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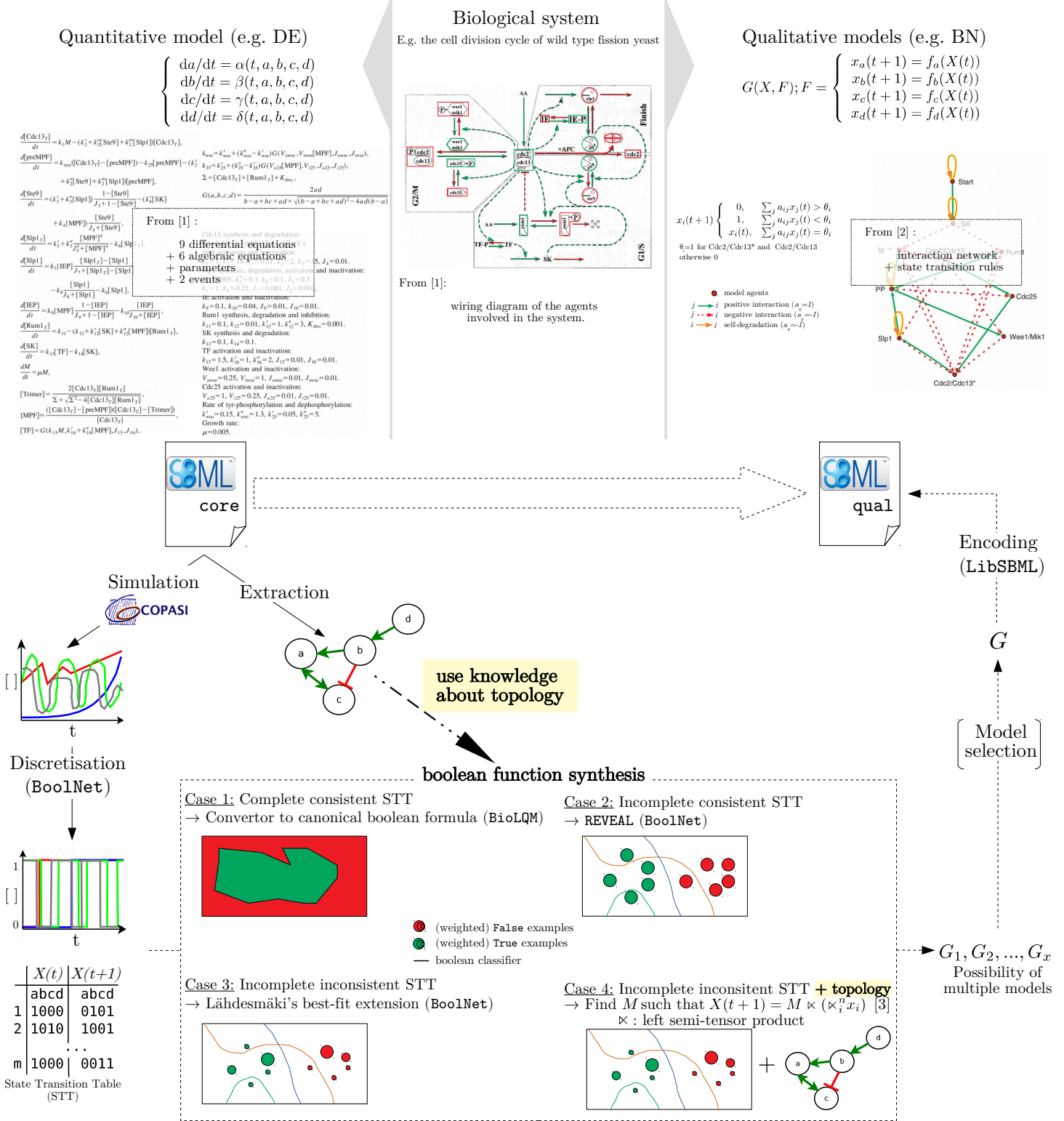
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Towards an automatic conversion from SBML core to SBML qual

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Abstract: The SBML format is the *de facto* standard to encode biological model in different formalisms. It was first developed to encode quantitative models like Differential Equations (DEs), but the current release allows the definition of packages extending the *core* format. One of these packages, named *qual*, encodes qualitative models like Boolean Networks (BNs). To the best of our knowledge, there is no automatic pipeline to convert a quantitative model encoded in SBML *core* into a qualitative model encoded with the *qual* package. Here, we explore such a pipeline on a relatively simple system: the cell division of fission yeast, which has been studied both with a set DEs [1] and with a BN [2]. Our approach consists in extracting the model topology from the set of DEs and in solving them numerically in order to retrieve the time course data of species' concentrations on which we apply a discretization. Then we extract from these data a scarce state transition table. We are currently investigating ways to synthesize a BN fitting both topology knowledge and state transitions.



Next objectives:

- Use the knowledge about topology derived from the kinetic model to synthesize boolean functions
- Define pipeline validation criteria such as attractor identification and matching
- Assess the pipeline on other models
- Fully automatize the pipeline → to be submitted to SBFC convertor

References:

- [1] Novak *et al.* 'Mathematical model of the cell division cycle of fission yeast', Chaos, Mar. 2001.
- [2] Davidich and Bornholdt, 'Boolean network model predicts cell cycle sequence of fission yeast', PLoS ONE, Feb. 2008.
- [3] Leifeld *et al.* 'Identification of Boolean Network Models From Time Series Data Incorporating Prior Knowledge', Front. Physiol., Jun. 2018.