

# W3C Semantic Web for Healthcare and Life Sciences

PRISM

Lambertville, NJ



Eric Neumann  
October 12, 2005

# Semantic Web

“--The Semantic Web is an extension of the current web in which information is given well-defined meaning, better enabling computers and people to work in cooperation.” - *Tim Berners-Lee*

# What is the Semantic Web?

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- **Focuses on Data Semantics rather than Syntax (Semantic Interoperability)**
- **Open-World Graph model of all information on the Web (or in your intranet)**
- **RDF - Web-based descriptive model of all information**
- **OWL - Web Ontology Language; 3 levels of expressivity**
- **New Semantic Browsers with logic-driven style-sheets**
- **Rules and Inference engines work great with OWL and RDF**

# Semantic Web Vision

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- Early goals
  - Using RDF-OWL technologies
  - Bottom-Up development
  - Interlinking of current ontologies
- Long-term goals
  - Intelligent connectivity of all of the Web
  - New level of services and transactions
  - Knowledge and Trust Networks

# What can the Semantic Web do NOW?

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- Data Integration via RDF triples and views
- Tagging of mined-Literature
- Data Federation (SPARQL)
- Knowledge Management of ideas (IP, hypotheses, decisions)
- Web service management (OWL-S)
- Business Workflow and Policy management using rules (SWRL)

# Semantic Web for Life Sciences Participants

MIT, Oct 27, 28 2004

Jackson Laboratories	<b>Berlex Biosciences</b>	<b>Novartis</b>	<b>Sanofi-Aventis</b>	Woods Hole Oceanographic Institute	Fred Hutchinson Cancer Research Center
<b>Infinity Pharmaceuticals</b>	<b>AstraZeneca R&amp;D</b>	Elsevier	<b>Millenium Pharmaceuticals</b>	Nature Publishing Group	Pacific Northwest National Laboratory
Stanford Medical Informatics	Harvard Partners	Affymetrix	Mayo Clinic	American Chemical Society	European Bioinformatics Institute
National Science Foundation	Hewlett-Packard	<b>Pfizer</b>	<b>Genentech</b>	MacArthur Foundation	National Center for Genome Resources
Oracle	BioGrid	SemantxLS	PRISM Forum	Swiss Institute of Bioinformatics	National Cancer Institute (Center for Bioinformatics)
Children's Hospital	IBM	INRIA	University of Michigan	University of Massachusetts Boston	Harvard Medical School
AGFA Healthcare	MIT / CSBi	KEVRIC	Chevron Texaco	University of Cambridge (UK)	Fujitsu Laboratories of America
Broad Institute / MIT	MITRE	Genstruct	Network Inference	Alzheimer's Research Forum	German Cancer Research Center
Stanford Medical Informatics	Annotea	BioPAX	HydroJoule	University of Manchester	VTT Finland
Matsushita / W3C	SkyPrise	Djinnisys	Siderean	Yale Center for Medical Informatics	MIND (University of Maryland)
DSTC Pty Ltd	Technion – Israel Institute of Technology	Columbia University	Intelligent Solutions	Panther Informatics	Image Bioinformatics Lab, University of Oxford
University of Colorado	Northeastern University	Tucana Technologies		University of Georgia	Japan Biological Information Consortium
University of Zurich	University of Michigan	Life Sciences Insights	Object Management Group	<b>De Novo Pharmaceuticals</b>	European Network of Excellence REWERSE

# W3C HCLSIG -

## Semantic Web for HealthCare and Life Sciences Interest Group

- An Open Scientific Forum for Discussing, Capturing, and Showcasing Best Practices
- Draft Charter open for comment:  
<http://www.w3.org/2005/05/swlsig-charter>
- To be formalized in the next few weeks
- First formal meeting planned for Dec 13-14
- SW Supporting Vendors: Oracle, IBM, HP
- Recent life science members: Pfizer, Merck, caBIG/NCI, TeraNode, Partners HealthCare
- Please join us!  
<http://www.w3.org/2005/04/swls/>

# HCLSIG First Set of Activities

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- **Core and Bridge Ontology work**
- **LSID refinement for SW**
- **Collect and Showcase Best Practices**
- **Construct powerful demonstrations in key areas**
- **Help create Work Groups in identified areas**

