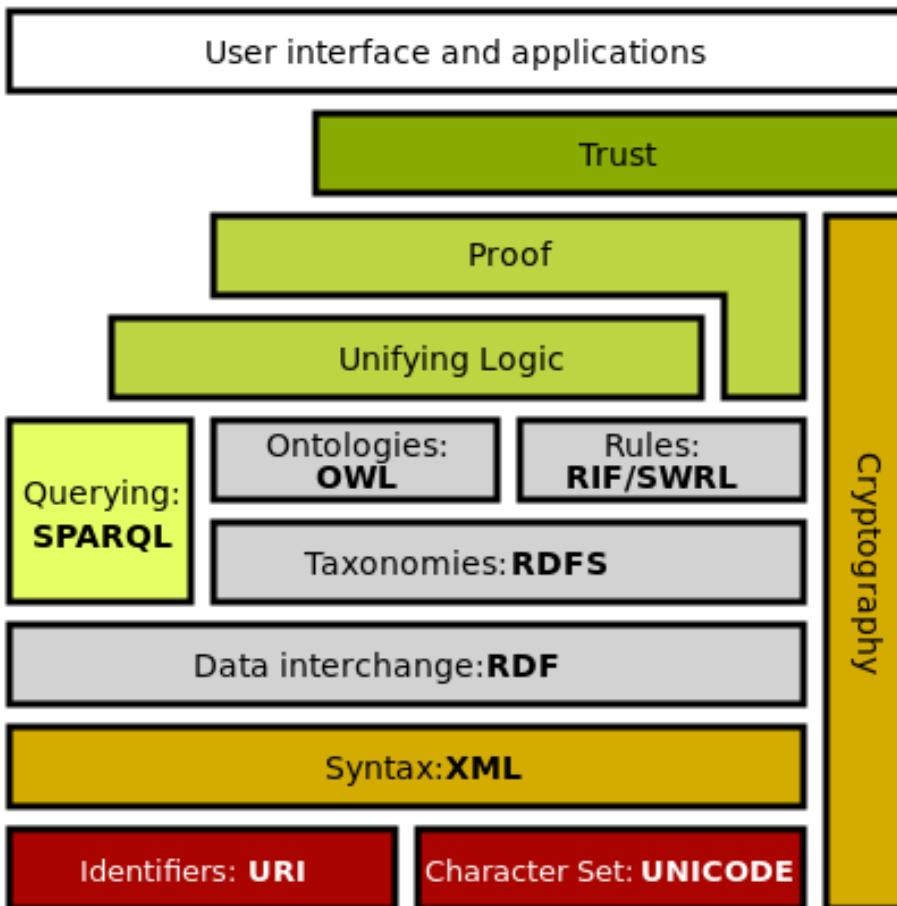


Semantic Web

The Semantic Web Stack



Sir Tim Berners-Lee
https://en.wikipedia.org/wiki/Semantic_Web_Stack



The Semantic Web Stack hierarchy of languages, where each layer exploits and uses capabilities of the layers below.

It shows how technologies that are standardized for Semantic Web are organized to make the Semantic Web possible.



Examples

Reference Ontology Examples

- BioPAX – Mid level – biological pathways
- Gene Ontology (“GO”) – Gene annotation

Application Ontology Example

- Influenza Ontology
- Translational Medicine Ontology

BioPAX

Biological PAthway eXchange



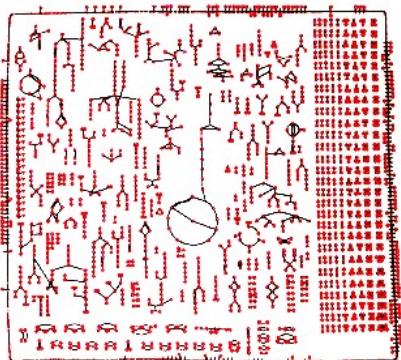
An abstract data model for biological pathway *integration* from multiple sources

