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# SBW TUTORIAL

# INSTALLATION

Install from the web site [sys-bio.org](http://sys-bio.org)

The screenshot shows the sys-bio.org website in a web browser. The browser's address bar displays 'sys-bio.org'. The website's header includes the 'sys-bio.org' logo and the text 'Computational Systems Biology Sauro Lab University of Washington'. A navigation bar contains links: Home, Downloads, News, Research, Papers, About Us, Contact Us, SBW Help, and Jobs. A search bar is located on the right side of the header.

The main content area features several sections:

- What is SBW**: A link to learn more about the workshop.
- Research Impact**: A link to explore the impact of the research.
- Published Papers**: A link to view published papers.
- Lab Members**: A link to meet the lab members.
- Available Positions**: A link to see available positions.
- CSB Links**: A link to connect with the Center for Systems Biology.
- Courses**: A link to find courses.
- Student Projects**: A link to view student projects.

On the left side, there are two additional sections:

- Online Services:** Includes links for SBML Layout Viewer, SBML Validation, SBML Simulation, SBML Translator, Web Service Creation, and Model Repository.
- Software Downloads:** Lists various software tools: 1. SBW, 2. JDesigner, 3. Jarnac, 4. WinSCAMP, 5. Matlab Interface, 6. Optimization, and 6. Bifurcation.

At the bottom left, it states 'maintained by Frank Bergmann' and provides a 'SOURCEFORGE.NET' link.

The central content area highlights the following:

- Announcing the Joint SBW & CompuCell3D Workshop August 2011**: A paragraph announcing the workshop and a link to the 'Workshop Page'.
- Version 2.8.3 SBW July 2011**: A paragraph announcing the release of version 2.8.3 of the Systems Biology Workbench.
- DOWNLOAD Windows version of Systems Biology Workbench: 2.8.3**: This link is circled in red. Below it, a link says 'Go to Sourceforge page for other OS specific downloads'.
- Announcement: Modeling Webinar Hosted by Rosa**: A paragraph about a webinar on modeling standards and software in biomedical systems.
- Group Blogs and Web Pages**: A section titled 'Visit our group blogs at:' with links to 'TinkerCell Blog by Deepak Chandran' and 'AnalogMachine Blog: Cells, Networks and Computation'.

The right sidebar contains several news items:

- May 09 2011: New Version of TinkerCell**: A paragraph about a new version of TinkerCell with features like ruby scripting, octave scripting, and a global sensitivity plugin.
- Feb 02 2011: Fan-out in Gene Regulatory Networks**: A paragraph discussing synthetic biology and gene regulatory circuits.
- Jan 14 2011: Nature Biotech Letter on Synthetic Biology**: A paragraph about a letter to Nature Biotechnology published for synthetic DNA sequences.
- Nov 22 2010: Robust Synthetic Circuits**: A paragraph about a new paper published in the Journal of Biological Engineering.

# INSTALLATION

From [jdesigner.sf.net](http://jdesigner.sf.net)

The screenshot shows the SourceForge project page for Systems Biology Software (jdesigner). The browser window has a single tab titled "Systems Biology Software". The address bar shows the URL [sourceforge.net/projects/jdesigner/](http://sourceforge.net/projects/jdesigner/). The SourceForge header includes navigation links: "Find Open Source Software", "Browse", "Blog", "Support", "Register", and "Log In".

Below the header, there are several banners: a "ZOLSK Find a Job. Get a Date." banner, a "Click Here for further information." banner, and a "Stephen Wellman's new blog: 'IT Matters: Doing More with Less'" banner.

The main content area is titled "Systems Biology Software Project by fbergmann, hsauro, ivan007, spaladug". It includes tabs for "Summary", "Files", "Reviews", "Support", "Develop", "Tracker", "Forums", and "Code".

The project description states: "This site hosts the source code for C++ version of the Broker for SBW, NOM module, advanced simulation suite, analysis applications and model editors."

Key project information is displayed in a grid:

- Project Home:** [jdesigner.sf.net](http://jdesigner.sf.net)
- Recommended By:** 4 users
- Last Update:** 2011-05-16
- Other Versions:** Browse all files
- Support:** [sf.net/project/memberlist.php?group\\_id=41646](http://sf.net/project/memberlist.php?group_id=41646)
- License:** BSD License
- More Detail:** Show

A red circle highlights the "Download" button, which is labeled "Download" and "SBW-2.9.2-win32.exe".

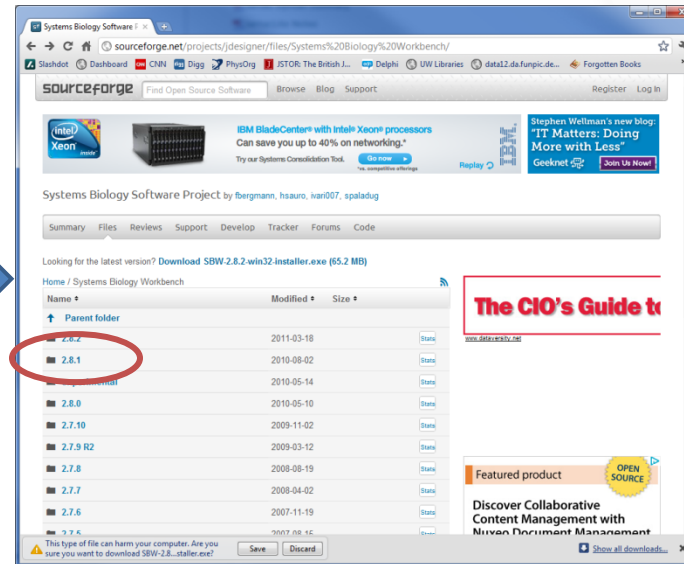
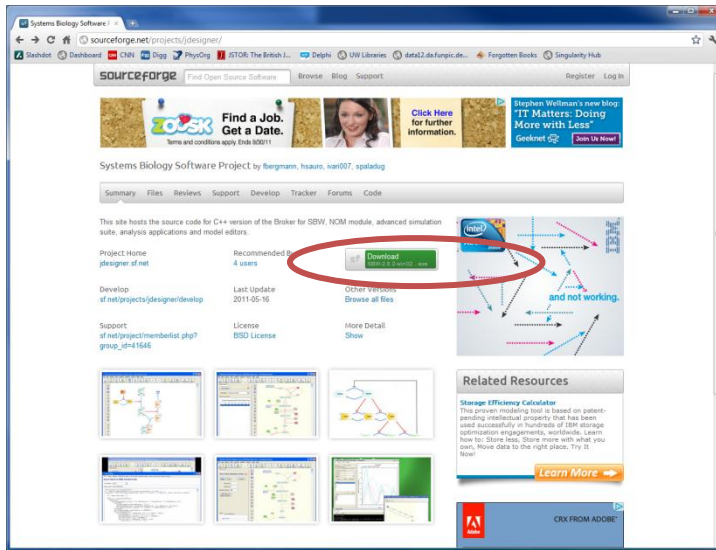
To the right of the download button is a diagram titled "and not working." showing a complex network of arrows and nodes, with an "Intel Xeon" logo in the top left corner.

Below the project information is a "Related Resources" section featuring a "Storage Efficiency Calculator" with a description and a "Learn More" button.

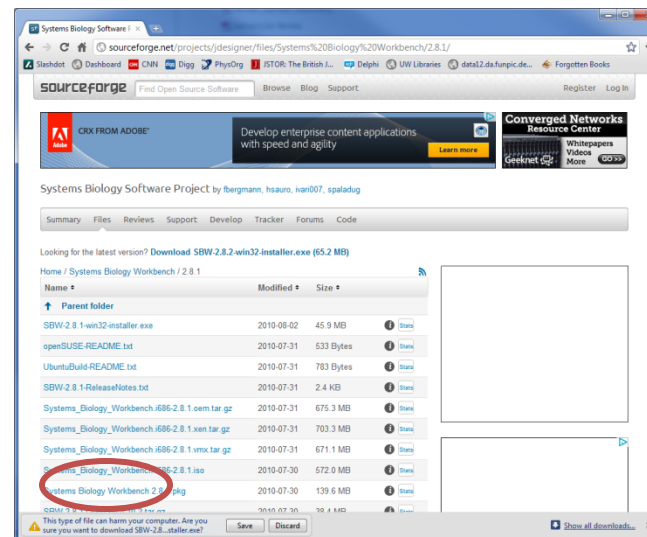
At the bottom right, there is an Adobe logo and the text "CRX FROM ADOBE".

# INSTALLATION FOR LINUX/OSX

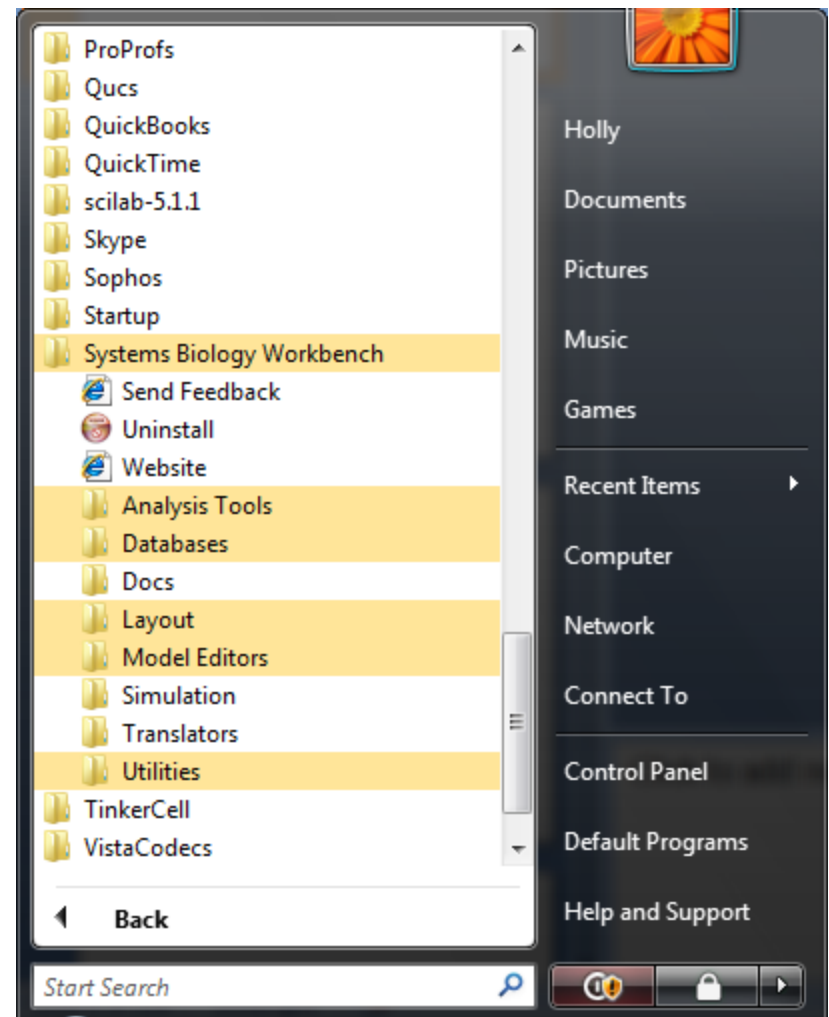
From jdesigner.sf.net



Linux/OSX is not the fully version due to porting difficulties. **Recommend** using the Windows version. A pure cross-platform version may be released next year.

