

# Ontologies for use in Systems Biology: SBO, KiSAO and TEDDY

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## BACKGROUND

The use of computational modeling in the description and analysis of biological systems is at the heart of Systems Biology. Besides the information stored in a core model, there is increasingly a need to provide additional semantic information: to identify model components, to assist in biological interpretation of models, to define simulation conditions and to describe simulation results. This information deficit can be addressed through the use of ontologies.

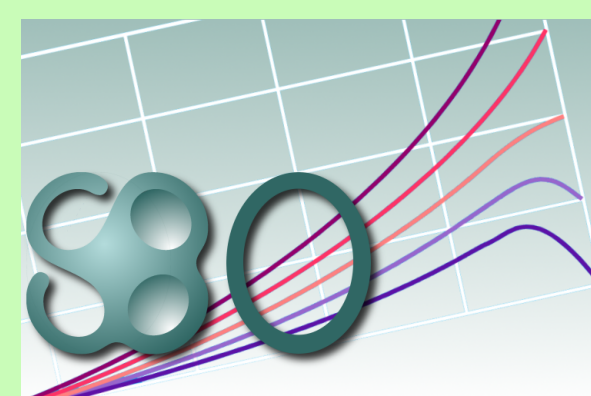
## OBJECTIVES

Computational modeling can be divided into three areas; model construction, concerned with the encoding of a process into a defined format; model simulation, with the precise set of operations to generate a specified result; model analysis, with the categorisation of observed system behaviours. We describe three ontologies created specifically to address the needs of the Systems Biology community in each division, and illustrate their practical use with the 'Repressilator' model [1]. The repressilator model can be found in BioModels Database [2] (BIOMD0000000012). COPASI [3] was used to generate the simulations shown.

### Systems Biology Ontology

SBO [4] seeks to describe the precise nature of each element of a model. It consists of six orthogonal branches, each of which forms a controlled vocabulary of terms for use in Systems Biology:

- Entity, e.g. *simple chemical, enzyme*
- Participant role, e.g. *inhibitor, substrate*
- Quantitative parameter, e.g. *kinetic constant, time interval*
- Modeling framework, e.g. *discrete, logical*
- Mathematical expression, e.g. *rate law, conservation law*
- Interaction, e.g. *transport reaction, cleavage*



### Kinetic Simulation Algorithm Ontology

KiSAO [5] classifies simulation algorithms applicable to biological models using different categories and a hierarchy of algorithm versions:

