Bridging data and modeling communities

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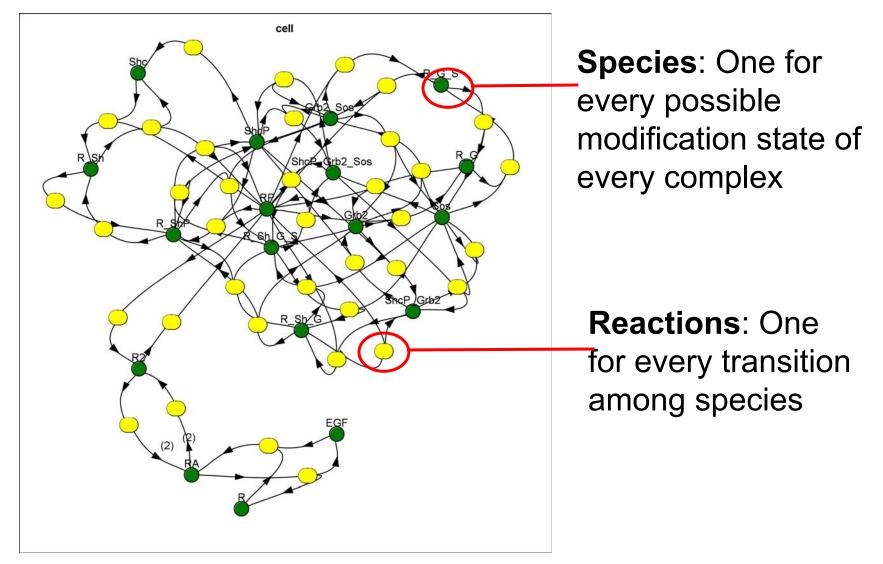
BioPAX and BioPAX OBO groups