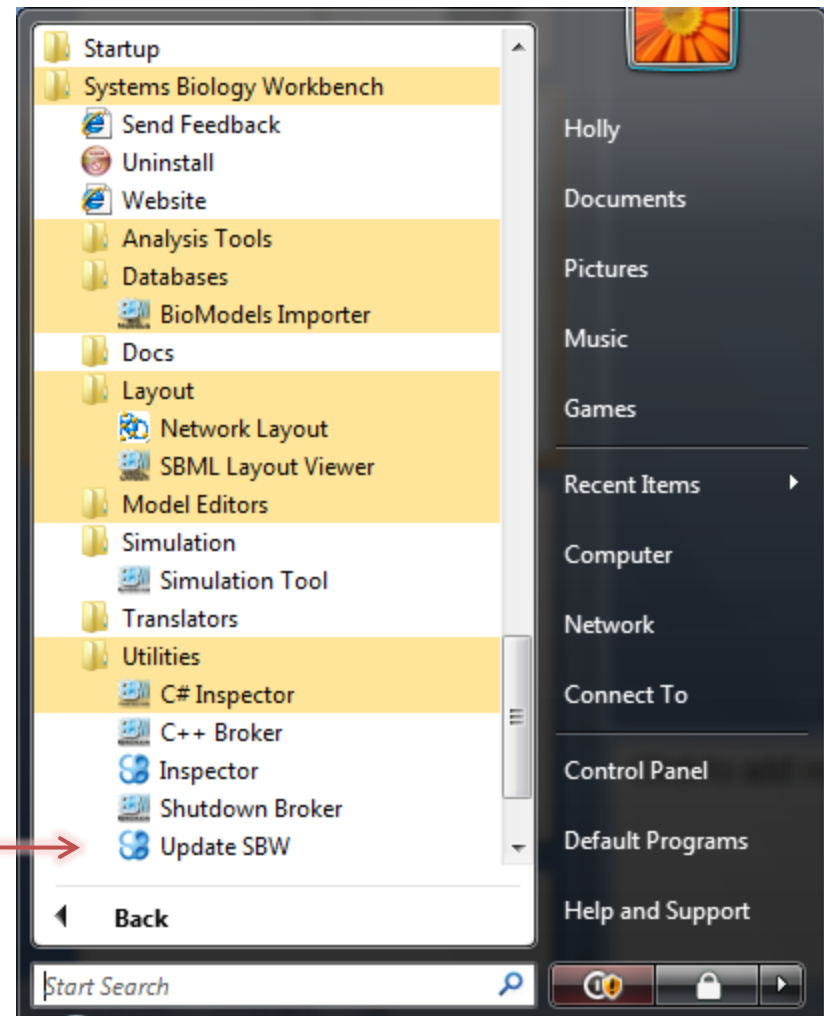


# Systems Biology Workbench



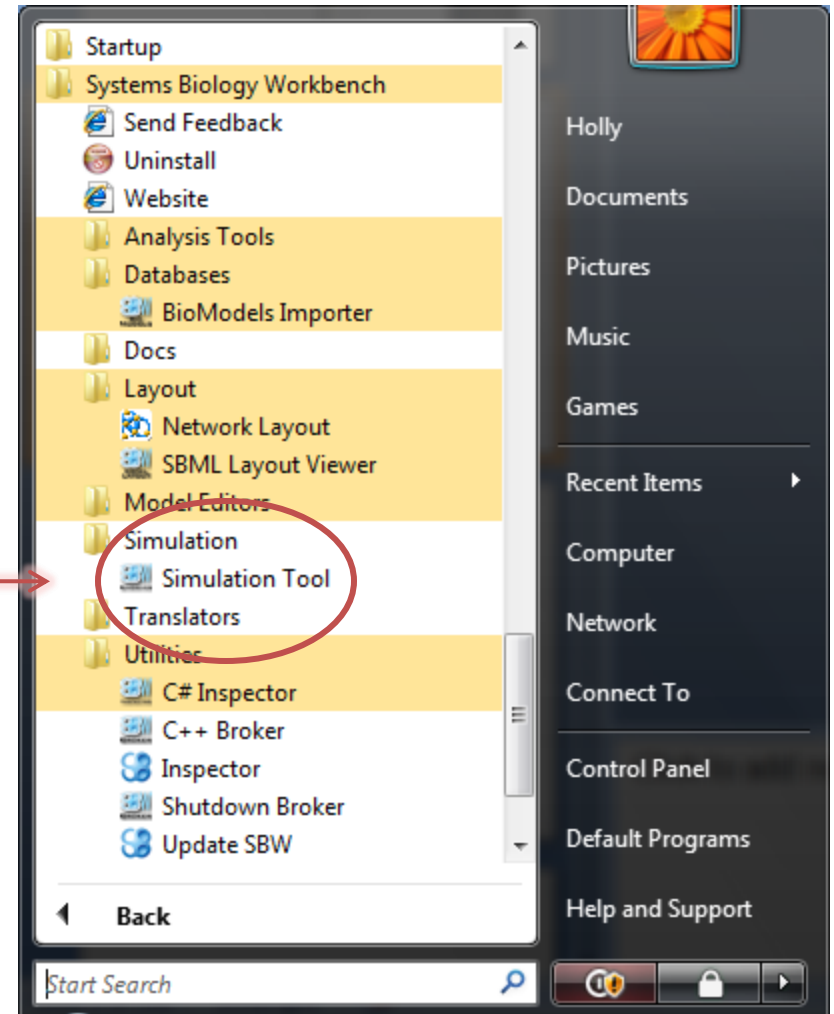
# Systems Biology Workbench

Auto Update



# Systems Biology Workbench

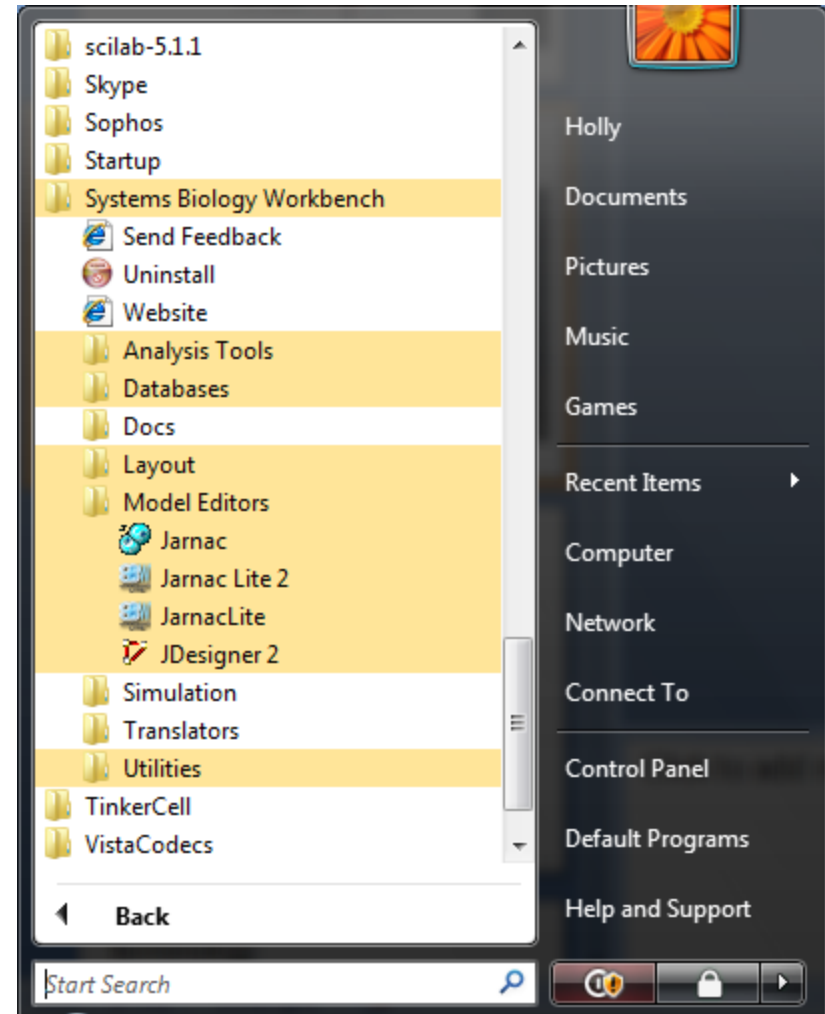
A main entry point for many users



# Systems Biology Workbench

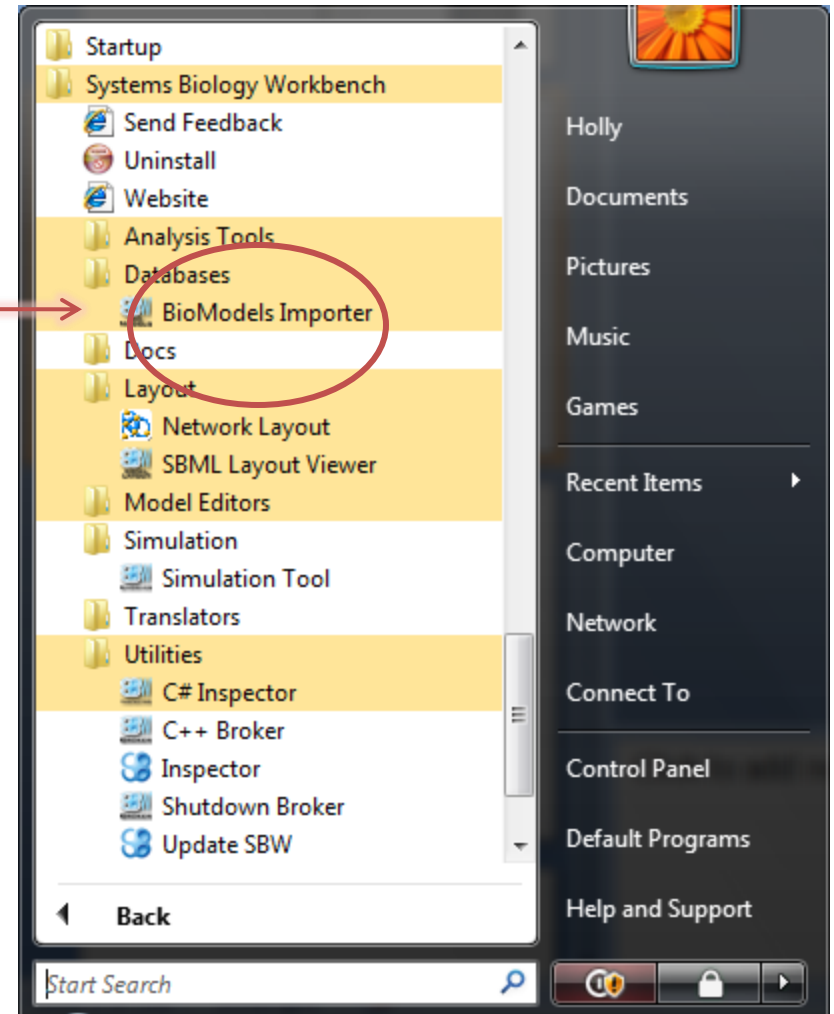
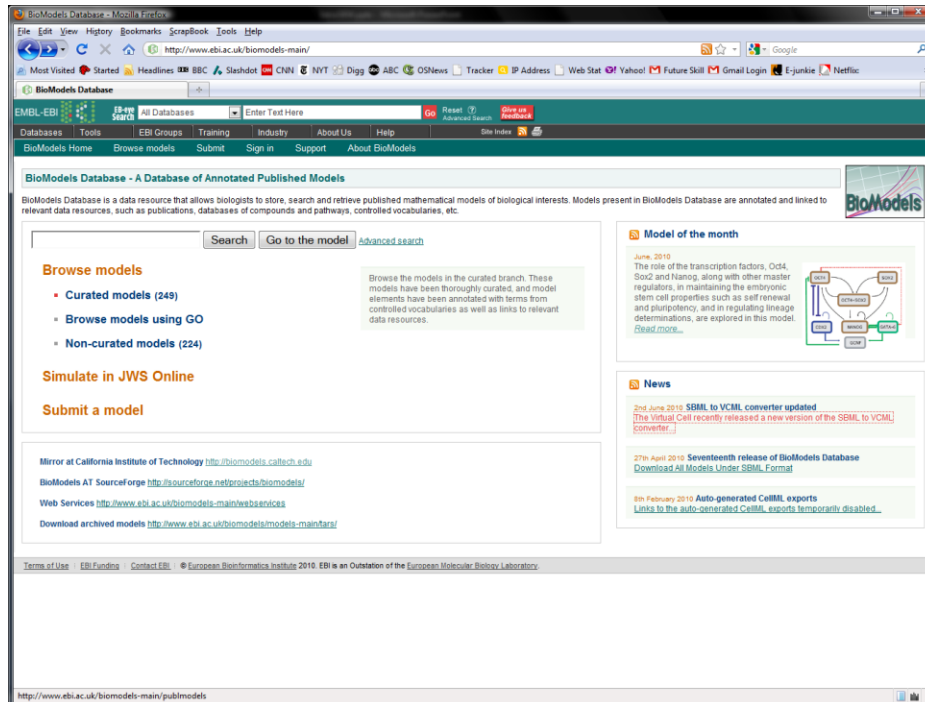
Other possible entry points

