

Pathway Commons and BioPAX, Validator Update + Factoid

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TORONTO



The Systems Biology Pyramid

Cary, Bader, Sander, FEBS
Letters 579 (2005) 1815-20

Biological
Systems

Predictions

Experiments

Computational
Models

Dynamic Simulation
Probability Networks
Propagation of Perturbation
Multiscale Coupling

Cytoscape
cPath2

Information
System

Analysis
Visualization
Searches
Information Classes
Data Storage

Pathway
Commons
BioPAX

Pathway & Process
Data

Molecular Interaction Surveys
Molecular & Genetic Profiles
Detailed Subsystem Measurements
Biological Knowledge

Chris Sander, MSKCC

http://pathguide.org

Vuk Pavlovic
Sylva Donaldson

Home

BioPAX

cBio

MSKCC

Pathguide» the pathway resource list

Navigation

Protein-Protein Interactions

Metabolic Pathways

Signaling Pathways

Pathway Diagrams

Transcription Factors / Gene Regulatory Networks

Protein-Compound Interactions

Genetic Interaction Networks

Protein Sequence Focused

Other

Search

Organisms

All

Availability

All

Standards

All

Reset

Search

Statistics

Analyze Pathguide

Contact

Comments, Questions, Suggestions are Always Welcome!

Complete Listing of All Pathguide Resources

Pathguide contains information about **222** biological pathway resources. Click on a link to go to the resource home page or 'Details' for a description page. Databases that are free and those supporting BioPAX, CellML, PSI-M, or SBML standards are respectively indicated.

If you know of a pathway resource that is not listed here, or have other questions or comments, please [send us an e-mail](#).

Get the Stats
Detailed Pathguide resource statistics now available

Pathguide Published
Please cite the [Pathguide](#).

Protein-Protein Interactions

Database Name (Order: alphabetically | [by web popularity](#))

	Full Record	Availability	Standards
3DID - 3D interacting domains	Details	Free	
ABCdb - Archaea and Bacteria ABC transporter database	Details	Free	
AfCS - Alliance for Cellular Signaling Molecule Pages Database	Details	Free	
AllFuse - Functional Associations of Proteins in Complete Genomes	Details	Free	
ASEdb - Alanine Scanning Energetics Database	Details	Free	
ASPD - Artificial Selected Proteins/Peptides Database	Details	?	
BID - Binding Interface Database	Details	Free	
BIND - Biomolecular Interaction Network Database	Details	Free	PSI-MI
BindingDB - The Binding Database	Details	Free	
BioGRID - General Repository for Interaction Datasets	Details		PSI-MI
BRITE - Biomolecular Relations in Information Transmission and Expression	Details	Free	
CA1Neuron - Pathways of the hippocampal CA1 neuron	Details	Free	
Cancer Cell Map - The Cancer Cell Map	Details	Free	BioPAX
CSP - Cytokine Signaling Pathway Database	Details	Free	
CTDB - Calmodulin Target Database	Details	Free	
DDIB - Database of Domain Interactions and Bindings	Details	Free	
DIP - Database of Interacting Proteins	Details		PSI-MI
Doodle - Database of oligomeri			
DopaNet - DopaNet			
DRC - Database of Ribosomal			
DSM - Dynamic Signaling Maps			
FIMM - Functional Molecular Im			
FusionDB - Prokaryote Gene Fu			

>320 Pathway Databases!

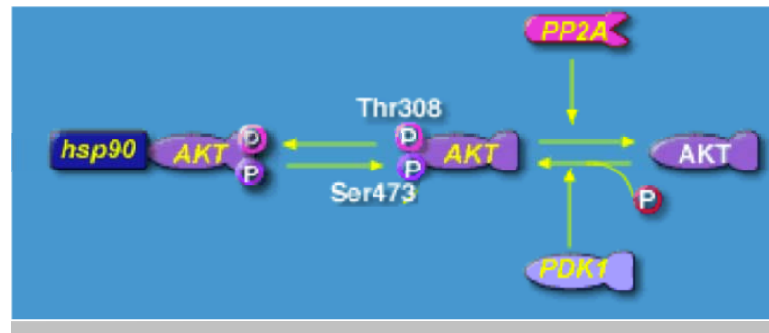
- Varied formats, representation, coverage
- Pathway data extremely difficult to combine and use

