

## Module 3: Biomedical Ontology

# Data Science for Drug Discovery, Health & Translational Medicine

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Indiana University School of Informatics and Computing



# Module 3: Ontologies

## Topics:

BioMedical Ontologies (also known as knowledge graphs)

Tools

## Learning Objectives:

Describe what an ontology is, how and why they are used in biomedicine.

Explain how ontologies help achieve semantic integration.

Know how to use an ontology look-up service.

# Ontology Overview

## Ontology Background

1. BioMed Domain – Health care and Life Science
2. Reference and Application
3. Ontology Granularity and Layout

## Examples

1. Reference Ontology Examples
  1. BioPAX – Mid level – biological pathways
  2. Gene Ontology (“GO”) – Gene annotation
2. Application Ontology Examples
  1. Influenza Ontology
  2. Translational Medicine Ontology
  3. Best Practices

## Conclusion

1. Process: Start with Use Case, develop prototype, Evaluation
2. Standards: BioMedical Ontology Best practices (BioPortal, BFO, SIO)

# Background

Domain: Health Care, Life Science, and People

1. Times have changed
2. Data Driven Medicine
3. Health Care Singularity

What are you building: Reference vs. Application

1. Ontology Spectrum
2. Reference vs Application Ontology

Why: Function (Use Case)

1. Link, Aggregate, Search, Integrate, etc.

# Scope: HCLS Domain

Health Care & Life Science

## The Open Biological and Biomedical Ontologies

<http://www.obofoundry.org>



Goal: a suite of orthogonal interoperable reference ontologies



Barry Smith  
U Buffalo, NCBO

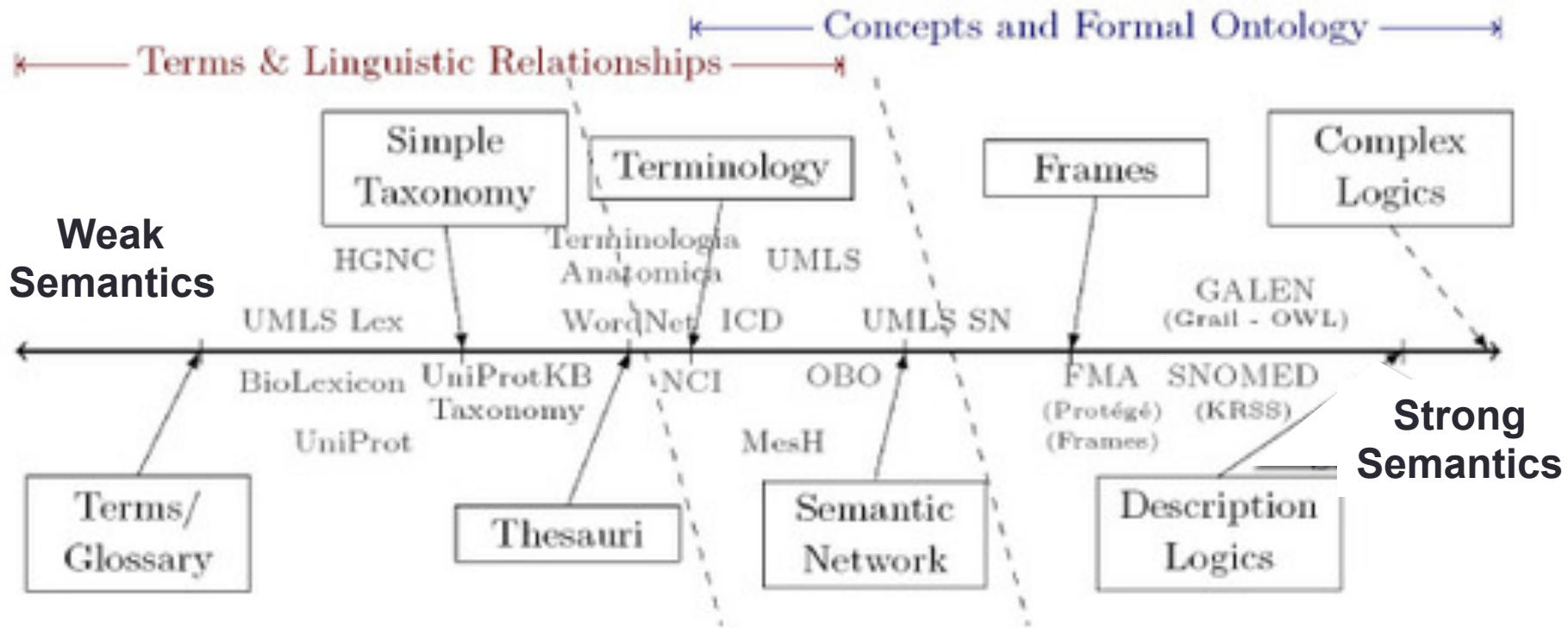
Table 1  
Coverage of initial Foundry ontologies

Granularity	Continuant			Occurrent
	Independent	Dependent		
Organ and organism	Organism (NCBI taxonomy or similar)	Anatomical entity (FMA, CARO)	Organ function (Physiology ontology, to be determined)	Organism-level process (GO)
Cell and cellular component	Cell (CL, FMA)	Cellular component (FMA, GO)	Cellular function (GO)	Phenotypic quality (PATO)
Molecule	Molecule (ChEBI, SO, RnaO, PRO)		Molecular function (GO)	Cellular process (GO)
				Molecular process (GO)

Down the left column is the granularities (spatial scales) of the entities represented in the ontologies; along the top is a dimension corresponding to the ways these entities exist in time.<sup>47</sup> 'Continuants' endure through time. 'Occurrents' (phenotypic qualities) unfold through time in successive stages. Continuants are divided into physical things, on the one

# Ontology Spectrum

Existing formalisms



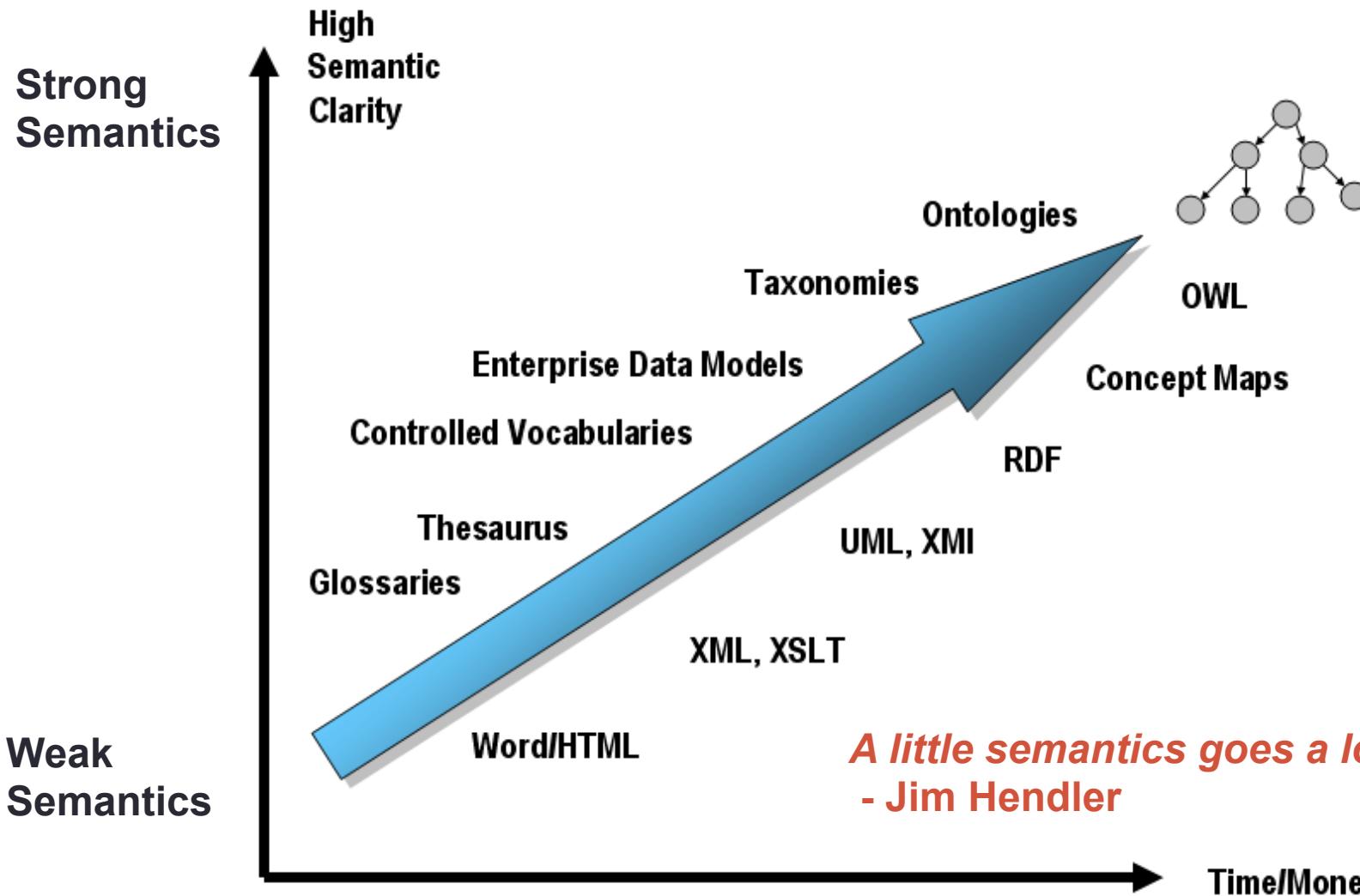
## Reuse of terminological resources for efficient ontological engineering in Life Sciences

by Jimeno-Yepes, Antonio; Jiménez-Ruiz, Ernesto; Berlanga-Llavori, Rafael; Rebholz-Schuhmann, Dietrich

Journal: BMC Bioinformatics Vol. 10 Issue Suppl 10

DOI: 10.1186/1471-2105-10-S10-S4

# Ontology Spectrum



# Application vs. Reference Ontology

## Reference Ontology

- Intended as an authoritative source
- True to the limits of what is known
- Used by others
- Application Ontology
  - Built to support a particular application (use case)
  - Reused rather than define terms
  - Skeleton structure to support application
  - Terms defined refine or create new concepts directly or through new classes based on inference

## Examples

### 2 Reference Ontology Examples

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

### 2 Application Ontology Example

- Influenza Ontology
- Translational Medicine Ontology

# The Open Biological and Biomedical Ontologies

<http://www.obofoundry.org>

Coverage of initial Foundry ontologies

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Molecule	Molecule (ChEBI, SO, RnaO, PRO)		Molecular function (GO)	Molecular process (GO)

# Overview

Introduction (10 minutes)

1. Background

1. BioMed Domain – Health care and Life Science
2. Reference and Application
3. Ontology Granularity and Layout

2. Examples: (40 minutes)

1. Reference Ontology Examples

## 1. BioPAX – Mid level – biological pathways (10)

2. Gene Ontology ("GO") – Gene annotation (5)

2. Application Ontology Examples

1. Influenza Ontology (5)
2. Best Practices (10)

3. Conclusion (5 minutes)

1. Process: Start with Use Case, develop prototype, Evaluation
2. Standards: BioMedical Ontology Best practices (BioPortal, BFO, SIO)
3. Conferences

## Examples

## 2 Reference Ontology Examples

- BioPAX – Mid level – biological pathways
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## 2 Application Ontology Example

- Influenza Ontology
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<http://www.obofoundry.org>

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# BioPAX

## Biological PAthway eXchange

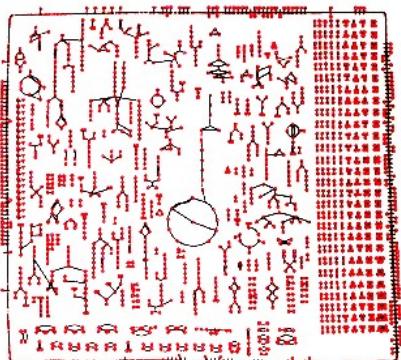
An abstract data model for biological pathway  
*integration*

