

Biological Pathway Exchange (BioPAX) Format and Pathway Commons Update

COMBINE
10/3/16

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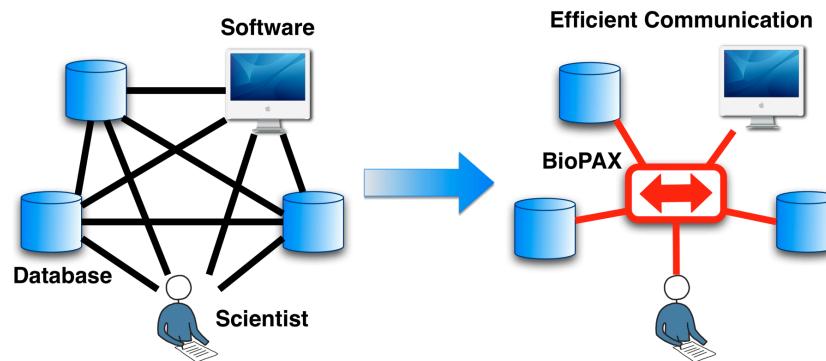
BioPAX: biopax.org
Paxtools: biopax.github.io/Paxtools
Pathway Commons: pathwaycommons.org
Tutorial Material: github.com/cannin/biopaxTutorial
SBGNViz: github.com/iVis-at-Bilkent/sbgnviz-js



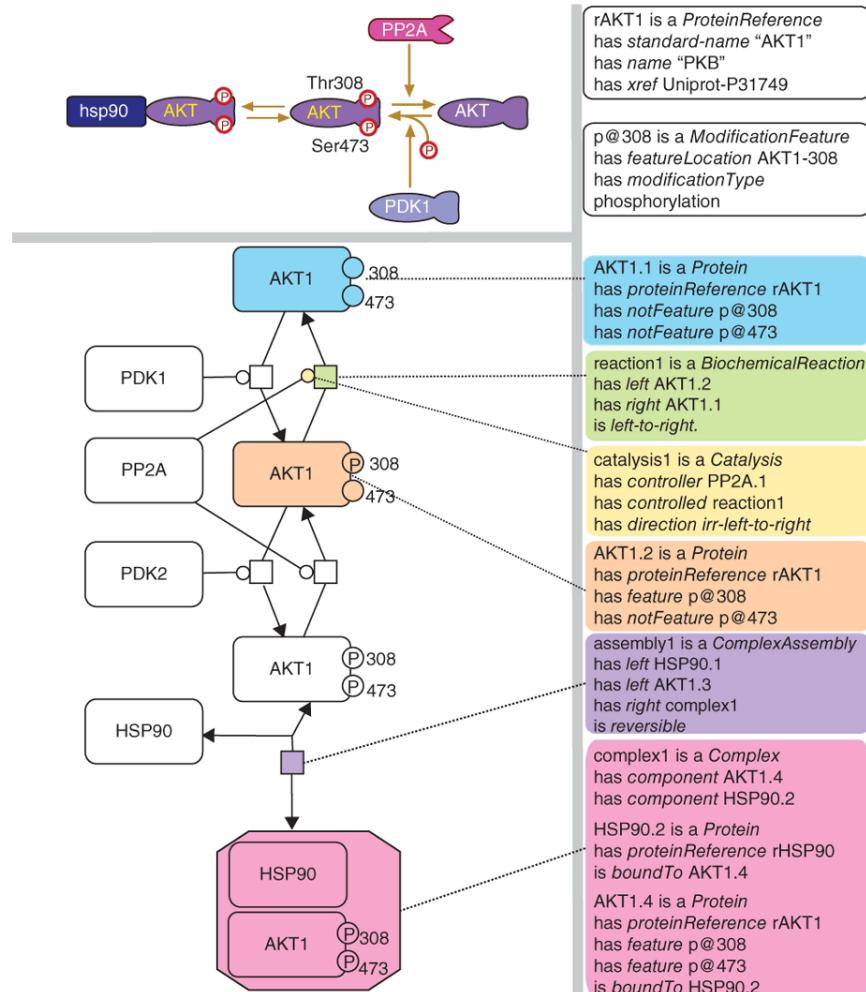
BioPAX Overview

BioPAX Scope/Goals

- To represent biological interactions and pathways
 - Pathways are collections of interactions that biologists have found useful to group together for organizational, historic, biophysical or other reasons
- Encourage a community-wide effort to distribute pathway data in standard format; over 500 databases listed on pathguide.org

