

# SigPath: Quantitative information management for cell signalling pathways and networks

Institute for Computational Biomedicine  
Weill Medical College of Cornell University  
New York, USA

# The SigPath Team & Sponsors



## Members of the Project

Institute for Computational Biomedicine and Department of Physiology and Biophysics (Weill Medical College of Cornell University)

- Harel Weinstein
- Fabien Campagne
- Eliza Chan
- Marko Srdanovic
- Piali Mukherjee
- Violet Chang

Department of Pharmacology and Biological Chemistry (Mount Sinai School of Medicine)

- Ravi Iyengar
- Susana Neves

## Past Contributors:

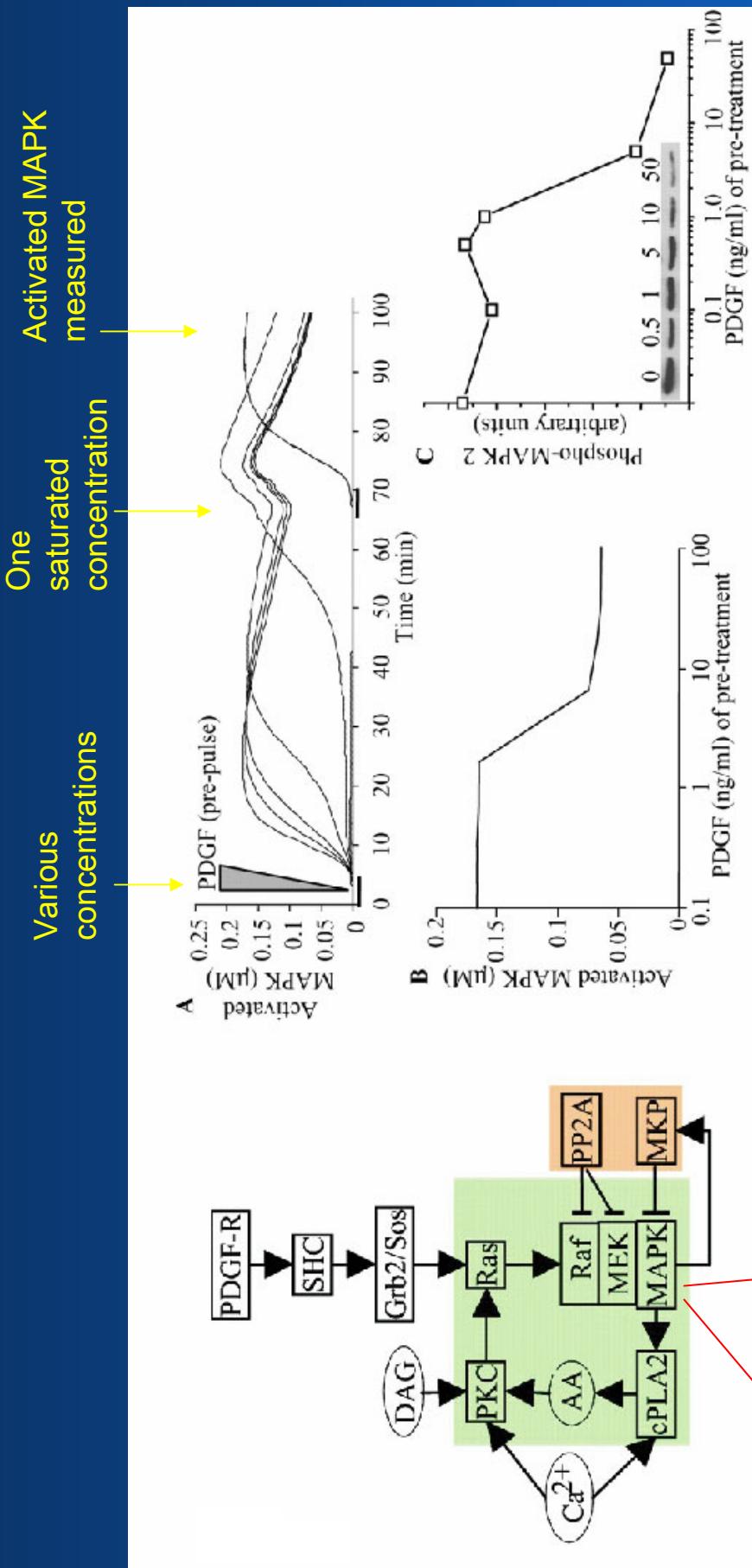
- Manuel Martin
- Ethan Cerami (now cbio/MSKCC)
- Anat Maoz (now WMC Graduate School)
- Benjamin Chiang
- Francois Le Feuvre (now Genoscope)
- Prahlad Ram (now Tulane University)
- Manda Wilson (now cbio/MSKCC)
- Lucy Skrabanek

NIH-NHLBI  
(Pre-NPEBC P20 program)  
NIH-NIDA  
(Signaling suppl. to P01 DA12923)  
Harel Weinstein

NIH-NCI (R01 CA-81050)  
NIH-NIGMS (R01 GM 54-508)  
Ravi Iyengar

Frueauff Foundation  
Fabien Campagne

# Modeling integrated biochemical systems



# Project goals

- Provide means to collaboratively organize biochemical information electronically (w/ links to the primary literature)
- Smoothly integrate with biochemical simulation tools.
- Smoothly integrate with sequence and other bioinformatics databases
- Provide a repository of facts/interpretations /hypotheses for interactions and models
- User-friendly web-based system
- Act as an educational resource
- Going beyond (standard) file formats
- Testing and developing new approaches to help manage biological information





## [ description ]

SigPath is a collaborative project of the Institute for Computational Biomedicine and the Department of Physiology and Biophysics at the Weill Medical College of Cornell University, and the Department of Pharmacology & Biological Chemistry at Mount Sinai School of Medicine.

SigPath is an information system designed to support quantitative studies on the signalling pathways and networks of the cell. [More](#)

Campagne F, Neves S, Chang CW, Skrabanek L, Ram PT, Iyengar R, Weinstein H. Quantitative information management for the biochemical computation of cellular networks. *Science* STKE. 2004; 248:PL11. [\[PubMed\]](#) [\[Full Text\]](#)

Srdanovic M, Schenk U, Schwieger M and Campagne F. Critical evaluation of the JDO API for the persistence and portability requirements of complex biological databases. *BMC Bioinformatics*. 2005; 6:5 [\[Abstract\]](#) [\[Full Text\]](#)

## [ documentation ]

Some novel or noteworthy **features** of SigPath include:

- ▶ Import of background information
- ▶ Full text search in background information
- ▶ BioWizard for submission of binding interactions
- ▶ BioWizard for submission of phosphorylation information
- ▶ Assemble and export simple quantitative models
- ▶ Exporting SigPath entities as XML
- ▶ Reviewing data in SigPath

The following **animated tutorials** highlight some basic uses of SigPath:

- ▶ Querying SigPath for interactions
- ▶ Querying SigPath for small molecules
- ▶ Querying SigPath for proteins
- ▶ Submitting phosphorylation reactions into SigPath using the BioWizard
- ▶ Submitting binding reactions into SigPath using the BioWizard
- ▶ Submitting Interactions into SigPath via XML upload
- ▶ Assembling a quantitative model using SigPath
- ▶ Exporting a SigPath model for iSIM
- ▶ Exporting a SigPath model for Kinetikit
- ▶ Exporting a SigPath model in SBML format
- ▶ Exporting a SigPath entity (models, reactions etc.) in XML format
- ▶ Reviewing data in SigPath