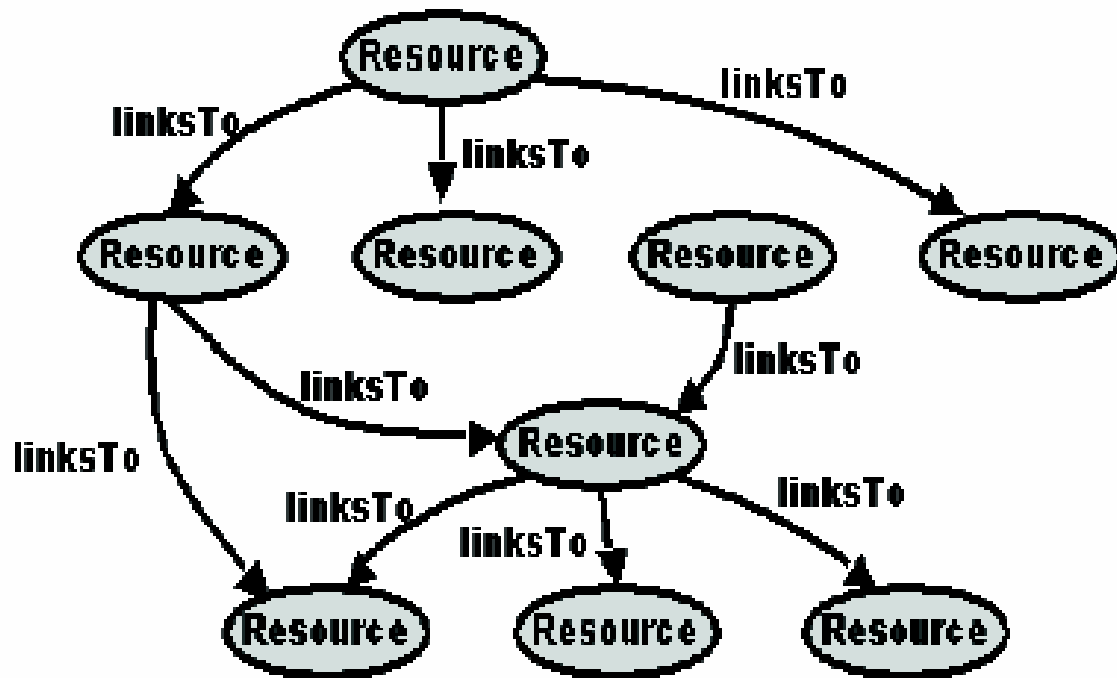




# Semantic Web Model

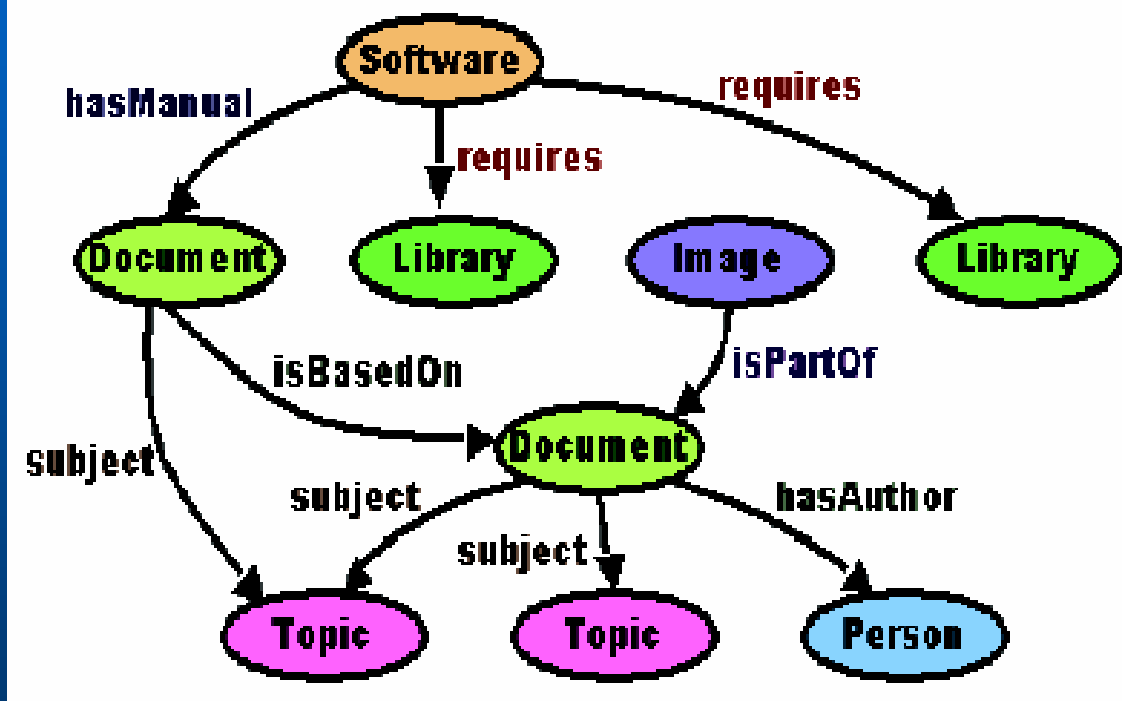


# The Current Web



- What the computer sees: “Dumb” links
- No semantics - `<a href>` treated just like `<bold>`
- Minimal machine-processable information

# The Semantic Web



- Machine-processable semantic information
- Semantic context published – making the data more informative to both humans and machines

# The Technologies: RDF

- Think: "Relational Data Format"
- W3C standard for making statements of fact or belief
- Descriptive statements are expressed as triples: (Subject, Verb, Object)
  - We call verb a “predicate” or a “property”