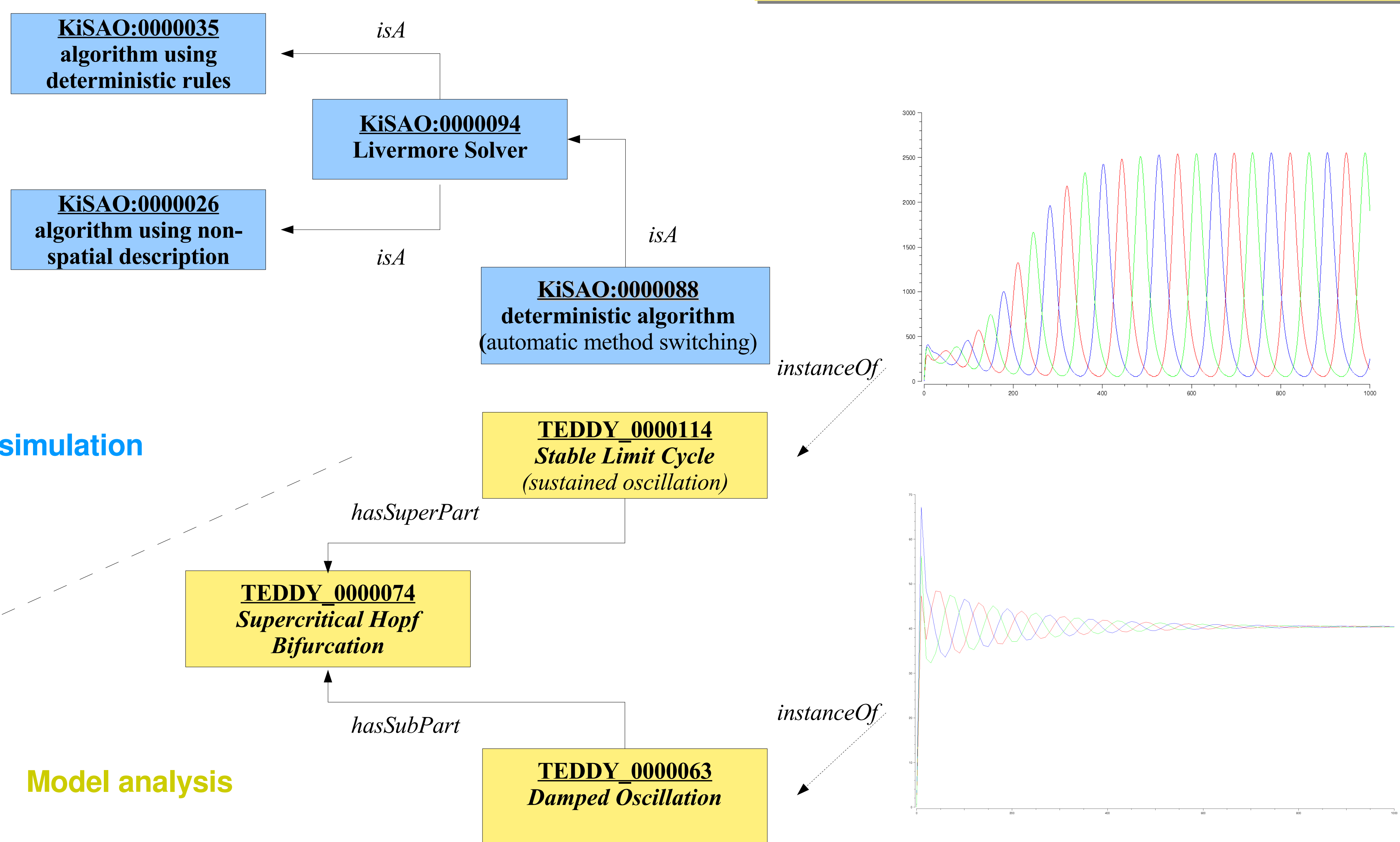
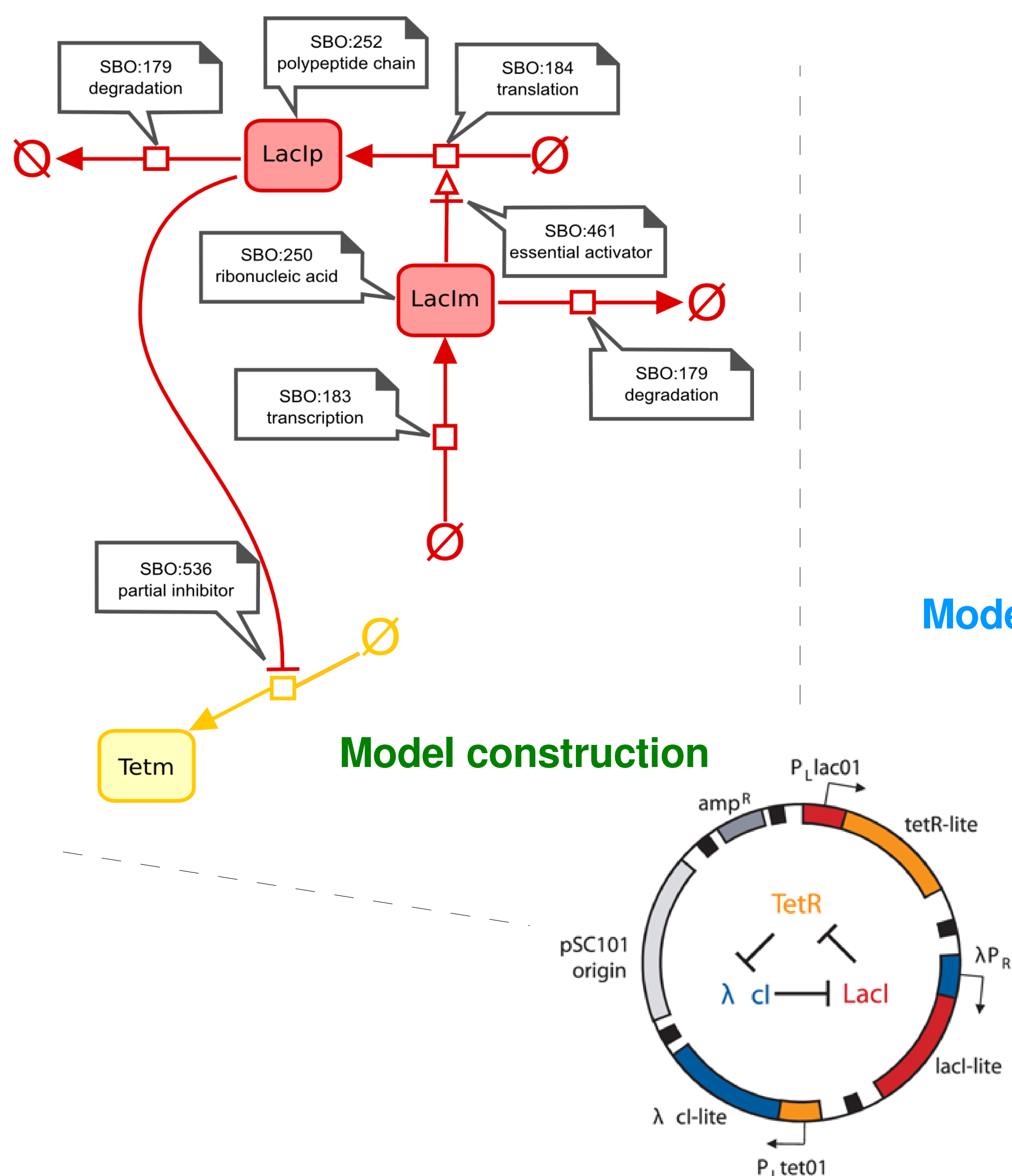
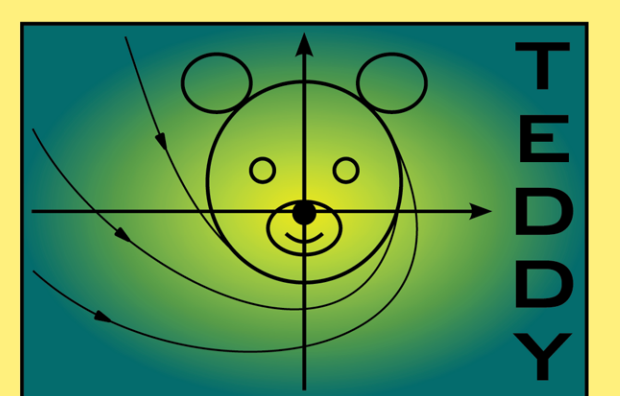
- Deterministic/Stochastic rules, e.g. *Euler forward vs. Smoluchowski equation based method*
- Spatial/Non-spatial approaches, e.g. *Green's function reaction dynamics vs. Euler forward*
- Discrete/Continuous variables, e.g. *Cellular automata vs. Livermore solver*
- Fixed/Adaptive time-step approaches, e.g. *Cellular automata vs. Green's function reaction dynamic*