Initiative *arose from the community*

# Biological Pathways of the Cell

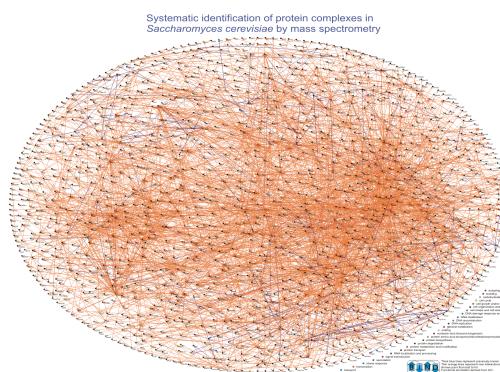
BioPAX

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



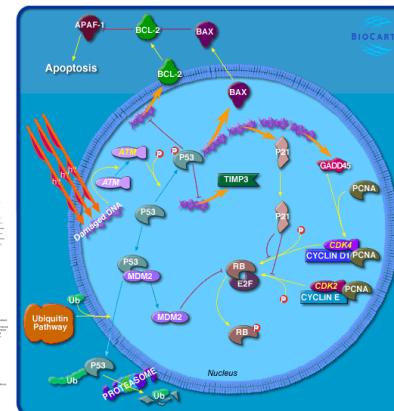
**Metabolic  
Pathways**

**BioPAX  
Level 1**



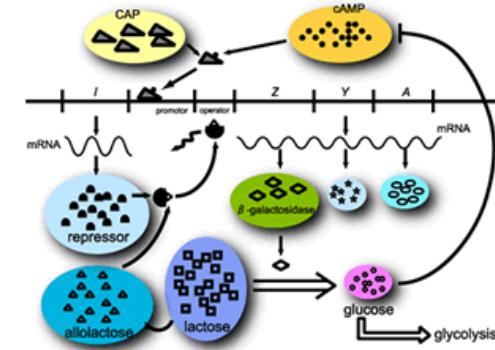
**Molecular  
Interaction  
Networks**

**BioPAX  
Level 2**



**Signaling  
Pathways**

**BioPAX  
Level 3**



**Gene  
Regulation**

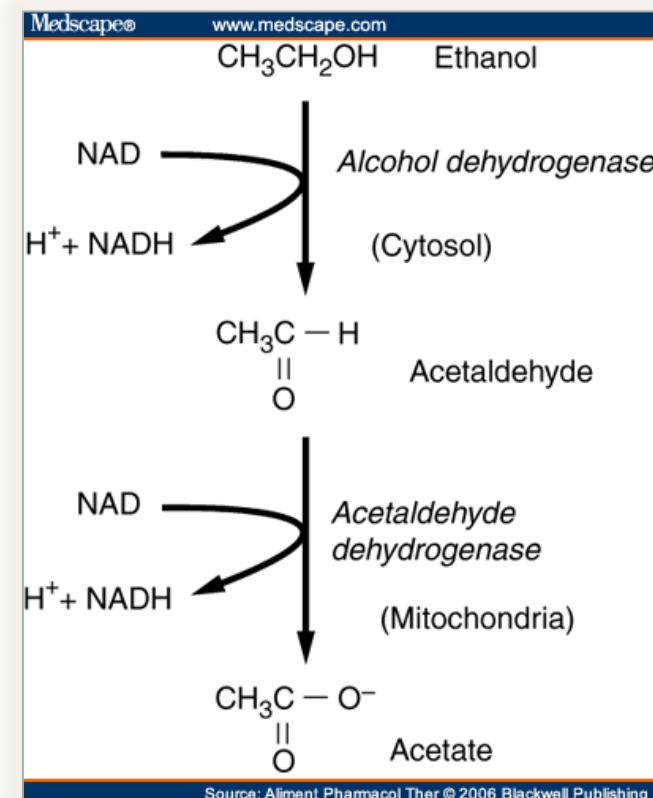
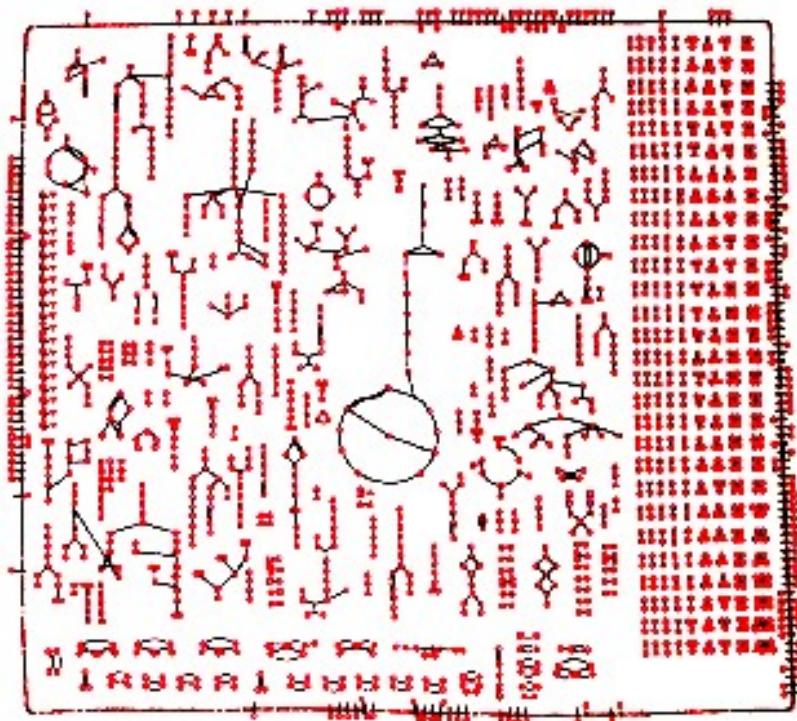
**BioPAX  
Level 4**

# Biological Pathways of the Cell

BioPAX

**BioPAX**  
Level 1

## Metabolic Pathways



A series of chemical reactions, catalyzed by enzymes

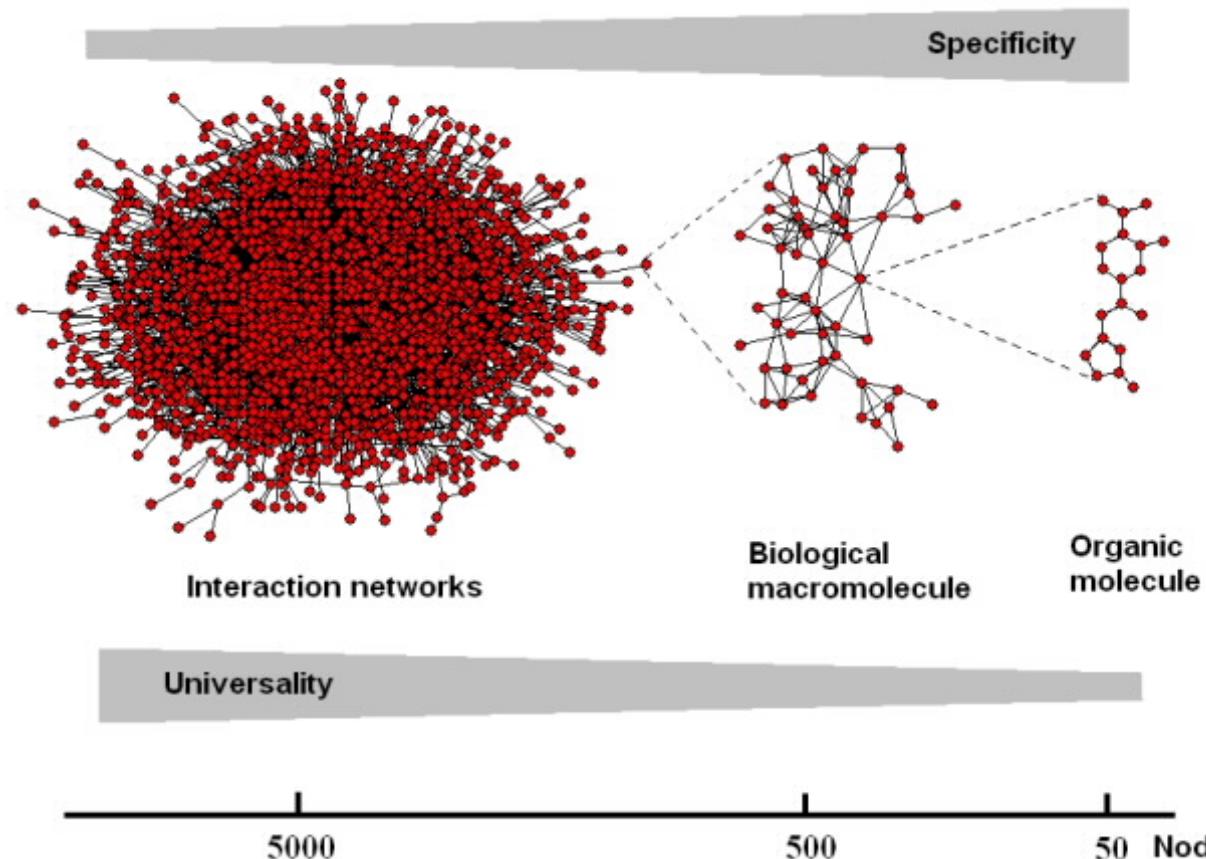
The products of one are the reactants of the next  
 e.g. Conversion, Transport

# Biological Pathways of the Cell

## Molecular Interaction Networks

BioPAX

BioPAX  
Level 2



<http://www.estradalab.org/research/>

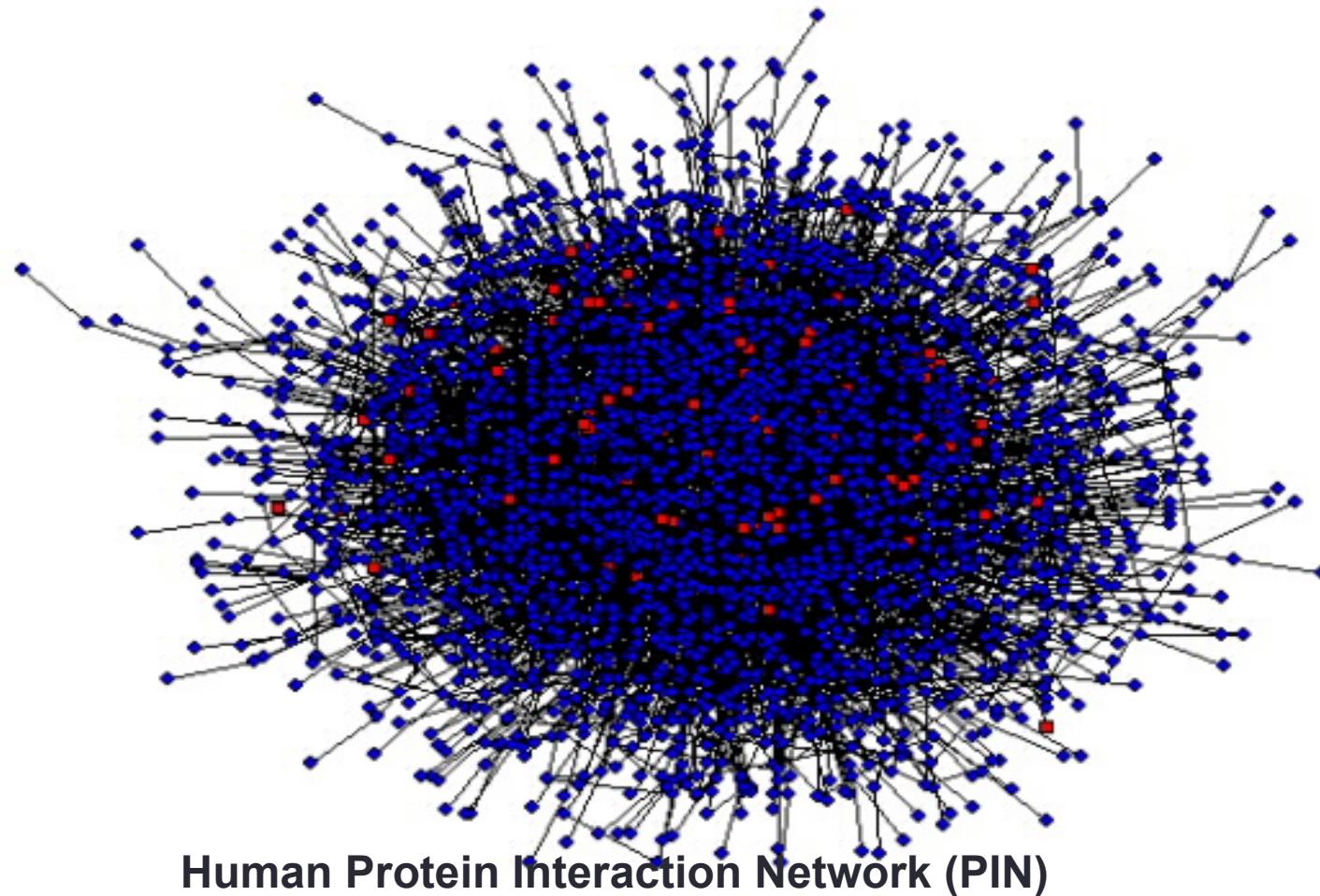
Cells are complex systems whose physiology is governed by an intricate network of Molecular Interactions (MIs) of which a relevant subset are protein–protein interactions (PPIs).