**Jarnac:** Script based modeling tool  
**JarnacLite:** Small version of above  
**JDesigner:** Visual design tool



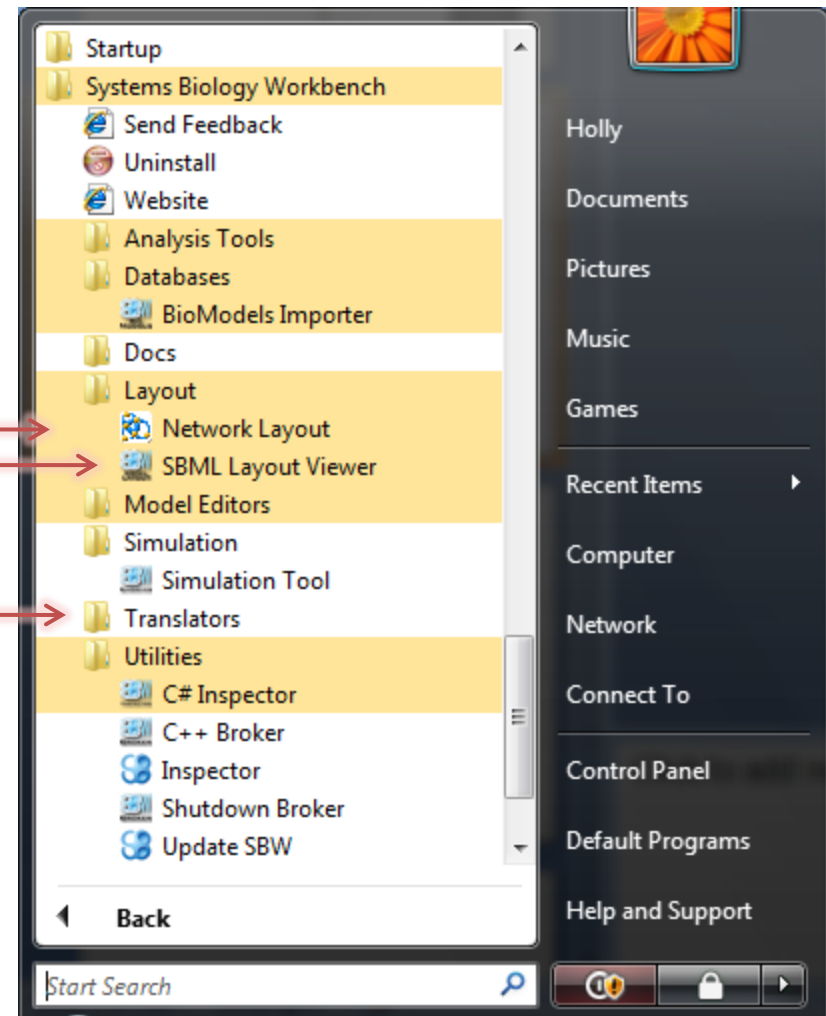
# Systems Biology Workbench

Access to biomodels



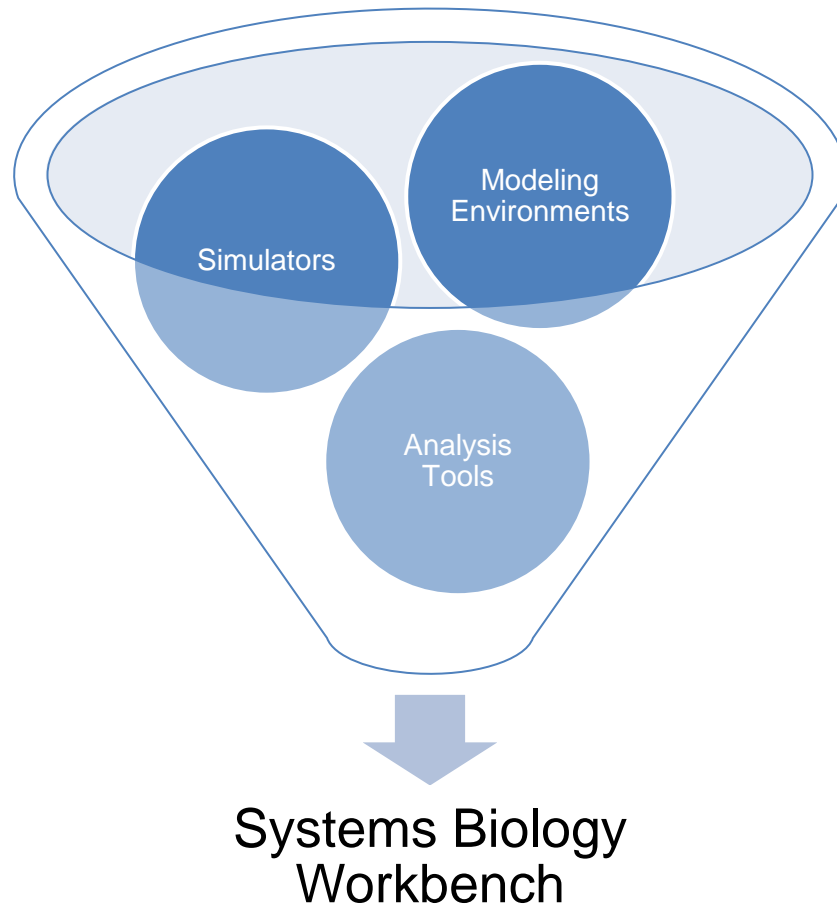
# Systems Biology Workbench

Layout networks  
General Network Viewer  
Models Translators to:  
Matlab, C, Java, C#, Jarnac,  
etc

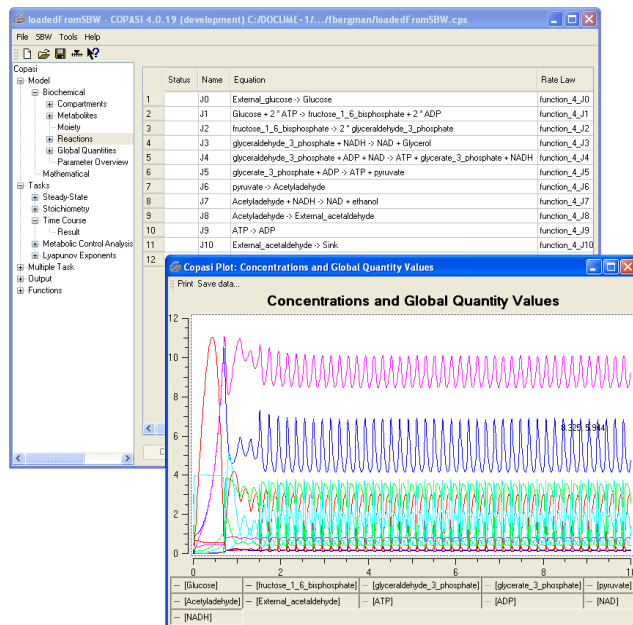


# Systems Biology Workbench

Collection of integrated tools.

