

## BIOUML – SOFTWARE FRAMEWORK FOR SYSTEMS BIOLOGY

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### Resume

*Motivation:* With the completion of several genomics initiatives, including the Human Genome Project, researchers are poised to begin the next phase of elucidating how living systems function. Systems biology, a synergistic application of experiment, theory and modeling towards understanding biological processes as whole systems, requires integrated software environment that spans the comprehensive range of capabilities including access to databases with experimental data, tools for formalized description of biological systems structure and functioning, as well as tools for their visualization and simulations.

*Results:* Here we describe architecture and structure of BioUML framework designed for formalized graphic notation of biological systems structure and functioning, their simulations and access to databases on biological pathways. BioUML meta model provides an abstract layer to present structure of any biological system as a clustered graph. BioUML viewer and editor provide visualization of these graphs as diagrams and their editing. To incorporate any databases on biological pathways into BioUML framework we introduce a module concept and demonstrate it by creating module for GeneNet database. BioUML modeler allows a user to create and modify visual diagrams of biological systems and provides automatic generation of their executable models as MATLAB M-files. Using MATLAB these models can be simulated and investigated.

*Availability:* <http://www.biosoft.ru/biouml.net/>; <http://groups.yahoo.com/group/biouml>.