# Biological Pathways of the Cell

## Molecular Interaction Networks

BioPAX

BioPAX  
Level 2



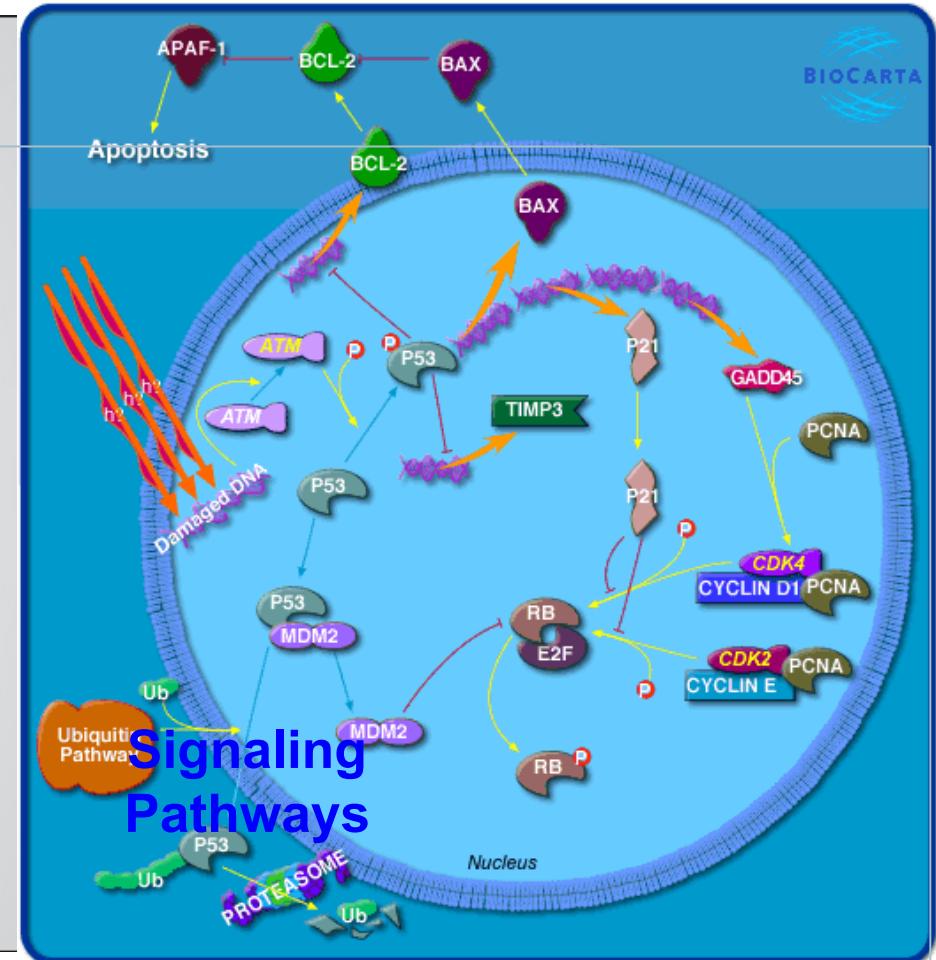
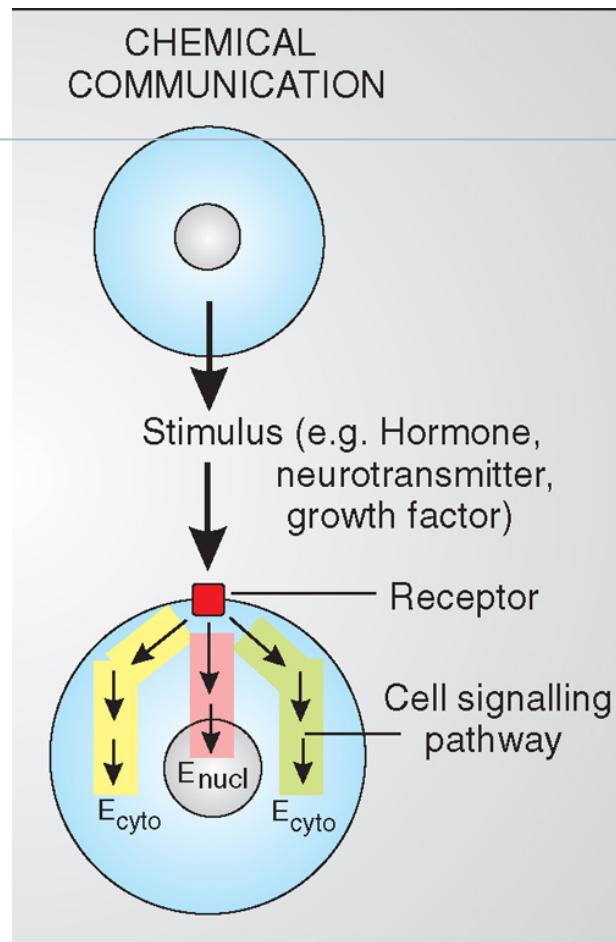
# Biological Pathways of the Cell

BioPAX

**BioPAX  
Level 3**

Signaling molecules trigger cellular responses.

Molecules bind to the cell surface causing a cascade of activation Reactions



**A activates B activates C....**

Adapted from Cell Signalling Biology - Michael J. Berridge - [www.cellsignallingbiology.org](http://www.cellsignallingbiology.org) - 2012  
and <http://www.hartnell.edu/tutorials/biology/signaltransduction.html>

# Biological Pathways of the Cell

## BioPAX

The modulation of any of the stages of gene expression that control:

which genes are switched on and off  
when, how long, and how much

Gene regulation may occur many stages:

Transcription

Post-transcriptional modification

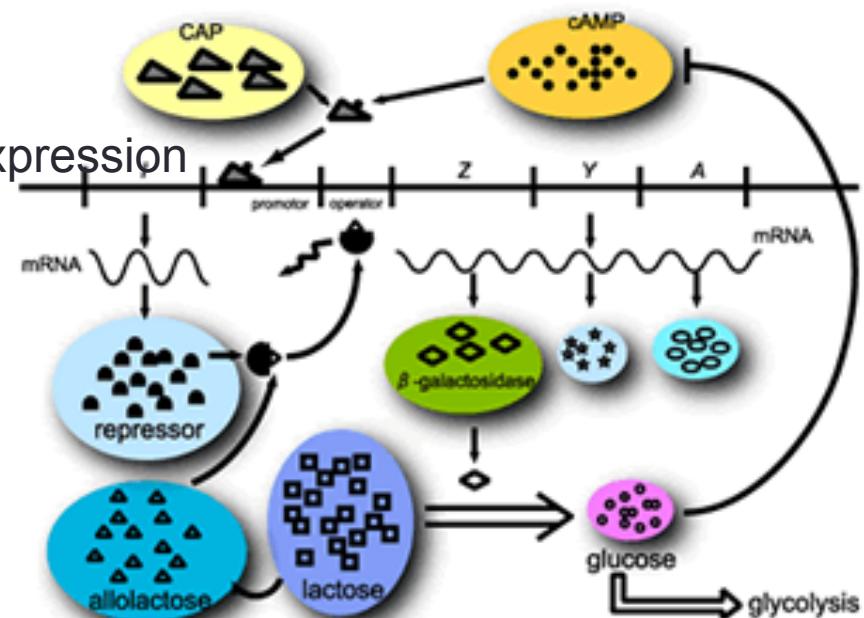
RNA transport

Translation

mRNA degradation

Post-translational modifications

among many others (more recently discovered!)



**Gene  
Regulation**

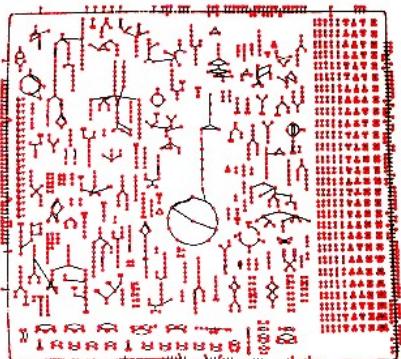
[http://en.wikipedia.org/wiki/Regulation\\_of\\_gene\\_expression](http://en.wikipedia.org/wiki/Regulation_of_gene_expression)

[http://www.biology-online.org/dictionary/Gene\\_regulation](http://www.biology-online.org/dictionary/Gene_regulation)

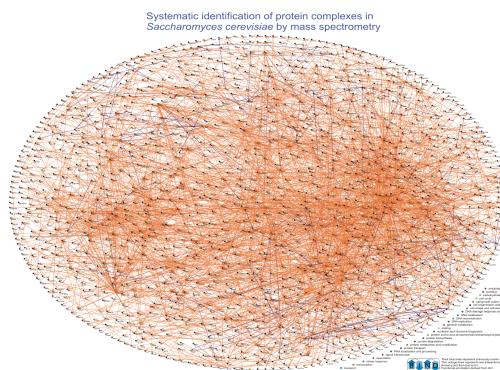
# Biological Pathways of the Cell

## BioPAX

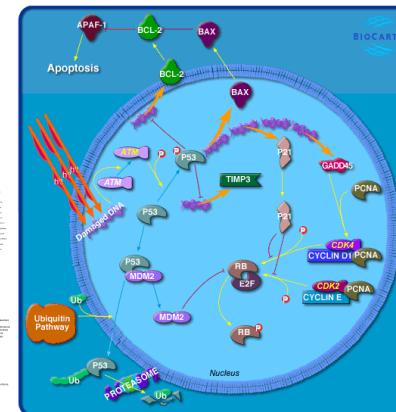
*What's a pathway?  
Depends on who you ask!*