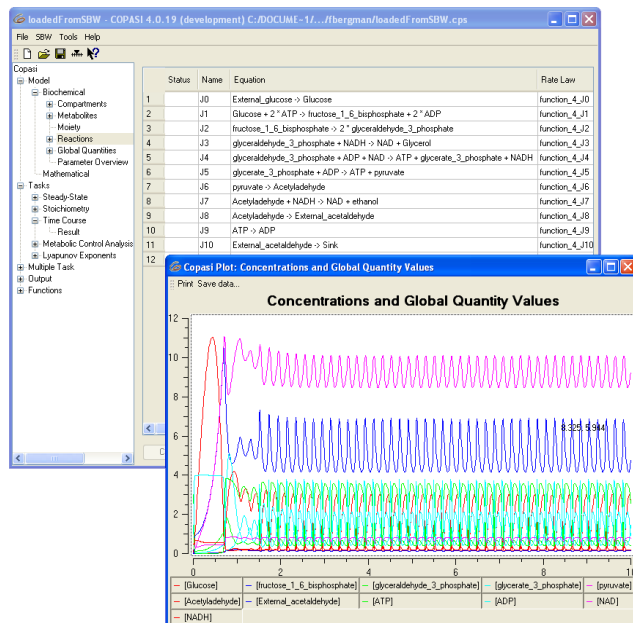


# Terminology



SBW Module

# Terminology

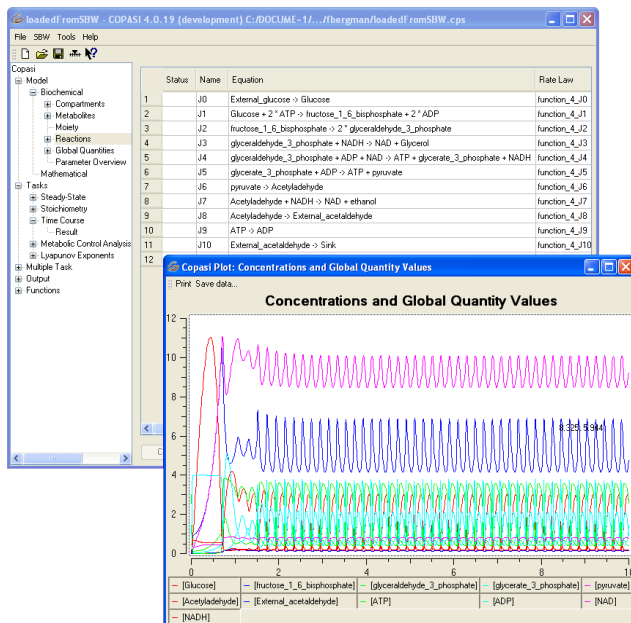


SBW Module

SBW Service

- Simulation
- Optimization
- Parameter Estimation

# Terminology



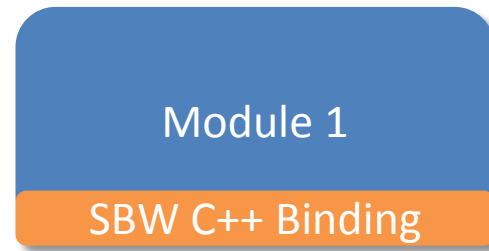
SBW Module

SBW Service

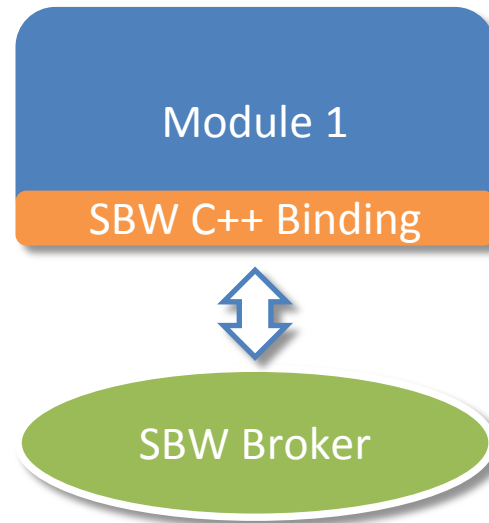
SBW Methods

- `loadSBML(model)`
- `setParameters(v)`
- `simulate()`

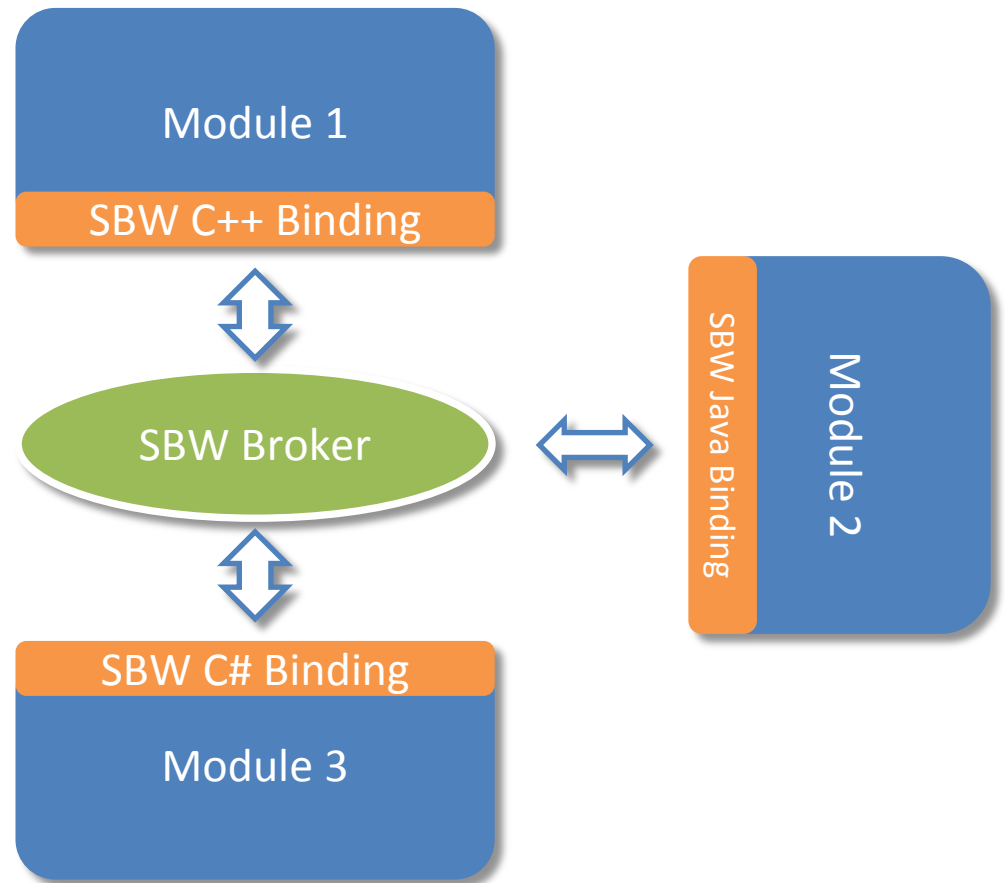
# Behind the Scenes



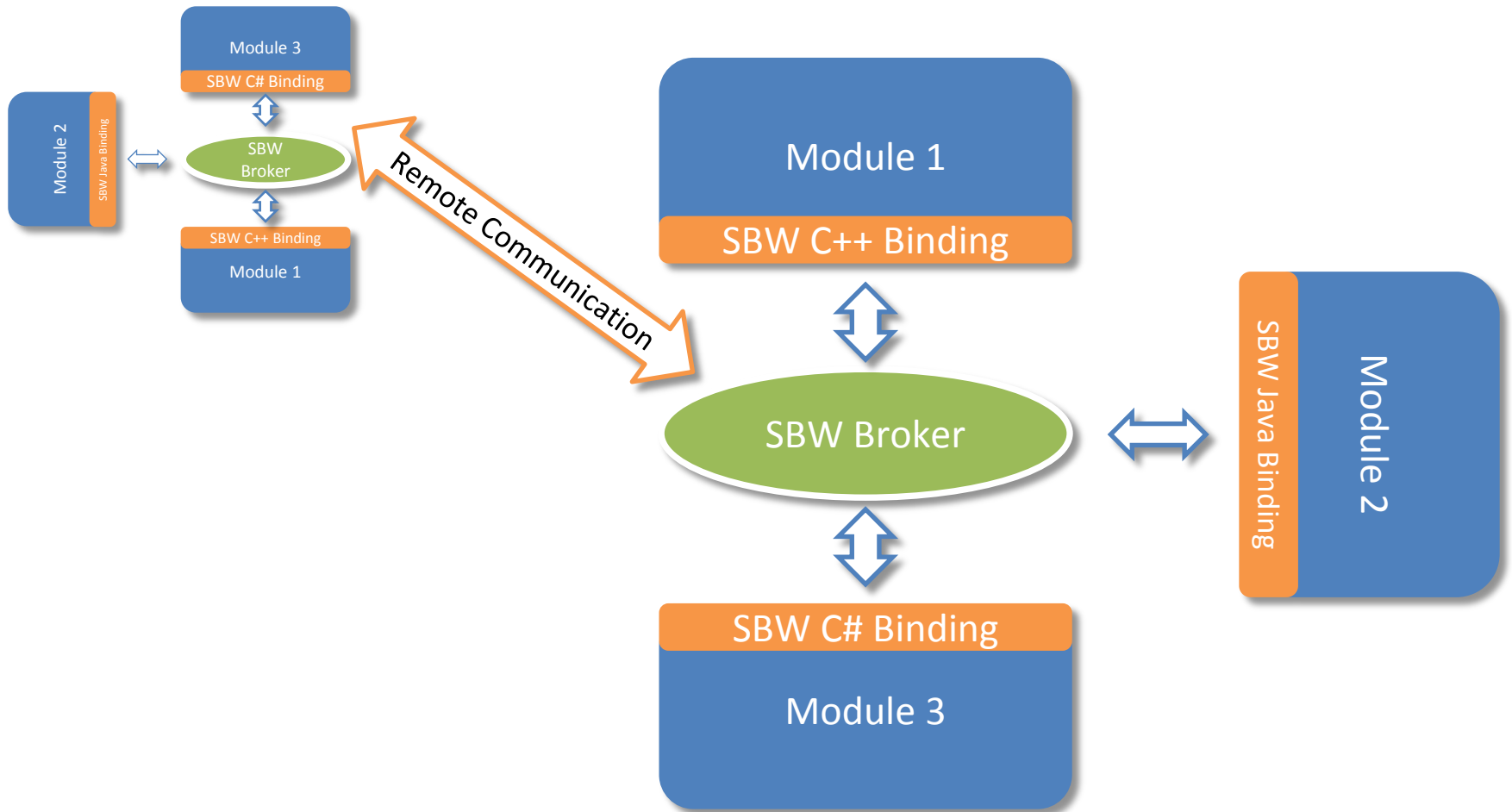
# Behind the Scenes



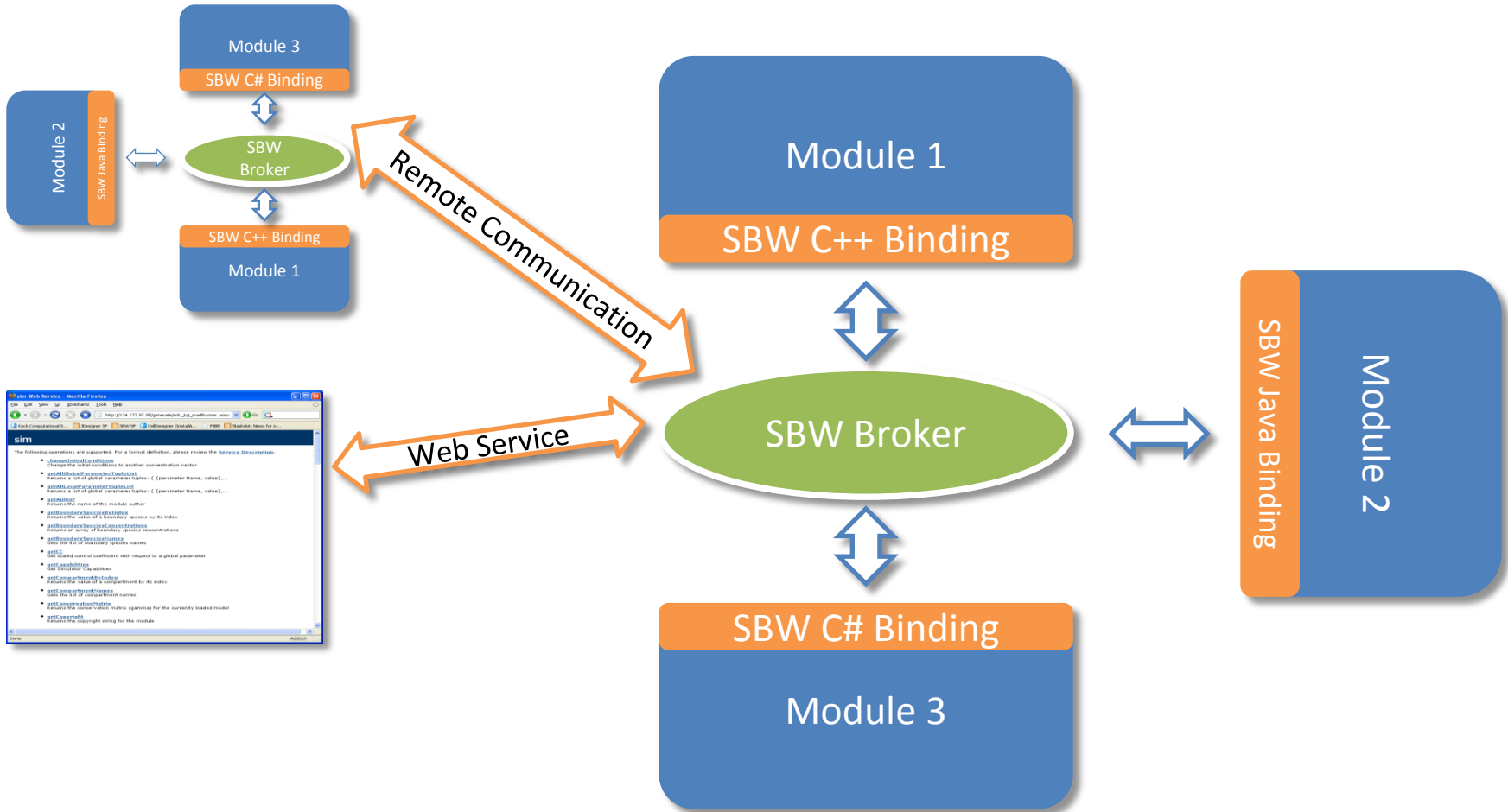
# Behind the Scenes



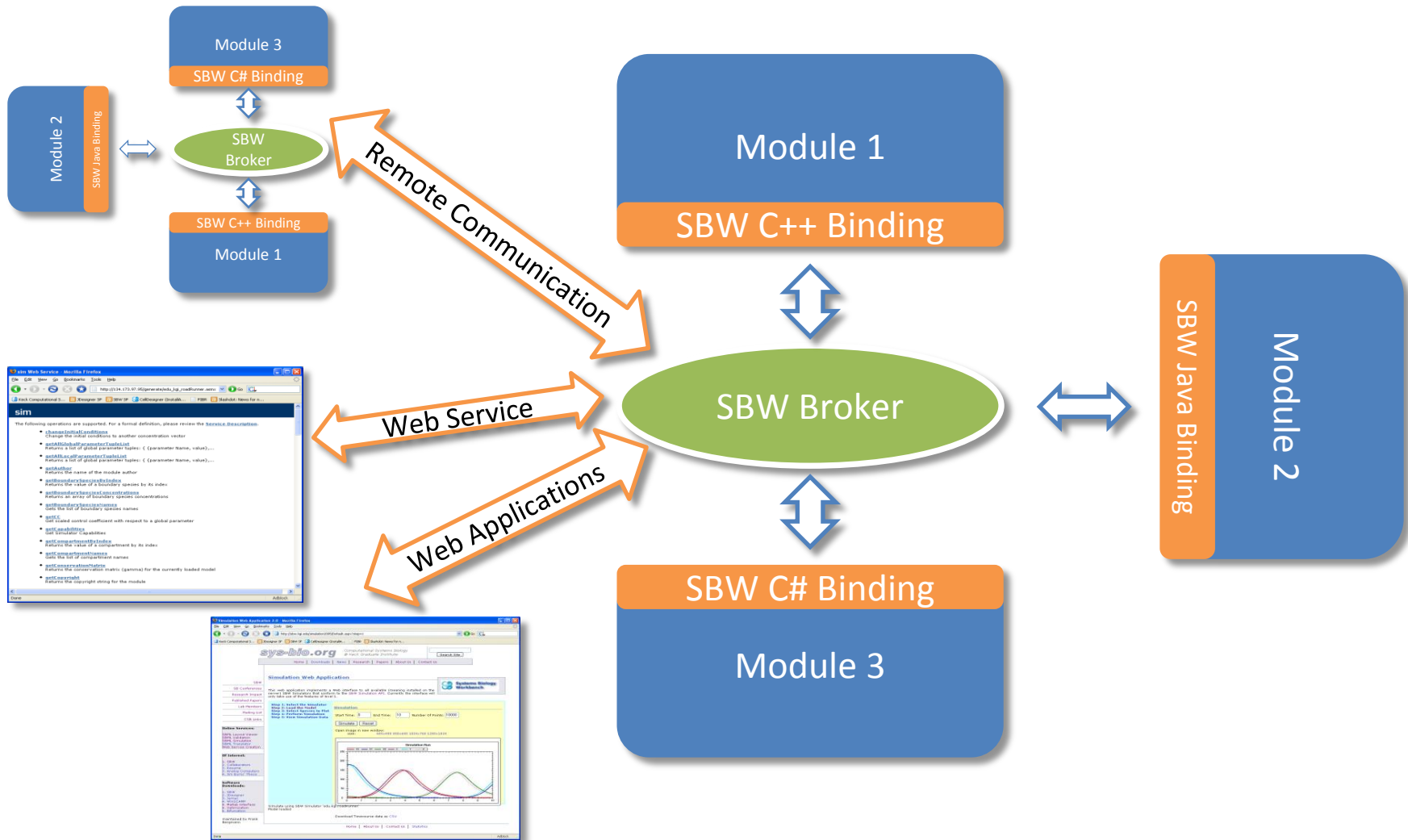
# Behind the Scenes



# Behind the Scenes



# Behind the Scenes



# Motivation



# Modular Approach

SBML Support

# Modular Approach

SBML  
Support

LAPACK  
Module

# Modular Approach

Structural Analysis

SBML  
Support

LAPACK  
Module

# Modular Approach

Simulator

Structural  
Analysis

LAPACK  
Module

SBML  
Support

# Modular Approach

## Modeling Environment

Simulator

Layout  
Module

Further  
Analysis  
Modules

SBML  
Support

LAPACK  
Module

Structural  
Analysis

SBML  
Layout  
Support

# How is interchange accomplished?

## By Community Agreed Standards

**SBML** (Systems Biology Markup Language): de facto standard for representing cellular networks. A large number (>200) of tools support SBML.

