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Qualitative analysis of biological oscillators as processing structures

ABSTRACT

In recent times there is a certain tendency in the field of computer science of trying to replace conventional processing platforms. Computer science is trying to escape the dependency of traditional electronic components. Research and ideas often point to the possibility of processing in biological systems. Whatever the future processing platform might be, computer science will most likely always need a component to synchronize processing elements. One of the basic elements to help with synchronization is an oscillator. Oscillator called repressilator was already realized as a biological system using gene regulatory networks. I will implement different deterministic models describing a repressilator and use it to qualitatively analyze repressilators with different number of repressors and different binding cooperativity. Using the results of this analysis I will compare different models as well as different sizes of repressilators for each model.

Key words: modeling, deterministic modeling, biological oscillator, repressilator, stability analysis, bifurcation analysis, bifurcation, gene regulatory network, ordinary differential equations