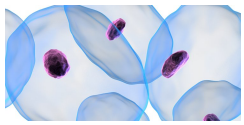
Laboratory of Systems and Synthetic Biology
www.wur.nl\ssb
www.systemsbiology.nl



Expanding and parallelising an evolutionary approach to model identification and design

Supervisors: Robert Smith

Contacts: robert1.smith@wur.nl

Type of thesis: Computational

Required competences: Knowledge of ordinary differential equations (ODEs) and their analysis, ability to simulate systems in MATLAB or Python. These are taught in courses, e.g., SSB30806, SSB31806, BCT20306, BCT31806.

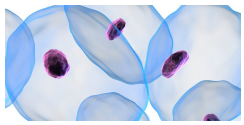
Acquired competences: Understanding optimisation of mathematical models, model analysis, parallel computing, computer programming skills.

Date: 30-06-2020

Description

Mathematical models are used in biology research as a means of describing and evaluating our current knowledge. If a model is able to accurately describe data we have available to us, it can then be used as a powerful tool to simulate new experimental hypotheses. In a number of biological, this feedback between conducting experiments and mathematical analysis has accelerated our understanding and knowledge about a given system. However, the model "design" process is not standardised – a model's design is influenced by the already available knowledge/data and prior beliefs as to how a system has been seen to, or is believed to, function. As such, the fairest means of finding the "correct" model is to evaluate a number of different mathematical systems and compare which ones match the given data the best, and produce the most accurate experimental hypotheses. The key question, then, is how do we find this subset of mathematical models to compare?

In previous work, we have looked to develop a computational (evolutionary) algorithm that can explore multiple model "designs" at once given a particular dataset to match. The result is a family of different models that can be compared and evaluated, either in comparison with data, or for the design of novel synthetic biology tools. In this



project, I wish to redesign this algorithm – using new computational methods that should improve the efficiency and rigour of our previous attempts. This will involve using already published optimisation algorithms and combining them in such a way that the resulting algorithm can be highly parallelised and utilise external/online storage facilities. Using experimental data from other currently ongoing projects, we can assess whether there are alternative mathematical interpretations of the biological data that may be worth exploring in future and have not, as of yet, been considered.

References

Smith RW, van Sluijs B, Fleck C (2017) Designing synthetic networks in silico: a generalised evolutionary algorithm approach. *BMC Syst Biol* **11:**118.

Penas DR, Henriques D, Gonzalez P, Doallo R, Saez-Rodriguez J, Banga JR (2017) A parallel metaheuristic for large mixed-integer dynamic optimization problems, with applications in computational biology. *PLoS One* **12**(8):e0182186

Villaverde AF, Frohlich F, Weindl D, Hasenauer J, Banga JR (2019) Benchmarking optimization methods for parameter estimation in large kinetic models. *Bioinformatics* **35**(5):830-838.