CellML: Stores models in mathematical form, therefore is quite general, but biological information is lost. Not possible to reconstruct network. Less than a hand-full of tools support CellML

SBGN: A proposed standard for visually representing cellular networks. No persistent format has yet been devised which limits its use in software.

## Open but 'non-standard' Representations

**Jarnac and JarnacLite**: Script based format for describing networks, can be easily translated to and from SBML.

Antimony: Script based modular format (extension of Jarnac) for describing networks, can be easily translated to and from SBML and Jarnac. (and soon CellML)

BioNetGen: Rule based scripting language for describing networks

# SBML

The screenshot shows the SBML.org website in a Mozilla Firefox browser window. The browser's address bar displays the URL [http://sbml.org/Main\\_Page](http://sbml.org/Main_Page). The website's header features the SBML.org logo and the title "The Systems Biology Markup Language". Below the header is a navigation menu with links to News, Documents, Downloads, Forums, Facilities, Community, Events, and About. A search bar is also present.

The main content area is divided into several sections:

- Welcome to the portal for the Systems Biology Markup Language (SBML),** a computer-readable format for representing models of biological processes. SBML is suitable for models of metabolism, cell signaling, and other processes, and has been evolving since 2000 thanks to an international community of researchers.
- For the curious**: What is SBML? Read our [introduction](#), then perhaps browse the [mailing lists](#) to get a sense of what's going on with SBML today.
- For modelers**: Looking for software that supports SBML? Our [software guide](#) lists over **180** systems today. Are you instead looking for models? Visit the [BioModels Database](#), where you can find hundreds!
- For software developers**: Interested in supporting SBML in your software? Read our [basic introduction](#) and then the [SBML specifications](#) to understand how to use SBML. After that, you may want to look at [libSBML](#).

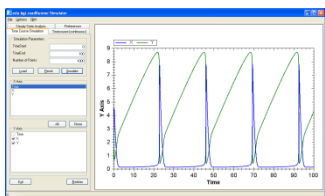
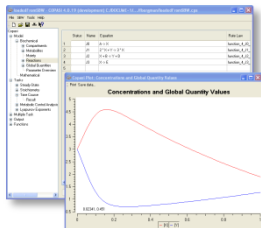
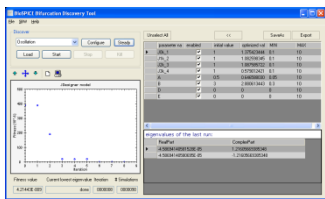
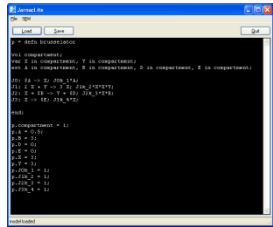
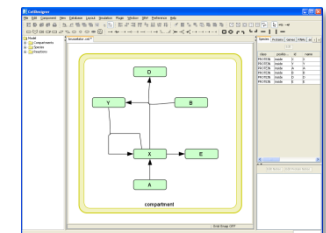
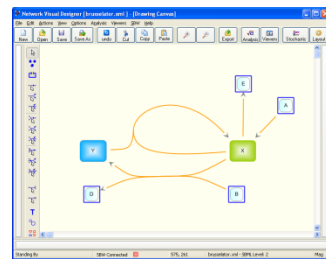
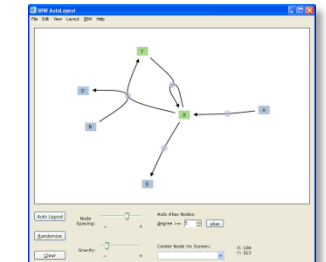
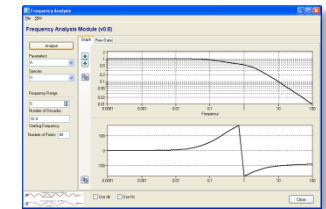
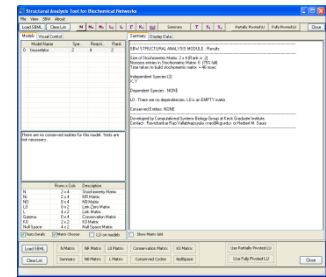
No matter how you use SBML, we invite you to sign up for news updates either through our [RSS feed](#), our [Twitter feed](#), or one of the [mailing lists](#), and get involved with [community efforts](#) to help keep improving SBML. You can also call attention to your project's support of SBML by displaying the [SBML logo](#).

SBML would not have been possible without support from [multiple agencies and organizations](#), as well as intellectual contributions from many motivated individuals, including the [major contributors](#) who are shaping SBML Level 3.

The right sidebar contains news updates:

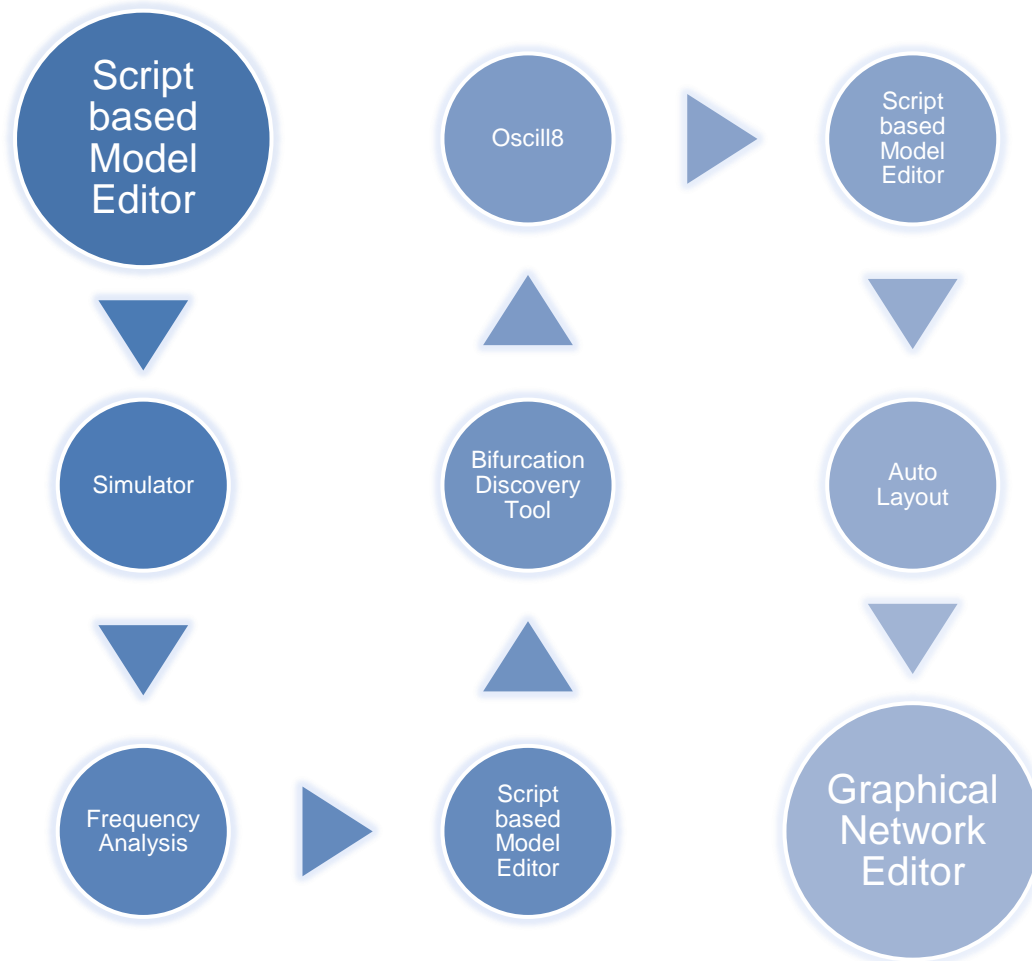
- SBML News**:
  - SBMLToolbox 3.1.2!** (27 Apr.'10) Another minor bug-fix release of our free MATLAB toolbox for SBML is now available.
  - SBMLToolbox 3.1.1!** (12 Apr.'10) A minor bug-fix release of our free MATLAB toolbox for SBML is now available.
  - Older news ...
- Community News**:
  - COPASI 4.6 Released** (22 Jul.'10) The new stable release of [COPASI](#) adds support for events, new stochastic algorithms, and SBML L2v4.
  - CellDesigner 4.1!** (30 Jun.'10) [CellDesigner](#) is a full-featured modeling environment with a GUI. This release adds SBML L2v4, SABIO-RK, MIRIAM, PANTHER, SBGN and other support.
  - Cain 1.4 released!** (31 May.'10) [Cain](#) is a stochastic simulator with highly efficient implementations of many methods.
  - Older news ...

The browser window shows various tabs and a search bar. The status bar at the bottom indicates "Done".

