GENE CIRCUITS MODELLING WITH KAPPA RULE BASED LANGUAGE

Abstract: Modeling biological interaction networks is a complex process that involves analyzing interactions of many agents and reviewing a lot of papers. The dynamics of living systems is usually modeled either by differential equations or by stochastic algorithms (such as Gillespie), while the models are written either in numeric (Matlab) or general purpose (Perl, Python, etc.), or in domain-specific (Kappa[1], BionetGen) languages .
Biological models written in Kappa language are usually faster and easier to read, integrate and reason about due to domain specialization. However, most of the time in the modelling process is spent not on code writing but on tuning parameters and interpreting papers: each rule and each variable must be backed by facts from the literature or by well defined modeling assumption. That is why I developed Kappa-Notebook software that connects to KaSim (Kappa simulator) and allows to run and collaborate on Kappa models online and connect Kappa rules to text fragments in papers ("nuggets" [2]), images and videos by semantic comment-based annotations.
In my presentation, using models of several gene-curcuites, I will:
➔demonstrate core features of Kappa language
➔show how to turn a plasmid map into a model
➔highlight the ways how researchers can benefit from Kappa modeling ➔show the limitations of Kappa simulator

REFERENCES:
[1] Vincent Danos, Jérôme Feret, Walter Fontana, Russell Harmer, Jean Krivine, Rule-Based Modelling of Cellular Signalling. CONCUR 2007, pp. 17-41
[2] Misirli G, Cavaliere M, Waites W, et al. Annotation of rule-based models with formal semantics to enable creation, analysis, reuse and visualization. Bioinformatics. 2016;32(6):908-17.