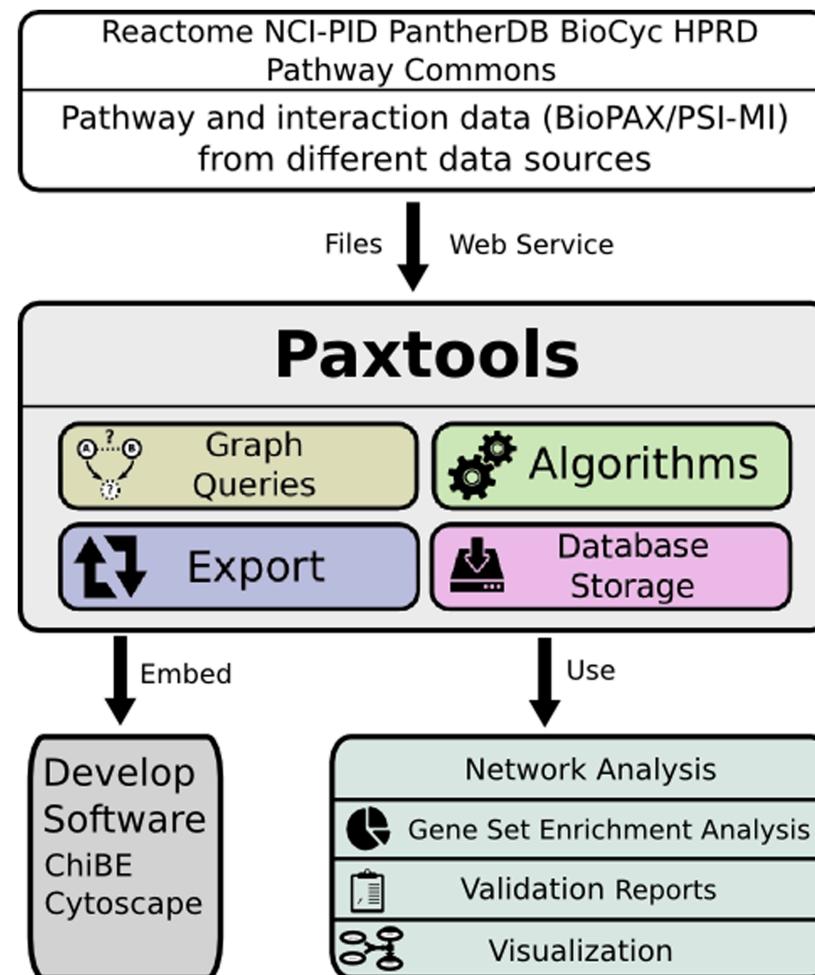


From Pathway Diagrams to BioPAX



BioPAX: biopax.org; Tutorial Material: github.com/cannin/biopaxTutorial

Paxtools: Biological Pathway Exchange (BioPAX) Format Java API



Paxtools: biopax.github.io/Paxtools; Demir et al (2013)