## SigPath Production

### SigPath Navigator

## Project Overview

### Contributing to SigPath

### Sigpath XML Schema

### Validation Data Set

#### For Developers

### Download SigPath

### JDO Benchmark

### Bug Tracker

### FAQ

### Project Members

### Sponsors

### News Archives

## SigPath News

## February 9th, 2005; New SigPath

### production release [Release info]

## December 9-11th, 2004;

### The First SigPath workshop was held in

### New York City. [Workshop info]

## November 3rd, 2004;

### New SigPath beta release [Release info]

## October 29th, 2004; New SigPath

### production released [Release info]

## Sept 22nd, 2004;

### New beta

### release of SigPath

### available for

### preview and testing. [Release info]

## Sep 3rd, 2004;

### A description of

### SigPath is now available in Science

### STKE. SigPath users may now cite

### it as Quantitative information

### management for the biochemical

### computation of cellular networks.

### Campagne F, Neves S, Chang CW,

### Skrabanek L, Ram PT, Iyengar R,

### Weinstein H, Science STKE

### 248:PL11. (2004). [SigPath]

## Mar 2nd, 2004;

### A new release of

### SigPath is now available. [SigPath]

## Mar 1st, 2004;

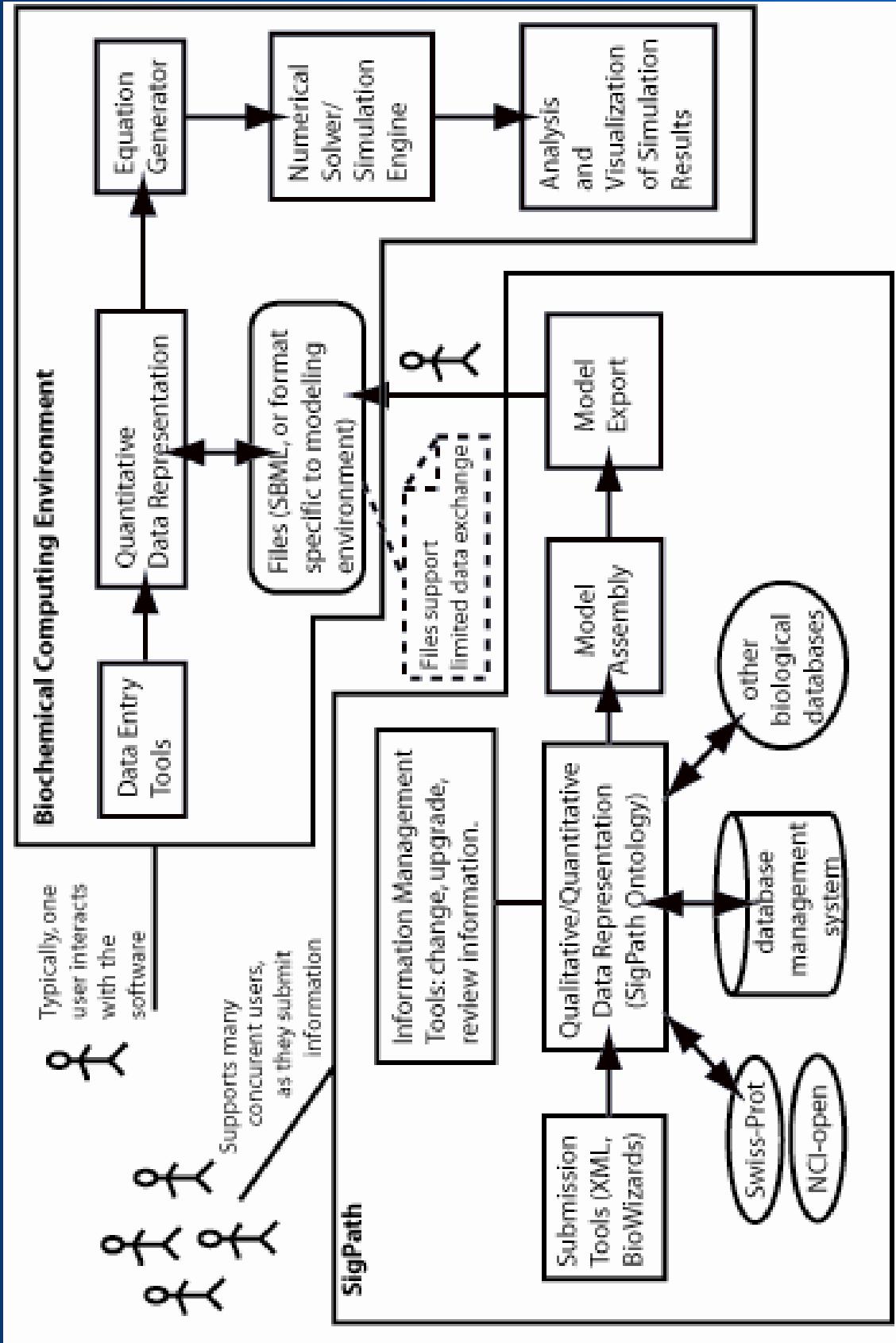
### SigPath is now

### released under the GNU General

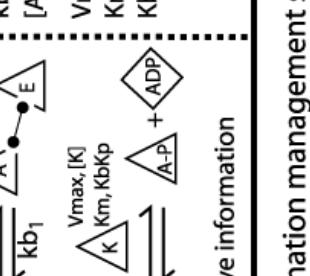
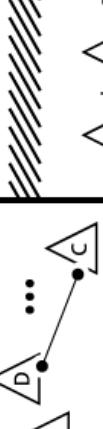
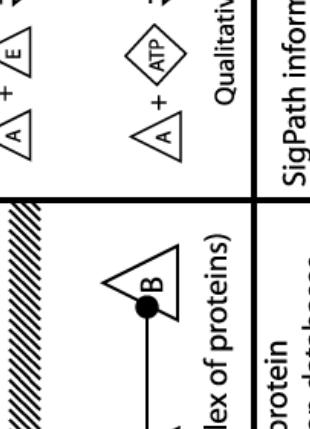
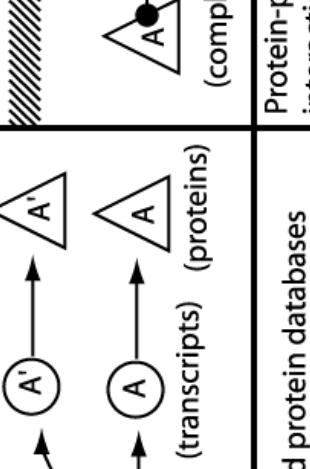
### Public License [download source]

