The ERATO Systems Biology Workbench

Michael Hucka, Andrew Finney, Herbert Sauro, Hamid Bolouri

ERATO Kitano Systems Biology Project
California Institute of Technology, Pasadena, CA, USA

Principal Investigators: John Doyle, Hiroaki Kitano

Collaborators:

Adam Arkin (BioSpice), Dennis Bray (StochSim),
Igor Goryanin (DBsolve), Andreas Kremling (ProMoT/DIVA),
Les Loew (Virtual Cell), Eric Mjolsness (Cellerator),
Pedro Mendes (Gepasi/Copasi), Masaru Tomita (E-CELL)

Overview of Tutorial

- **Short intro to the Systems Biology Workbench (SBW)**
  - Motivations
  - Technology
- **SBW from a user's perspective, demonstration of**
  - SBW core components & features
  - Currently available SBW-enabled modules
- **Programming with SBW**
  - Using Java
  - Using C, C++

Motivations

- **No single package answers all needs of modelers**
  - Different packages have different niche strengths reflecting expertise & preferences of the developing group
  - Strengths are often complementary to those of other packages
- **No single tool is likely to do so in the near future**
  - Range of capabilities needed is large
  - New techniques (⇒ new tools) are evolving too rapidly
- Researchers are likely to continue using multiple packages for the foreseeable future
- **Problems with using multiple tools:**
  - Simulations & results often cannot be shared or re-used
  - Duplication of software development effort

Goal & Approach

- **Systems Biology Workbench project goal: provide software infrastructure that**
  - Enables sharing of simulation/analysis software & models
  - Enables collaboration between software developers
- **Initially focused on biochemical modeling**
- **Two-pronged approach:**
  - Develop a common model exchange language
    - SBML: Systems Biology Markup Language
      - XML-based representation of biochemical networks
  - Develop an environment that enables tools to interact
    - SBW: Systems Biology Workbench
      - Uses SBML to transfer models between tools
      - Supports resource sharing

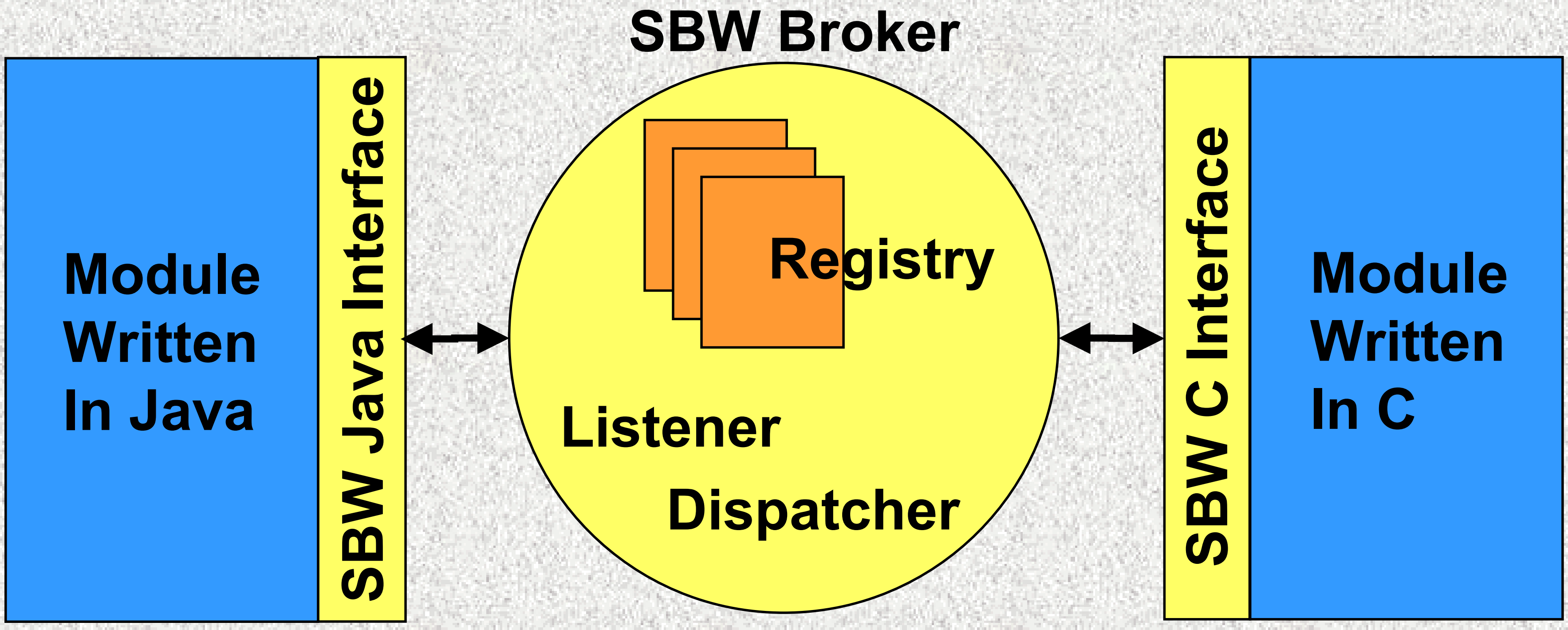
Systems Biology Workbench

- **Open-source, integrated software environment that enables sharing of computational resources**
  - Allows software developers to easily build interprocess communications facilities into their applications
- **From the user's perspective:**
  - One SBW-enabled application can interact with another
  - Each application or module offers services to others
    - E.g.: optimization, time-based simulation, visualization, etc.

