

Beyond Structure: KiSAO and TEDDY – Two Ontologies Addressing Pragmatical and Dynamical Aspects of Computational Models in Systems Biology Dagmar Köhn<sup>1</sup>  $\diamond$  Nicolas Le Novère<sup>2</sup>  $\diamond$  Christian Knüpfer<sup>3,4</sup>

# Introduction

Computational models are becoming more and more the central scientific paradigm for understanding the complexity of living systems. With the increasing number and size of these models there is a growing need for model reuse and exchange. Furthermore, detailed models are not manageable without computer support. There are efforts to formalise the mathematical structure of models (e.g. SBML) and to standardise the kinetic and biological meaning of model components (e.g. SBO, GO, UniProt). However, formalising only the structure of computational models is not sufficient to easily exchange and reuse models and to achieve full computer support for modelling. We also need to formalise the pragmatical and dynamical aspects of models. For this purpose we propose two ontologies: The Kinetic Simulation Algorithm Ontology (KiSAO) and the TErminology for the Description of DYnamics (TEDDY).

# **KiSAO**

KiSAO classifies simulation algorithms applicable to biological models using different categories and a hierarchy of algorithm versions. Each term contains information about synonyms, a definition and a publication reference.

## Classification

Simulation algorithms are classified wrt. the following dimensions:

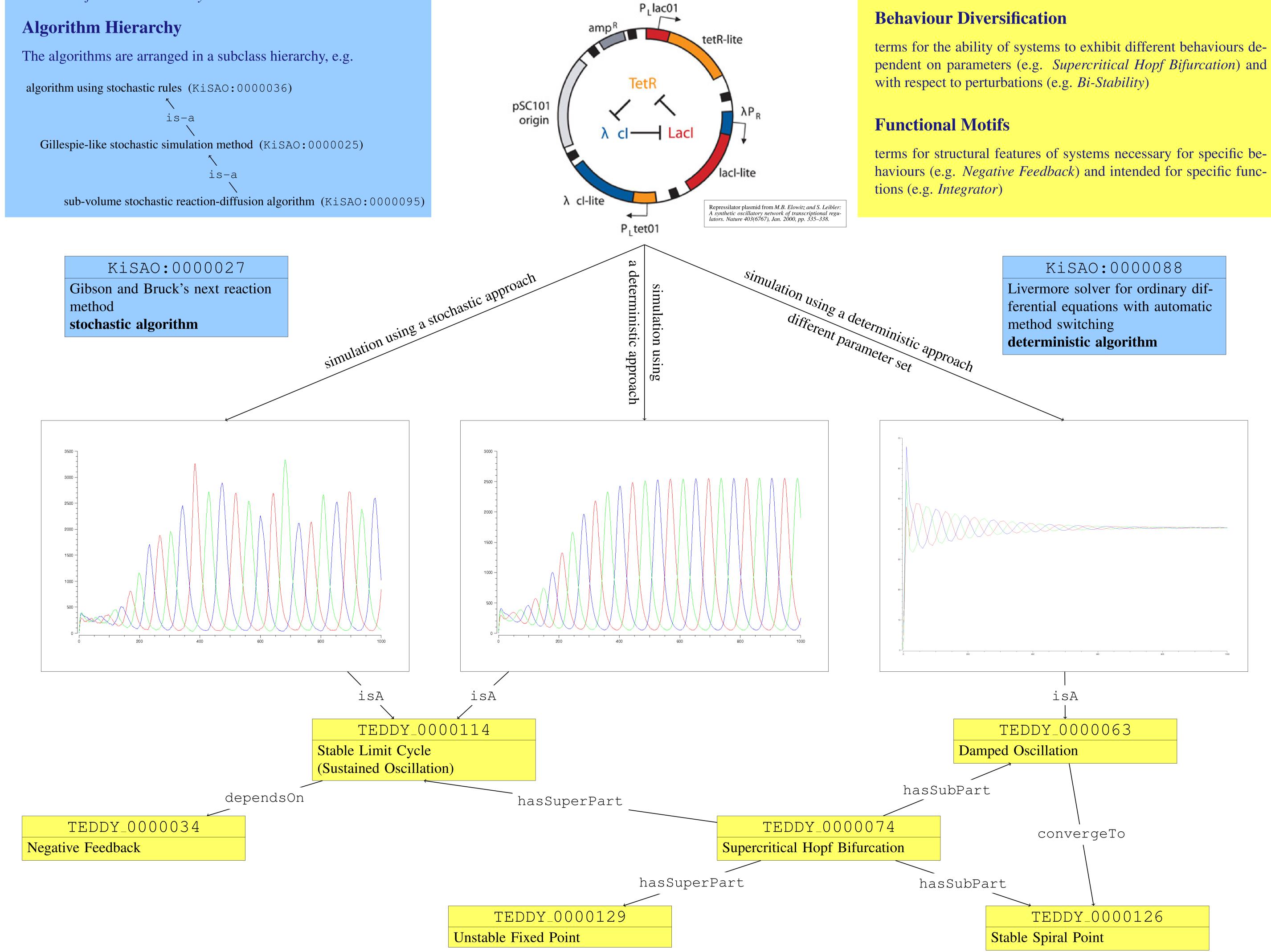
- algorithm using deterministic/stochastic rules, e.g. Euler forward vs. Smoluchowski equation based method
- Spatial/non-spatial approaches, e.g. Green's function reaction dynamics vs. Euler forward
- discrete/continuous variables, e.g. Cellular automata vs. Livermore solver
- fixed/adaptive time-step approaches, e.g. *Cellular automata* vs. *Green's function reaction dynamics*

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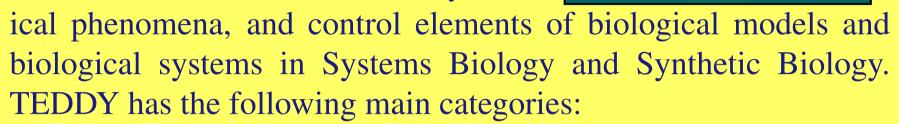
For demonstration of KiSAO and TeDDY annotations, we use the well-known example of the "Repressilator" as published by Elowitz and Laiber (2000). The mathematical model describes a negative-feedback loop consisting of three repressor genes and their promoters. The model does not describe a natural system but in contrast is an artificial oscillating network. It is used to show how the ability of the system to oscillate depends on critical parameters. Furthermore, the influence of stochastic effects of the system behaviour is investigated. The model is build up of three different mRNA concentrations and the corresponding protein concentrations. The species are involved in transcription, translation and degradation processes.

The repressilator model can be found in BioModels Database (BIOMD0000000012). We use COPASI for the simulations shown on this poster.



## **TEDDY**

The aim of TEDDY is to provide terms for describing and characterising dynamical behaviours, observable dynam-



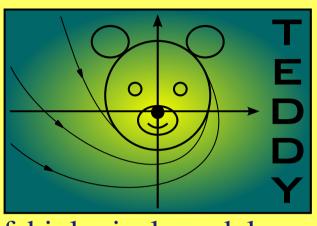
## **Temporal Behaviour**

terms for the actual (temporal) dynamical behaviour of models, e.g. Damped Oscillation, Stable Fixed Point

### **Behaviour Characteristic**

terms for characterising concrete behaviours (e.g. Period) and for discriminating between types of behaviours (e.g. Stable vs. Unstable)

pendent on parameters (e.g. Supercritical Hopf Bifurcation) and



http://www.ebi.ac.uk/compneur-srv/kisao

http://teddyontology.sourceforge.net/