Getting started with BioPAX and Paxtools API

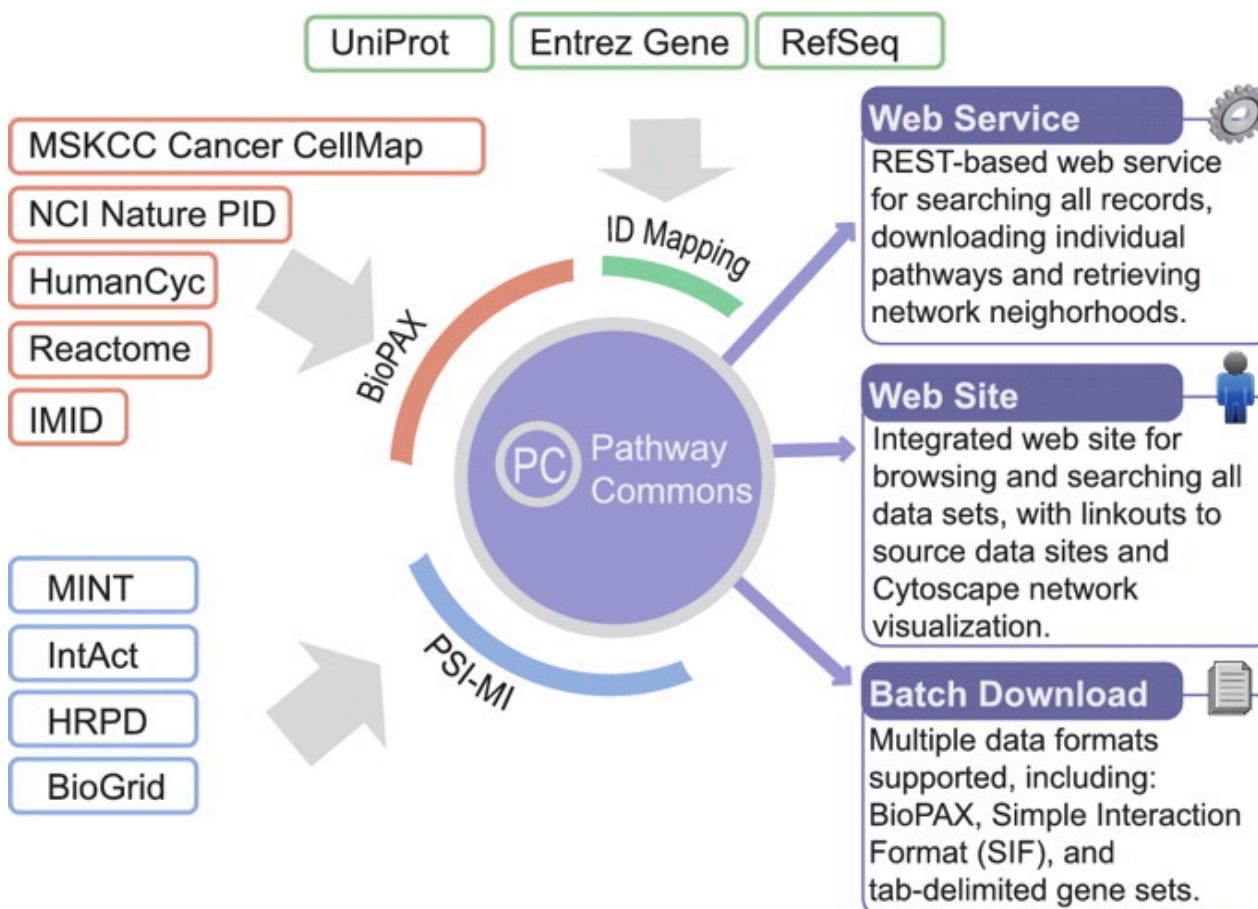
- Paxtools Web Console: pk0iye.appspot.com

The screenshot shows the BioPAX Web Console interface. It features a central workspace divided into several sections:

- Code Editor:** A large blue box containing Java code for reading a BioPAX file and printing BiochemicalReactions.
- BioPAX OWL File:** A blue box displaying the generated OWL code.
- Output:** A blue box showing the results of the executed code, including two BiochemicalReaction URIs.
- Code Examples:** A blue box listing various Groovy scripts available for download.
- Navigation and Tools:** A top navigation bar with links for "BioPAX Web Console", "Run", "View BioPAX File", and "About". Below the navigation are tabs for "BioPAX" and "Pathway Commons".
- Code Snippets:** A sidebar on the right listing other Groovy scripts: listFiles_0.groovy, firstModel_1.groovy, simpleIO_2.groovy, basicTraversal_3.groovy, and merging_7.groovy.

