

simBio

*simBio is a simulator for biological systems such as cardiac cells, epithelial cells, and pancreatic # cells.
simBio is written in Java, uses XML and can solve ordinary differential equations.*

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1. Introduction

In the field of medical biology, extensive research results regarding molecular and cellular level functions have been accumulated, but the mechanisms of these complex cell functions cannot be explained quantitatively. Due to this fact, a quantitative dynamic model that can integrate experimental data and reproduce biological mechanisms on computers is important. We developed simBio in order to have a tool for an easy creation of cell models employing object-oriented principles. In simBio, mathematical models such as a myocyte model that are described using ordinary differential equations are split into function elements such as ion channels and variables such as ion concentrations. In this new way of developing cell models, function elements are equally independent, and can be grouped according to biological classifications. Moreover, the correlations of variables and function elements can be described as a graph. The aim is a tool with which various cellular functions and mechanisms based on the experimental results can easily be combined to a more complex cellular structure or even a whole cell which is suitable for exploring new hypotheses.

2. License

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The LGPL original text is <http://www.gnu.org/copyleft/lesser.html>.

3. References

1. Nobuaki Sarai, Satoshi Matsuoka and Akinori Noma
simBio: a Java package for the development of detailed cell models
[Progress in Biophysics and Molecular Biology 90: 360-377,2006](#)

4. Contributors

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