→

# SigPath complements biochemical modeling environments



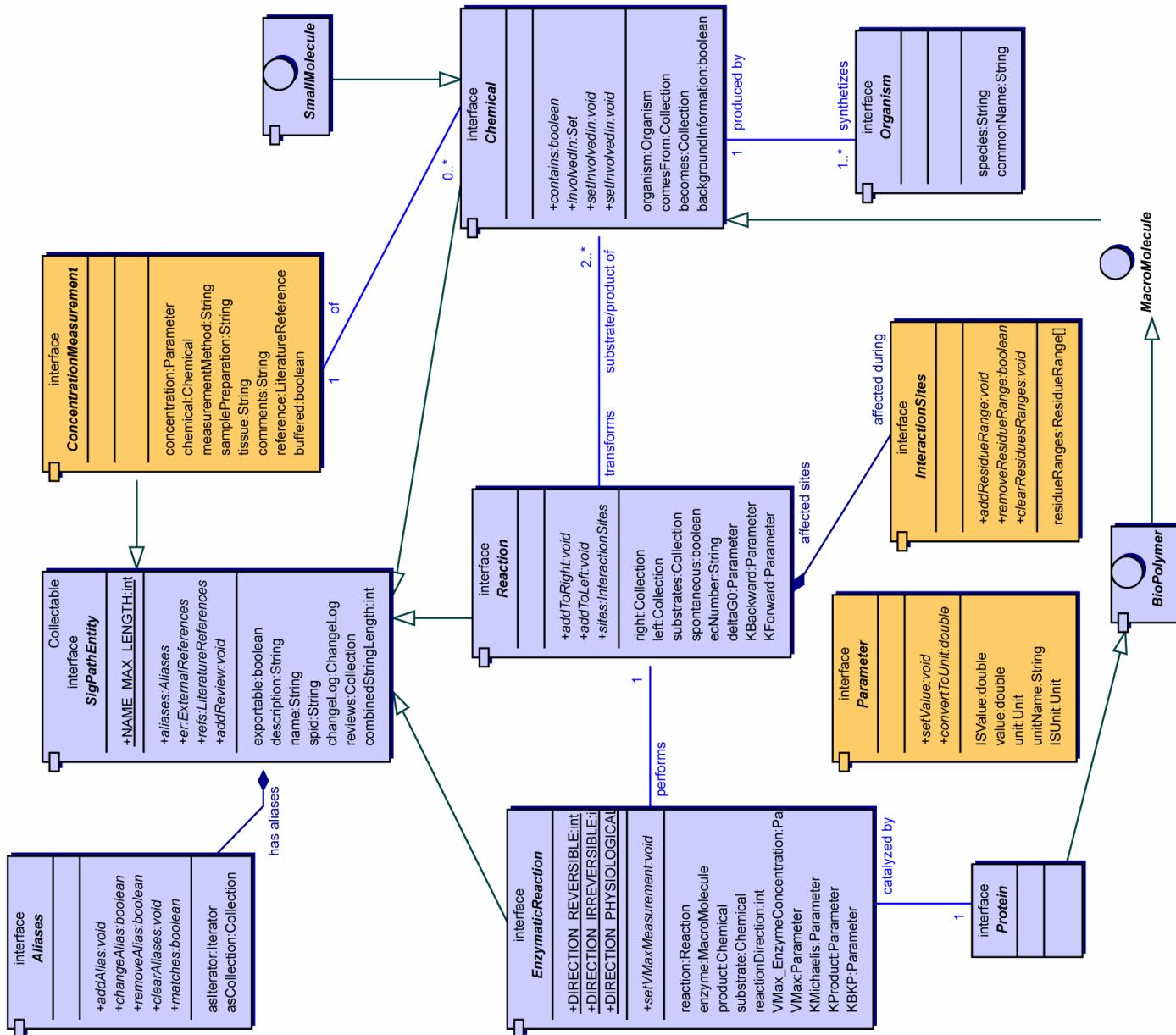
## Comparison to other types of data and databases

	 <p><b>Genomic and protein databases</b></p>	<p>Graph-like data, one or two types of biochemical entities</p>
	 <p><b>Protein-protein interaction databases</b></p>	<p>Graph-like data, many types of biochemical entities</p>
	 <p><b>SigPath information management system</b></p>	<p>Graph-like data, many types of biochemical entities</p>

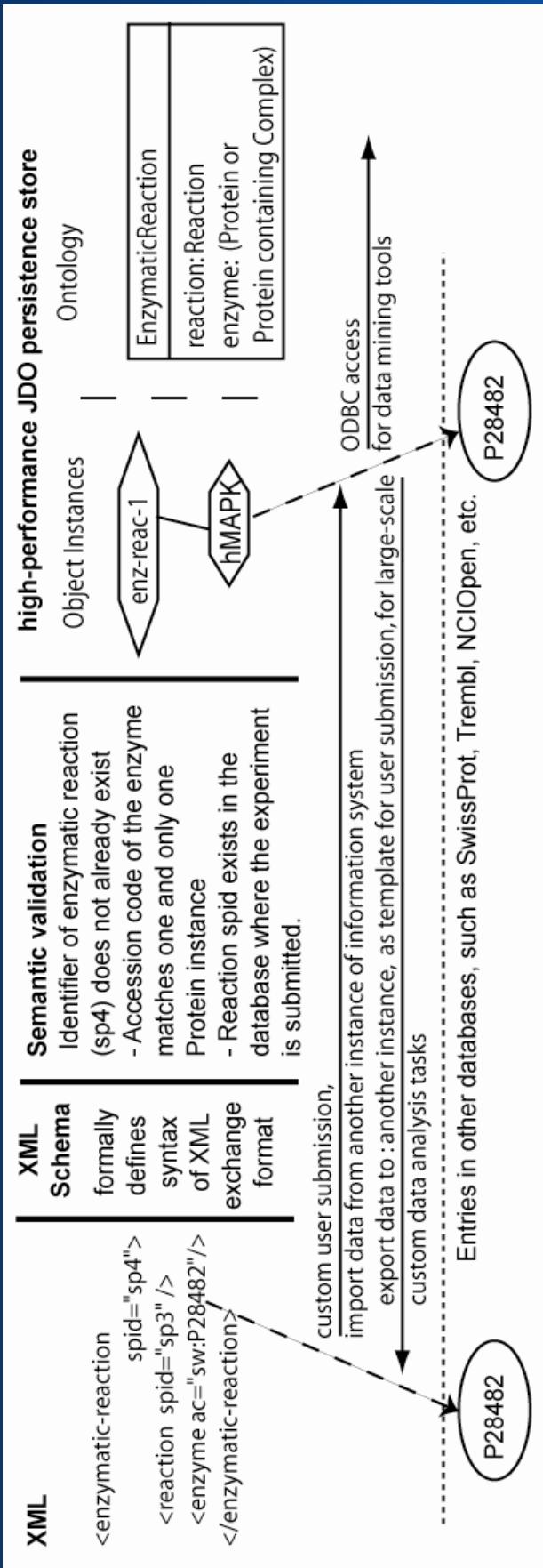
The SigPath ontology is derived from the EcoCyc ontology (Karp P), but includes many extensions. For instance, to represent quantitative features

(e.g., rates, concentrations) and context of the measurements.