Pathway Commons

Pathway Commons Database (pathwaycommons.org)



Includes signaling, drug/target, metabolic, regulatory, etc DBs

Reactome	11924
NCI PID	16017
PhosphoSitePlus	13642
HumanCyc	7024
HPRD	40618
PantherDB	5282
DIP	7102
BioGRID	244843
InAct	98347
BIND	35566
TRANSFAC	261624
miTarBase	51214
DrugBank	19159
Recon X	10910
CTD	313174
KEGG	4472
Total Interactions	1140918

Cerami et al (2011)

Pathway Commons Tools

Pathway Commons

Download

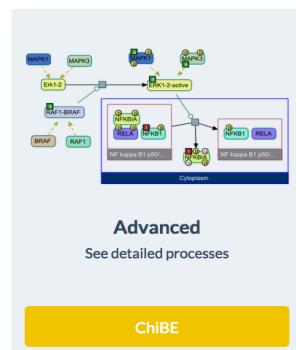
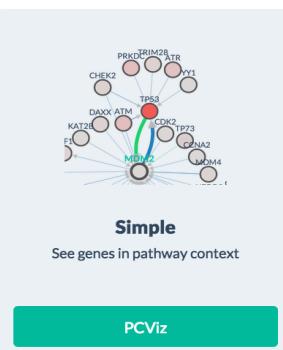
F.A.Q.

Publications

Contact

For biologists

Search, visualize and download Pathway Commons pathways as part of an integrated network analysis ([more](#))



For computational biologists and software developers

Download all pathways in BioPAX, SIF and other formats for pathway and network analysis. Build software on top of Pathway Commons using our web service API ([more](#))



<http://www.pathwaycommons.org/>

biopax.org

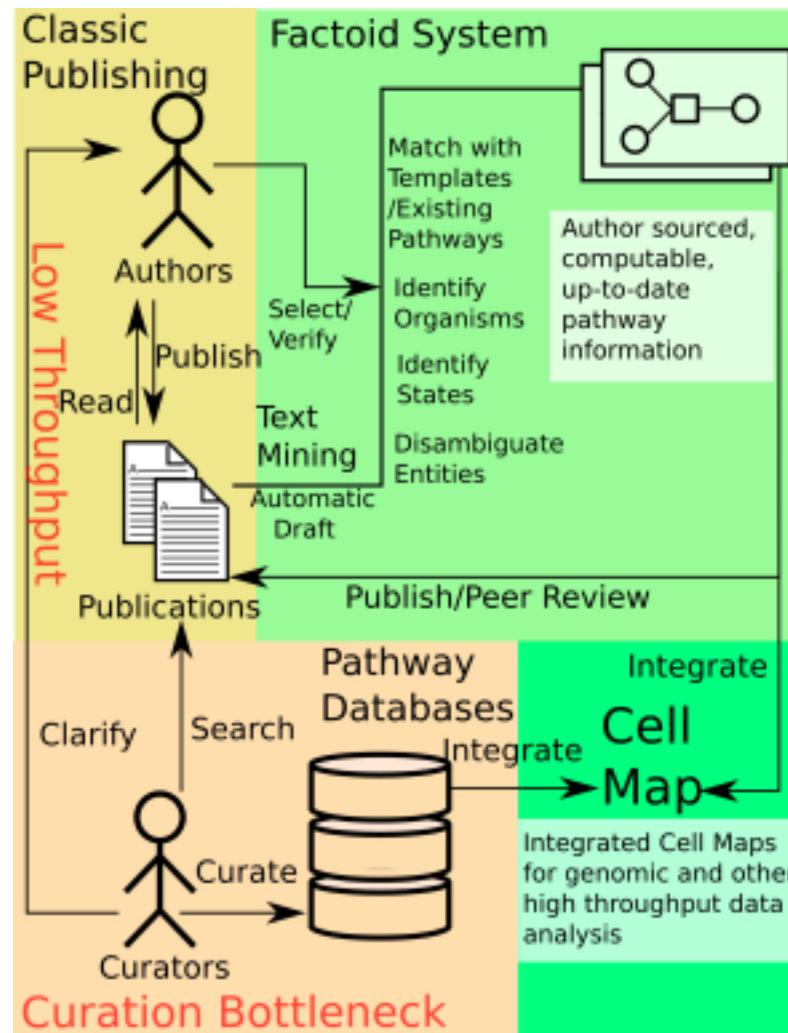
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Expanding Pathway Commons

Expanding Pathway Commons

- Manual
 - BioPAX data creation from diagrams to simplify content creation
- Automated
 - Use natural language processing

