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Taverna workflows for systems biology

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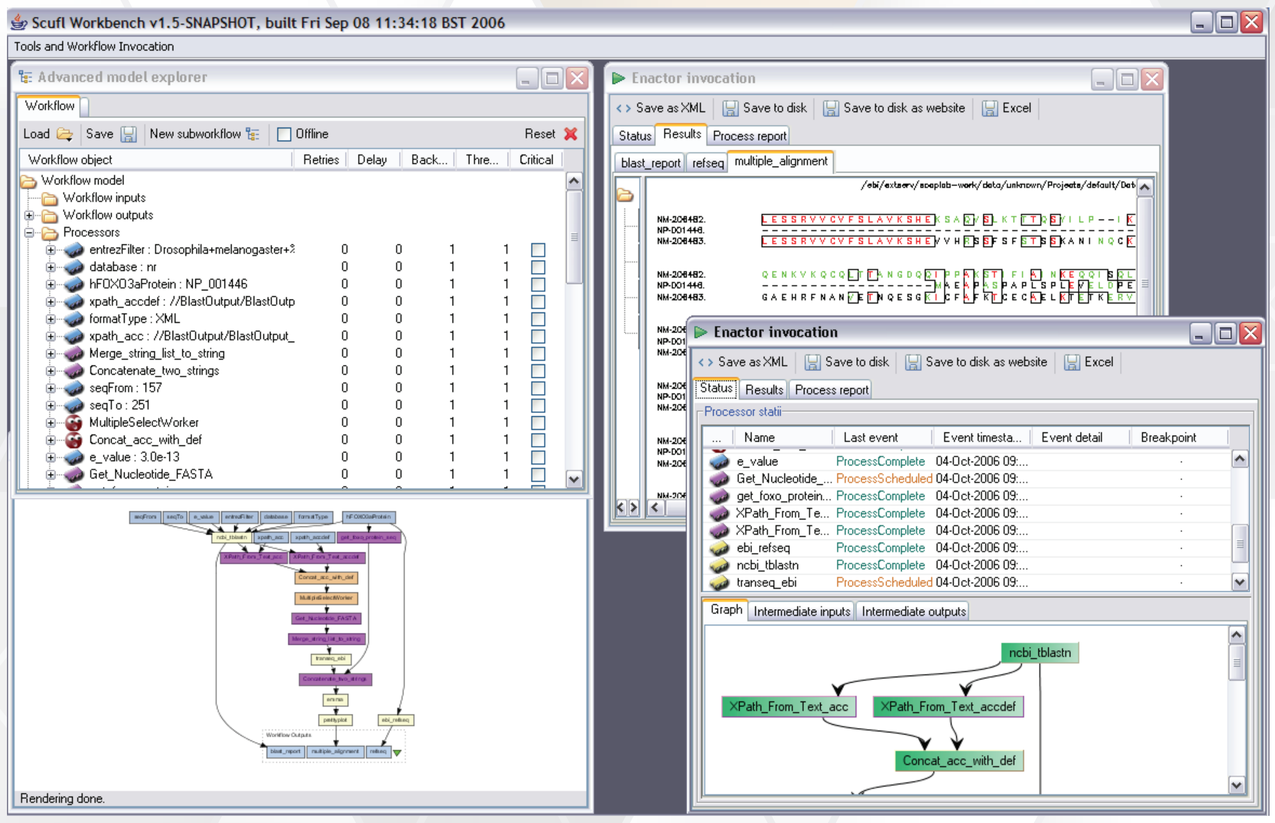
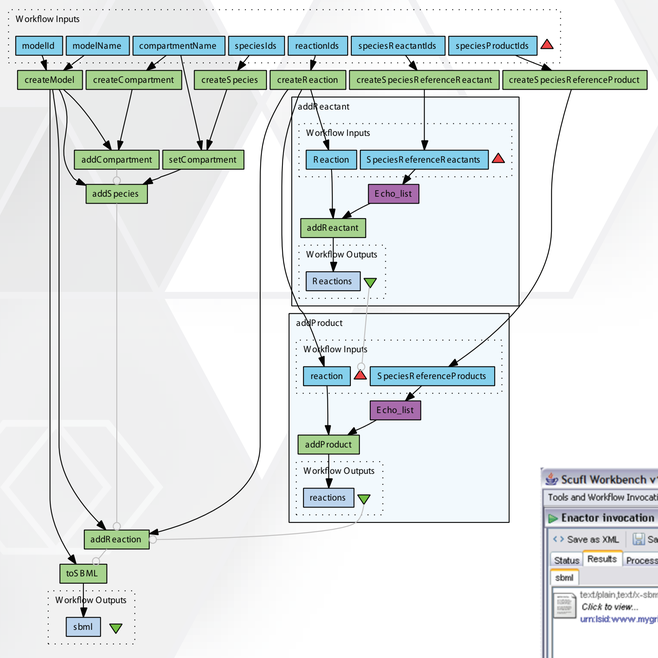
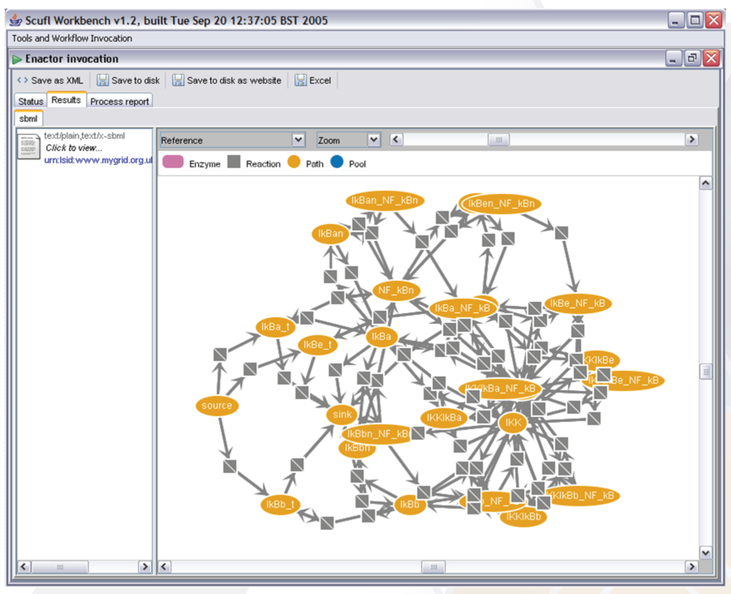
Introduction