BioPAX Pathway Language

- Represent:
 - Metabolic pathways
 - Signaling pathways
 - Protein-protein, molecular interactions
 - Gene regulatory pathways
 - Genetic interactions
- Community effort: pathway databases distribute pathway information in standard format

www.biopax.org

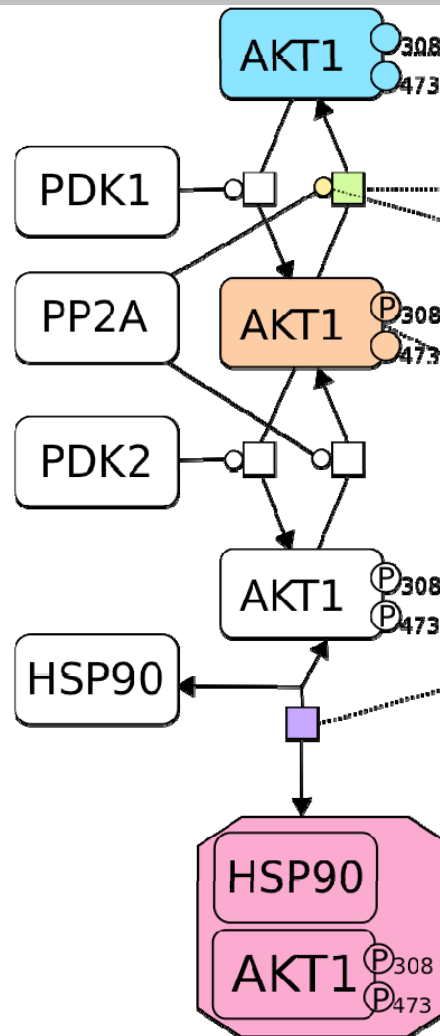
BioCarta



rAKT1 is a *ProteinReference*
has standard-name "AKT1"
has name "PKB"
has xref **Uniprot-P31749**

p@308 is a *ModificationFeature*
has featureLocation **AKT1-308**
has modificationType
phosphorylation

SBGN.org



AKT1.1 is a *Protein*
has proteinReference **rAKT1**
has notFeature **p@308**
has notFeature **p@473**

reaction1 is a *BiochemicalReaction*
has left **AKT1.2**
has right **AKT1.1**
is left-to-right.

catalysis1 is a *Catalysis*
has controller **PP2A.1**
has controlled **reaction1**
has direction irr left-to-right

AKT1.2 is a *Protein*
has proteinReference **rAKT1**
has feature **p@308**
has notFeature **p@473**

assembly1 is a *ComplexAssembly*
has left **HSP90.1**
has left **AKT1.3**
has right **complex1**
is reversible

complex1 is a *Complex*
has component **AKT1.4**
has component **HSP90.2**

HSP90.2 is a *Protein*
has proteinReference **rHSP90**
is boundTo **AKT1.4**

AKT1.4 is a *Protein*
has proteinReference **rAKT1**
has feature **p@308**
has feature **p@473**
is boundTo **HSP90.2**

BioPAX

Emek Demir

BioPAX Level 3 Support

- Reactome
- NCI/Nature PID
- PANTHER
- PhosphositePlus
- RegulonDB
- HumanCyc (and other BioCyc's)
- BioModels.net
- PSI-MI to BioPAX converter (HPRD, IntAct, MINT, DIP, BIND, etc.)
- Spike
- PharmGKB
- NetPath
- KEGG to BioPAX converter (Clemens Wrzodek, Tuebingen)