Programming SBW

- **Numerous desirable features**
  - Small application programming interface (API)
  - Simple message-passing architecture
    - Easy to make cross-platform compatible
    - Easy to make distributed
  - Language-neutral architecture
    - We provide C, C++, Java, Python libs for Windows & Linux
    - … but libs can be implemented for any language
  - A registry of services for applications to query
  - Use of well-known, proven technologies

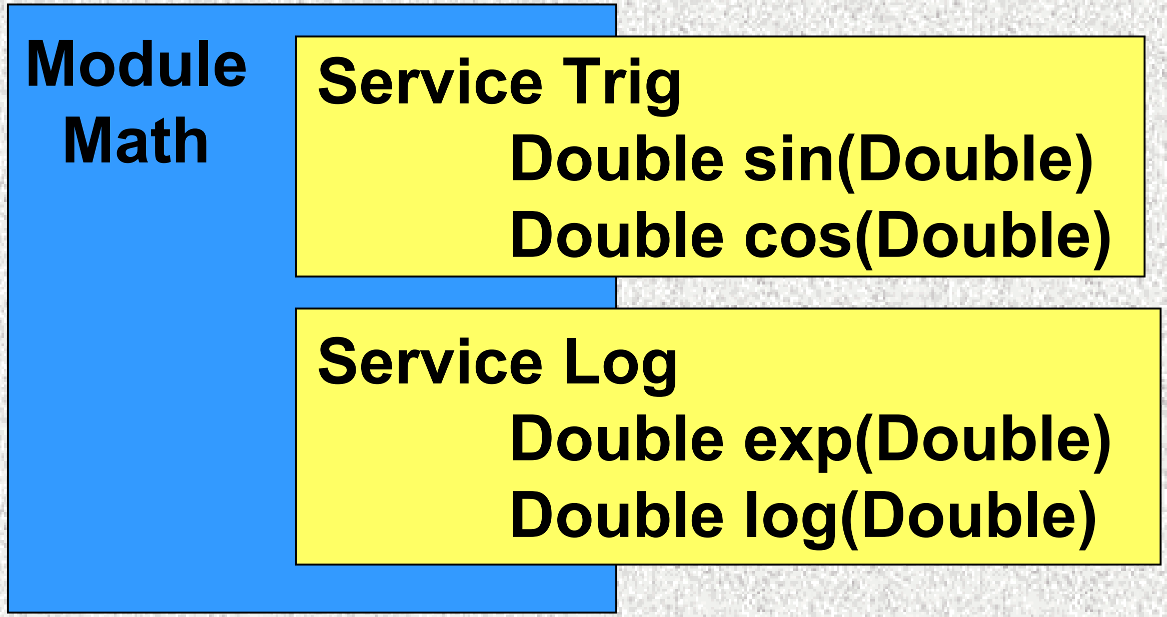
The SBW Framework



- **SBW libraries implement RPC mechanisms**
  - Provide language bindings for SBW
    - C, C++, Java, Python, etc.
  - Implement underlying message-passing protocols

Modules & Services in SBW

- Modules are separately compiled executables
- Modules may offer one or more *Services*
- Services consist of one or more *Methods*



Module Math

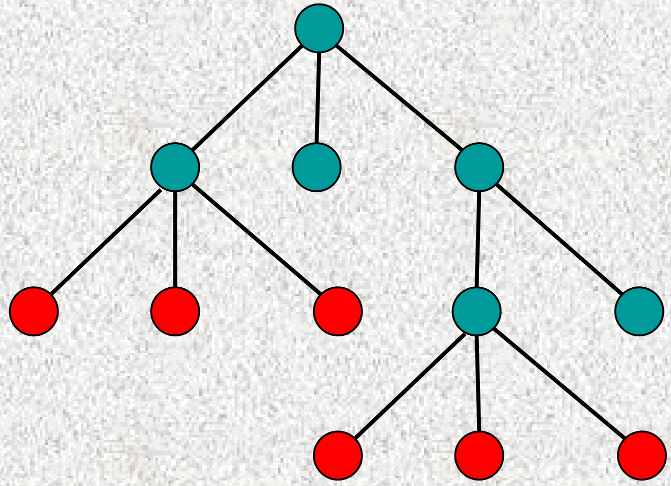
Service Trig
Double sin(Double)
Double cos(Double)

Service Log
Double exp(Double)
Double log(Double)

- Services are categorized into *Service Categories*
- Services do not have to be categorized

The SBW Registry

- **Registry records information about modules**
  - Module name
  - How to start module
  - What services the module provides
  - The categorization of those services
- **Hierarchy of service categories**



Service Categories **(Interface Hierarchy)**

Services **(Interfaces)**

Why?

- **Why not use CORBA?**
  - Complexity, size, compatibility
  - SBW scheme does not require an elaborate compiled IDL
  - No fully-compliant open-source CORBA ORB that supports more than one programming language
  - But: we plan to provide a gateway between CORBA & SBW
- **Why not use SOAP or XML-RPC?**
  - Performance, data type issues, implementation quality
- **Why not Java RMI?**
  - Java-specific
- **Why not COM?**
  - Microsoft-specific, low portability

SBW Status

- **Available Now:**
  - **LGPL open-source beta release from**
    http://www.bioinformatics.org/sbw/
  - **Java, C, C++, Python libraries**
  - **Tutorials, developer's manuals, examples**
  - **Modules:**
    - SBML Network Object Model
    - Gepasi optimization module
    - Jarnac ODE simulator + MCA
    - Plotting
    - Gibson stochastic simulator
    - MATLAB model generator
    - JDesigner visual editor

SBW Future

- **To deliver by April 2002**
  - LGPL production release
    - Improve quality of beta release code, GUIs & docs
  - C# and Perl libraries
  - Secure distributed operation
  - CORBA access
- **Third-party modules under development**
  - Bifurcation analysis module
  - Gillespie “Tau-Leap” module
  - GENESIS interface