Data integration is key in systems biology if we are to understand how biological systems function. However, integrating information in the life sciences is problematic due to the fact that the data is heterogeneic and distributed amongst many databases. Workflows offer a loosely coupled approach for integrating distributed data. Taverna is an example of a workflow system which can orchestrate the flow of data between web services-enabled resources. We have investigated how data from different levels of biological complexity can be integrated using taverna.





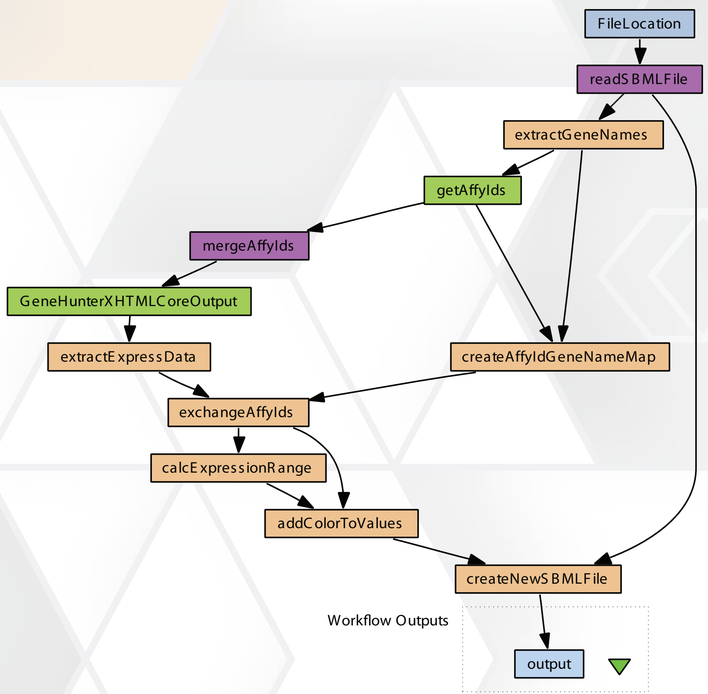


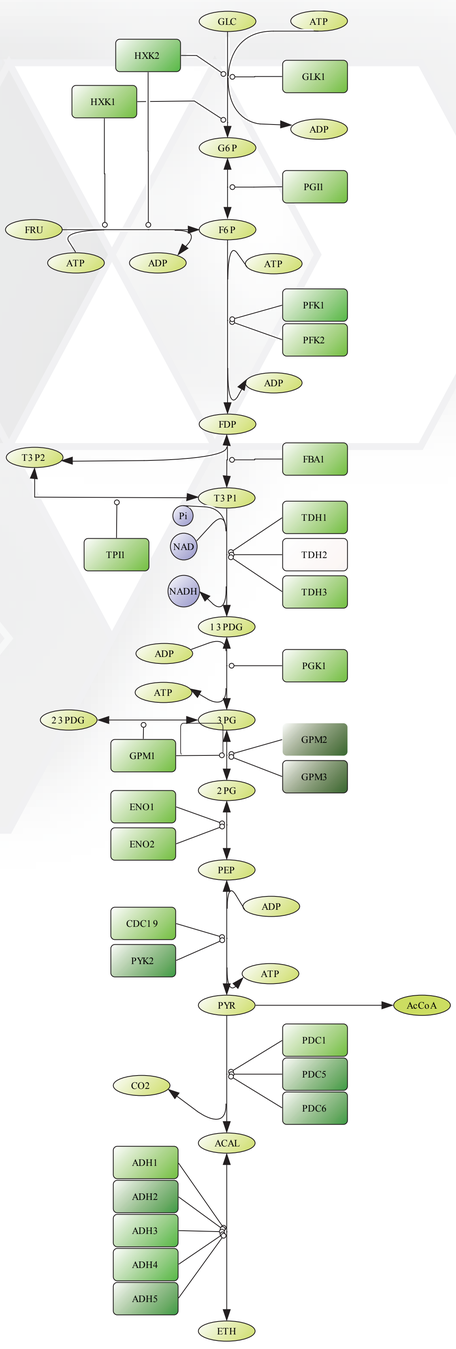
Construction of models in SBML

Workflows have been developed which demonstrate how biological pathways can be automatically constructed using distributed data from databases such as KEGG and BIND in a generic fashion on an ad hoc basis. Pathway models were created in SBML which was made possible by using Taverna's API consumer functionality which allows the import of the Java API of libSBML as workflow components. SBML models were visualized from within Taverna as graphs using GraphViz as well as an interactive graph viewer called SharkView which is able to focus at specific sections of SBML graphs and traverse along reaction edges of interest.

Integration of array data onto pathway maps

Taverna workflows have also been written to retrieve data from the MaxD microarray database and superimpose it onto pathway maps such as metabolic networks. The integration of microarray data and pathway information and its subsequent visualization is a process which enables changes in the expression of genes to be visualised from the context of a biological system represented as a molecular interaction network.





Acknowledgements

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