



Traditio et Innovatio



Exploiting Equation-Free Analysis for Multi-Level Agent-Based Models in Cell Biology Kai Budde*, Tom Warnke*, Fiete Haack*, Ilias Panagiotopoulos°, Eric Schätz*°,

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Abstract

Multi-level modeling approaches have been successfully applied in systems biology to model complex systems with different levels of organization. Unfortunately, the effort required for comprehensive simulation studies with complex multi-level models is often prohibitive. Equation-free analysis reduces the demand for simulations and facilitates numerical analysis of the macroscopic behavior of a system.

We present the integration of equation-free analysis through control-based continuation into the simulation language SESSL to analyze multistability of biochemical models. It combines ideas from numerical continuation and feedbackcontrol to stabilize the system state and track unstable phenomena. The resulting bifurcation diagram divides parameter space into regions of qualitatively different behavior and is a key element in understanding nonlinear dynamics. We use a Wnt shuttling model as a case study.

Wnt signaling is imperative for embryonic development and homeostatic selfrenewal in a number of adult tissues [2]. It has been shown that multistability that arises within the cross-talk of Wnt and other signaling pathways such as Notch is related to cell fate selection [5]. Since β -catenin acts as intracellular signal transducer, it is the primerary protein to observe.

Experimental Design

Biochemical model defined in the multi-level modeling language ML-Rules [4]
 Declarative description with Simulation Experiment Specification via a Scala Layer (SESSL) [3]
 SESSL takes care of stochasticity of the model and model observation

Method: Control-Based Continuation

- Consider a microscopic model $\dot{u} = f(u)$ in the form of a high-dimensional system of *N* differential equations (or described by reaction rules), which quickly converges to a low-dimensional object (macroscopic system)
 - Goal: Track unobservable (unstable) steady states of macroscopic system F (depending on parameter μ) with assumed model: $\dot{x} = F(x, \mu)$
 - Add control term [1] (shown in red) to stabilize unstable steady states: $\dot{x} = F(x, \mu) + a(y - x)$
 - Add control target equation [7, 8] to have an adaptive, reference-free control technique for locating unknown steady states: $\dot{y} = b(y - x)$
- If a steady state is observed → control term vanishes → steady state of the original system found
- \circ Requirements to track unstable ('un-observable') steady states: $0 < b \ll a$
- \circ In our case:
 - > β -catenin is part of the microscopic model, but it behaves on a different time scale than the other variables \rightarrow good choice for a macroscopic variable

Case Study: Wnt Shuttling Model

Automated bifurcation analysis

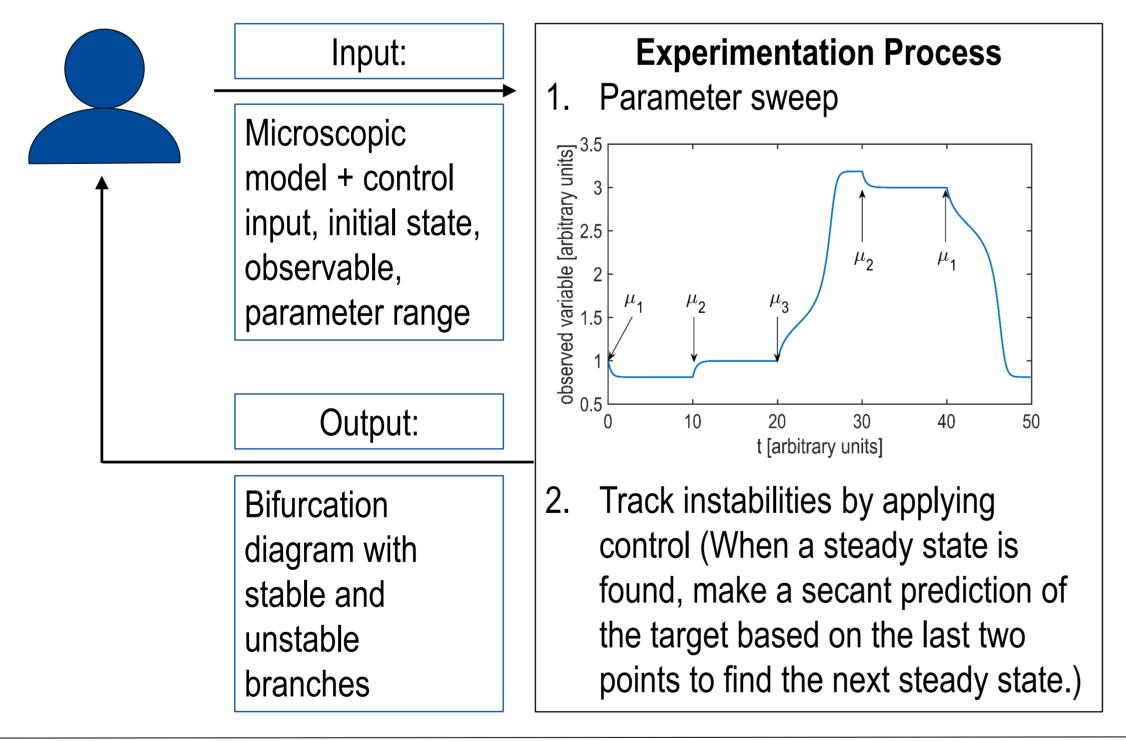


Fig. 1: Outline of the equation-free analysis with SESSL. The plot (inside the experimentation process) shows an example parameter sweep with hysteresis.

Open Questions & Outlook

How to automate the entire analysis process?
How to generate control-terms automatically?