BioPAX provides a consistent format for biological pathway data

Biological Pathways of the Cell

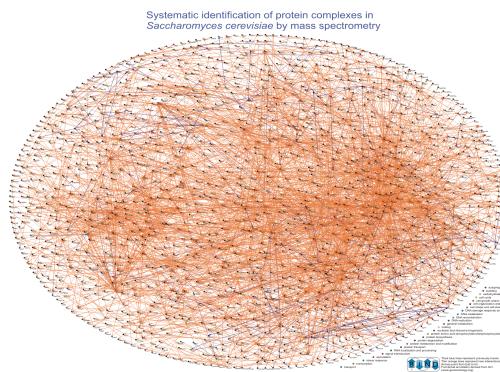
BioPAX

*What's a pathway?
Depends on who you ask!*



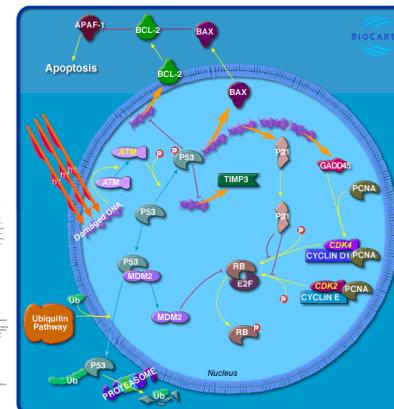
**Metabolic
Pathways**

**BioPAX
Level 1**



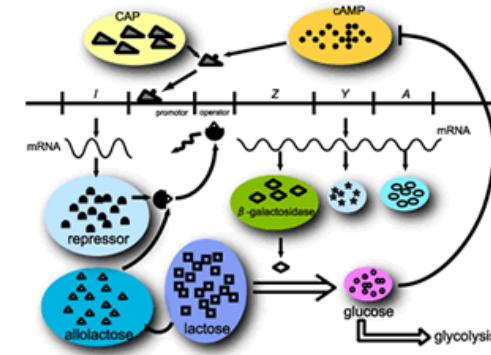
**Molecular
Interaction
Networks**

**BioPAX
Level 2**



**Signaling
Pathways**

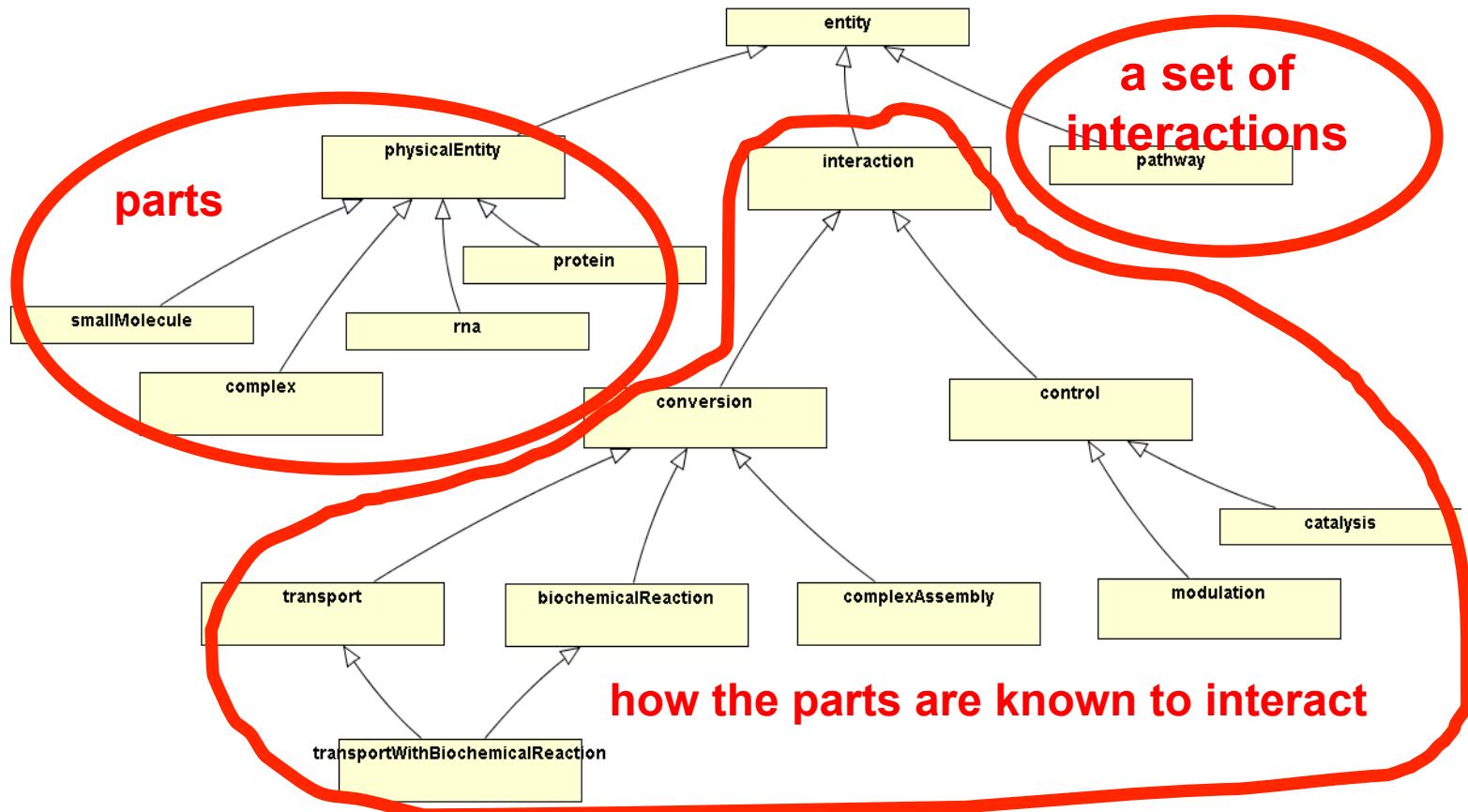
**BioPAX
Level 3**



**Gene
Regulation**

**BioPAX
Level 4**

BioPAX Ontology



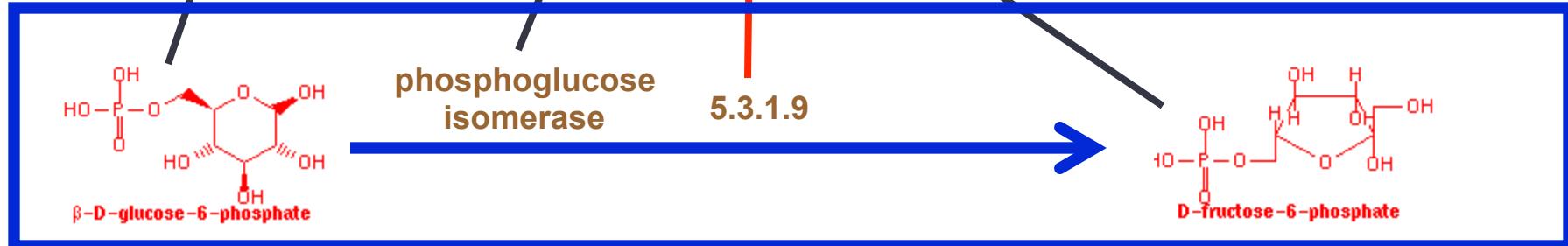
Level 1 v1.0 (July 7th, 2004)

BioPAX Biochemical Reaction



