

Abstract Title

New possibilities of BioUML workbench

Abstract Text

Objective: reconstruction of complex biological systems requires integrated software that provides:

1. integration with a wide range of biological databases
2. integration with omics data
3. powerful search capabilities
4. visual modelling approach
5. client-server architecture for team work.

Results: BioUML (<http://www.biouml.org>) is an open source integrated Java workbench for systems biology. Its core is a meta model that provides an abstract layer for comprehensive formal description of wide range of biological and other complex systems. New version of BioUML workbench provides:

1. graphic notation editor – it allows an advanced user to create new graphic notation or extend an existing one. As an example SBGN graphic notation was created.
2. composite database module – allows to a user to specify set of databases that he would like to use simultaneously as a source of components during creation and editing of diagrams.
3. EBI data pack – database modules for main databases supported by EBI: Ensembl, UniProt, ChEBI, Reactome, IntAct, GO, BioModels, SBO. These databases are installed on the special BioUML server and can be easily searched and used by BioUML workbench (client).
4. Microarray data analysis - allows a user to load his microarray data, identify up/down regulated genes and highlight diagram elements according to microarray data or results of this data analysis.
5. BioHub – an approach that allows to arrange relationships between different biological objects formally (it is conceptually similar with MIRIAM standard) and use this information for searching. Results of such search can be presented as an editable graph.
6. Composite diagrams – allows a user to join several existing diagrams/models into a bigger one.
7. Experiment diagram type – allows to specify conditions (initial values, parameters, external stimulus, etc.) for virtual experiments on the diagram.

Conclusion: we believe that new version of BioUML workbench will greatly simplify, speed up and improve the process of formal description and reconstruction of biological pathways.

Topic

011 DEDICATED SESSIONS - Software tools

Presentation Preference

Oral presentation

Author Details

Tolstyh, Nikita, Institute of Systems Biology, Design Technological Institute of Digital Techniques, Novosibirsk, Russian Federation (Presenting); Lapukhov, Sergey, Institute of Systems Biology, Design Technological Institute of Digital Techniques, Novosibirsk, Russian Federation; Kiselev, Ilya, Institute of Systems Biology, Design Technological Institute of Digital Techniques, Novosibirsk, Russian Federation; Shadrin, Aleksey, Institute of Systems Biology, Design Technological Institute of Digital Techniques, Novosibirsk, Russian Federation; Kolpakov, Fedor, Institute of Systems Biology, Design Technological Institute of Digital Techniques, Novosibirsk, Russian Federation