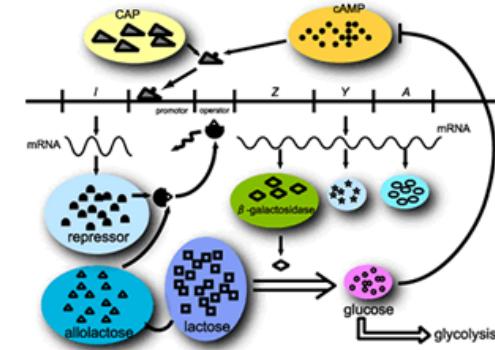
**Metabolic Pathways**



**Molecular Interaction Networks**



**Signaling Pathways**



**Gene Regulation**

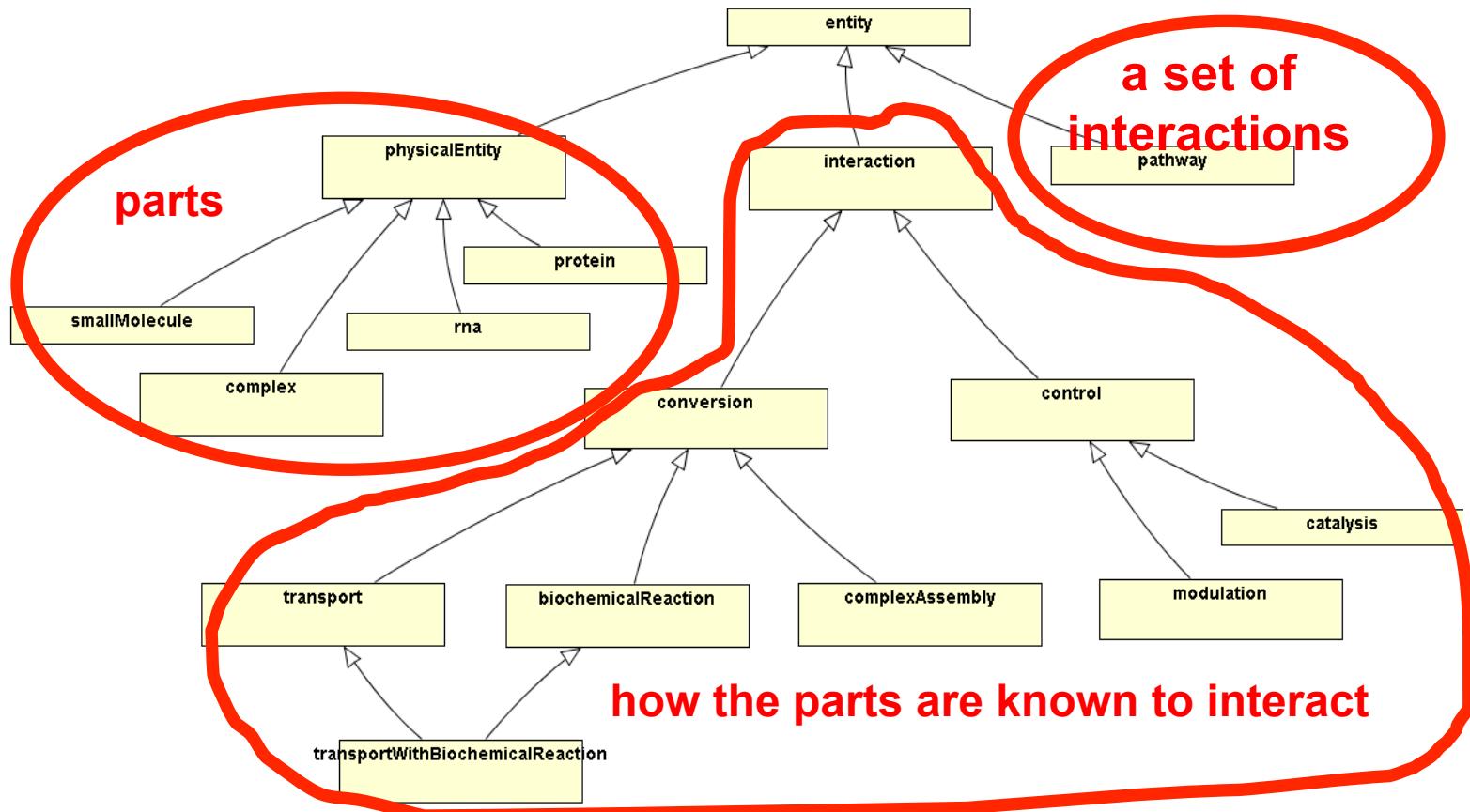
**BioPAX  
Level 1**

**BioPAX  
Level 2**

**BioPAX  
Level 3**

**BioPAX  
Level 4**

# BioPAX Ontology

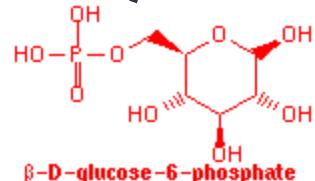
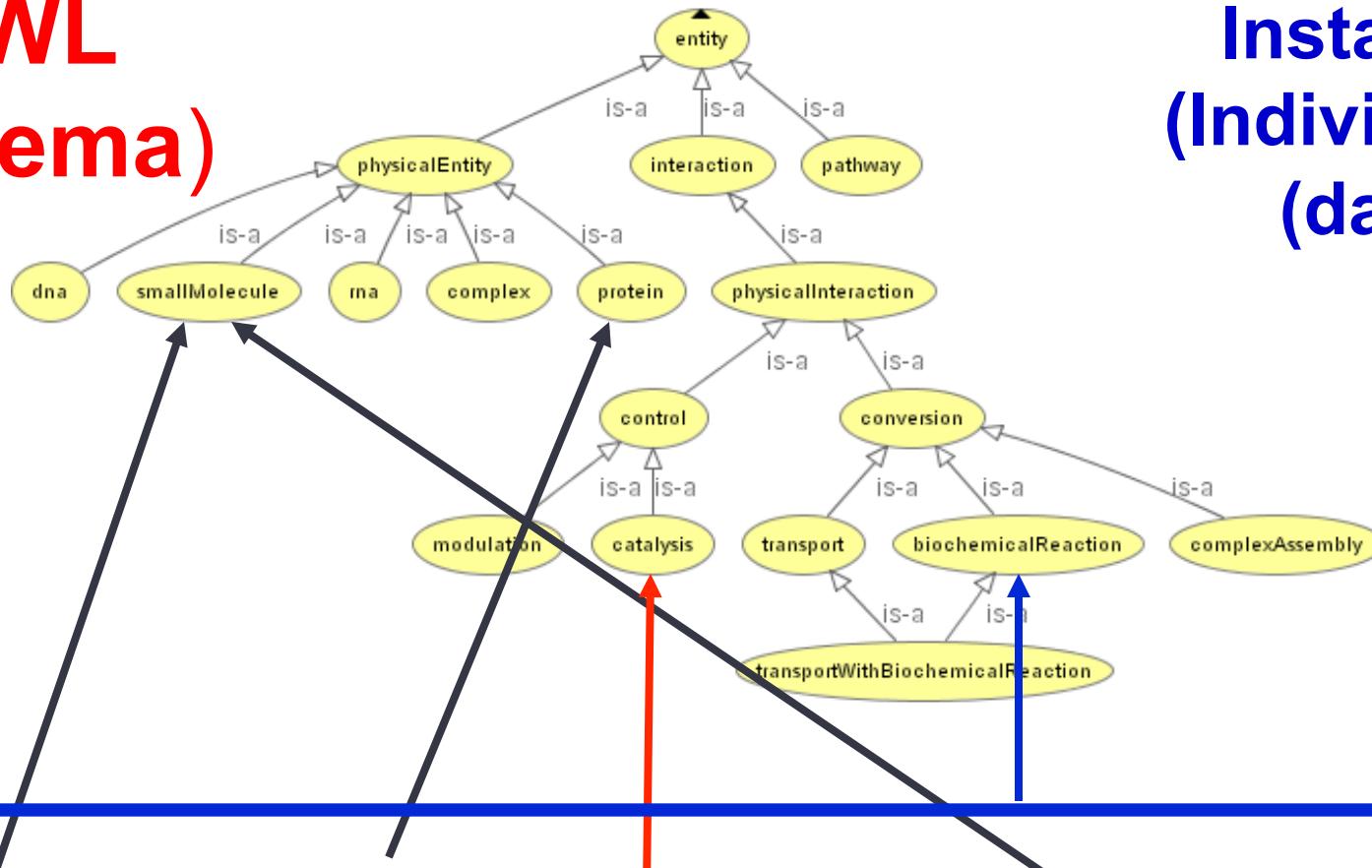


Level 1 v1.0 (July 7th, 2004)

# BioPAX Biochemical Reaction

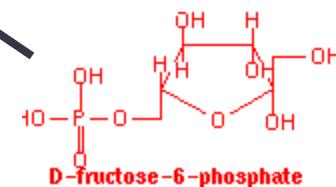
**OWL  
(schema)**

**Instances  
(Individuals)  
(data)**



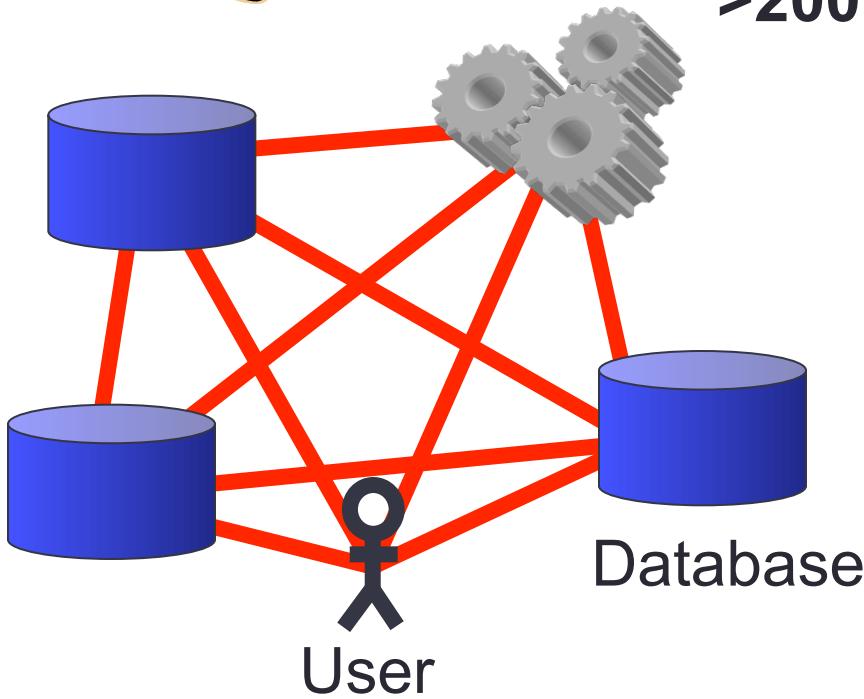
**phosphoglucose  
isomerase**

5.3.1.9



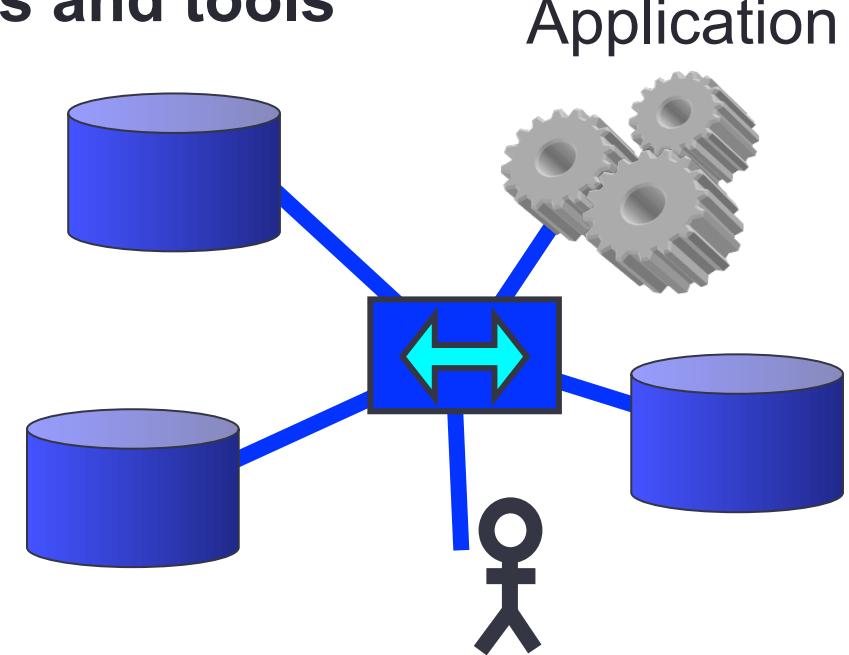


# BioPAX - Simplify



Before BioPAX

>200 DBs and tools



With BioPAX

Common “computable semantic” enables scientific discovery

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    1. UMLS – High level across biomedicine (5)
    2. BioPAX – Mid level – biological pathways (10)
    3. Gene Ontology (“GO”) – Gene annotation (5)
  2. Application Ontology Examples
    1. Influenza Ontology (5)
    2. Best Practices (10)
3. Conclusion (5 minutes)
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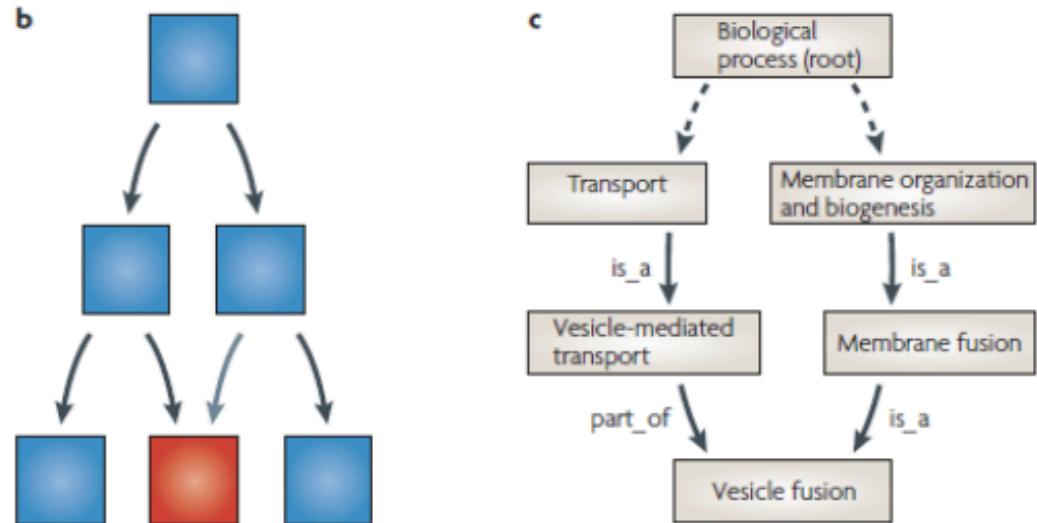
# Gene Ontology (GO)

Standard representations:

- Gene and gene product attributes
- Across species and databases

Structured controlled vocabularies organized as 3 independent Ontologies

- Molecular Interactions
- Biological Processes
- Cellular Location



[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](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
- Use to annotate genomes to enable the analysis of the genome through the annotation terms.