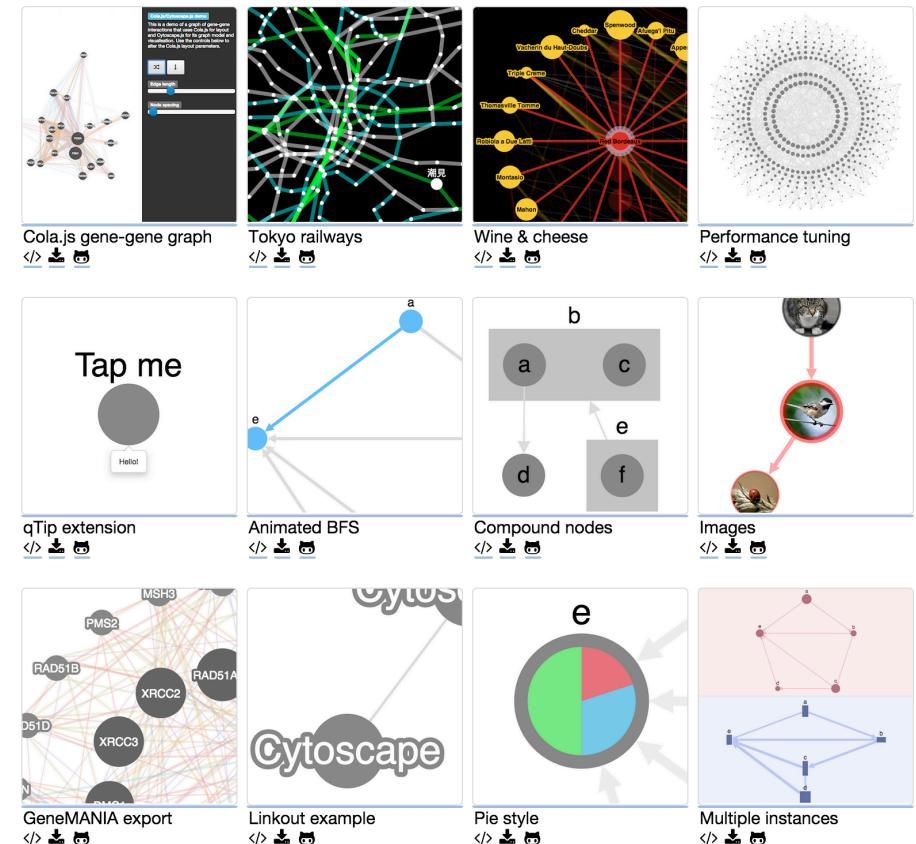
Factoid: Expanding Pathway Commons During Manuscript Submission Process