Just a glimpse..  
>80 classes in the  
current ontology



# Data integration approach used for SigPath



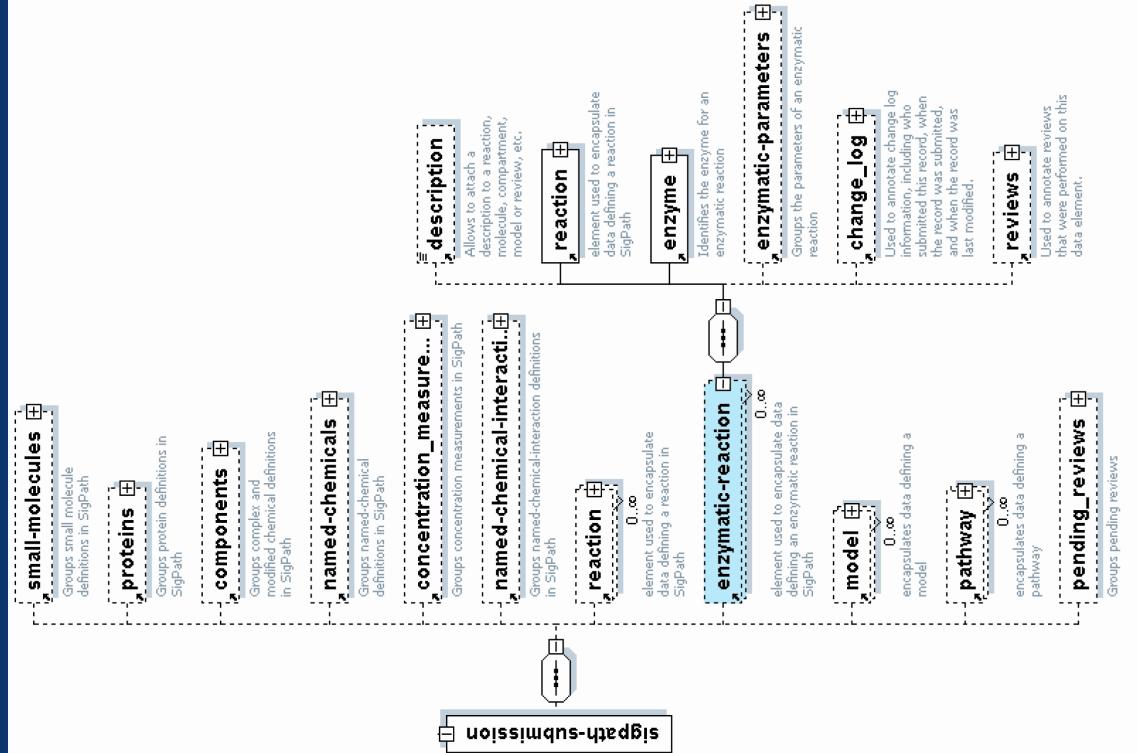
**The ontology is implemented in the semantic validation layer and the Java Data Object-compliant database backend.**

(For JDO, see Srdanovic M et al. Critical evaluation of the JDO API for the persistence and portability requirements of complex biological databases. BMC Bioinformatics. 2005 Jan 10;6(1):5.)

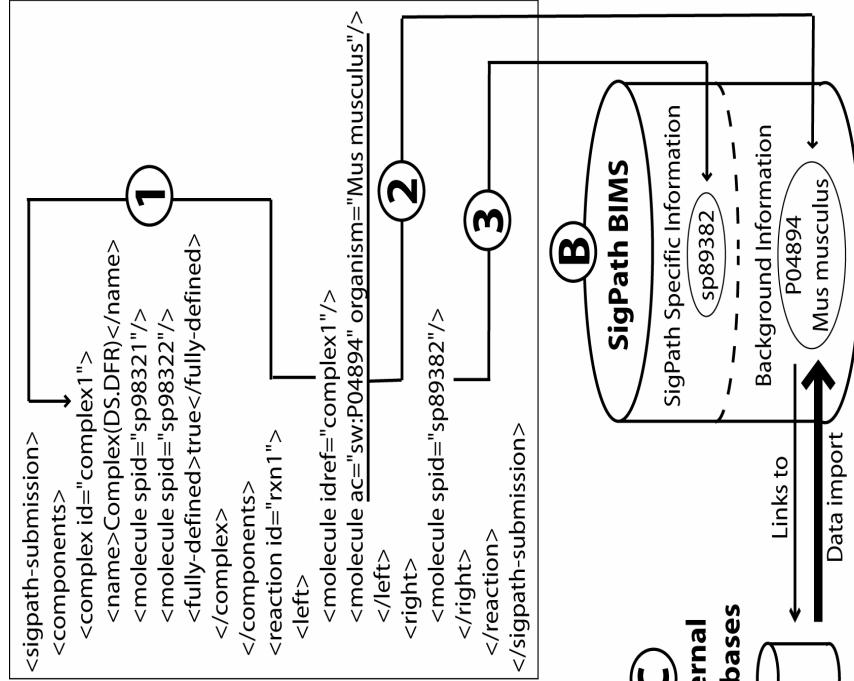
The approach is

- Scalable (amount of data, # concurrent users)
- Leverages open standards (e.g., XML, JDO)
- Supports customized web-based user interfaces, web services, and batch processes

# SigPath XML exchange format



```
-- GBB4_MOUSE + GBG2_MOUSE &lt;...&gt; Gbeta4gamma2 -->
reaction id="rxn221" spid="sp106" 
<description>Gbeta4 gamma2 dimerization</description>
<left>
  <molecule spid="bid79897" ac="sw:P29387" organism="Mus musculus">
    <name>GBB4_MOUSE</name>
  </molecule>
</left>
<right>
  <molecule spid="bid0024" ac="sw:Q9TS47" organism="Mus musculus">
    <name>GBG2_MOUSE</name>
  </molecule>
</right>
<parameters/>
<publications/>
<change_log>
<user_name>wiletchang</user_name>
<dateSubmitted>2003-03-30T18:00:00-05:00</dateSubmitted>
<dateLastModified>2003-03-30T18:01:59-000-05:00</dateLastModified>
<change_log>
```



# SigPath provides tools for user communities

These users are not curators, they are end-users who submit and edit information in SigPath.

View Users (109)		
<u>name</u>	<u>username</u>	<u>affiliation</u> ▲
Anja Hartmann	anjaregina	Uni Rostock
Harvey Florman	hflorman	Univ Massachusetts Medical School
Chris Brinkerhoff	chrisbrink	Univ of Michigan
Alasdair Gibb	a.gibb	University College London
Lily Mirels	mirels	University of California, Berkeley
Marc Birtwistle	rmbirdy857	University of Delaware
Takako Takai	taka	University of Tokyo
Jun-ichi Narukawa	nalchan	University of Tokyo
joseph mclaughlin	micreynolds	Vanderbilt
Lixin Shen	lixin	Vanderbilt University
Masha Niv	MashaNiv	WCMC

We designed SigPath to be a tool to manage data about work in progress. This requirement and the type of data managed raise interesting information management questions:

- Is the submitter ownership policy the best option to encourage data sharing and data reuse?
- How to best support different communities of users at different times

# SigPath provides tools for user communities

The screenshot shows the SigPath web application interface. At the top, there's a header with the ICB logo, the text "institute for computational biomedicine", the "SigPath" logo, and the word "CORNELL". Below the header, a message says "You are logged in as: [Campaign](#) [Logout](#)". On the left, a sidebar has links for "SigPath Home", "View User", and "View All Users". The main content area displays a table of "Submission" entries:

<u>Submission</u>	<u>Name</u>	<u>Institution:</u>	<u>Type</u>	<u>Submitted</u>	<u>Modified</u>
<a href="#">sp3490</a>	Generic Tyrosine Phosphatase	NamedChemical		12/11/04 11:08 AM	12/11/04 11:10 AM
<a href="#">sp3506</a>	inositol 1,4,5 triphosphate			12/11/04 3:28 PM	12/11/04 3:28 PM
<a href="#">sp3513</a>	EGFR_EGF	ComplexImpl		12/10/04 5:36 PM	12/11/04 10:31 AM
<a href="#">sp3518</a>	(EGF_EGFR)_2	ComplexImpl		12/10/04 5:48 PM	12/11/04 10:35 AM
<a href="#">sp3531</a>	DO NOT USE	ComplexImpl		12/11/04 10:18 AM	12/11/04 10:35 AM
<a href="#">sp3539</a>	PLCgamma-(EGFR_EGF)_2_P	ComplexImpl		12/11/04 11:55 AM	12/11/04 11:56 AM
<a href="#">sp3555</a>	Grb2-SOS	ComplexImpl		12/11/04 2:03 PM	12/11/04 2:03 PM
<a href="#">sp3570</a>	Grb-SOS	ComplexImpl		12/11/04 3:20 PM	12/11/04 3:20 PM
<a href="#">sp3571</a>	x1	ComplexImpl		12/14/04 2:45 PM	12/14/04 2:46 PM
<a href="#">sp3572</a>	Complex(EGF_EGFR)	ComplexImpl		12/14/04 2:45 PM	12/14/04 2:45 PM
<a href="#">sp3585</a>	(EGFR_EGF)_2_P	ProteinImpl		12/11/04 12:17 PM	12/11/04 12:17 PM

To the right of the table, a text box contains the following text:

Registered users can track data they submitted

spXXXX values are SigPath identifiers (spids for short).

spids behave like accession codes and can be cited in articles.

