Advanced SubCellular Simulation Capabilities with the Systems Biology Workbench

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Computational modeling and simulation of biochemical networks is a central part of systems biology. The Systems Biology Workbench (SBW) is a software application for modeling and simulation of biochemical networks. The workbench comprises of two primary applications, Jarnac, a script based modeling tool and JDesigner, a visual network based modeling tool. Both tools build on our backend simulator called roadRunner. Both Jarnac and JDesigner are widely used in both academia and industry. Both tools support import and export of SBML together with export to Matlab. RoadRunner supports an extensive API that includes ODE simulation, Stochastic simulation, steady state analysis, stoichiometric analysis, sensitivity and frequency analysis and data fitting capabilities. In addition to being used by Jarnac and JDesigner we also support a roadRunner Python interface to allow users to drive the same simulation engine directly from Python or R. This for example can be used with CompuCell3D to make it much easier to develop multiscale models. In the near future bifurcation analysis will also be included. JDesigner is a visual design tool that allows users to draw networks on screen using the mouse. Networks can be decorated with many different visual cues. Jarnac incorporates a powerful scripting language that allows user to develop reproducible models together with import/export to and from SBML. Models can be seamlessly transferred between Jarnac and Designer. For the future, we plan addition features including version control, model tracking and real-time interactive modeling.