### Terminology for the Description of Dynamics

TEDDY [6] provides terms for describing and characterising dynamical behaviours, observable dynamical phenomena, and control elements of biological models and biological systems in Systems Biology:

- Temporal dynamical behaviour, e.g. *Dampened Oscillation, Stable Fixed Point*
- Concrete behaviours, e.g. *Periods*, and types of behaviours e.g. *Stable and Unstable*
- Behaviour Diversification, e.g. *Supercritical Hopf Bifurcation* (parameter dependent) and *Bistable behaviour*
- Functional Motifs, e.g. *Negative feedback*



## CONCLUSION

The provision of semantic information extends model longevity and facilitates their reuse. It can provide useful insight into the biology of modelled processes, or be used to make informed decisions on subsequent simulation experiments. The ontologies described are freely available to view or download at the websites indicated, or through BioPortal [7].

## REFERENCES

- [1] Elowitz and Leibler (2000), A synthetic oscillatory network of transcriptional regulators. *Nature* 403(6767):335-8.
- [2] BioModels Database: <http://biomodels.net/database/>
- [3] COPASI: <http://www.copasi.org/>
- [4] SBO: <http://biomodels.net/sbo/>
- [5] KiSAO: <http://biomodels.net/kisao/>
- [6] TEDDY: <http://biomodels.net/teddy/>
- [7] BioPortal: <http://bioportal.bioontology.org/>