# Web-based Visualization (reaction)

**SigPath** institute for computational biomedicine

CORNELL

You are logged in as: [campaign](#) [Logout](#)

[View Reaction: sp3697](#)

The table below shows the elements of your reaction

Description: Phospho-Shc-Grb-Aktive EGFR binding to SOS

Left Side	Right Side	Reaction Parameters
• SOS1_HUMAN	• (EGFR_EGF)_2_P-Shc_P-Grb	KForward: 10.0 microM <sup>-1</sup> .sec <sup>-1</sup>
	• (EGFR_EGF)_2_P-Shc_P-Grb-SOS	KBackward: 0.0214 sec <sup>-1</sup>

[Edit](#) [View XML](#)

**Reaction mechanism and kinetics**

**Links to the literature**

**User comments**

**Change tracking**

View XML | Edit

General Information		Substrate/ Product Links		Web-based Visualization (molecule)																							
SPID:	<b>bid339261</b>	Accession Code(s):	<b>PROSITE: PS50898</b>	Concentrations measured for this molecule																							
Name:	<b>RAF1_RAT</b>	Organism:	Rattus norvegicus (Rat)																								
Description:	<b>RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.37) (Raf-1) (C-RAF) (cRaf)</b>	Aliases:	<b>RAF1_RAT</b>																								
<b>Basic Information</b>																											
<p><b>Comes From, Becomes, Contains:</b></p> <table border="1"> <tr> <td>Comes From:</td> <td>• None</td> </tr> <tr> <td>Becomes:</td> <td>• <a href="#">sp217675: active cRaf-1</a> • <a href="#">sp217735: active cRaf-1</a></td> </tr> <tr> <td>Contains:</td> <td>• None</td> </tr> </table> <p><b>Involved in Reactions:</b></p> <ul style="list-style-type: none"> <li>• <a href="#">SP217980: ATP + RAF1_RAT &lt;...&gt; ADP + active cRaf-1</a></li> <li>• <a href="#">SP3651: RAF1_RAT + Ras.GTP &lt;...&gt; Activated_c_Raf</a></li> <li>• <a href="#">SP217849: GTP-Ras + RAF1_RAT &lt;...&gt; Complex(GTP-Ras.KRAF_RAT)</a></li> <li>• <a href="#">SP218019: ATP + active cRaf-1 &lt;...&gt; ADP + RAF1_RAT [Enzyme: P2AA_CHICK]</a></li> <li>• <a href="#">SP218018: ATP + active cRaf-1 &lt;...&gt; ADP + RAF1_RAT</a></li> <li>• <a href="#">SP217979: ATP + RAF1_RAT &lt;...&gt; ADP + active cRaf-1 [Enzyme: active membrane bound PKC]</a></li> <li>• <a href="#">SP217904: Raf*-p'ase &lt;...&gt; RAF1_RAT + DUS1_RAT</a></li> <li>• <a href="#">SP218104: RAF1_RAT + Ras.GTP &lt;...&gt; Activated_c_Raf</a></li> <li>• <a href="#">SP217901: RAF1_RAT + Ras-GTP &lt;...&gt; Raf-Ras-GTP</a></li> <li>• <a href="#">SP217978: ATP + RAF1_RAT &lt;...&gt; ADP + active cRaf-1</a></li> <li>• <a href="#">SP217981: ATP + RAF1_RAT &lt;...&gt; ADP + active cRaf-1 [Enzyme: active PKC-DAG-AA]</a></li> <li>• <a href="#">SP217959: ATP + MPK1_RAT &lt;...&gt; ADP + p-MPK1_RAT [Enzyme: RAF1_RAT]</a></li> </ul> <p><b>Concentrations</b></p> <table border="1"> <thead> <tr> <th>SPID</th> <th>Concentration</th> <th>Tissue</th> <th>Method of Measurement</th> <th>Sample Preparation</th> <th>Comments</th> <th>Pub Med Reference</th> <th>Action</th> </tr> </thead> <tbody> <tr> <td>sp218126</td> <td>0.0664 micromoles/l</td> <td>HeLa cells</td> <td>staining with semi-quantitative electrophoresis (western, etc.)</td> <td>Not Specified</td> <td>Calculated from molecules per cell, assuming 1e-9 cubic centimeters</td> <td>Birgit Schoeberl, Claudia Eichler-Jonsson, Ernst Dieter Gilles, Gertraud Müller</td> <td>Delete</td> </tr> </tbody> </table>						Comes From:	• None	Becomes:	• <a href="#">sp217675: active cRaf-1</a> • <a href="#">sp217735: active cRaf-1</a>	Contains:	• None	SPID	Concentration	Tissue	Method of Measurement	Sample Preparation	Comments	Pub Med Reference	Action	sp218126	0.0664 micromoles/l	HeLa cells	staining with semi-quantitative electrophoresis (western, etc.)	Not Specified	Calculated from molecules per cell, assuming 1e-9 cubic centimeters	Birgit Schoeberl, Claudia Eichler-Jonsson, Ernst Dieter Gilles, Gertraud Müller	Delete
Comes From:	• None																										
Becomes:	• <a href="#">sp217675: active cRaf-1</a> • <a href="#">sp217735: active cRaf-1</a>																										
Contains:	• None																										
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sp218126	0.0664 micromoles/l	HeLa cells	staining with semi-quantitative electrophoresis (western, etc.)	Not Specified	Calculated from molecules per cell, assuming 1e-9 cubic centimeters	Birgit Schoeberl, Claudia Eichler-Jonsson, Ernst Dieter Gilles, Gertraud Müller	Delete																				

## Web-based Visualization (molecule)

General Information

SPID: **bid339261**

Name: **RAF1\_RAT**

Description: **RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.37) (Raf-1) (C-RAF) (cRaf)**

### Basic Information

Accession Code(s): **PROSITE: PS50898**

Organism: Rattus norvegicus (Rat)  
Aliases: **RAF1\_RAT**

### Comes From, Becomes, Contains:

Comes From:	• None
Becomes:	• <a href="#">sp217675: active cRaf-1</a> • <a href="#">sp217735: active cRaf-1</a>
Contains:	• None

### Involved in Reactions:

- [SP217980: ATP + RAF1\\_RAT <...> ADP + active cRaf-1](#)
- [SP3651: RAF1\\_RAT + Ras.GTP <...> Activated\\_c\\_Raf](#)
- [SP217849: GTP-Ras + RAF1\\_RAT <...> Complex\(GTP-Ras.KRAF\\_RAT\)](#)
- [SP218019: ATP + active cRaf-1 <...> ADP + RAF1\\_RAT \[Enzyme: P2AA\\_CHICK\]](#)
- [SP218018: ATP + active cRaf-1 <...> ADP + RAF1\\_RAT](#)
- [SP217979: ATP + RAF1\\_RAT <...> ADP + active cRaf-1 \[Enzyme: active membrane bound PKC\]](#)
- [SP217904: Raf\\*-p'ase <...> RAF1\\_RAT + DUS1\\_RAT](#)
- [SP218104: RAF1\\_RAT + Ras.GTP <...> Activated\\_c\\_Raf](#)
- [SP217901: RAF1\\_RAT + Ras-GTP <...> Raf-Ras-GTP](#)
- [SP217978: ATP + RAF1\\_RAT <...> ADP + active cRaf-1](#)
- [SP217981: ATP + RAF1\\_RAT <...> ADP + active cRaf-1 \[Enzyme: active PKC-DAG-AA\]](#)
- [SP217959: ATP + MPK1\\_RAT <...> ADP + p-MPK1\\_RAT \[Enzyme: RAF1\\_RAT\]](#)