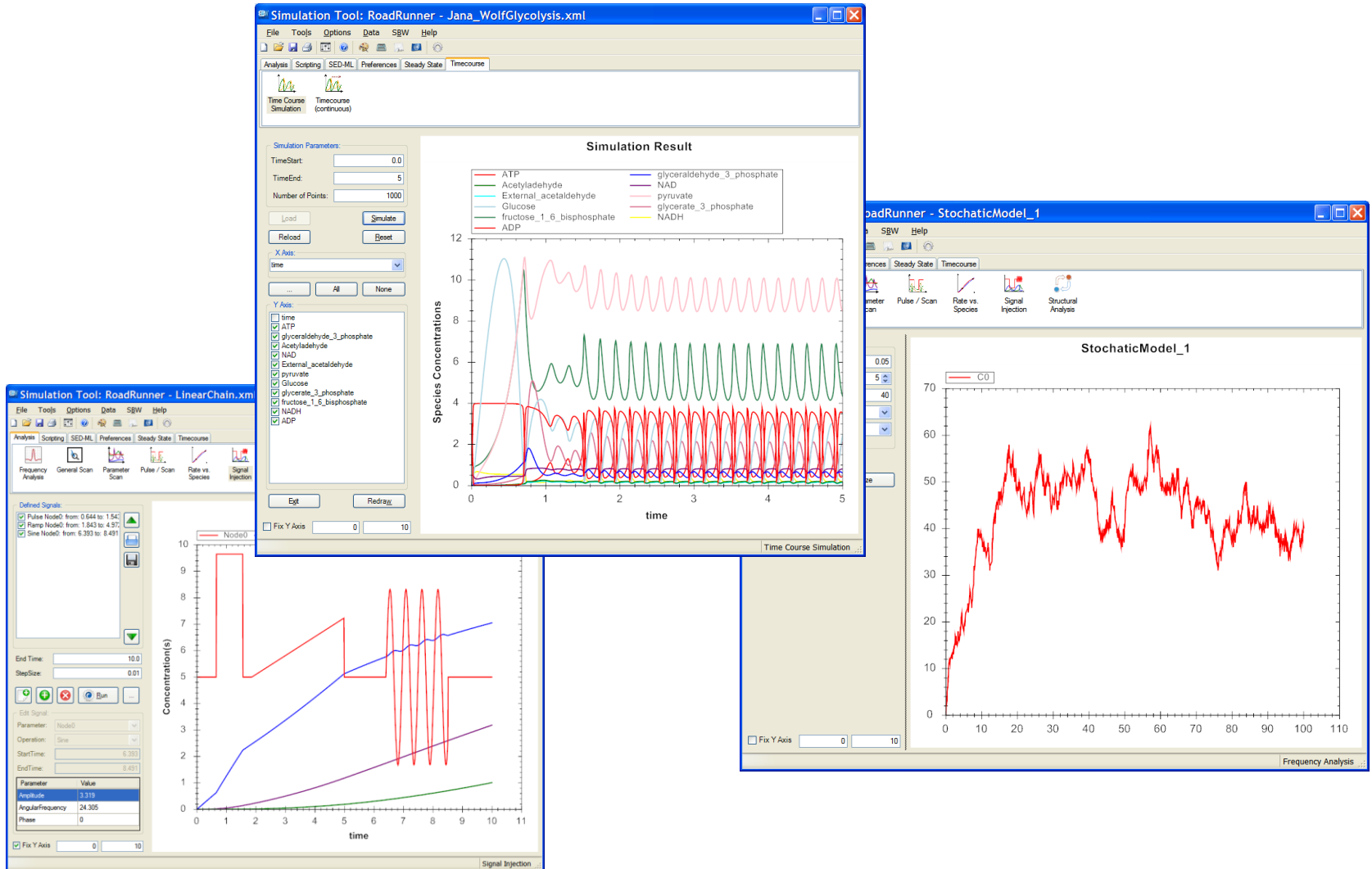


- Bifurcation Discovery Tool
- Chemical\_Langevin\_Equation Simulation Service
- COPASI (SBW Dev. Version)
- CVODE Simulation Service
- Dizzy Simulation Service
- edu.kgi.roadRunner Simulation Service
- Frequency Analysis Module
- Gibson\_NRM Simulation Service
- Gillespie\_DM Simulation Service
- Gillespie\_FRM Simulation Service
- GillespieGUI
- JacobianViewer
- Jarnac Simulation Service
- JDesigner
- Layout Network
- LSODA Simulation Service
- Oscill8 GUI
- Save Model as Matlab ODE Function File
- Save Model as Matlab SimuLink Function File
- SBML layout reader (GUI)
- Simulate 3D (OpenGL)
- Structural Analysis Tool

# Example Workflow



# General Simulation Tool



# General Simulation Tool

Gillespie  
Library

Structure  
Analysis

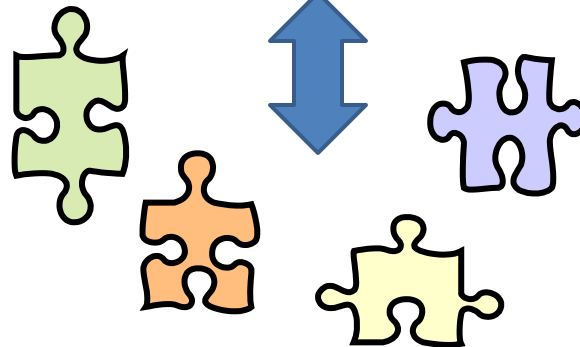
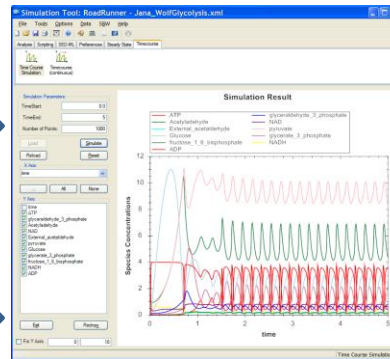
Biomodels  
DB

Simulator  
RoadRunner

SBML  
Support

Python  
Plugin

To SBW



Other Types of  
Plugins, eg GUI  
(See next slide)

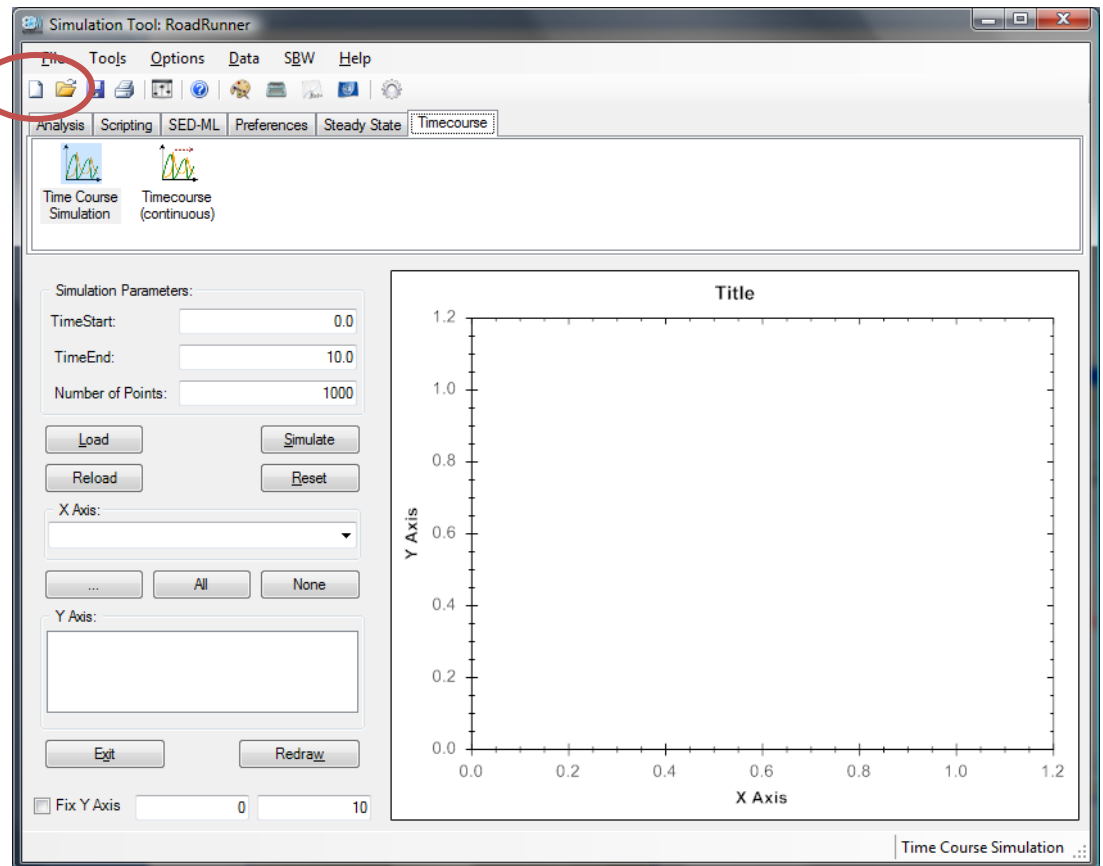
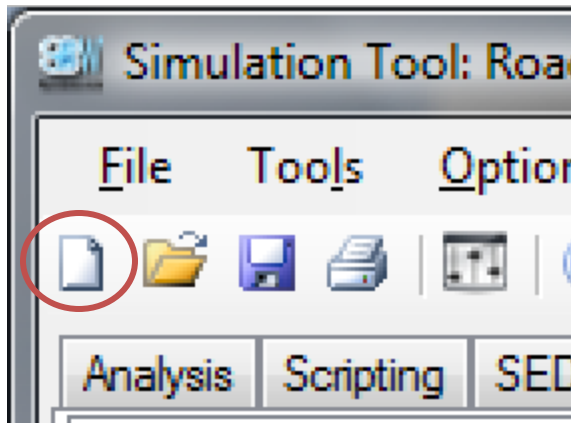
# General Simulation Tool

Current Set of Plugins:

1. Time Course Simulation
2. Steady State including MCA
3. Parameter Scans
4. Signal Injection
5. Frequency Analysis
6. Analysis of Stoichiometry Matrix
7. SED-ML (describing simulation experiments (experimental!))
8. Species versus rate tool
9. Python Scripting with access to the internal object model