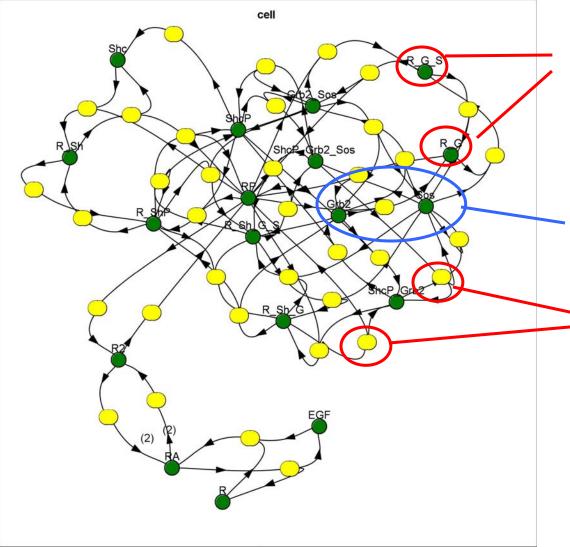
NRCAM meeting February 23rd, 2009



The Virtual Cell representation of chemical reactions



Better and reusable representation

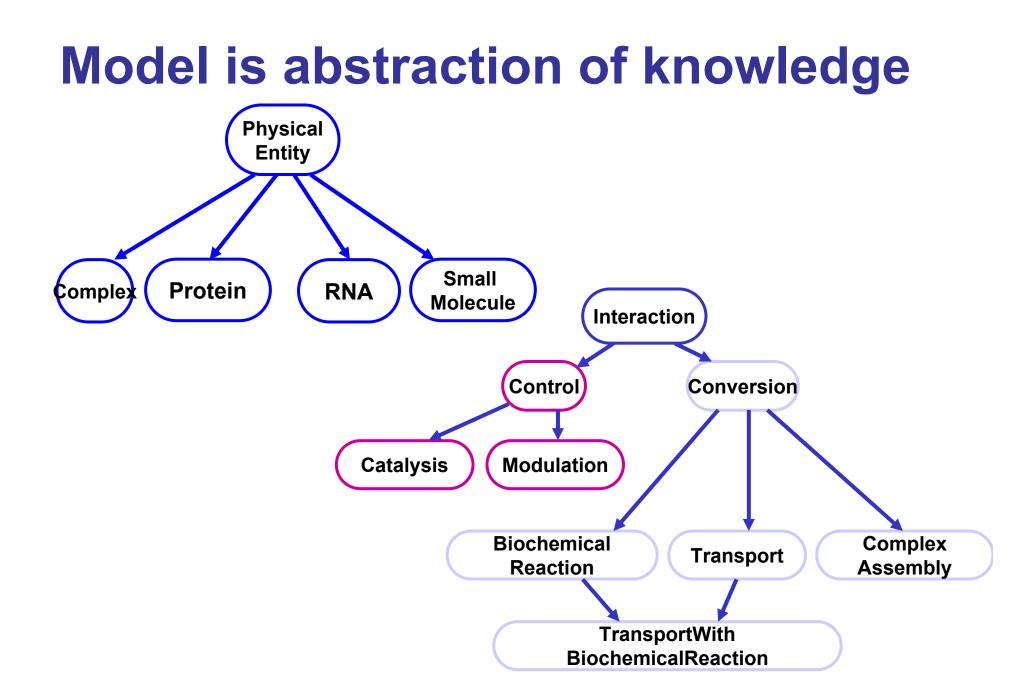


Different types of species: proteins, small molecules, complexes.

User-specified grouping: ligandbinding module, Grb2 interactions

Different types of reactions:

biochemical reaction, complex assembly



World of models

- Over 100 software tools support import and/or export of models in SBML format
- Database of models in SBML format <u>http://BioModels.net</u> contains more than 200 curated models
- VCell database contain more than 600 publicly available models including about 50 curated models. Many of them can be exported to SBML.

World of pathway databases

Data Source	Protein(SwissProt)	Coverage (SwissProt)	Interaction	Citation
Reactome	1229 (1194)	5% (8%)	21394	Vastrik <i>et al</i> , 2007
Panther	2997 (1670)	12% (12%)	75694	Mi <i>et al</i> , 2007
CellMap	567 (567)	2% (4%)	1195	cancer.cellmap.org
INOH	719 (711)	3% (5%)	11759	Kushida <i>et al</i> , 2006
NCI-Nature	593 (592)	2% (4%)	2900	pid.nci.nih.gov
NCI-BioCarta	936 (936)	4% (6%)	4752	pid.nci.nih.gov
KEGG	2033 (1947)	8% (13%)	11144	Kanehisa <i>et al</i> , 2004
<u>Total</u>	5283 (3847)	21% (27%)	118867	

World of ontologies

- **BioPAX** = <u>**Bio**</u>logical <u>**PA**</u>thway e<u>X</u>change
- **GO** = Gene Ontology
- **ChEBI** = Chemical Entities of Biological Interest
- RO (OBO) = Relation Ontology (Open Biomedical Ontologies))
- **SBO** = Systems Biology Ontology
- **BFO** = Basic Formal Ontology

Two worlds

Modeling Community

- Do the math so that it can be Link information so that it • calculated
- Quantities
- Simulate and fit
- Data models •

SBML

- <u>System Biological Markup</u> Language
- Quantitative information
- XML •
- http://www.sbml.org/ •

Pathway Community

- can be found
- Relationships
- Reason and query
- Ontologies •

BioPAX

- Biological PAthway e**X**change
- Qualitative, no kinetics
- RDF / OWL
- http://www.biopax.org/ ullet

Can BioPAX and SBML work together?

Conversions

- Binom (Cytoscape))
- Sbml2biopax

Annotation

- Use BioPAX for annotations in SBML
- Add dummy elements to SBML to describe BioPAX features