factoid.baderlab.org

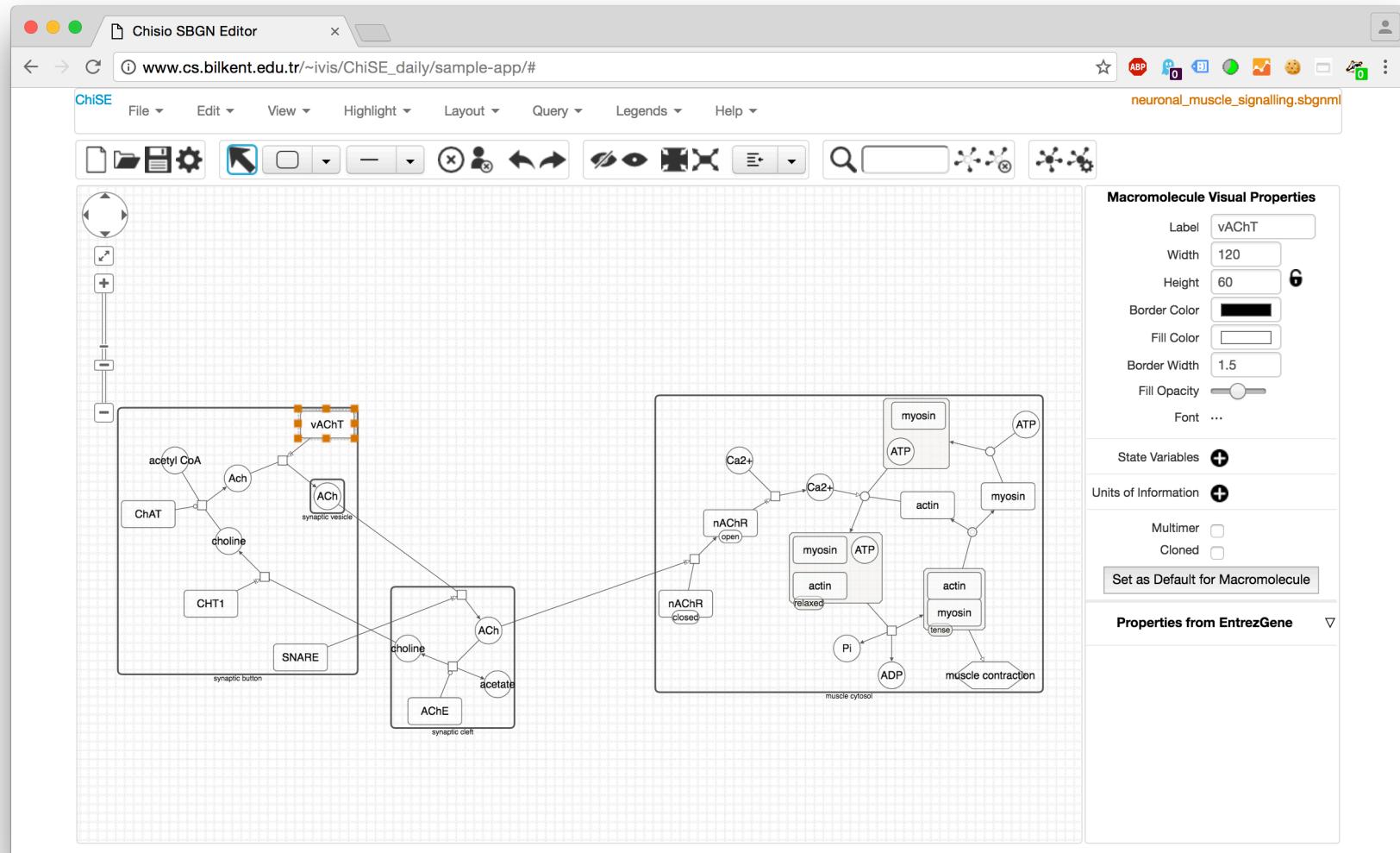
Cytoscape.js: A Javascript library for analysis and visualization of networks

- Can handle large networks
- Provides analysis algorithms
- Provides various layouts
- Customizable features
 - Colors
 - Tooltips
 - Linkouts
 - Node images
 - Compound nodes
 - ...
- Basis for other projects
 - PCViz
 - SBGNViz



