

Jarnac: An SBW Compliant Systems Biology Simulation Tool

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ABSTRACT

Jarnac is a general purpose scripting based simulation tool for modeling and analyzing biochemical networks [1]. Jarnac employs a BASIC like scripting language hosted in a friendly GUI environment. In addition, basic built-in simulation and analysis tools are provided, including time course simulation, steady state analysis, metabolic control analysis, network structural analysis, together with extensive mathematical and matrix arithmetic facilities.

The Systems Biology Workbench (SBW) is a distributed system for sharing computational resources [2]. Its chief characteristics are language and platform neutrality. In addition, the workbench architecture has been designed so that interfacing to the workbench is very straightforward. In fact under Jarnac, SBW remote resources appear transparently to the user as normal Jarnac resources, which can be controlled and manipulated using the Jarnac scripting language like any other built-in Jarnac resource.

In this poster I wish to describe the modifications to Jarnac, which allows it to be a resource provider and consumer in the ERATO Systems Biology Workbench. In addition, an example application is given illustrating how the functionality of Jarnac can be easily extended to include facilities such as stochastic, optimization analyses and network layout and visualization tools.

REFERENCES

- [1] Sauro, H. M. (2000). "Jarnac: a system for interactive metabolic analysis." In: *Animating the Cellular Map 9th International BioThermoKinetics Meeting* (eds: Hofmeyr, J-H. S., Rohwer, J. M., and Snoep J. L.). Stellenbosch, University Press, ISBN 0-7972-0776-7.
- [2] Hucka, M., Sauro, H. M., Finney, A., Bolouri, H, Doyle, J. and Kitano, H, The ERATO Systems Biology Workbench: An Integrated Environment for Multiscale and Multitheoretic Simulations in Systems Biology, *Foundations of Systems Biology*, **6**, 2001, In press