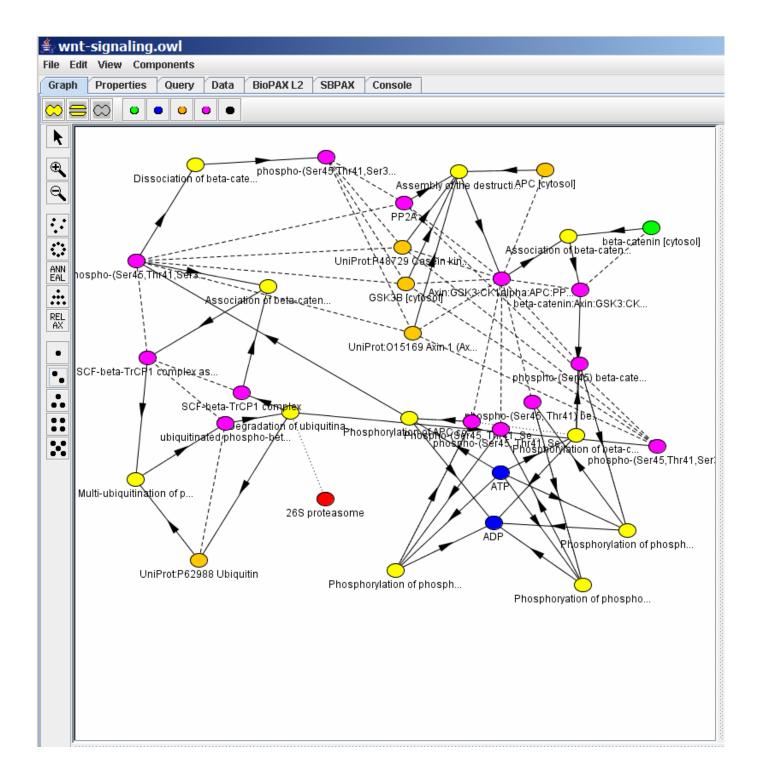
Direct conversion may be impossible

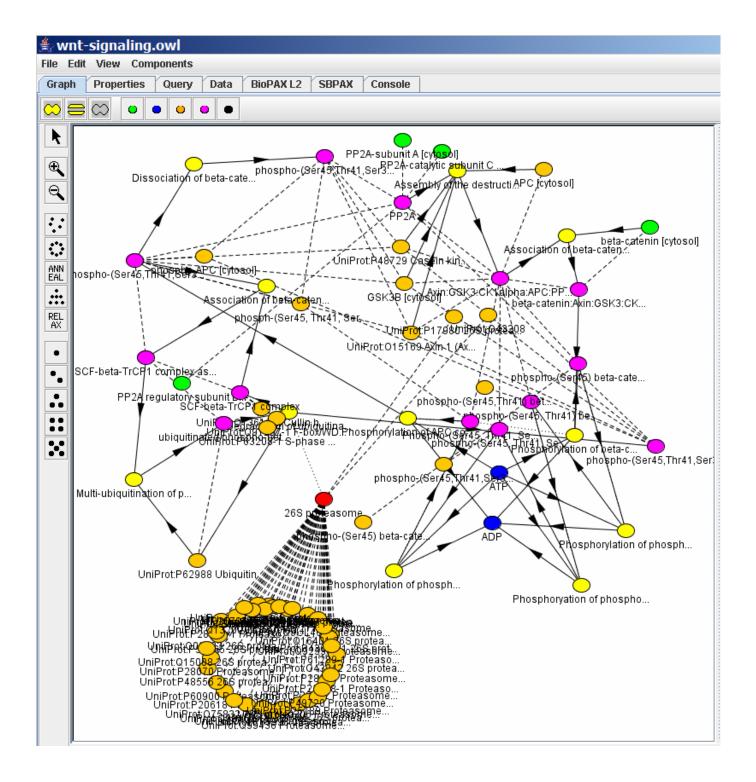
- An entity in BioPAX corresponds to multiple species in SBML (e.g. a protein in varying phosphorylation states)
- A species in SBML corresponds to multiple entities in BioPAX (e.g. generic participants in transport, translation and transcription)