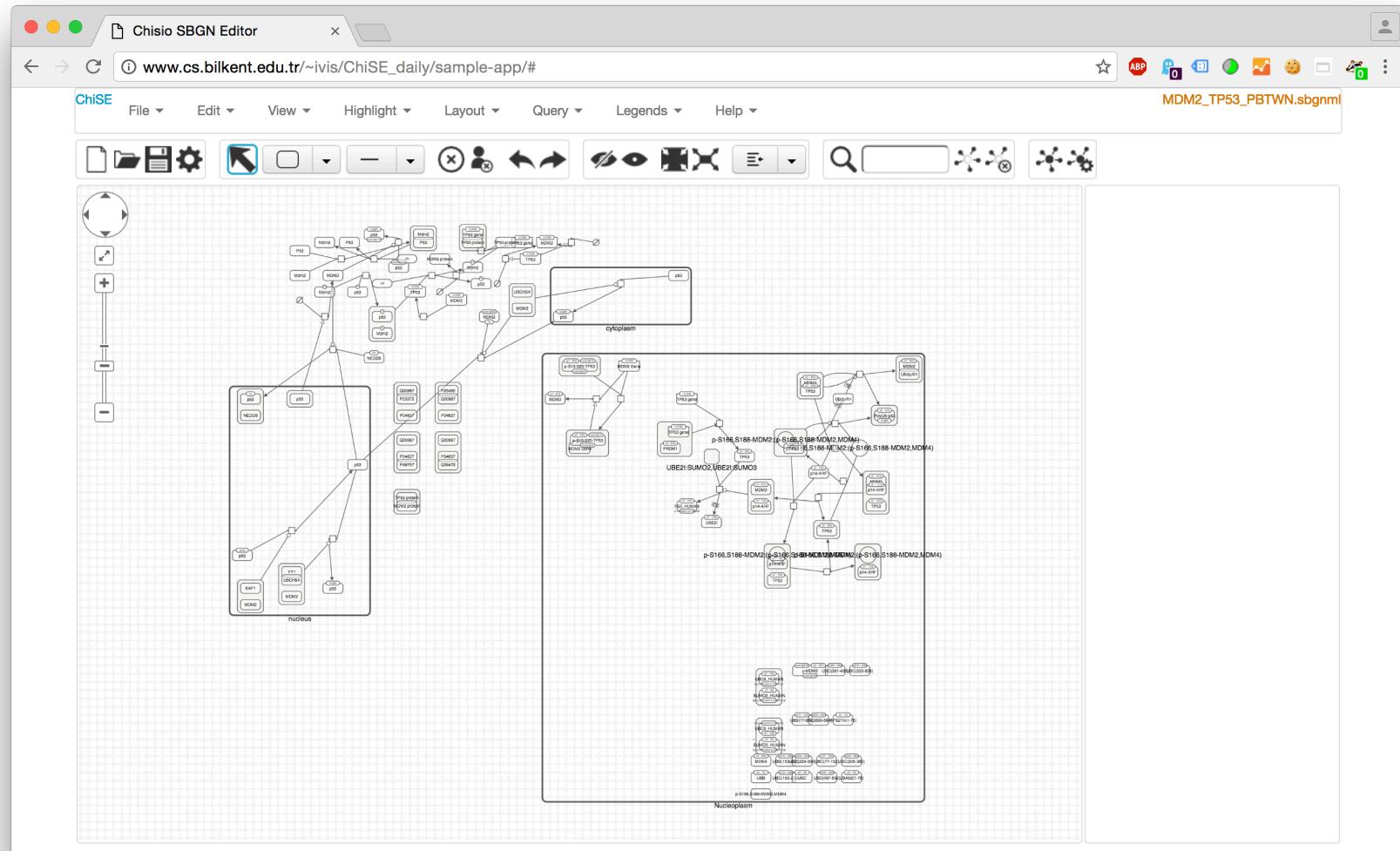
<http://js.cytoscape.org/>

SBGNViz.js (Standalone SBGN Viewer) and Chisio SBGN Editor (Editor)