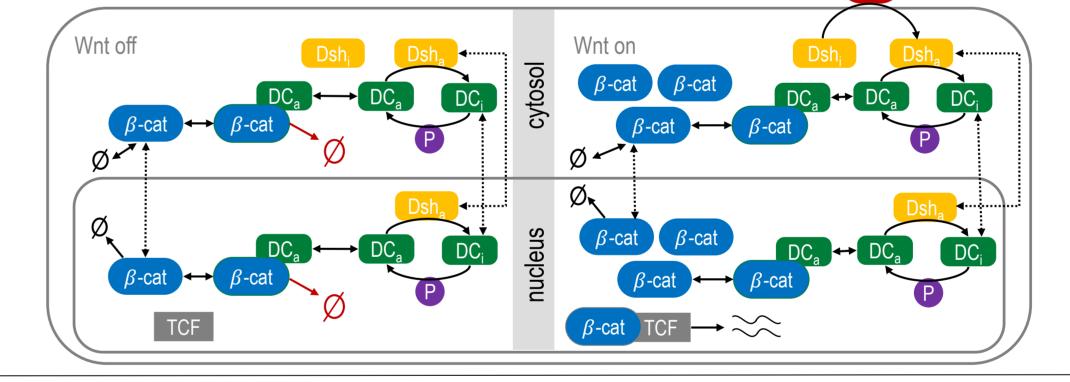


Fig. 2: Wingless and INT-1 (Wnt) model (19 ordinary differential equations / 31 reaction rules) with focus on the processes of shuttling and degradation [6]. Wnt is turned on for simulation.

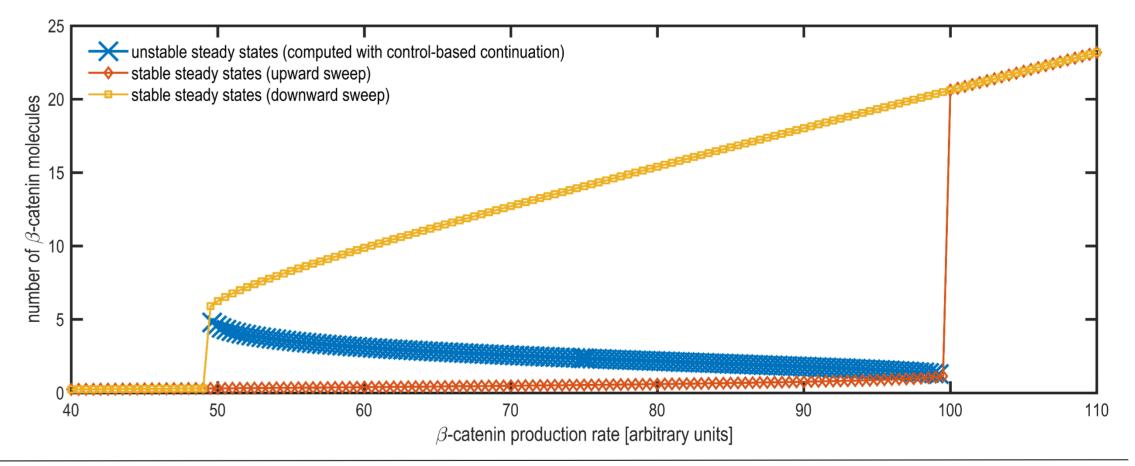


Fig. 3: Bifurcation diagram of hysteresis behavior of β -catenin depending on its production rate, which shows bistability of Wnt shuttling model. The unstable branch (blue) was tracked by using control-based continuation with a=50, b=0.01.

References

[1] Bureau, E., F. Schilder, I. Santos, J. J. Thomsen, and J. Starke. 2011. "Experimental bifurcation analysis for a driven nonlinear flexible pendulum using control-based continuation". In 7th European Nonlinear Dynamics Conference.
[2] Clevers, H. (2006). "Wnt/β-catenin signaling in development and disease". Cell, 127(3), 469-480.
[3] Ewald, R., and A. M. Uhrmacher. 2014. "SESSL: A domain-specific language for simulation experiments". ACM Transactions on Modeling and Computer Simulation (TOMACS), 24(2), 11.
[4] Helms, T., T. Warnke, C. Maus, and A. M. Uhrmacher. 2017. "Semantics and Efficient Simulation Algorithms of an Expressive Multi-Level Modeling Language". ACM Trans. Model. Comput. Simul. 27 (2): 8:1–8:25.
[5] Kay, S. K., H. A. Harrington, S. Shepherd, K. Brennan, T. Dale, J. M. Osborne, D. J. Gavaghan, and H. M.Byrne. 2017. "The role of the Hes1 crosstalk hub in Notch-Wnt interactions of the intestinal crypt". PLoS computational biology 13 (2): e1005400.
[6] MacLean, A. L., Z. Rosen, H. M. Byrne, and H. A. Harrington. 2015. "Parameter-free methods distinguish Wnt pathway models and guide design of experiments". Proceedings of the National Academy of Sciences, 112(9), 2652-2657.
[7] Pyragas, K., V. Pyragas, I. Z. Kiss, and J. L. Hudson. 2004. "Adaptive control of unknown unstable steady states of dynamical systems". Physical Review E, 70(2), 026215.
[8] Wang, H. O., and E. H. Abed. 1995. "Bifurcation control of a chaotic system". Automatica, 31(9), 1213-1226.

- How to find regions (initial state and parameter values) of multistability?
 How to track the branch around fold bifurcation points?
- How to adapt the control-based continuation method in order to work with dynamically nested multi-level models?

Next steps:

- Develop a set of benchmark models
- Application and comparison of other methods of equation-free analysis (e.g. using lifting and restriction operators)
- Test realistic model that combines intra- und intercellular dynamics to predict behavior on cell population level
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