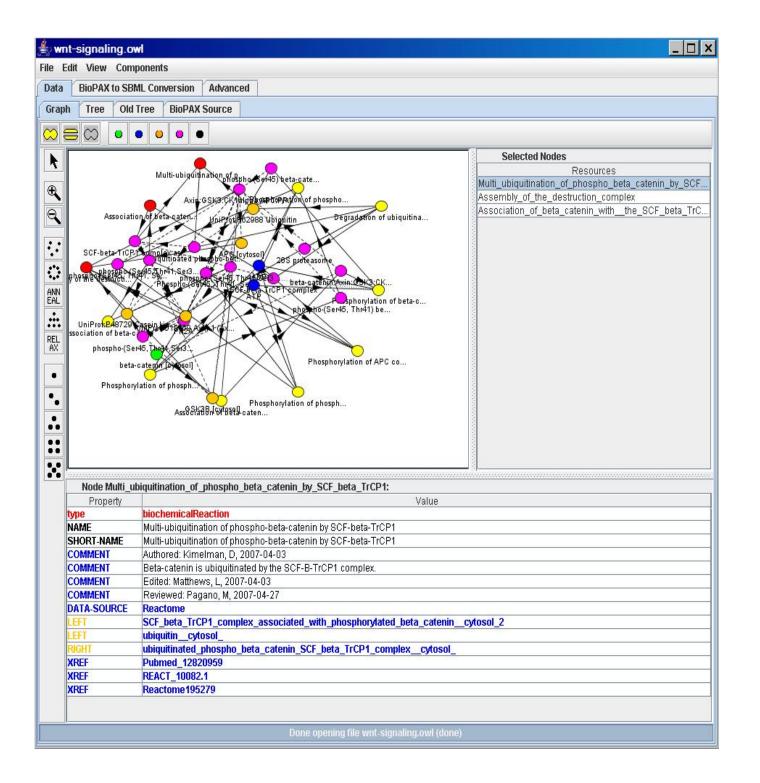
- <u>http://vcell.org/biopax</u>
- SyBiL provides capabilities for:
 - Visualizing, analyzing and querying pathway data represented in BioPAX
 - Creating computational model (SBML) from qualitative description (BioPAX)
 - Converting, gluing and merging data and models about pathways coming from different sources, such as BioPAX and SBML.
 - Intelligent visualizing and modular presentation of VCell model.

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🚖 wnt-signaling.owl
File Edit View Components
Data BioPAX to SBML Conversion Advanced
Conversion Criteria Reactions and Participants Compartments
Criteria for conversion of BioPAX data to SBML model Here you can select which Physical Entities Participants in BioPAX file will be converted to separate speciesTypes in SBML file. Depending on whether location is the same or different, Physical Entity Participants are assigned the same or different species. Below you can select assumptions about generic conversion. Later you can override these assumptions.
More about conversion criteria More about BioPAX and SBML
 None - None of Physical Entity Participants is assigned a separate SpeciesTypes. Manually assign species to each Physical Entity on the next screen. Some - Some types of PhysicalEntities are directly converted to speciesTypes.
🗌 Substance 🗹 rna 🗹 dna 🗹 smallMolecule 🗹 protein 🔲 complex
○ All - All Physiscal Entity Participants are converted to a separate SpeciesType.
Reset Process and Proceed