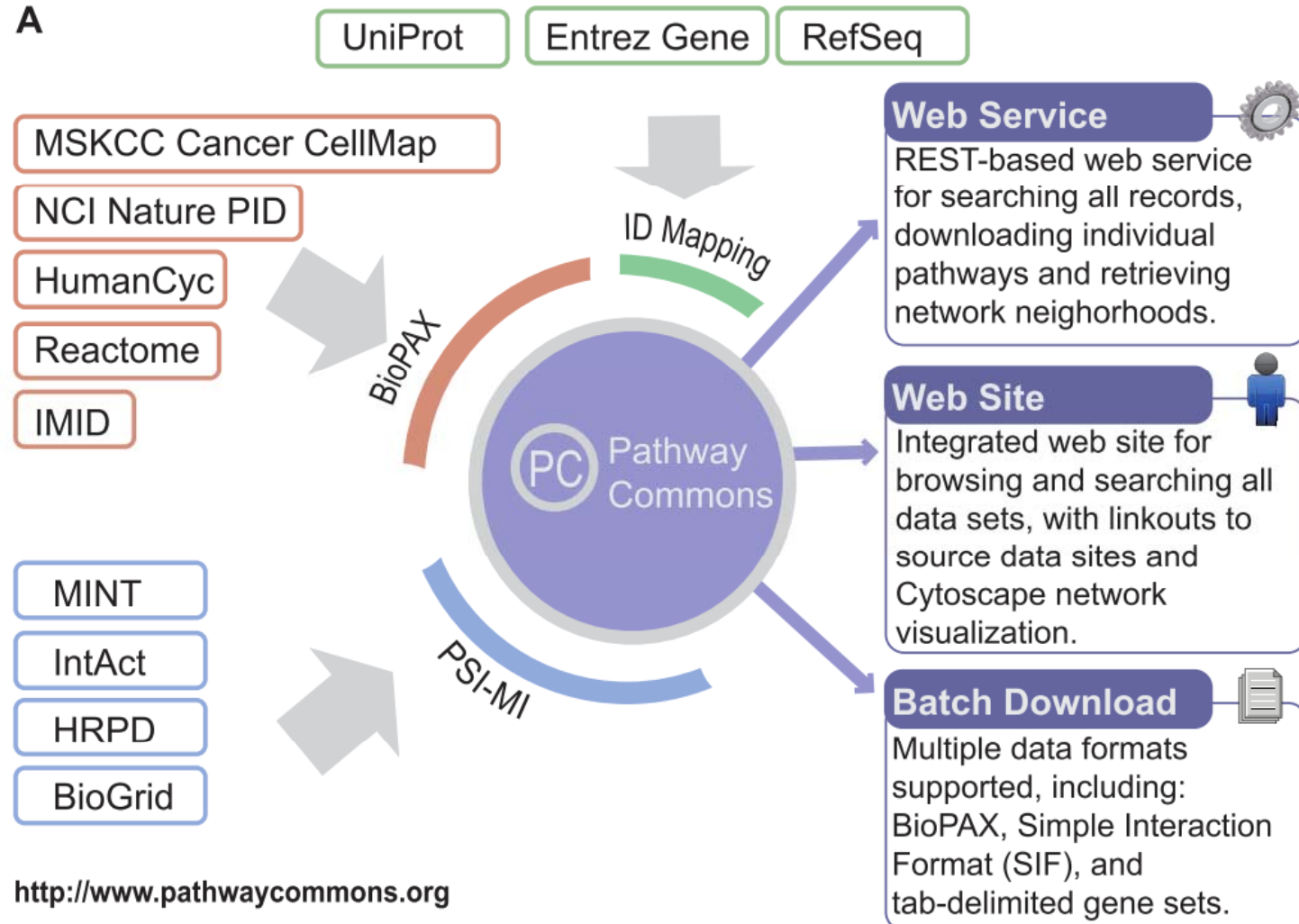
BioPAX future plans

- **Editors: Peter D'Eustachio, Oliver Ruebenacker and Andrea Splendiani, Emek Demir and Huaiyu Mi**
- Update software and databases
- Maintain the format
 - Extensions
 - Minor updates
- Think about level 4
 - Semantic web technology
- Add new data
- BioPAX Validator
 - Validation profiles catering to different use cases
 - We need your help
- PaxTools (Emek will talk next)

Aim: Convenient Access to Pathway Information

<http://pathwaycommons.org>

A



Facilitate creation and communication of pathway data
Aggregate pathway data in the public domain
Provide easy access for pathway analysis

Long term: Converge
to integrated cell map

Pathway Commons: cPath²

- <http://www.pathwaycommons.org/pc2-demo/>
- <http://awabi.cbio.mskcc.org/pc2-demo/>