### Concentrations

SPID	Concentration	Tissue	Method of Measurement	Sample Preparation	Comments	Pub Med Reference	Action
sp218126	0.0664 micromoles/l	HeLa cells	staining with semi-quantitative electrophoresis (western, etc.)	Not Specified	Calculated from molecules per cell, assuming 1e-9 cubic centimeters	Birgit Schoeberl, Claudia Eichler-Jonsson, Ernst Dieter Gilles, Gertraud Müller	Delete

## View Model

[View XML](#) | [Edit](#)

## General Information

### Model Information:

Model SPID: sp7  
Model Name: MAPK cascade  
Model Description: Map kinase cascade. Starting from activated Ra, micromoles/l  
Target Unit: micromoles/l

### Selected Reactions:

- sp218110 Enzymatic Reaction: ATP + P-MEK1 <...> ADP + P-P-MEK1 [Enzyme: Activated\_C\_Raf]
- sp218119 Enzymatic Reaction: P-P-MEK1 <...> P-MEK1 [Enzyme: P2AA\_RAT]

## Reactions

## Initial Concentrations

## Exporting to Modeling Environments

## Web-based Visualization (model)

(details omitted)

DUS1\_RAT\_Default\_Compartment 4.0E-4 micromoles/l  
P-MARK1 0.0 mol/l  
MWP = model Will Provide

[Export to Kinetikit](#)

[KineticKit home page](#) from National Center for Biological Sciences (Bangalore, India)

[Export to JSim](#)

[JSim Documentation](#) from University of Washington (Seattle, USA)

[Export to SBML](#)

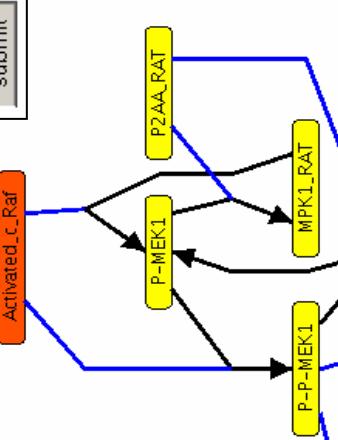
[SBML reference site](#) from the SBML format development group (includes many research groups).

[GIF](#) [Select Image Format](#)

- Compact: enzyme view
- Compact: complex view
- Show ATP and ADP (for enzymatic reactions)

[View Model Image](#)

The following options are  
Please choose which option  
Export below to download t  
used with modelling environ  
**Select options below and**  
 Level 1 version 1  
 Level 1 version 2  
 Level 2 version 1  
 Include diagram layout (

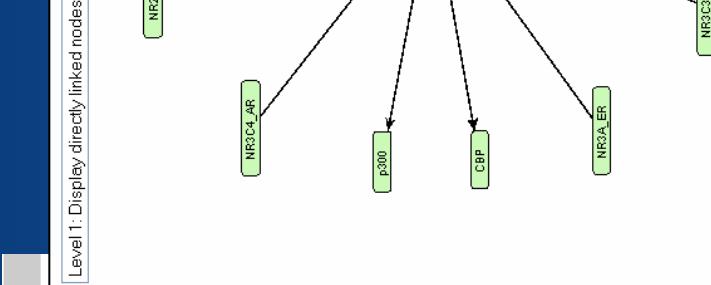
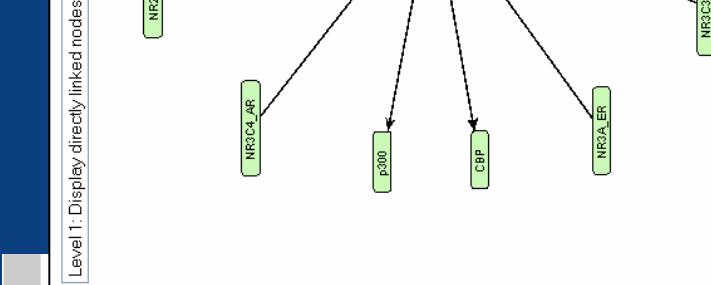


Model Schematic (automatically generated)