# Gene Ontology Evidence Codes

Manually-assigned evidence codes fall into

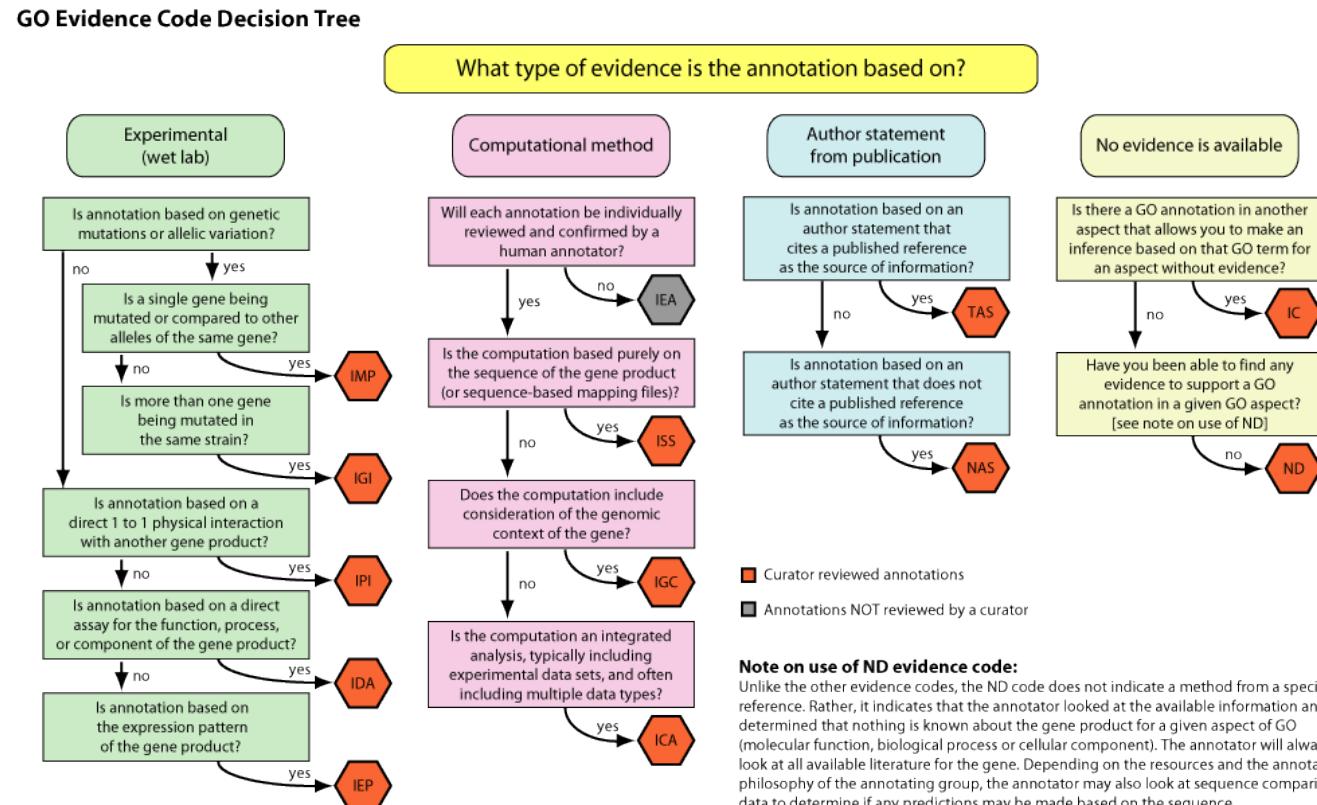
Four categories:

Experimental

Computational analysis

Author statements,

Curatorial statements



Inferred from Electronic Annotation (IEA) is not assigned by a curator.

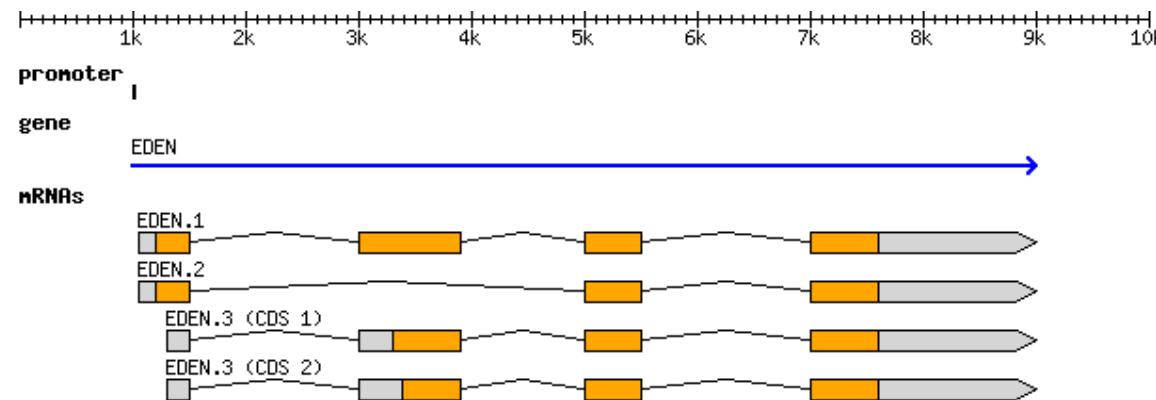
Adapted from: [http://people.oregonstate.edu/~knausb/rna\\_seq/annot.pdf](http://people.oregonstate.edu/~knausb/rna_seq/annot.pdf)

Rhee, S.Y, Wood, V., Dolinski, K. and Draghici, S. 2008. Use and misuse of the gene ontology annotations. Nature Reviews Genetics 40: 509-515.  
See also: <http://www.geneontology.org/GO.evidence.shtml>

# 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!)



(snuck this one in as another example)

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# **Application Ontology**

## **Influenza Ontology**

# **Ontology Support for Influenza Research and Surveillance**

**Joanne Luciano, PhD,  
Lynette Hirschman, PhD, Marc Colosimo, PhD**

Approved for Public Release; Distribution Unlimited.

28 April 2008 Case Number 08-0738



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# Application Ontology

## Influenza Ontology

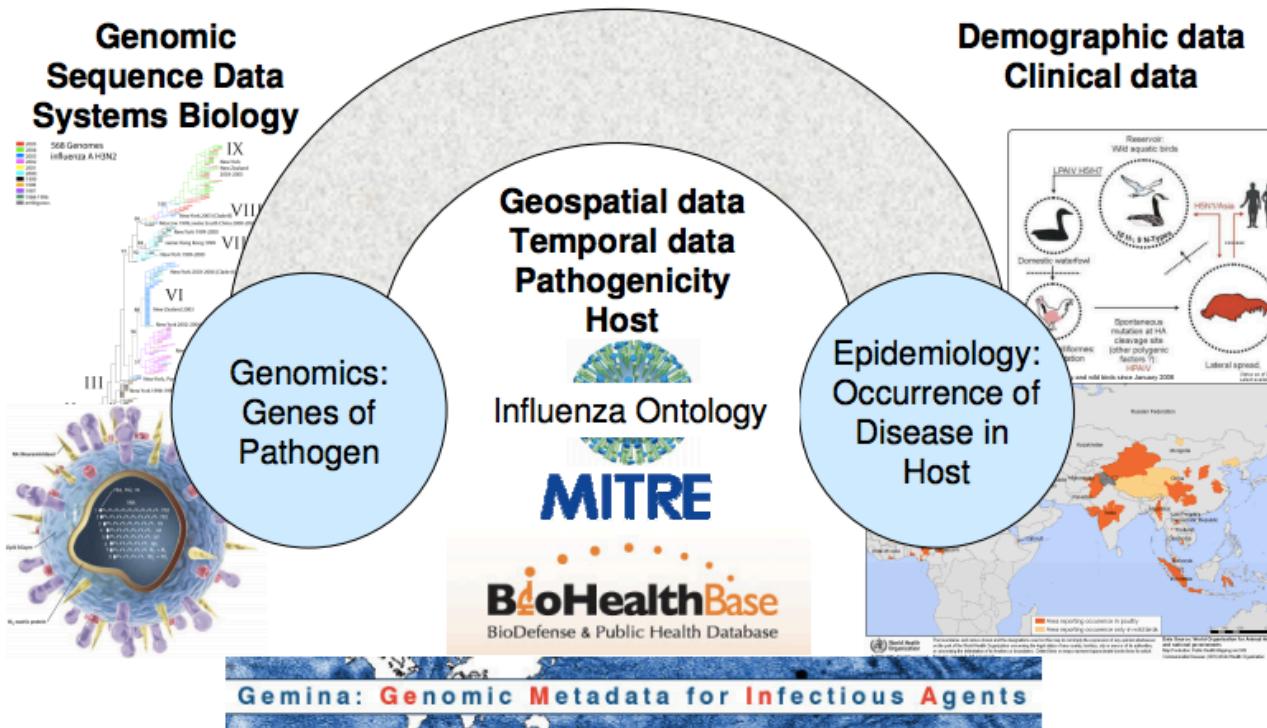
### Case Study 2: UK

- Outbreak of H5N1 in the UK at a turkey farm Feb 1, 2007
- What is the source of the outbreak?
  - Contact with infected wild birds?
    - But turkeys were in an enclosed “biosecure” unit
    - No H5N1 detected in the region in the 2 previous months
  - Govt. veterinarian suggested turkey meat from Hungary might be source of infection
    - Turkey farm is adjacent to a poultry packing plant that had processed poultry products from Hungary
    - Hungary had reported an H5N1 outbreak 2 weeks earlier
- Sequence data showed that strain infecting the turkeys was 99.96% identical to strain that had infected Hungarian birds
- Conclusion: Infected Hungarian poultry was source of H5N1 infection
  - Open question (relevant to food defense):  
how did H5N1 spread from processing plant to live turkeys?

# Application Ontology

## Influenza Ontology

### Research Question: Bridging the Gap - Connecting Genomics and Epidemiology



MITRE

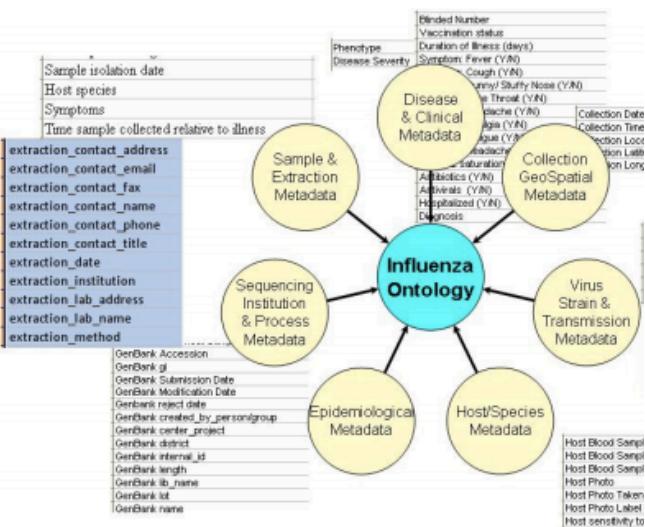
4  
© 2008 The MITRE Corporation. All rights reserved.