OWL Instance
(Individual)
(datum)

OWL class



Ontology Metadata



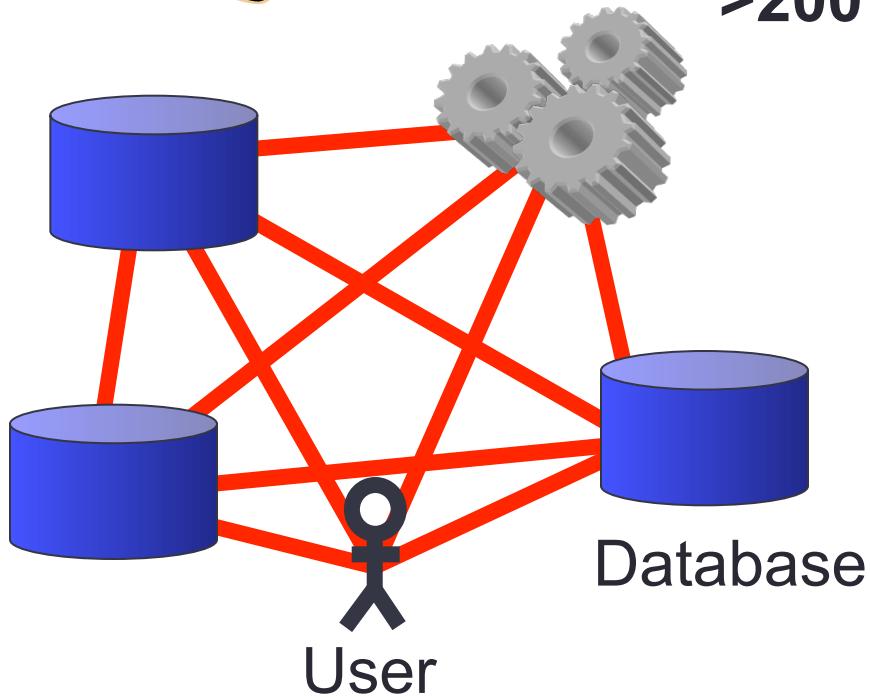
```
▼<owl:DatatypeProperty rdf:id="EC-NUMBER">
  <rdfs:domain rdf:resource="#biochemicalReaction"/>
  ▼<rdfs:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
    The unique number assigned to a reaction by the Enzyme Commission of the
    International Union of Biochemistry and Molecular Biology. Note that not all
    biochemical reactions currently have EC numbers assigned to them.
  </rdfs:comment>
  <rdfs:range rdf:resource="http://www.w3.org/2001/XMLSchema#string"/>
</owl:DatatypeProperty>
```

