

# Overview of SBW developments

**Andrew Finney<sup>1,2</sup>, Mike Hucka<sup>1</sup>,  
Herbert Sauro<sup>1</sup>, Hamid Bolouri<sup>1,2</sup>**

<sup>1</sup> California Institute of Technology

<sup>2</sup> University of Hertfordshire

# What is SBW

In case you didn't know

- **Systems Biology Workbench (SBW)** provides a mechanism for the integration of software
- SBW has a message-passing broker architecture
- A **SBW module** is an executable linked with a **client library**
  - Client libraries exist for C, C++, Java, Delphi, Perl and Python
- **SBW itself does not contain any representations of biology nor user interface (UI) components**
  - Modules do provide UIs and representations of biology

# Lastest SBW Release

- **Version 1.0.2**
- **New Core Features**
  - Distributed computation
    - Mike will describe
  - Perl
    - Andrew will describe
  - CORBA
    - Andrew will describe
- **New Modules**
  - Herbert will describe
- **More Installation options**
- **More Documentation**

# Installation <http://www.cds.caltech.edu/erato/sbw/downloads>

- **Installers with and without source code**
- **Windows and Linux installers**
- **3<sup>rd</sup>-Party modules available separately**

# New Documentation

- **Separate programming manuals for:**
  - Java, C, C++, Perl, Delphi and Python
- **Manuals describing:**
  - Module programming interfaces
  - CORBA gateway
  - User interface

# SBW and You

- **Feedback**
  - Distributed computing
  - Installation
  - API
    - Implementation of modules
    - Exercising modules
- **Service Categories**
  - Module APIs

# Plans

- **Set up web repository of SBML models**
  - Herbert and Maria
- **Make SBW a community development**
  - Already on bioinformatics.org
- **New Modules**
  - Integrations of 3<sup>rd</sup> party modules
  - Develop modules from scratch
- **Strategy**
  - Focus on requirements of Systems Biologists and Experimentalists