# Application Ontology

## Influenza Ontology

### Reuse of existing ontologies & metadata standards

200 controlled vocabulary terms covering several fields



OBI – Ontology of Biomedical Investigations

EnvO – Environmental Ontology (habitat of pathogen)

GAZ – Gazetteer (geographic locations)

FMA – Foundational Model of Anatomy

DC – Dublin Core (publication metadata)

PATO – Phenotype

SO – Sequence Ontology (sequence features)

Cell – Cell Ontology (types of cells)

DO – Disease Ontology

IDO – Infectious Disease Ontology

# Metadata (simplified)

## Biochemical Reaction

```
<reaction
    id="pyruvate_dehydrogenase_rxn">
    <listOfReactants>
        <speciesRef species="NADP+"/>
        <speciesRef species="CoA"/>
        <speciesRef species="pyruvate"/>
    </listOfReactants>
    <listOfProducts>
        <speciesRef species="NADPH"/>
        <speciesRef species="acetyl-CoA"/>
        <speciesRef species="CO2"/>
    </listOfProducts>
    <listOfModifiers>
        <modifierSpeciesRef
            species="pyruvate_dehydrogenase_E1"/>
    </listOfModifiers>
</reaction>
```

## Synonyms

```
<species id="pyruvate" metaid="pyruvate">
    <annotation xmlns:bp="http://biopax.org/releasedataformat">
        <bp:smallMolecule rdf:ID="#pyruvate" >
            <bp:SYNONYMS>pyroracemic acid</bp:SYNONYMS>
            <bp:SYNONYMS>2-oxo-propionic acid</bp:SYNONYMS>
            <bp:SYNONYMS>alpha-ketopropionic acid</bp:SYNONYMS>
            <bp:SYNONYMS>2-oxopropanoate</bp:SYNONYMS>
            <bp:SYNONYMS>2-oxopropanoic acid</bp:SYNONYMS>
            <bp:SYNONYMS>BTS</bp:SYNONYMS>
            <bp:SYNONYMS>pyruvic acid</bp:SYNONYMS>
        </bp:smallMolecule>
    </annotation>
</species>
```

# Metadata (Webified)

## Instead of textual labels

```
<bp:smallMolecule rdf:ID="#pyruvate">
  <bp:Xref>
    <bp:unificationXref rdf:ID="#unificationXref119">
      <bp:DB>LIGAND</bp:DB>
      <bp:ID>c00022</bp:ID>
    </bp:unificationXref>
  </bp:Xref>
</bp:smallMolecule>
```

## Use actual URLs

gene	pathway
<a href="http://lsrn.org/KEGG:hsa:7498">http://lsrn.org/KEGG:hsa:7498</a>	<a href="http://lsrn.org/KEGG_PATHWAY:hsa00983">http://lsrn.org/KEGG_PATHWAY:hsa00983</a>
<a href="http://lsrn.org/KEGG:hsa:7498">http://lsrn.org/KEGG:hsa:7498</a>	<a href="http://lsrn.org/KEGG_PATHWAY:hsa00230">http://lsrn.org/KEGG_PATHWAY:hsa00230</a>
<a href="http://lsrn.org/KEGG:hsa:7498">http://lsrn.org/KEGG:hsa:7498</a>	<a href="http://lsrn.org/KEGG_PATHWAY:hsa04146">http://lsrn.org/KEGG_PATHWAY:hsa04146</a>
<a href="http://lsrn.org/KEGG:hsa:7498">http://lsrn.org/KEGG:hsa:7498</a>	<a href="http://lsrn.org/KEGG_PATHWAY:hsa01100">http://lsrn.org/KEGG_PATHWAY:hsa01100</a>
<a href="http://lsrn.org/KEGG:hsa:7498">http://lsrn.org/KEGG:hsa:7498</a>	<a href="http://lsrn.org/KEGG_PATHWAY:hsa00232">http://lsrn.org/KEGG_PATHWAY:hsa00232</a>
<a href="http://lsrn.org/GenelD:7498">http://lsrn.org/GenelD:7498</a>	<a href="http://lsrn.org/GO:0006144">http://lsrn.org/GO:0006144</a>
<a href="http://lsrn.org/GenelD:7498">http://lsrn.org/GenelD:7498</a>	<a href="http://lsrn.org/GO:0009115">http://lsrn.org/GO:0009115</a>
<a href="http://lsrn.org/GenelD:7498">http://lsrn.org/GenelD:7498</a>	<a href="http://lsrn.org/GO:0055086">http://lsrn.org/GO:0055086</a>
<a href="http://lsrn.org/GenelD:7498">http://lsrn.org/GenelD:7498</a>	<a href="http://lsrn.org/GO:0006195">http://lsrn.org/GO:0006195</a>

# Metadata (Webified)

**Query results  
return  
links to the original  
data!**

http://lsrn.org/Kt:GG:hsa:7498 http://lsrn.org/Kt:GG:PATHWAY:hsa00U232

http://lsrn.org/GenelD:7498 http://lsrn.org/GO:0006144

http://lsrn.org/GenelD:7498 http://lsrn.org/GO:0009115

http://lsrn.org/GenelD:7498 http://lsrn.org/GO:0055086

http://lsrn.org/GenelD:7498 http://lsrn.org/GO:0006195

**Kegg** PATHWAY: hsa00983

<b>Entry</b>	hsa00983	Pathway
<b>Name</b>	Drug metabolism - other enzymes - Homo sapiens (human)	
<b>Class</b>	Metabolism; Xenobiotics Biodegradation and Metabolism	<b>BRITE hierarchy</b>
<b>Pathway map</b>	hsa00983 Drug metabolism - other enzymes	
	<a href="#">All organisms</a>	<a href="#">Ortholog table</a>
<b>Disease</b>	H00193 Dihydropyrimidine dehydrogenase deficiency H00199 Dihydropyrimidinase deficiency	

**the Gene Ontology** AmiGO

xanthine catabolic process

Term Information

Accession	GO:0009115
Ontology	Biological Process
Synonyms	exact: xanthine breakdown exact: xanthine catabolism exact: xanthine degradation
Definition	The chemical reactions and pathways resulting in the breakdown of xanthine, 2,6-dihydroxypurine, a purine formed in the metabolic breakdown of guanine but not present in nucleic acids.
Comment	None
Subset	Prokaryotic GO subset

Adapted from Mark Wilkinson webscience20-120829124752-phpapp01

# Research to Practice Timeline

(earlier work: 10 years in Software Research & Development and Product Development)

World Congress on  
Neural Networks,  
July 11-15, 1993,  
Portland, Oregon SIG  
Mental Function and  
Dysfunction  
Sam Levin

Thesis Proposal  
Approved

1995

PhD

US Patents  
No. 6,063,028  
Awarded

1997

BioPAX

EMPWR

2001 2006

Patents Offered at  
Ocean Tomo  
Auction Chicago, IL

Patents Sold  
to Advanced  
Biological  
Laboratories  
Belgium

U Pitt  
Greg Siegle  
Collaboration

Yuezhang  
Xiao  
Master's  
Thesis  
(RPI)

**Center for  
Proactive  
Depression  
Treatment**

Jackie Samson,  
Mc Lean Hospital  
Depression  
Research

Workshop Neural Modeling of  
Cognitive and Brain Disorders

Poster Presented  
ISMB 1997  
PSB 1998

US Patent No.  
6,317,73  
Awarded

Linked Data  
W3C HCLS  
BioDASH  
EPOS

Rensselaer  
(RPI)

Brendan Ashby  
Master's Thesis (RPI)  
Actively  
SEEKING FUNDING  
Nightingale

Actively  
SEEKING  
FUNDING  
Nightingale

2008

2009

2010

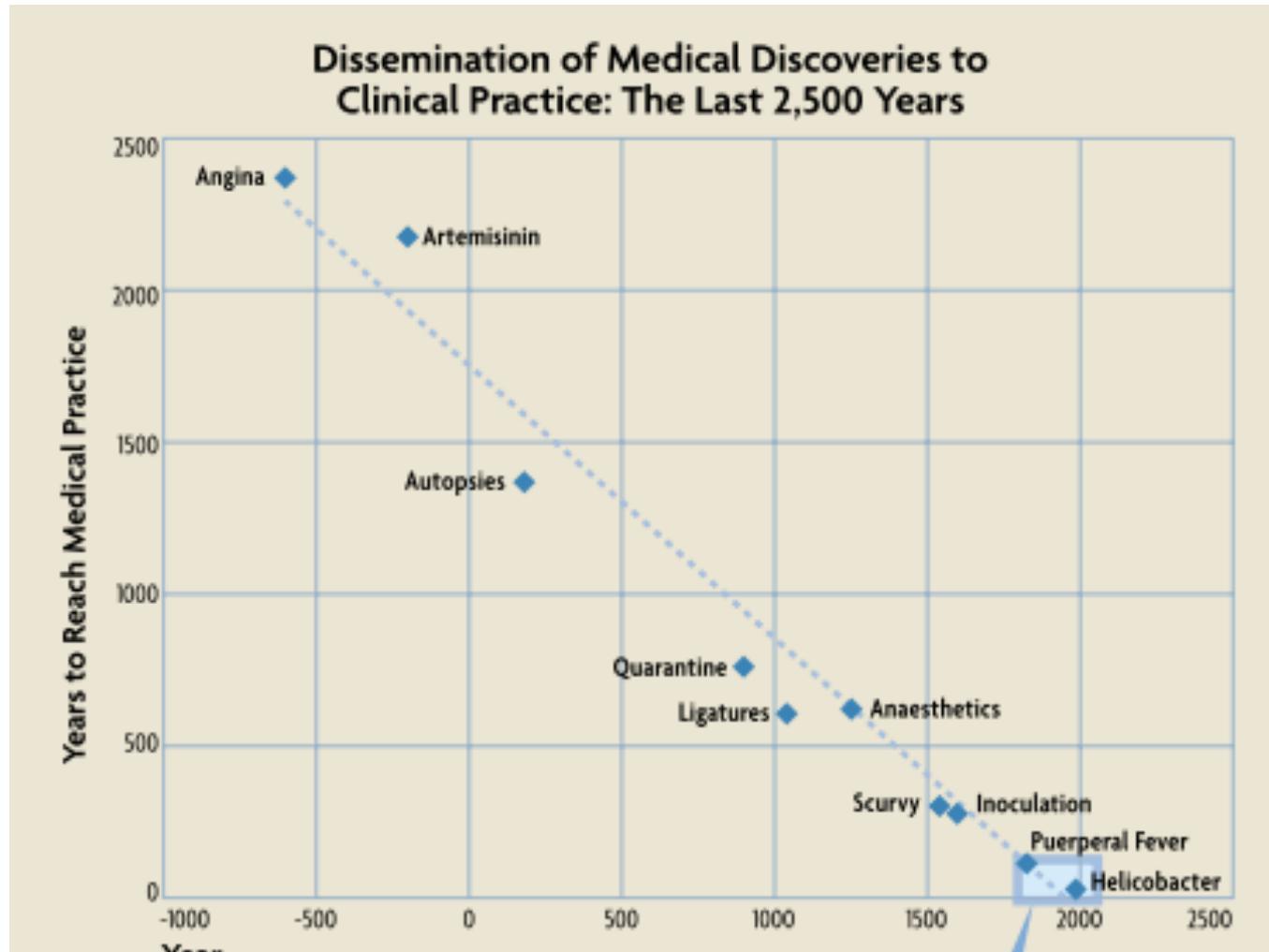
2011

2012

2013

?