# RDF Example (Gene)

RDF

Subject

N3

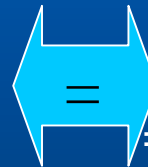
```
<Gene
  rdf:about="http://www.w3.org/2005/04/swls/gsk3b/gsk
  #GSK3b">
    <rdfs:label>Glycogen Synthase Kinase 3
    beta</rdfs:label>
  <translatedAs>
    rdf:resource="http://www.w3.org/2005/04/swls/gsk3b/g
    sk#GSK3betaProt"/>
    <dc:source>http://www.ncbi.nlm.nih.gov/entrez/query.
    fcgi?db=gene&#38;cmd=Retrieve&#38;dopt=Graphics
    &#38;list_uids=2932</dc:source>
  <exonSet rdf:parseType="Resource">
    <rdf:first
      rdf:resource="http://www.w3.org/2005/04/swls/gsk3b/g
      sk#ex1"/>
    </exonSet>
  <genomeLoc>14q3.2</genomeLoc>
  <hasAnnotation>Single locus </hasAnnotation>
  <hasTranscriptVariant
    rdf:resource="http://www.w3.org/2005/04/swls/gsk3b/g
    sk#GSK3betaSV"/>
  <isImplicatedIn
    rdf:resource="http://www.w3.org/2005/04/swls/gsk3b/g
    sk#Alzheimers"/>
  <isImplicatedIn
    rdf:resource="http://www.w3.org/2005/04/swls/gsk3b/g
    sk#DiabetesType2"/>
</Gene>
```

Verb

Object

gsk:GSK3b

```
  rdf:type :Gene ;
  <rdfs:label "Glycogen Synthase Kinase 3 beta" ;
  :translatedAs gsk:GSK3betaProt ,
  <dc:source
    "http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=ge
    ne&#38;cmd=Retrieve&#38;dopt=Graphics&#38;list_ui
    ds=2932" ;
  <exonSet @( gsk:ex1 ) ;
  :genomeLoc "14q3.2" ;
  :hasAnnotation "Single locus"
  :hasTranscriptVariant gsk:GSK3betaSV ;
  :isImplicatedIn gsk:Alzheimers ;
  :isImplicatedIn gsk:DiabetesType2 .
```



N3 form is isomorphic  
with RDF, but more  
readable



# Statements Structure

**ApoA1** ...

- ... is produced by **the Liver**
- ... is expressed less in **Atherosclerotic Liver**
- ... is correlated with **DKK1**
- ... is cited regarding **Tangier's disease**
- ... has Tx Reg elements like **HNFR1**

Subject ↗ Verb ↗ Object

# RDF-XML





# RDF vs. XML example

Wang et al., Nature Biotechnology, Sept 2005

AGML

QuickTime™ and a  
TIFF (LZW) decompressor  
are needed to see this picture.

HUPML

## RDF Stripe Mode

Document 1:

```
<rdf:RDF
  xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
  xmlns:cce="http://www.charlestoncore.org/ontology/example#">
```

```
<cce:shape>
```

```
<cce:x-radius>1.1067</cce:x-radius>
```

```
<cce:y-radius>0.6465</cce:y-radius>
```

```
<cce:center>
```

```
<cce:x-position>5.2820</cce:x-position>
```

```
<cce:y-position>9.5478</cce:y-position>
```

```
</cce:Point>
```

```
</cce:center>
```

```
</cce:Ellipse>
```

```
</cce:shape>
```

```
</cce:Spot>
```

```
</rdf:RDF>
```

Document 2:

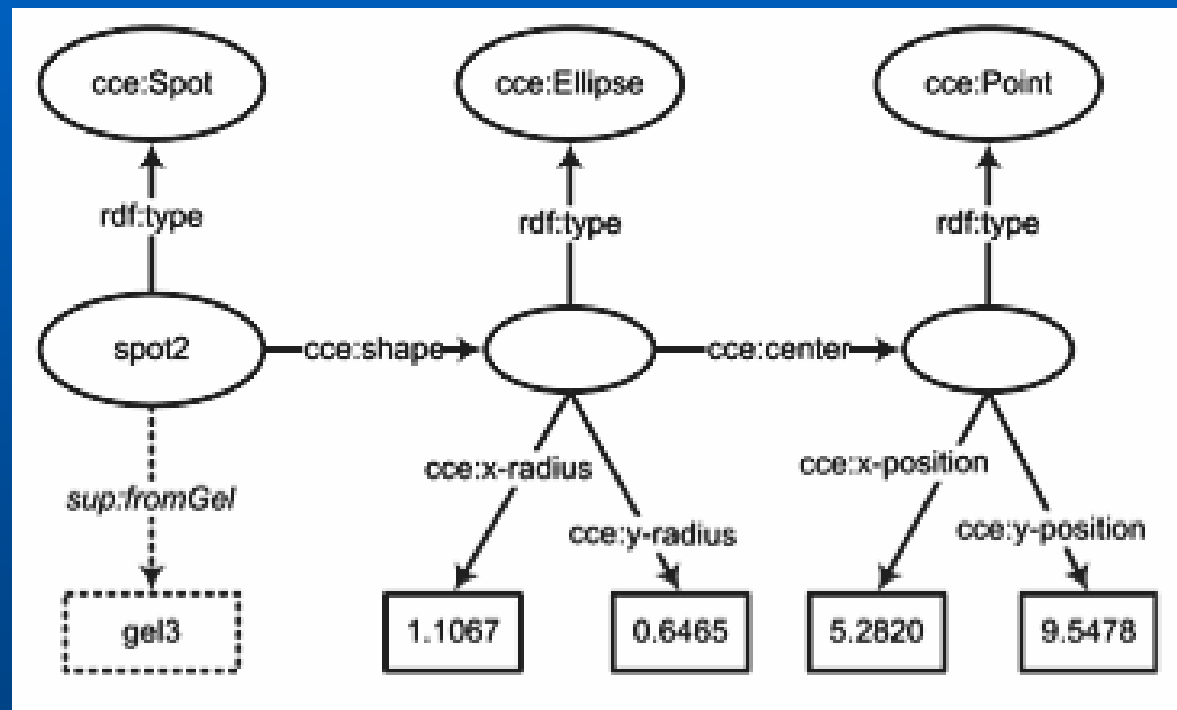
```
<rdf:RDF
  xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
  xmlns:cce="http://www.charlestoncore.org/ontology/example#"
  xmlns:sup="http://www.charlestoncore.org/ontology/supplement#">
```

```
<sup:virtualGel
```

```
</cce:Spot>
```

```
</rdf:RDF>
```

