Evaluation of an Open Source Electrical Circuit Simulator in a Biological Context

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Abstract

It was shown that tools and methods used in microelectronics are adaptable to the modelling and simulation of biological functions for example in the design of gene regulatory networks (GRN) [1]. Up to now, a commercial simulator, namely Spectre® from Cadence® design suite is being used for the simulation.

In this paper, we evaluate NGSPICE an open source electronic simulator for the modelling and simulation of these biological functions. In our tool, we developed a translator that converts the description of the biological system given in a text file into a Spice netlist, which NGSPICE takes as input. The netlist contains the biological circuit topology, its corresponding elements and the simulation control structures. The output is a file or graphical plot showing the results of the simulation.

To simulate the biological functions, we represent by analogy the molecule concentration as a voltage, flux or synthesis or consumption of a molecule as a voltage-controlled current source (VCCS), molecule decay as a resistor, accumulation of molecules as a capacitor. Thus, an electrical node can represent a protein whose concentration is determined by the generalised Kirchhoff laws.

We used and compared two approaches in our simulation. First, we implemented elementary biological functions as sub-circuits composed of basic electronic components (resistor, capacitor, and VCCS). Alternatively, we use the XSPICE code-model interface, which allows us to describe in C-language the models of these functions.

Furthermore, we modelled the motion of molecules between cells as a diffusion phenomenon. We solve this spatio-temporal behaviour by dividing the space into compartments (an adaptive mesh) such that in each compartment, the problem is reduced to only a time-dependent differential equation. The motion of molecules was modelled through different diffusion equations from compartments to compartments [2]. This approach which has already been validated with Spectre® generates a lot of equations which poses a challenge to the simulator.

Our results show good agreement with the expected outcome, and faster computation time

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when compared to COPASI, a biochemical system simulator standard in systems biology. NGSPICE is available online at http://ngspice.sourceforge.net

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