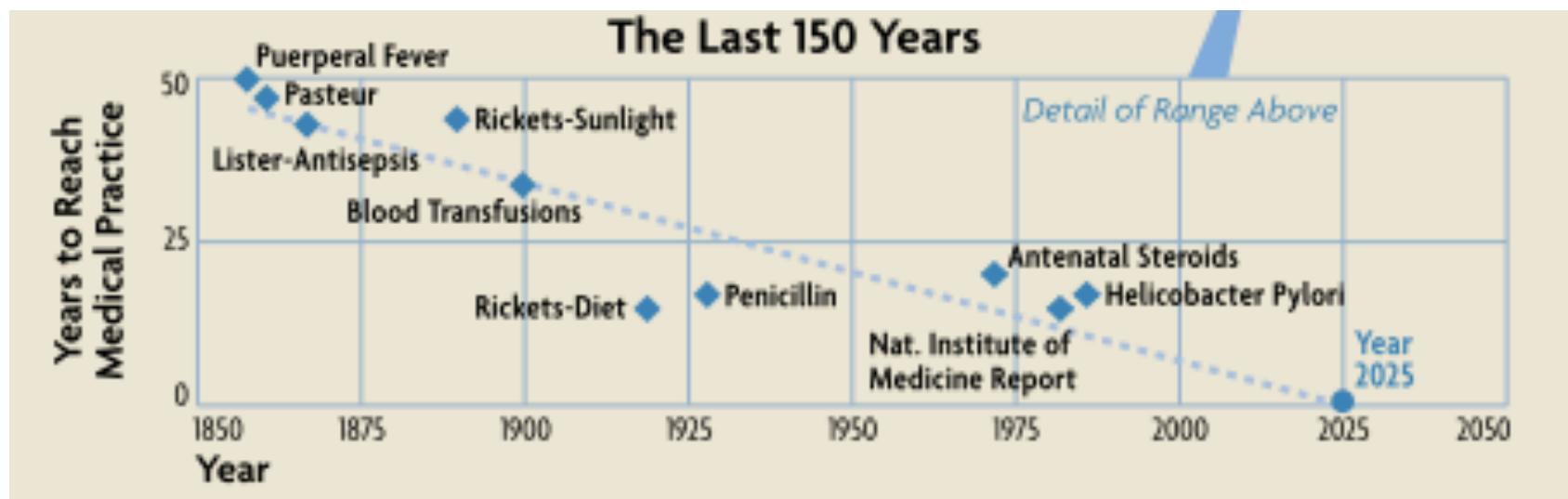
# Healthcare Singularity and the age of Semantic Medicine



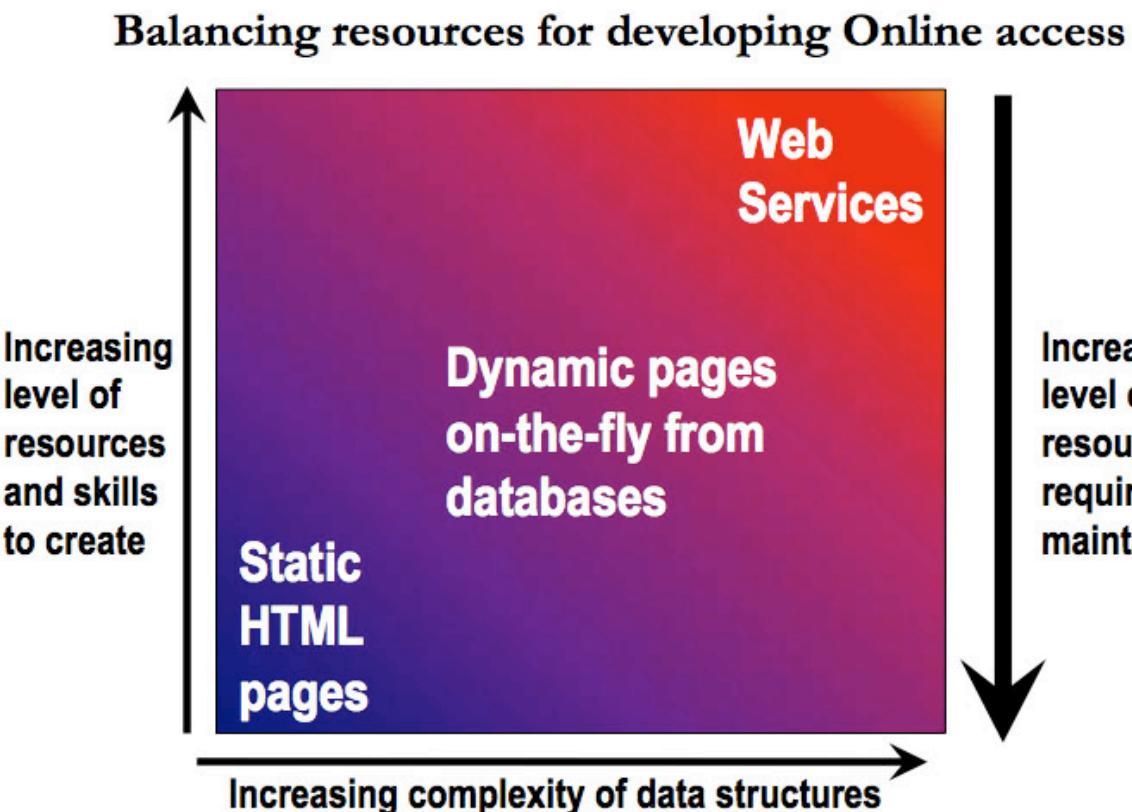
2,300 years after the first report of angina for the condition to be commonly taught in medical curricula, modern discoveries are being disseminated at an increasingly rapid pace.

# Healthcare Singularity and the age of Semantic Medicine

Focusing on the last 150 years, the trend still appears to be linear, approaching the axis around **2025**.



# Shifts in Data Access



The burden of making data accessible is shifting from the user of the data to the provider of the data

Other people help too!

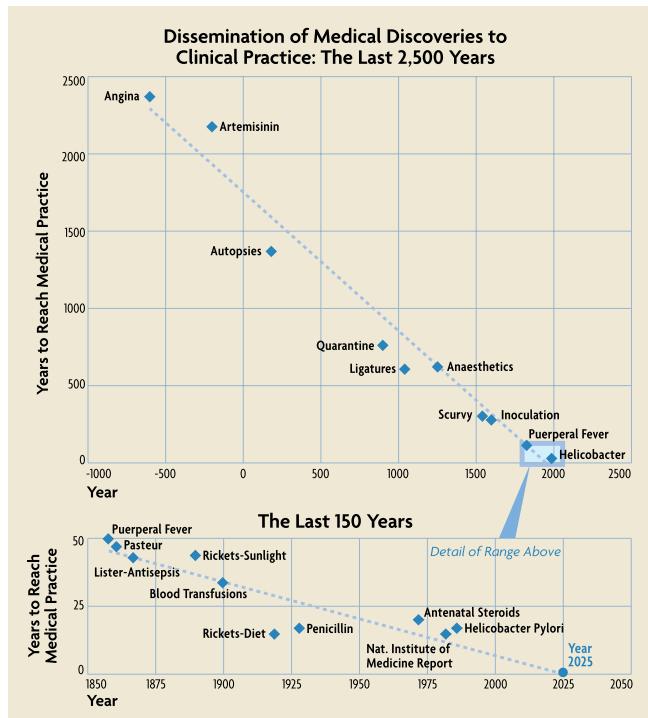
CSV2RDF4LOD

## “Web Driven Medicine”

“While it took 2,300 years after the first report of angina for the condition to be commonly taught in medical curricula, modern discoveries are being disseminated at an increasingly rapid pace. Focusing on the last 150 years, the trend still appears to be linear, approaching the axis around 2025.”

The Healthcare Singularity and the Age of Semantic Medicine,  
Michael Gillam, et al, *The Fourth Paradigm: Data-Intensive  
Scientific Discovery* [Tony Hey \(Editor\), 2009](#)

Slide adapted with permission from Joanne Luciano, Presentation  
at Health Web Science Workshop 2012, Evanston IL, USA  
June 22, 2012.



# Computing in WWW

Conducting  
*in silico*  
research  
*in*  
the Web



SADI  
Find. Integrate.  
Analyze.

# DEEPER DIVE

Web Science 2.0

Conducting *in silico* research *in* the Web  
from hypothesis to publication

*Mark Wilkinson*

 Isaac Peral Senior Researcher in Biological Informatics  
Centro de Biotecnología y Genómica de Plantas, UPM, Madrid, Spain

 Adjunct Professor of Medical Genetics, University of British Columbia  
Vancouver, BC, Canada.

<http://www.slideshare.net/markmoby/web-science-sadi-and-the-singularity>

# Overview

## Introduction (10 minutes)

1. Background
  1. BioMed Domain – Health care and Life Science
  2. Reference and Application
  3. Ontology Granularity and Layout
2. Examples: (35 minutes)
  1. Reference Ontology Examples
    1. BioPAX – Mid level – biological pathways (10)
    2. Gene Ontology (“GO”) – Gene annotation (5)
  2. Application Ontology Examples
    1. Influenza Ontology (5)
    2. Best Practices (10)
3. Conclusion (5 minutes)
  1. Process: Start with Use Case, develop prototype, Evaluation
  2. Standards: BioMedical Ontology Best practices (BioPortal, BFO, SIO)
  3. Conferences

## Examples

### 2 Reference Ontology Examples

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

### 2 Application Ontology Example

- Influenza Ontology
- Translational Medicine Ontology

# Application vs. Reference Ontology

## Reference Ontology

- Intended as an authoritative source
- True to the limits of what is known (which does change!)
- Used by others
- Application Ontology
  - Built to support a particular application (use case)
  - Reused rather than define terms
  - Skeleton structure to support application
  - Terms defined refine or create new concepts directly or through new classes based on inference

# Translational Medicine Ontology

The Translational Medicine Ontology and Knowledge Base:  
driving personalized medicine by bridging the gap between bench  
and bedside

Luciano et al. Journal of Biomedical Semantics 2011, 2(Suppl  
2):S1 <http://www.jbiomedsem.com/content/2/S2/S1>

# Individuals, Not Populations



## A 2D barcode that helps predict a patient's personal response to medical therapy

A **Medicine Safety Code** captures data about a patient's 400 most important pharmacogenomic markers and allergies as a 2D barcode. It can help to predict how medications are metabolized and tolerated by the patient. Medical doctors can use this information to make the delivery of medications safer and more effective.



