheel.de

REFERENCES

- [1] T. Maiwald, J. Timmer. Dynamical modeling and multi-experiment fitting with PottersWheel. *Bioinformatics* 24, 2008, 2037-2043
- [2] A. Raue, C. Kreutz, T. Maiwald, J. Bachmann, M. Schilling, U. Klingmüller, J. Timmer. Structural and practical identifiability analysis of partially observed dynamical models by exploiting the profile likelihood. *Bioinformatics* 25, 2009, 1923-1929