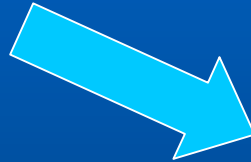
# RDF Graph



# Mapping from Current Formats



Table Conversion



**XML**

XSLT



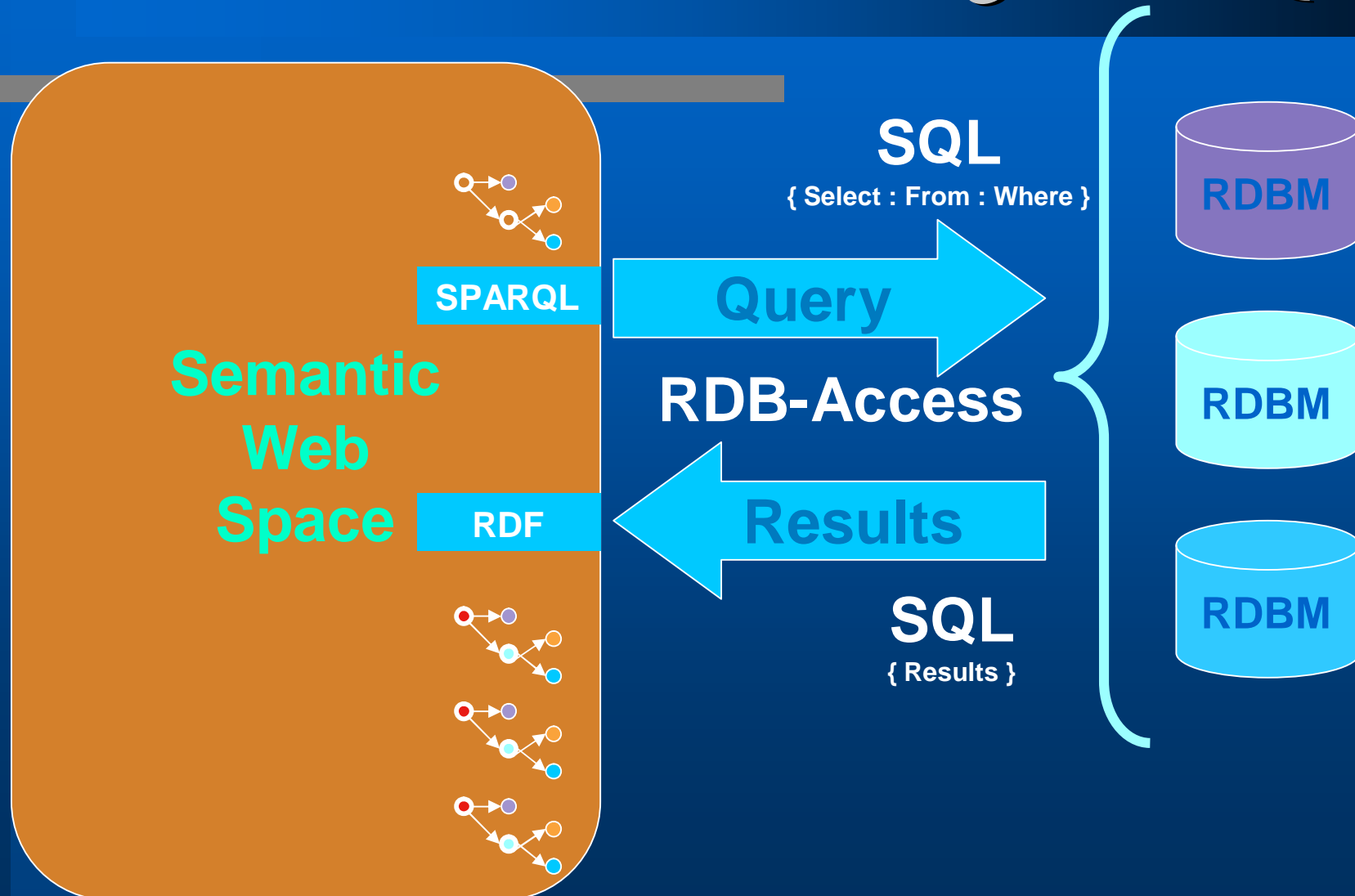
**RDF-OWL**



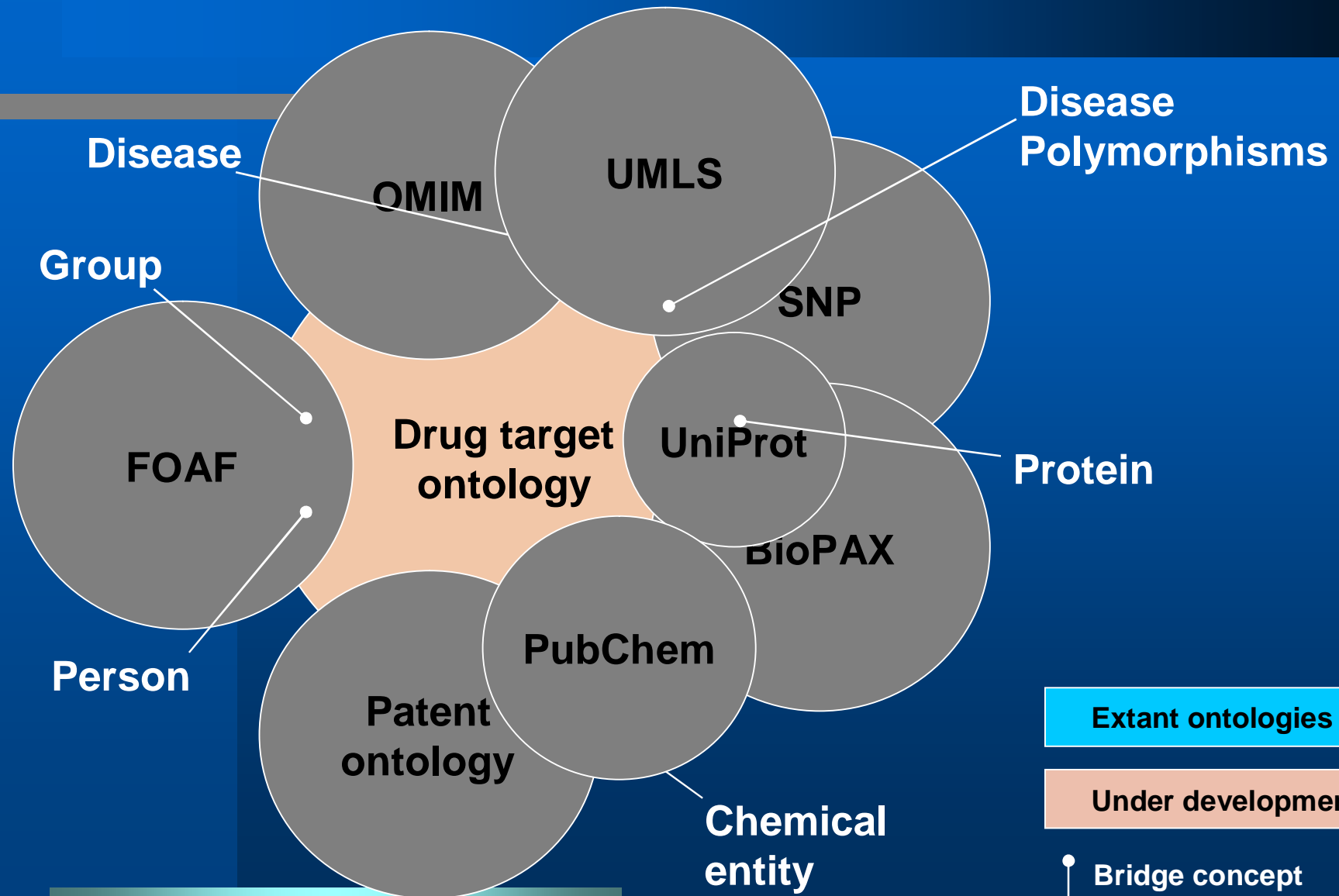
RDB-Access



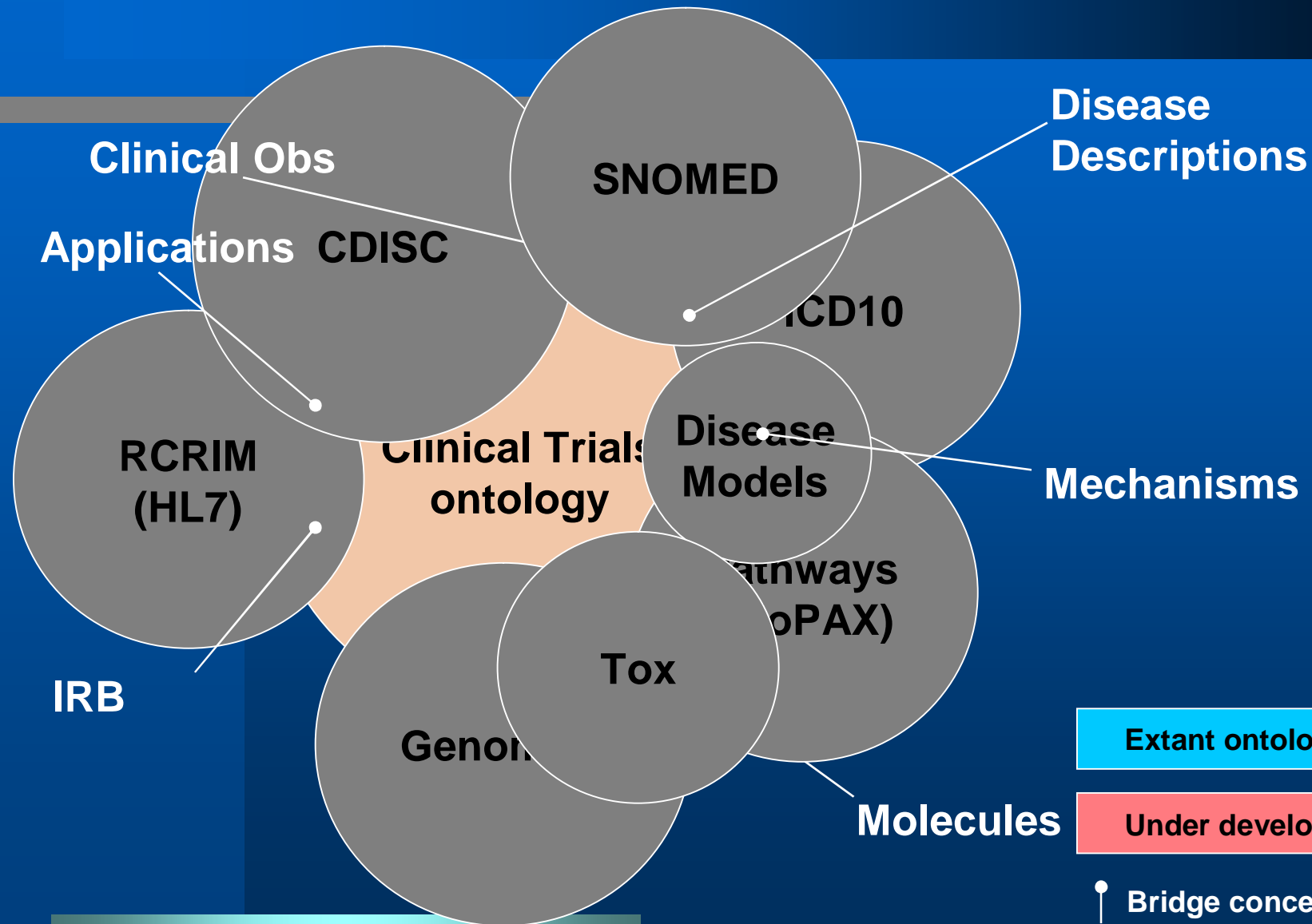
# Semantic Federation using SPARQL



# Multiple Ontologies Used Together



# Potential Linked Clinical Ontologies



# Applications of Ontologies

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- Controlling vocabulary (ala GO)
- Controlling data types (concepts)
- Integrating data (instance serialization)
- Tagging of text to associate meta-data (publishing and search)
- Reasoning over aggregated information
- Web-service categorization



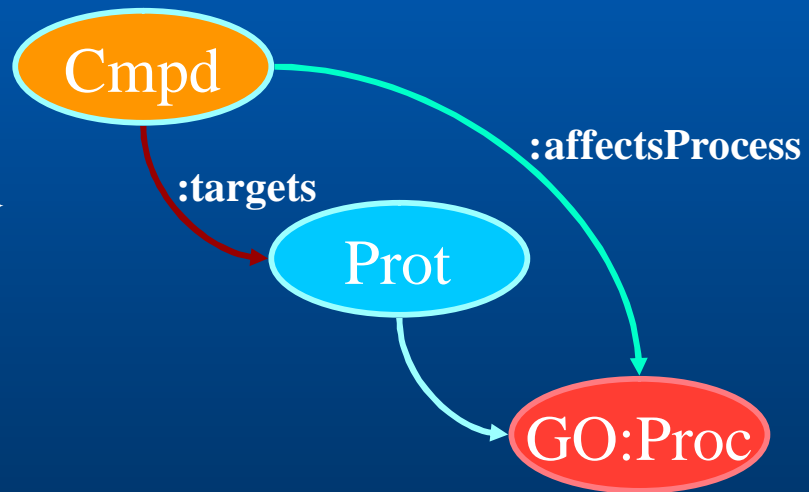
# Bridging Domains via Rules

*Projecting protein properties onto compounds*