<http://safety-code.org/>

Photo: <http://www.flickr.com/photos/sepblog/4014143391/>



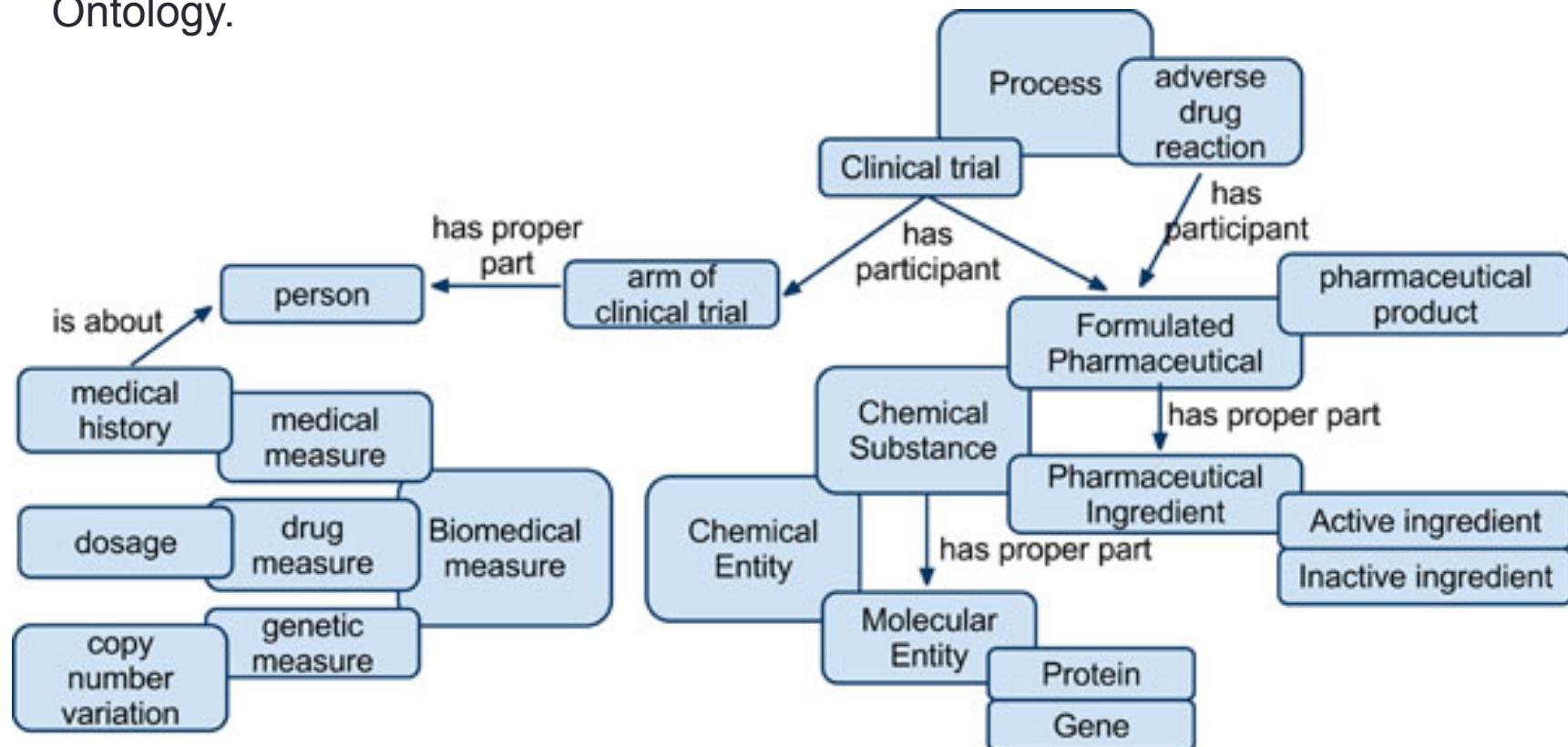
Distinguished paperMedInfo 2013

Quickly retrieve pharmacogenomic markers of patients when needed

No central storage of data is necessary, giving patients full control over their personal health information.

# Translational Medicine Ontology

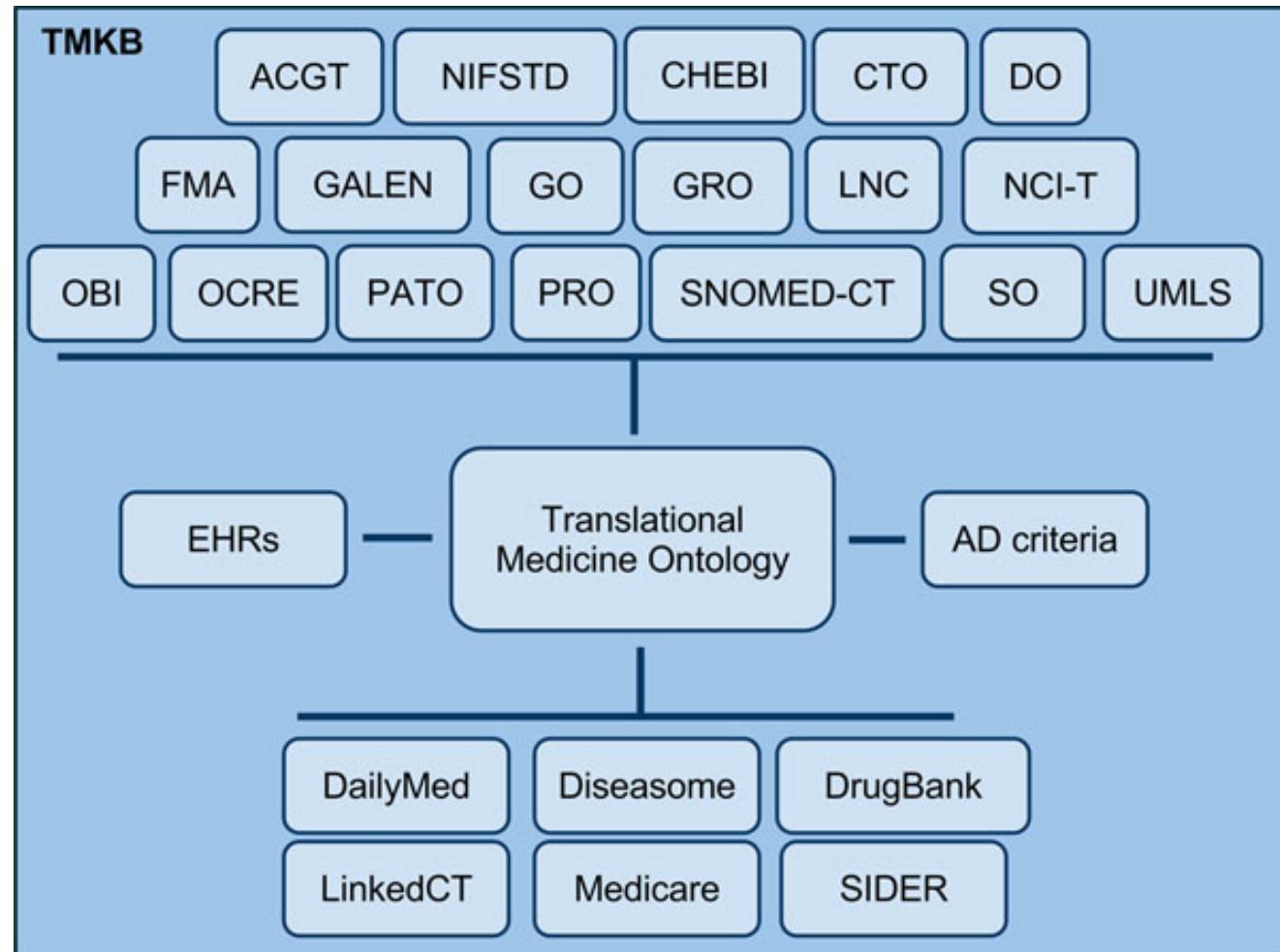
Overview of selected types, subtypes (overlap) and existential restrictions (arrows) in the Translational Medicine Ontology.



# Translational Medicine Knowledge Base

Translational  
Medicine Ontology  
with mappings to  
ontologies and  
terminologies listed  
in the NCBO  
BioPortal.

The TMO provides a  
global schema for  
Indivo-based  
electronic health  
records (EHRs) and  
can be used with  
formalized criteria for  
Alzheimer's Disease.  
The TMO maps  
types from Linking  
Open Data sources.



# Overview

## Introduction (10 minutes)

### 1. Background

1. BioMed Domain – Health care and Life Science
2. Reference and Application
3. Ontology Granularity and Layout

### 2. Examples: (40 minutes)

#### 1. Reference Ontology Examples

1. UMLS – High level across biomedicine (5)
2. BioPAX – Mid level – biological pathways (10)
3. Gene Ontology (“GO”) – Gene annotation (5)

#### 2. Application Ontology Examples

1. Influenza Ontology (5)
2. Best Practices (10)

### 3. Conclusion (5 minutes)

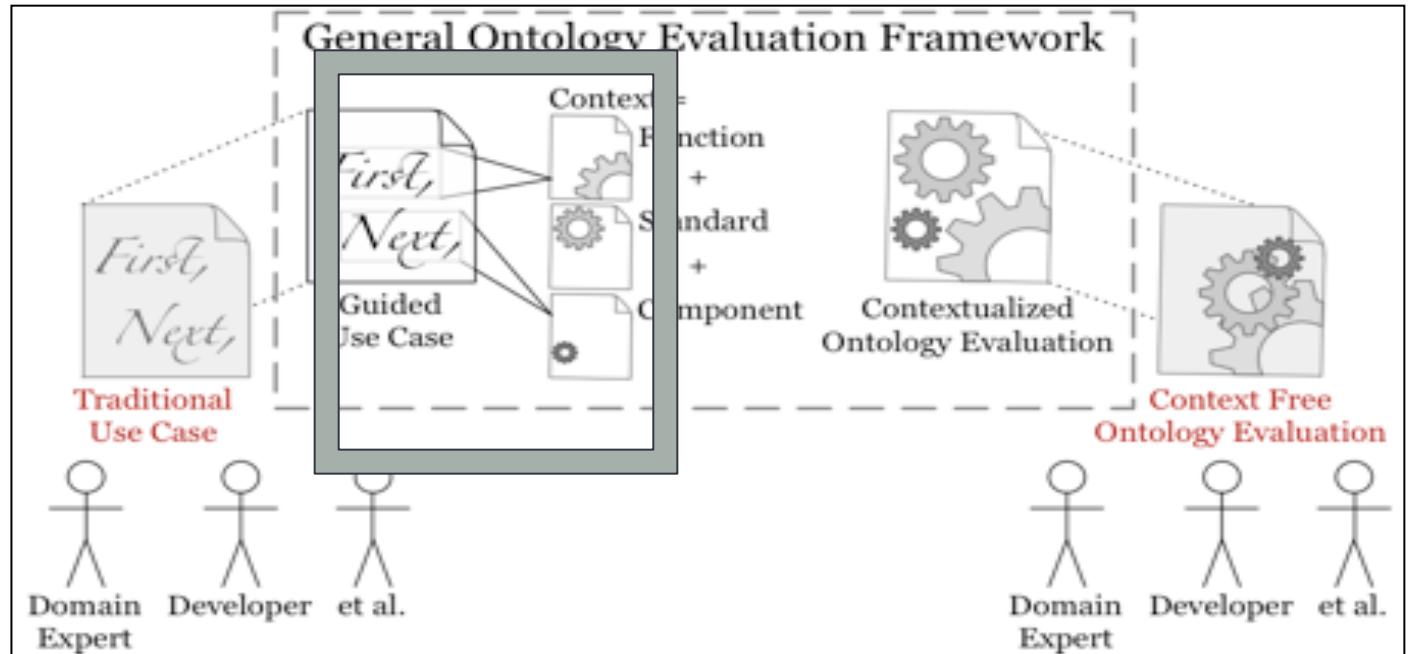
1. Process: Start with Use Case, develop prototype, Evaluation
2. Standards: BioMedical Ontology Best practices (BioPortal, BFO, SIO)
3. Conferences

# Best Practices

## Semantic Web Methodology & Technology Development Process



# Generalized Ontology Evaluation Framework (GOEF)



Two stages:

1. Recast use case into its components:  
Three Levels of Evaluation
2. Evaluate components using objective metrics

# BioPortal

<http://bioportal.bioontology.org/>

Provides access to commonly used biomedical ontologies and to tools for working with them. BioPortal allows you to

- **Browse**
  - the library of ontologies
  - mappings between terms in different ontologies
  - a selection of projects that use BioPortal resources
- **Search**
  - biomedical resources for a term
  - for a term across multiple ontologies
- **Receive recommendations**
  - on which ontologies are most relevant for a corpus
- **Annotate text**
  - with terms from ontologies

All information available through the BioPortal Web site is also available through the NCBO Web service REST API. Please see REST API documentation for more information.

[http://www.bioontology.org/wiki/index.php/NCBO\\_REST\\_services](http://www.bioontology.org/wiki/index.php/NCBO_REST_services)

# Backup Slides

# HL-7 and RIM

HL-7 and RIM: <http://www.w3.org/2013/HCLS-tutorials/RIM/#%286%29>

- **RDF RIM Tutorial** [Eric Prud'hommeaux, <eric@w3.org>](mailto:eric@w3.org)
- Basic understanding of the structure of how data written in HL7's RIM can be expressed in RDF.
- It is not a substitute for HL7's documentation, but instead the author's notion of a quick way to familiarize oneself with the concepts and terms used in the RIM and how the graph structure of RDF is a natural way to represent this data.

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[Usage policies apply.](#)

# Scope

## Ontology Uses

- Knowledge Management
  - Annotate data (such as genomes)
  - Access information (search, find, and access)
  - Map across ontologies relate
- Data integration and exchange
  - Model dynamic cellular processes
  - Identify Drug Interactions
- Decision support
  - SafetyCodes
  - Diabetic Care
  - Lab Alerts

(Bodenreider YBMI 2008)

<http://themindwobbles.wordpress.com/2009/05/04/olivier-bodenreider-nlm-best-71-practices-pitfalls-and-positives-cbo-2009/>