Web Service API:

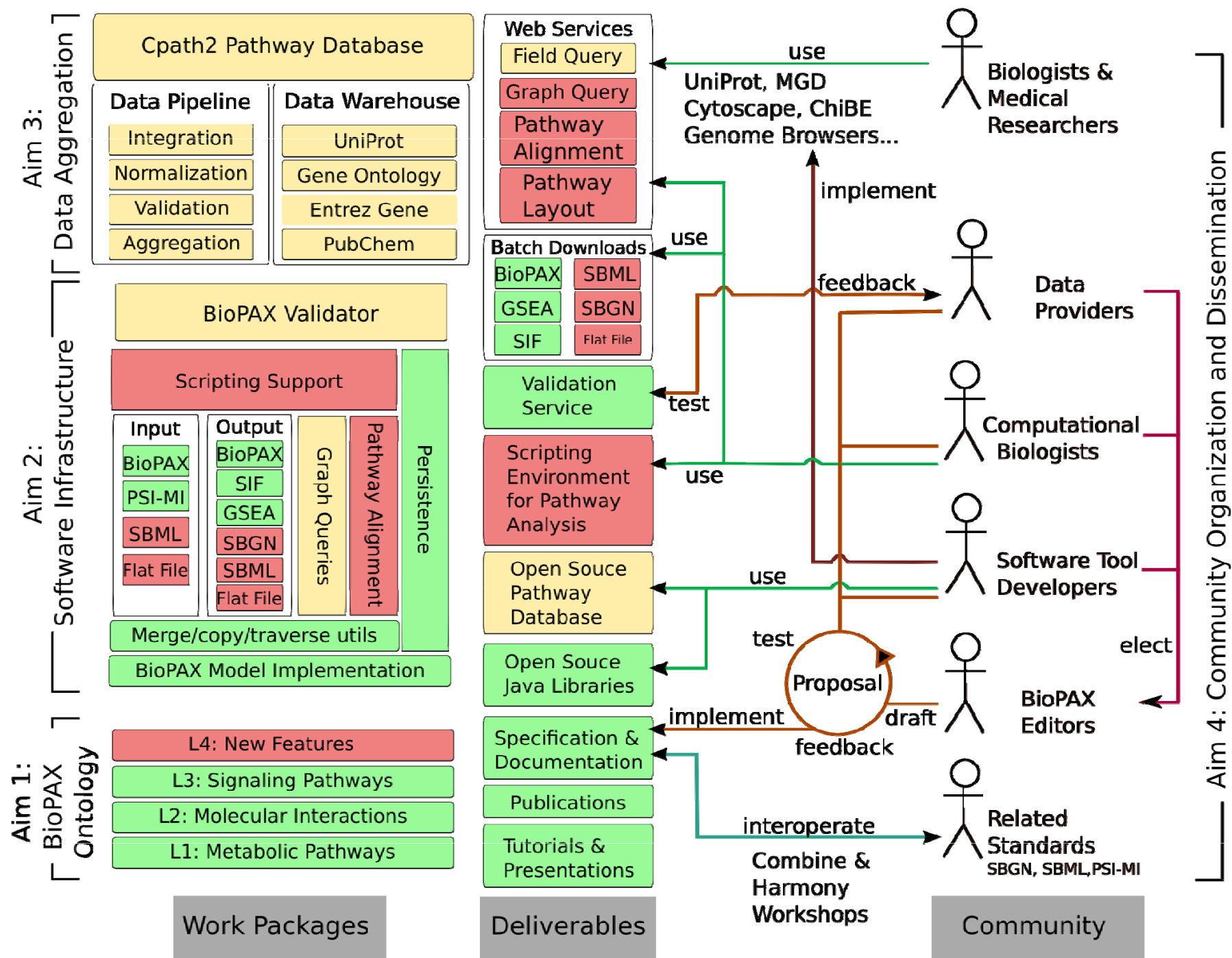
You can programmatically access the data within Pathway Commons using the Pathway Commons Web Service Application Programming Interface (API). This page provides a reference guide to help you get started.