```
{:cmpd :targets ?prot .  
  ?prot :bio-process ?proc}
```



```
{:cmpd :affectsProcess  
  ?proc}.
```



# Semantic Browsers

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- Next generation browsers extend viewing functionality to semantic information via “semantic lenses”
- Renders OWL-RDF, XML, and HTML documents
- Lenses act as info aggregators and style-sheets
- Most lenses require no Java, C, or perl programming; similar to how HTML can be rendered by any browser today
- New lenses can easily be created and added
- BioDash uses the Haystack browser from MIT

# BioDASH Semantic Browser

<http://www.w3.org/2005/04/swls/BioDash>

The screenshot displays the BioDASH Semantic Browser interface for the 'GSK3beta Topic'. The interface includes a sidebar with commands and available views, a main content area with a target overview diagram, a group members table, and a primary disease section.

**Compound:** A chemical structure is highlighted in the target overview diagram.

**Target:** The 'GSK-3beta' node is highlighted in the target overview diagram.

**Team Member:** The table below lists team members:

Title	role	Department	E-mail
John Tegler	Medicinal Chemist	Chemistry	john.tegle
Steve Smith	Synthetic Chemist	Chemistry	steve.smit
Tim Gross	Molecular Modeler	Cheminformatics	tim.gross

**Primary Disease:** The 'Type 2 Diabetes' section is highlighted, showing details for **#125853** **DIABETES MELLITUS, NONINSULIN-DEPENDENT; NIDDM**. Alternative titles include: DIABETES MELLITUS, TYPE II; NONINSULIN-DEPENDENT DIABETES MELLITUS; MATURITY-ONSET DIABETES; INSULIN RESISTANCE, SUSCEPTIBILITY TO, INCLUDED. The gene map locus is [20q12-q13.1, 20q12-q13.1](#).