# Try a Simple Simulation

1. Start the Simulation Tool
2. Click on the new button (top left)



# Try a Simple Simulation

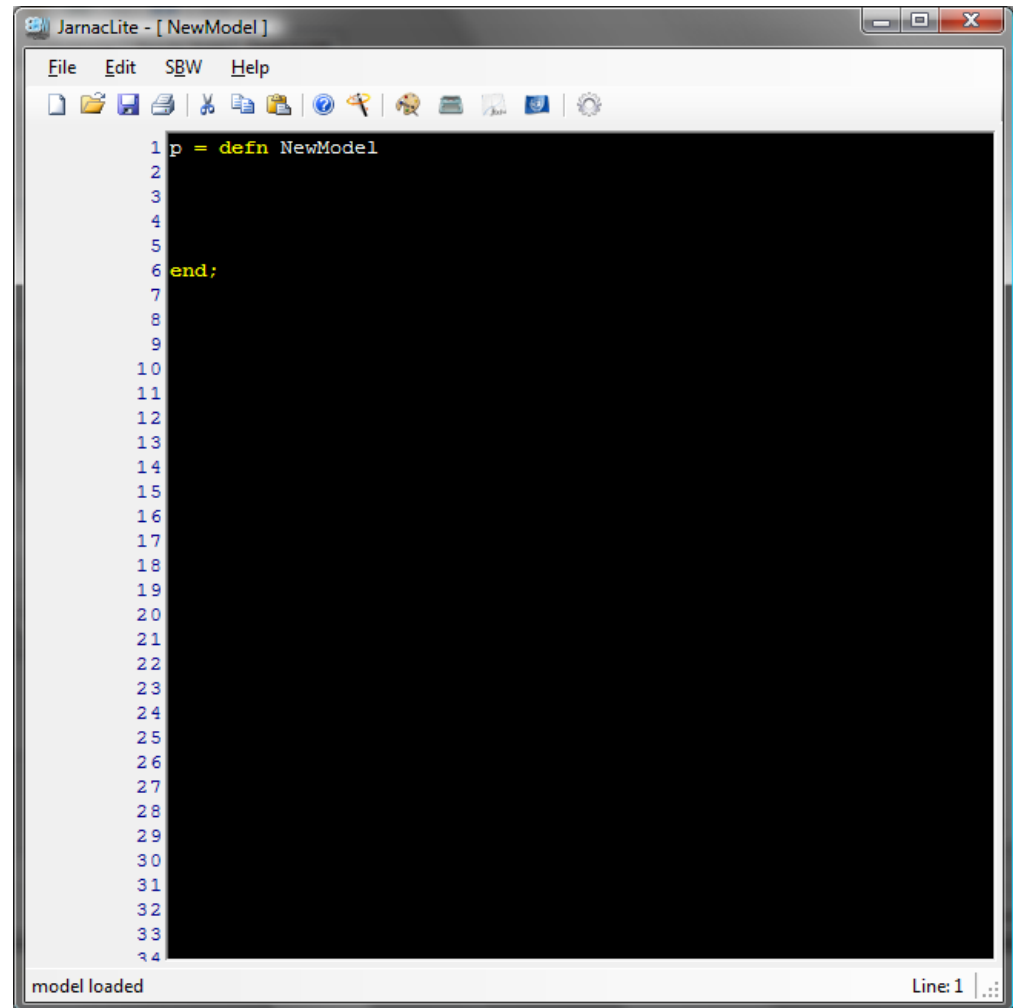
The model editing window should appear,  
type the following in the window:

```
p = defn cell
    S1 -> S2; k1*S1;
    S2 -> S3; k2*S2;
end;
```

```
p.S1 = 10;
p.S2 = 0;
p.S3 = 0;
```

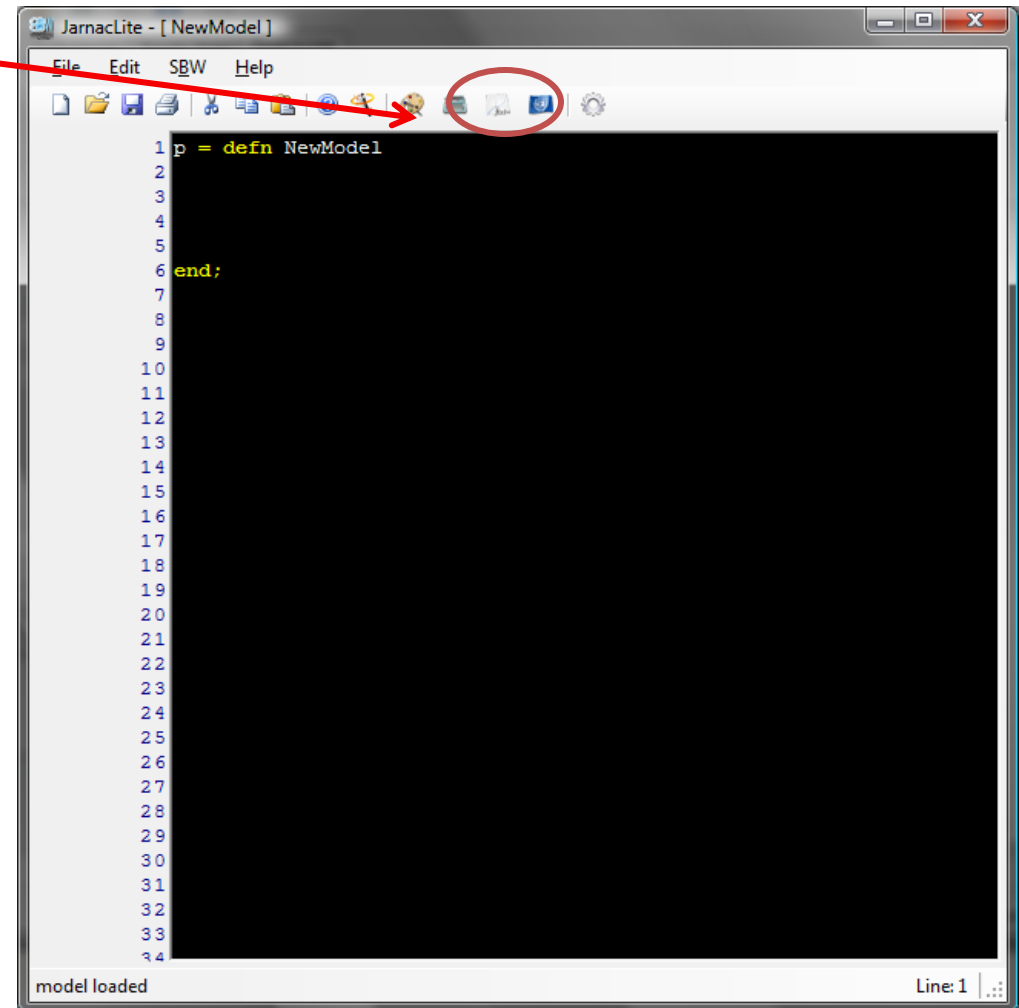
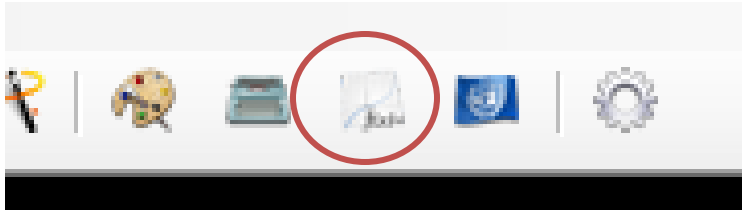
```
p.k1 = 0.34;
p.k2 = 1.3;
```

Make sure you hit return after  
the last line!



# Try a Simple Simulation

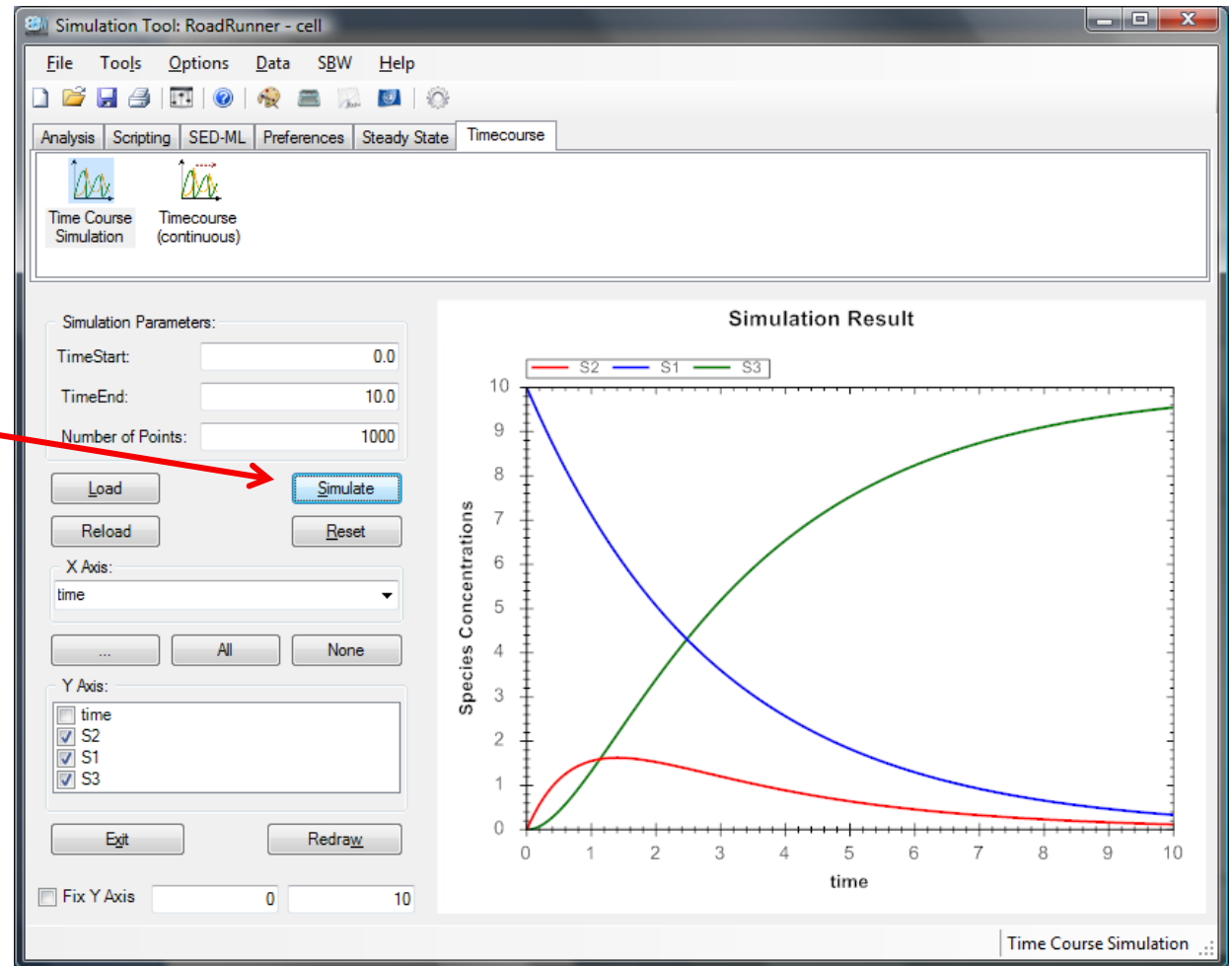
Move the mode to the simulation  
Tool by clicking on:



Third button from the right.

# Try a Simple Simulation

Click to run simulation



# Access Data

Copy simulation data to  
the clipboard or load into Excel