1. [Command: SEARCH](#)
2. [Command: GET](#)
3. [Command: GRAPH](#)
4. [Command: TRAVERSE](#)
5. [Command: TOP_PATHWAYS](#)
6. [Command: HELP](#)

**Emek Demir, Igor Rodchenkov, Chris Sander Ozgun Babur, Arman Aksoy,
Onur Sumer, Ethan Cerami, Ben Gross**

Demo

- <http://awabi.cbio.mskcc.org/pc2-demo/>
- CyPath2 App for Cytoscape 3.0
- ChiBE



The Factoid Project

- Publishing in science
 - Highly inefficient
 - Outdated technology, difficult to search and compute
- <http://www.elseviergrandchallenge.com/>
 - Winner: <http://reflect.ws/>
- Pathway and network information database curation
 - Highly inefficient
- The factoid project
- Game?

Pathway and Network Analysis

1. Gene set: pathway enrichment analysis
2. Network: network regions (modules), regulation
3. Process model: classical pathways
4. Simulation model: detailed models



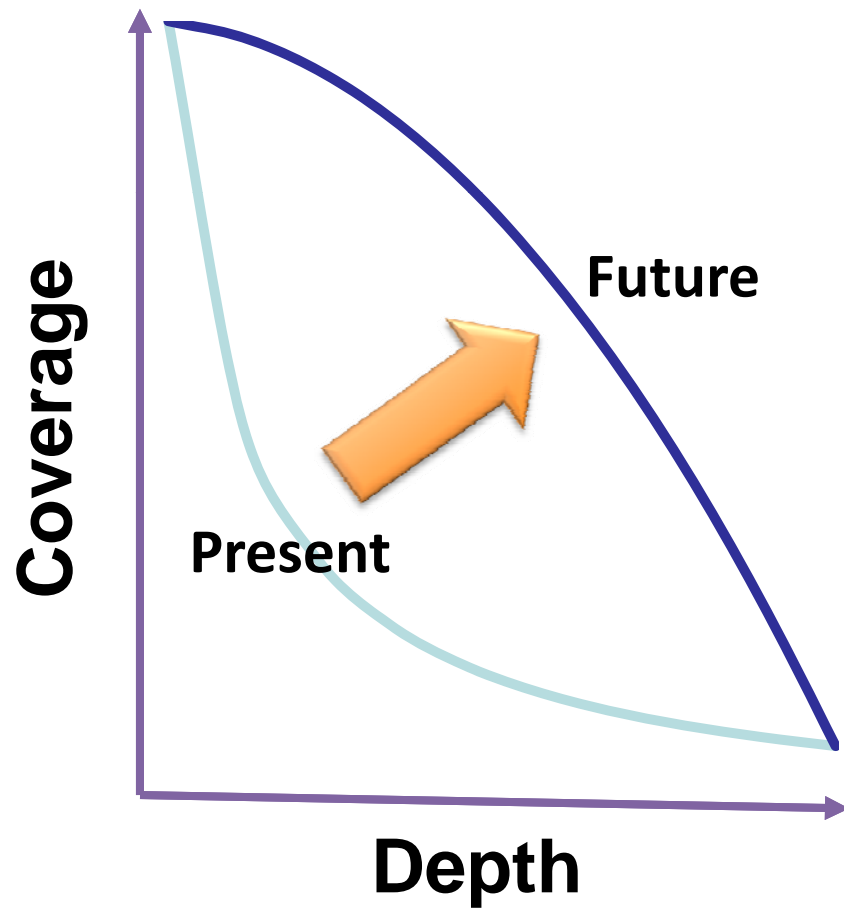
**Genome Coverage
And use**



**Mechanistic
Understanding**

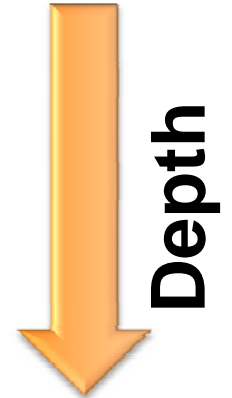
Increase Coverage and Depth

Data and analysis methods



Cellular Process Representation

- Gene set
- Network
- Process model
- Simulation model



- Analysis methods need to keep up!