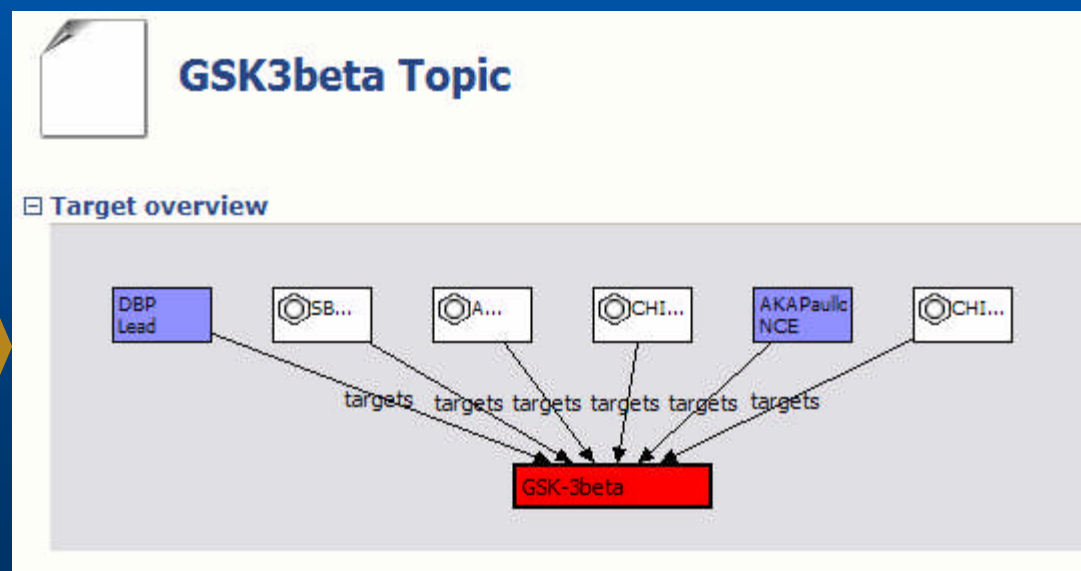
# BioDASH Semantic Browser

All viewed information is in RDF, which is then rendered according to “semantic lenses” to GUI components.

```
:Target gsk:GSK3beta  
  :rdfs:label "GSK-3beta" ;  
  :contextDisease gsk:DiabetesType2 ;  
  :targetFor gsk:AKAP ;  
  :targetFor gsk:ARA014418 ;  
  :targetFor gsk:CHIR98014 ;  
  :targetFor gsk:CHIR99021 ;  
  :targetFor gsk:DBP ;  
  :targetFor gsk:SB216763 ;  
  :inPathway gsk:Wnt ;  
  :references gsk:GSK3b ;  
  :xref
```

LENS

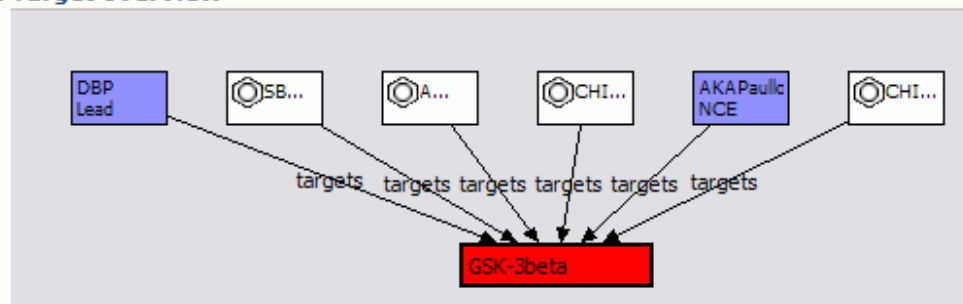
```
<urn:lsid:uniprot.org:lsid.biopathways.org:uni  
prot:P49841>
```



# Bridging Chemistry and Molecular Biology

- Different Views have different semantics: Semantic Lenses
- When a correspondence between objects is determined, a semantic binding is made