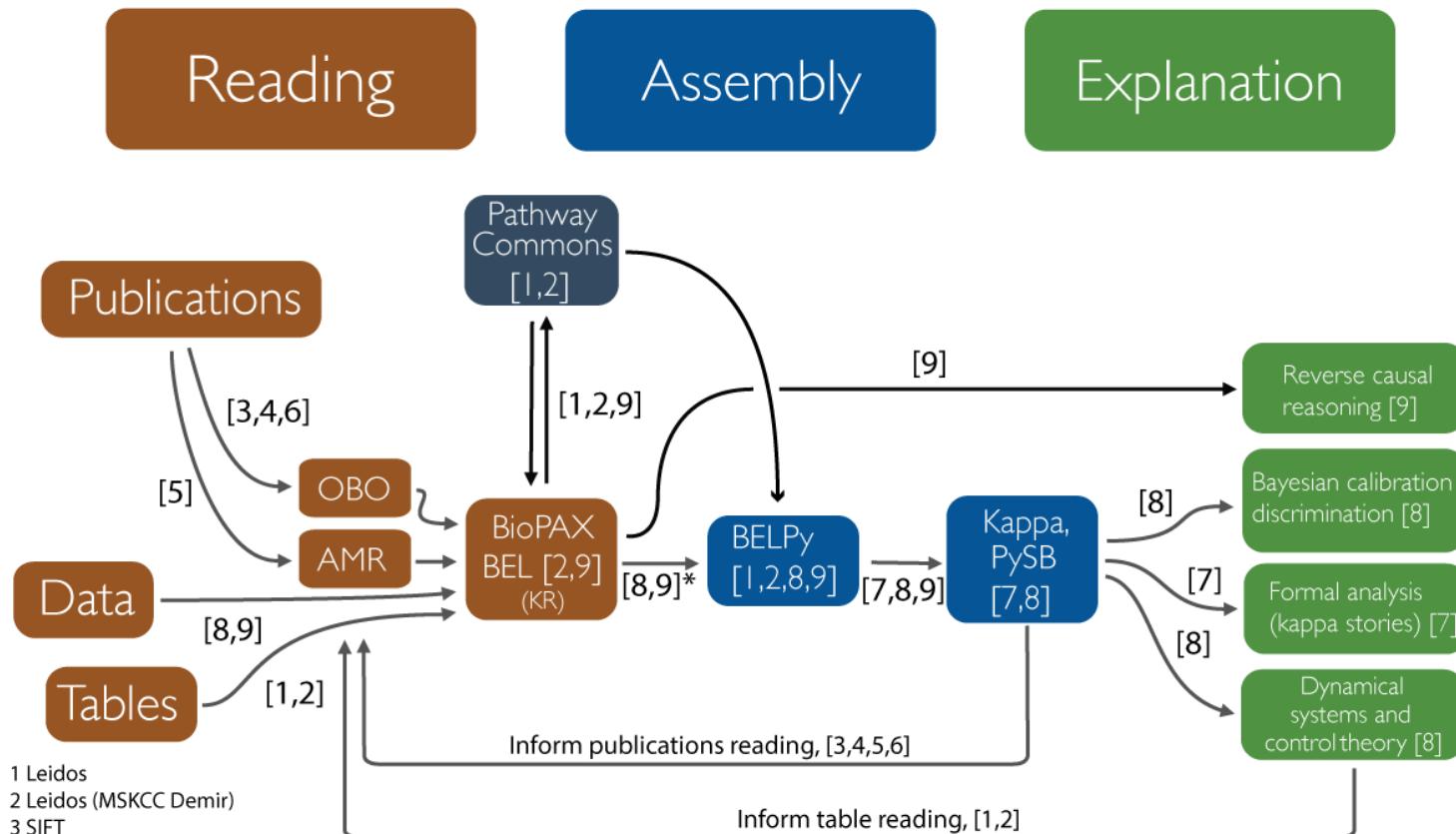
Editing Glyph Properties and Alignment to Grid. (www.cs.bilkent.edu.tr/~ivis/ChiSE_daily/sample-app/)

Querying Pathway Commons Using SBGNViz



Pathway Commons Interactions Involving TP53-MDM2

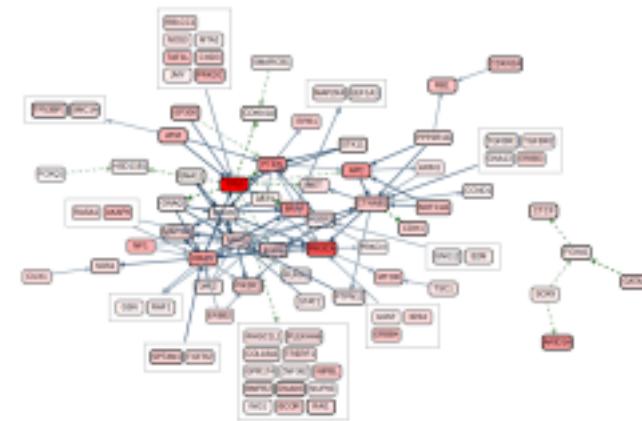
Novel Data Acquisition Through the DARPA Big Mechanism Project



<http://www.darpa.mil/our-research>

Molecular Interaction Information Extraction (IE) Using ODIN/REACH

- ODIN: Rule-based, domain independent IE framework
- REACH: ODIN-based system with rules for biomedical literature
- Used to process ~300K open access publications



PC Without REACH (87/300 genes)



PC With REACH (141/300 genes)

Website: github.com/clulab/reach

Next Steps

- Continued development of Pathway Commons
 - Data expansion and web-based tools to simplify usage
- Application of SBGNViz in new use cases
 - Online visualization of SBML models
- BioPAX Updates
 - New use cases through SBOL?

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 - Emek Demir
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