Application of Coloured Petri Nets to Model Communication, Movement, Death and Duplication of Unicellular Organisms

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Abstract

Background: Studying complex biological systems *in vivo* is time and money consuming. Computational biology simplifies the study of biological systems by modelling these systems *in silico* in a more efficient way to describe, predict and analyse behaviour to make this process faster and less expensive. The aim of the research reported in this paper is to explore how Petri nets can be used to model complex biological systems and also to identify methods to analyse such models.

Methods: In this study, a library of model components was constructed in Coloured Petri nets using Snoopy and Spike software (part of the PetriNuts* tools platform), to yield a multi-level, multi-scale, multidimensional environment supporting models of the dynamic behaviour of single cell organisms in a 2D or 3D spatial context. The library includes model components of varying complexities. Alone, these models describe a simple behaviour, such as chemotaxis. But these models can be combined with each other to create more complex models that describe a range of different but simultaneous behaviours. An example is a model at an abstract level that demonstrates chemotaxis, duplication and death of motile microorganisms where location is represented using cartesian coordinates on a 2D or 3D grid. Optimisation methods such as hill climbing and simulated annealing were employed to tune models to achieve expected behaviours; further analysis was performed using R and Python.

Results: The library of models, available in GitHub, has been designed using sound engineering principles: construction and re-design of models, the use of abstraction in representing communication and the response to it (e.g. quorum sensing and biofilm formation) as well as movement, chemotaxis, reproduction and death in unicellular microorganisms such as bacteria and Dictyostelium. While studying each model individually, we also can combine them to create a system that describes all these system elements in one. By defining objectives for each model, we confirm the usability of the models to execute the objectives as expected, based on biological studies.

Conclusion: The simplicity and practicality of Petri nets make them an ideal tool for users with little or no computational background; this study is an example of how this technique can be applied into biology. With a focus on a small set of interesting biological behaviours, creating libraries, and investigating the behaviour of the models, covered in the current study is a starting point for further modelling and analysis of more complex biological systems in biology.

References:

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* https://www-dssz.informatik.tu-cottbus.de/DSSZ/Software/Software

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