🚔 wnt-signaling.owl

File Edit View Components

Data BioPAX to SBML Conversion Advanced

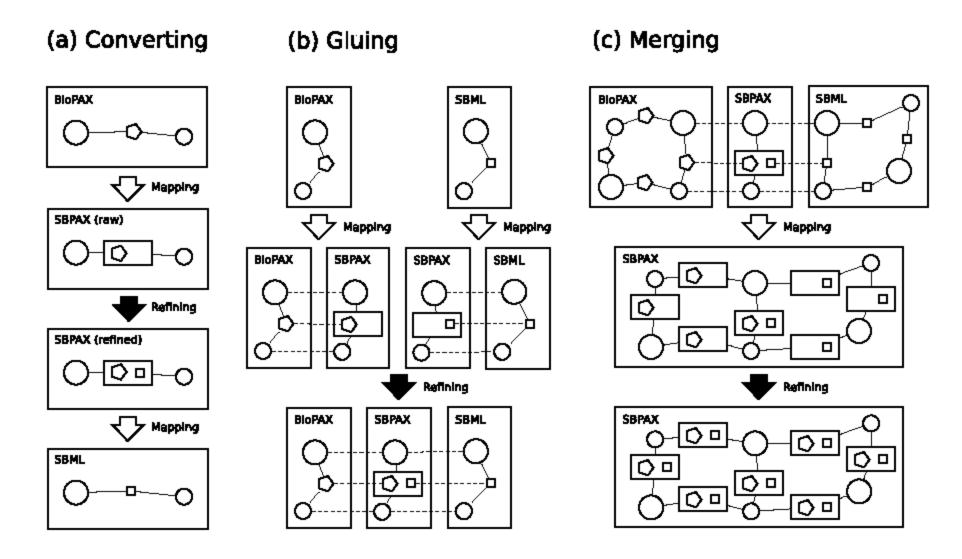
Process (BP)/	Participants	3		Entity Class	Stoich.	SpeciesTyp	Location	-
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	and the second	3 CK1aln		complex	1.0	[none]		-
Phosphorylation of beta-ca			ADP	smallMolecule	1.0	[new]	cytosol	-
		catenin		complex	1.0	and the second se	cytosol	-
				complex	[none]	[none]	a toool	-
hosphorylation of phosph		<u></u>	ATP	smallMolecule	1.0	beta-cateni	cytosol	-
		catenin		complex	1.0	[none]	cytosol	
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		1 heta		complex	1.0	[none]	cytosol	-
				complex	[none]	[none]	cvtosol	-
hosphoryation of phosph			ATP	smallMolecule	1.0	ATP	cvtosol	-
		1 heta		complex	1.0	[none]	cvtosol	-
			phospho-(Ser45, Thr41, Ser37) beta-ca		1.0	[none]	cvtosol	-
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						[none]	cytosol	-
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ssembly of the destructio				protein	1.0	UniProt:O		_
ssembly of the destructio			PP2A	complex	1.0	[none]	cytosol	_
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		_Ser37		complex	1.0	[none]	cytosol	_
Phosphorylation of APC co			ADP	smallMolecule	1.0	ADP	cytosol	_
				complex	[none]	[none]	cytosol	_
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				complex	1.0	[none]	cytosol	_
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		beta_cat		complex	1.0	[none]	cytosol	_
hosphorylation of phosph			ATP	smallMolecule	1.0	ATP	cytosol	_
	o phosphoSer45Thr4	1Ser3		complex	1.0	[none]	cytosol	_
hosphorylation of phosph			ADP	smallMolecule	1.0	ADP	cytosol	
1 / /	o Phospho_Ser45_Thr4			complex	1.0	[none]	cytosol	
hosphorvlation of phosph	o Phospho Ser45 Thr	1 Ser3	Phospho-(Ser45, Thr41, Ser37, Ser33)	complex	[none]	Inonel	cvtosol	_
Re	set and Save		Process and Save		Proce	ss and Proceed	i	

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File Edit View Con Data BioPAX to SE	nponents IML Conversion Advanced			
Conversion Criteria	Reactions and Participants	Compartments		
Compartment/			Spatial	Surrounding /
Location			Dims	Outside 3 [none]
910501				[none]
				cytosol
	Reset and Save		Process and Save	Process and proceed

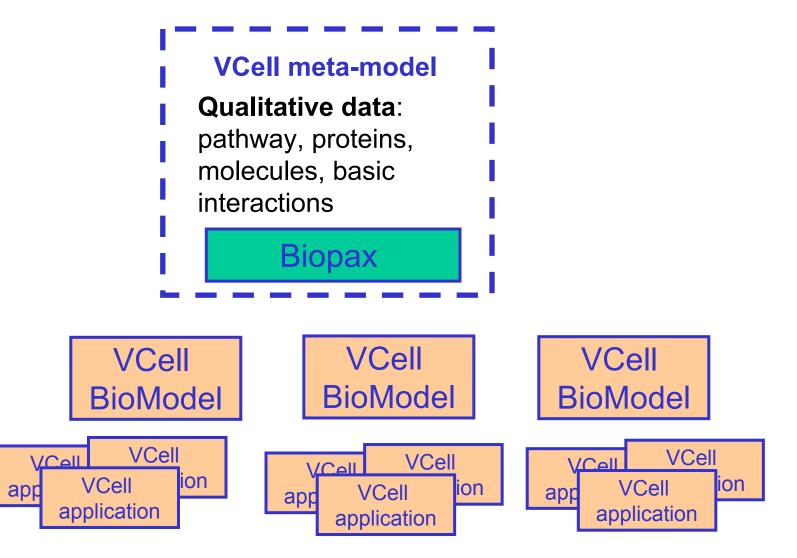
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Systems Biology Pathway Exchange (SBPAX)



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Extension of the Virtual Cell: meta-model



Acknowledgements

BioPAX

- C. Sander (Memorial Sloan-Kettering Cancer Center)
- Emek Demir (Memorial Sloan-Kettering Cancer Center)
- G. Bader (University of Toronto).

BioPAX OBO

- Alan Ruttenberg (Science Commons)
- Jeremy Zucker (Harvard)
- Joanne Luciano (Harvard)