# Visualizing interactions is key for the end-user, but is still an open problem...

## Involved in Reactions:

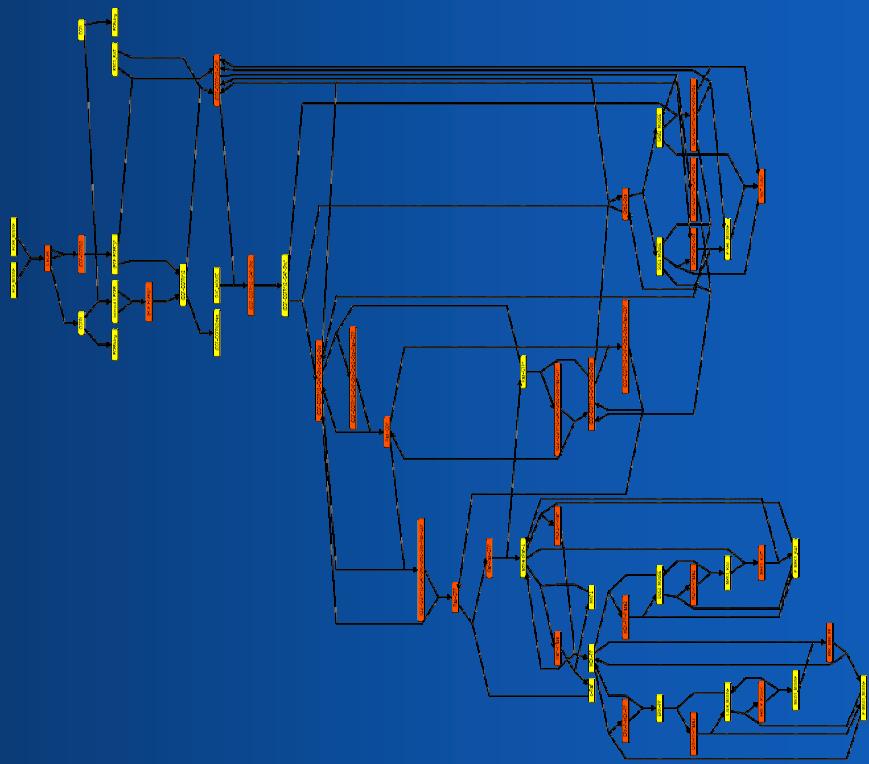
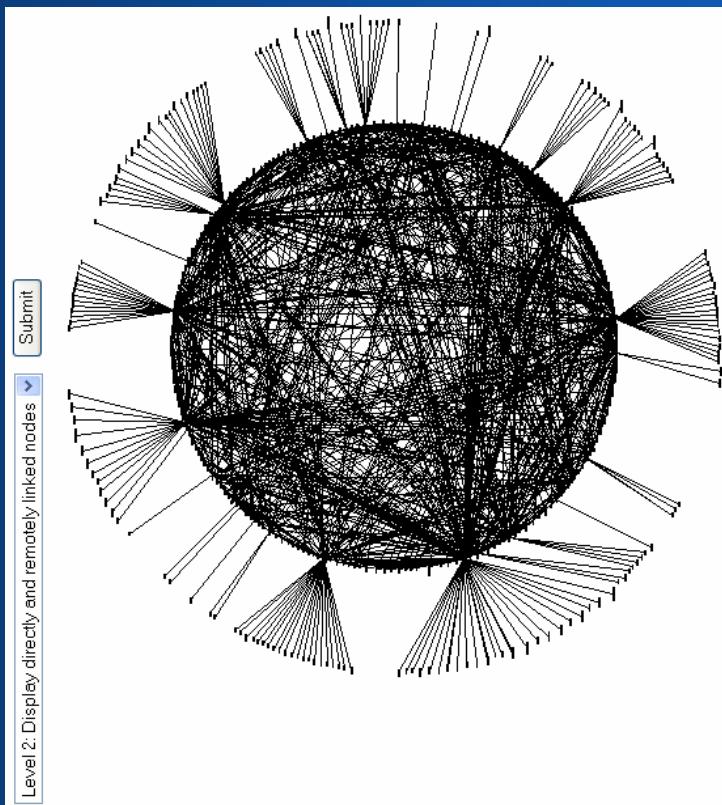
- [View](#) SP2832: NR2B\_RXR interacts with NFkappaB\_subunitp65
- [View](#) SP3257: NR3C3\_PR interacts with NFkappaB\_subunitp65
- [View](#) SP1640: NR2B\_RXR binds NFkappaB\_subunitp65
- [View](#) SP720: NR3C4\_AR interacts with NFkappaB\_subunitp65
- [View](#) SP639: NFkappaB\_subunitp50 forms complex with NFkappaB\_subunitp65
- [View](#) SP2566: NR3C1\_GR interacts with NFkappaB\_subunitp65
- [View](#) SP2624: NR3C1\_GR dimerizes with NFkappaB\_subunitp65
- [View](#) SP2933: NR3C1\_GR links to NFkappaB\_subunitp65
- [View](#) SP2282: NR3C1\_GR associates with NFkappaB\_subunitp65
- [View](#) SP3261: NFkappaB\_subunitp65 forms complex with CBP
- [View](#) SP2894: NR3C1\_GR precipitates with NFkappaB\_subunitp65
- [View](#) SP1571: NR1C3\_PPARgamma binds NFkappaB\_subunitp65
- [View](#) SP2838: NFkappaB\_subunitp50 dimerizes with NFkappaB\_subunitp65
- [View](#) SP1207: NFkappaB\_subunitp65 has implied interaction with p300
- [View](#) SP896: NR3C1\_GR binds NFkappaB\_subunitp65
- [View](#) SP1253: NR3C1\_GR has implied interaction with NFkappaB\_subunitp65
- [View](#) SP1790: NR1C1\_PPARalpha interacts with NFkappaB\_subunitp65
- [View](#) SP2965: NR3A\_ER forms complex with NFkappaB\_subunitp65
- [View](#) SP3016: NFkappaB\_subunitp65 dimerizes with NFkappaB\_subunitp50
- [View](#) SP668: NR3C4\_AR forms complex with NFkappaB\_subunitp65
- [View](#) SP1972: NR3C4\_AR associates with NFkappaB\_subunitp65
- [View](#) SP1279: NR3A\_ER interacts with NFkappaB\_subunitp65

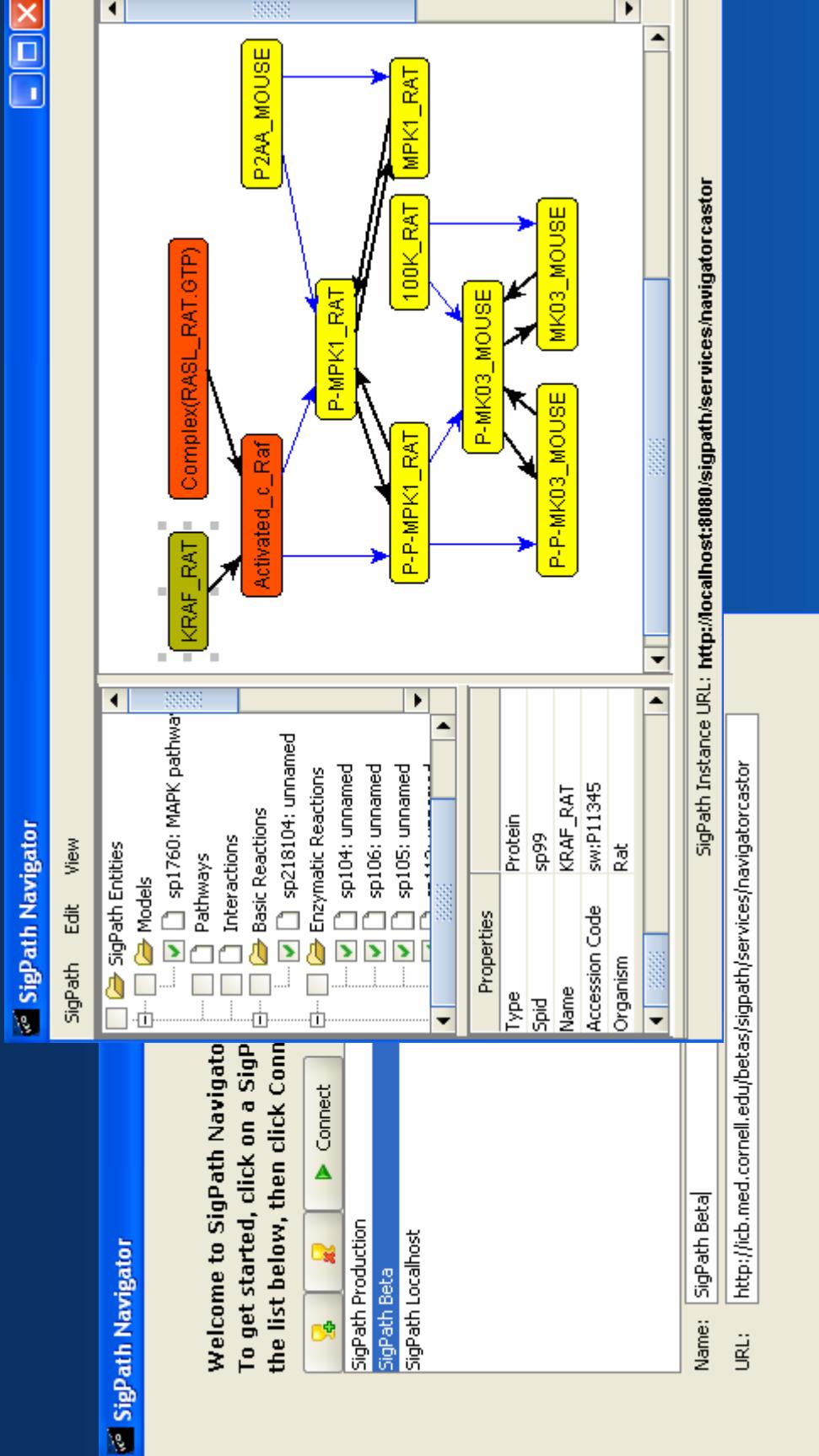


Data reproduced with permission from:

- Sylvie Albert, Sylvain Gaudan, Heidrun Knigge, Andreas Raetsch, Asuncion Delgado, Bettina Huhse, Harald Kirsch, Michael Albers, Dietrich Rebholz-Schuhmann, Manfred Koegl  
Computer-assisted generation of a protein-interaction database for nuclear receptors.  
Mol Endocrinol. 2003 Aug; 17 (8): 1555-67. [View Abstract](#)

Visualizing interactions is key for  
the end-user, but is still an open  
problem...