<http://www.biopax.org/release/biopax-level1.owl>

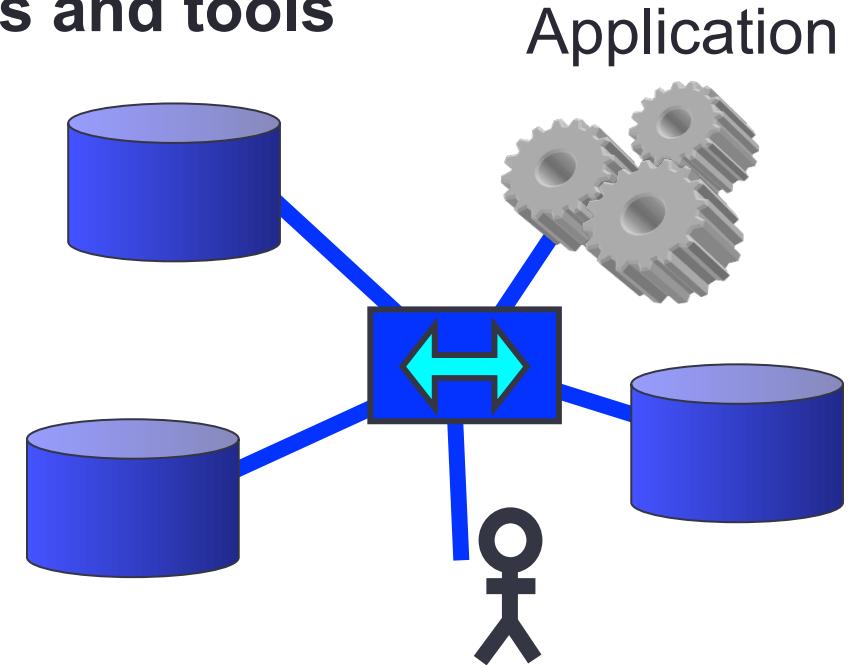


BioPAX - Simplify

>200 DBs and tools



Before BioPAX



With BioPAX

Common “computable semantic” enables scientific discovery

Gene Ontology (GO)



Standard representations:

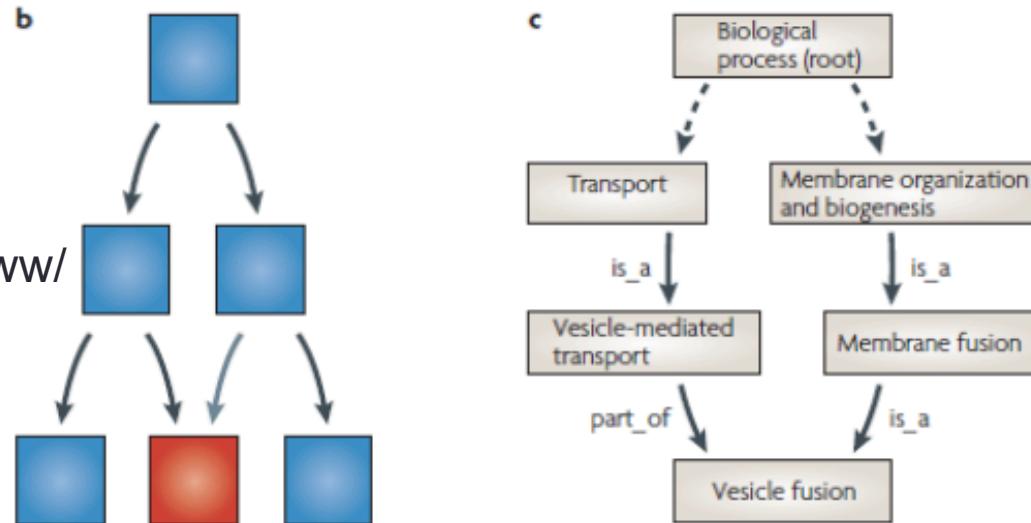
- Gene and gene product attributes
- Across species and databases

<ftp://ftp.geneontology.org/pub/go/www/GO.doc.shtml>

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

Structured controlled vocabularies organized as 3 independent Ontologies

- Molecular Interactions
- Cellular Location
- Biological Processes



[1] Rhee, S.Y, Wood, V., Dolinski, K. and Draghici, S. 2008. Use and misuse of the gene ontology annotations. Nature Reviews Genetics 9:509-515.

[2] http://people.oregonstate.edu/~knausb/rna_seq/annot.pdf

Gene Ontology



Two Key Uses:

Resource

to look up genes with similar functionality or location within the cell to help characterize the function of a sequence or structure

Standard Vocabulary

to annotate genomes to enable the analysis of the genome through the annotation terms.

Sequence Ontology



Sequence Ontology (SO) ‘terms and relationships used to describe the features and attributes of biological sequence.’ (E.g., binding_site, exon, etc.)

- sequence_attribute
- feature_attribute
- polymer_attribute
- sequence_location
- variant_quality
- sequence_feature
- junction
- region
- sequence_alteration
- sequence_variant
- functional_variant
- structural_variant
- Relationship (lots!)