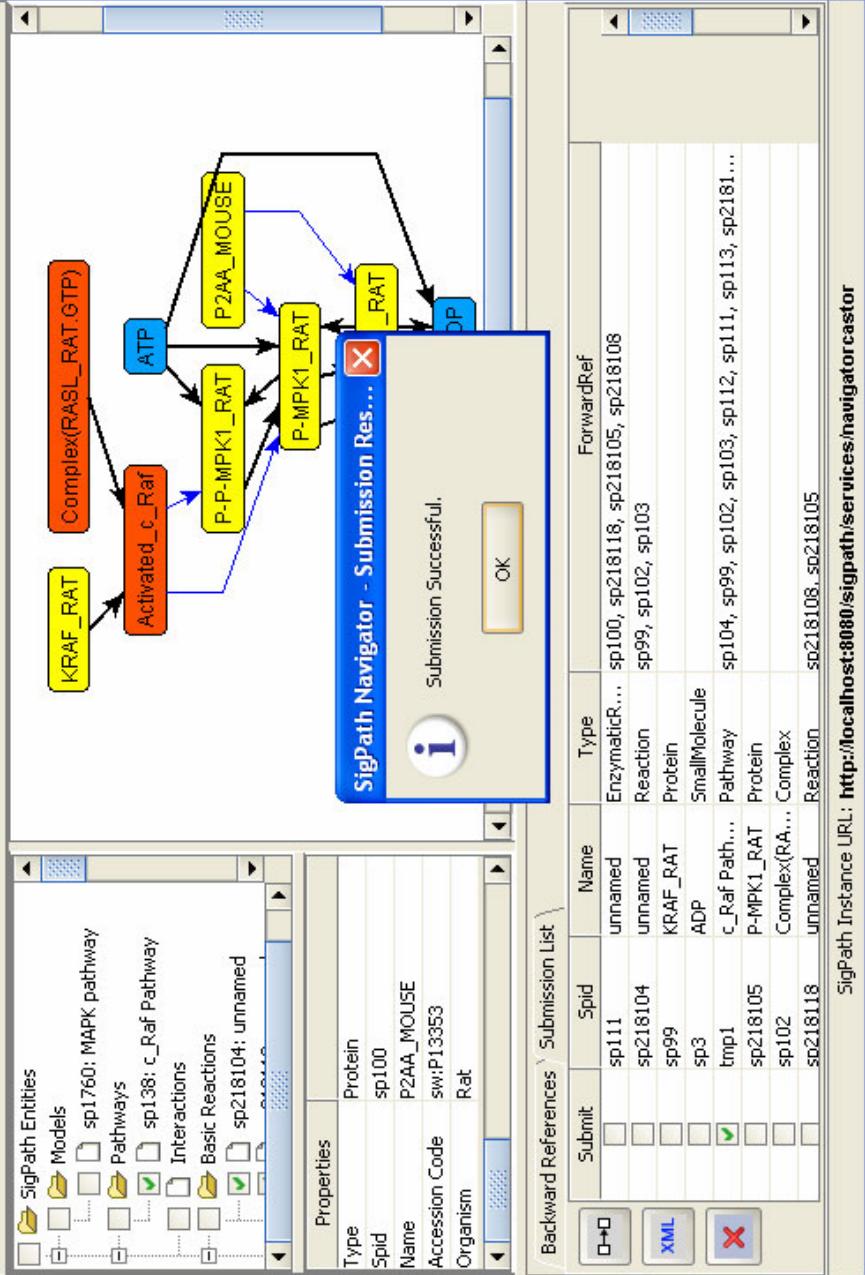


# SigPath Navigator

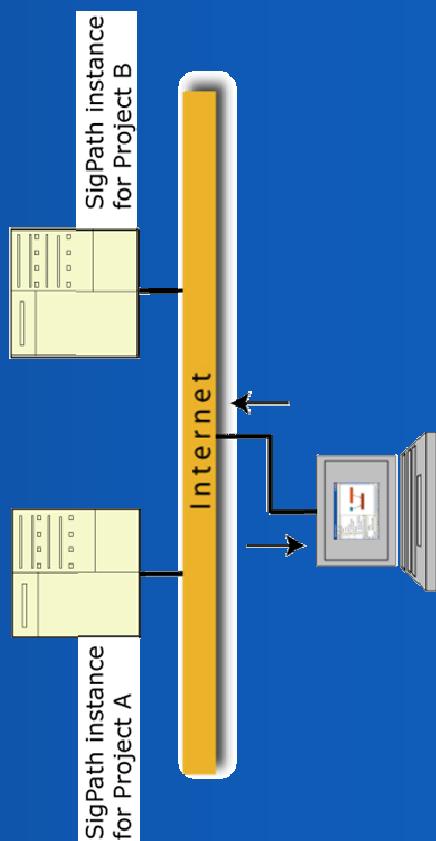
- Helps users navigate data relationships and create custom views of the data, interactively
  - Desktop tool, connects to several SigPath instances
  - Cross-platform, Java WebStart (auto install&updates)

# SigPath Navigator

- Submit pathways interactively
- Inspect connectivity of entries before deleting or editing data



- Select SigPath entries and transfer to another SigPath instance



# SigPath and Open Source

- SigPath is distributed under the GPL
- Leverages the JDO API, an open standard for database portability (object/relational databases, commercial *and* open-source)
- An open-source JDO implementation is on the way (see [www.JPOX.org](http://www.JPOX.org))  
  
(See ISMB Poster C-37)
- Towards a bio-database framework (reusing the SigPath code base for bio-database projects with similar requirements).
- Interested in the project? Contact us!

# Acknowledgments

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Manuel Martin  
Marko Srdanovik  
Piali Mukherjee

SBML:  
Mike Hucka,  
Andrew Finney

Check out our other open-source bioinformatics projects:

TissueInfo – High-throughput tissue expression profiling with ESTs  
Textractor – Direct protein name dictionary construction from full-text (Poster B-11)

<http://icb.med.cornell.edu>

# A few of the tools that help us build SigPath



## sigpath/mapping

Current directory [Development] / sigpath / mapping  
Files shown: 5

### Open-source

### Free for open-source projects



### Concurrent Versions System

The open standard for version control

Logged in as : campaigne (Fabien Campaigne - administrator)

[Main | My View | View Issues | ReportIssue | Logout]

04-25-2005 16:33 EDT

[First Prev 1 2 3 4 Next Last ]

Viewing Issues (1 - 50 / 179) [Print Reports] [CSV Export]

Search: [ ]

Search: [ ]

Reset Filter [ ]

Save Current Filter [ ]

Summary [ ]

Updated [ ]

Status [ ]

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Reporter [ ]

Monitored By: [ ]

Assigned To: [ ]

Category: [ ]

Severity: [ ]

Priority: [ ]

Product Version: [ ]

Fixed in Version: [ ]

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No [ ]

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Show [ ]

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Slides after this are for questions.

# Related work

At least three systems share goals similar to SigPath's

- **ProcessDB** Robert Phair and Ann Chason ([commercial, free for academia](http://www.integrativebioinformatics.com/processdb.html)  
<http://www.integrativebioinformatics.com/processdb.html>)  
(Focus is on modeling capabilities, rough UI)
- **Monod** David Soergel, Brian George, Ross Morgan-Linial, Roger Brent, and Drew Endy ([open-source](http://monod.molsci.org/docs/Monod-June-2003.pdf) <http://monod.molsci.org/docs/Monod-June-2003.pdf>)  
(No quantitative data)
- **BioModels.net** Le Novère et al. <http://www.ebi.ac.uk/biomodels/> (April 2005)  
(open / closed source?)

These systems differ in their approaches and capabilities