## Target overview

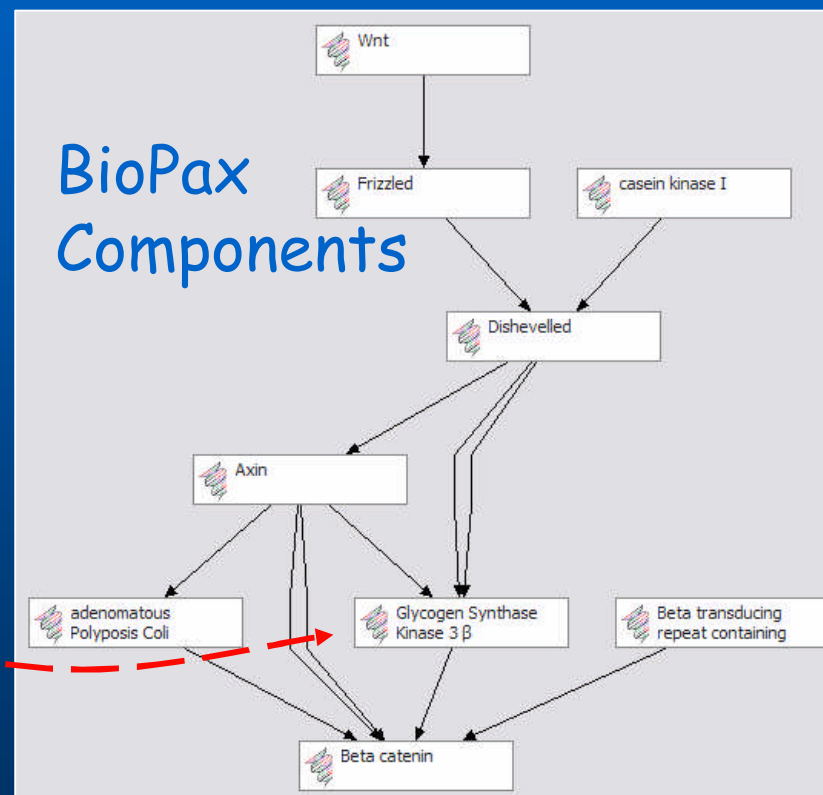


[urn:lsid:uniprot.org/uniprot:P49841](http://urn:lsid:uniprot.org/uniprot:P49841)

## Apply Correspondence Rule:

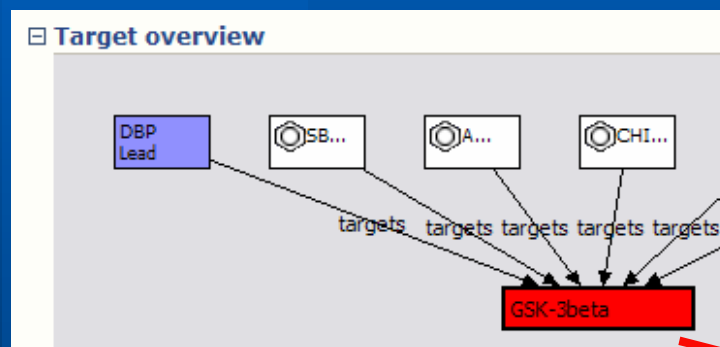
if ?target.xref.lsid == ?bpx:prot.xref.lsid  
then ?target.correspondsTo.?bpx:prot

## BioPax Components

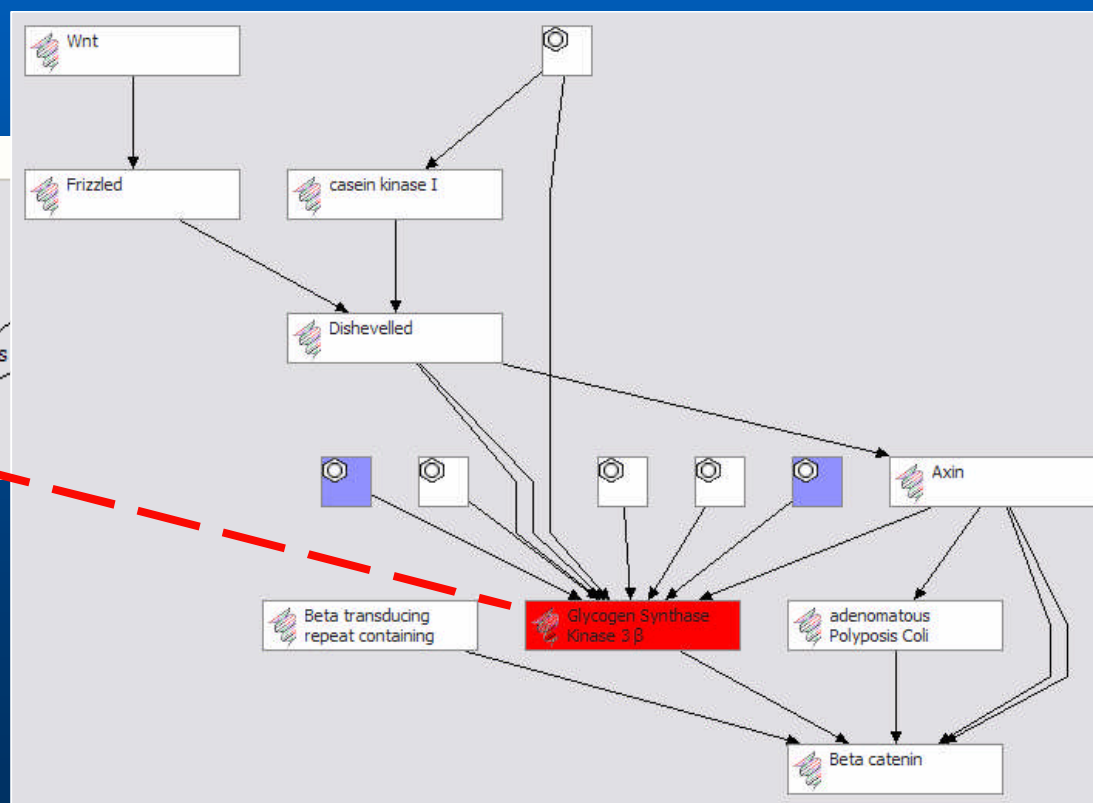


# Bridging Chemistry and Molecular Biology

- Lenses can aggregate, accentuate, or even analyze new result sets
- Behind the lens, the data can be persistently stored as RDF-OWL

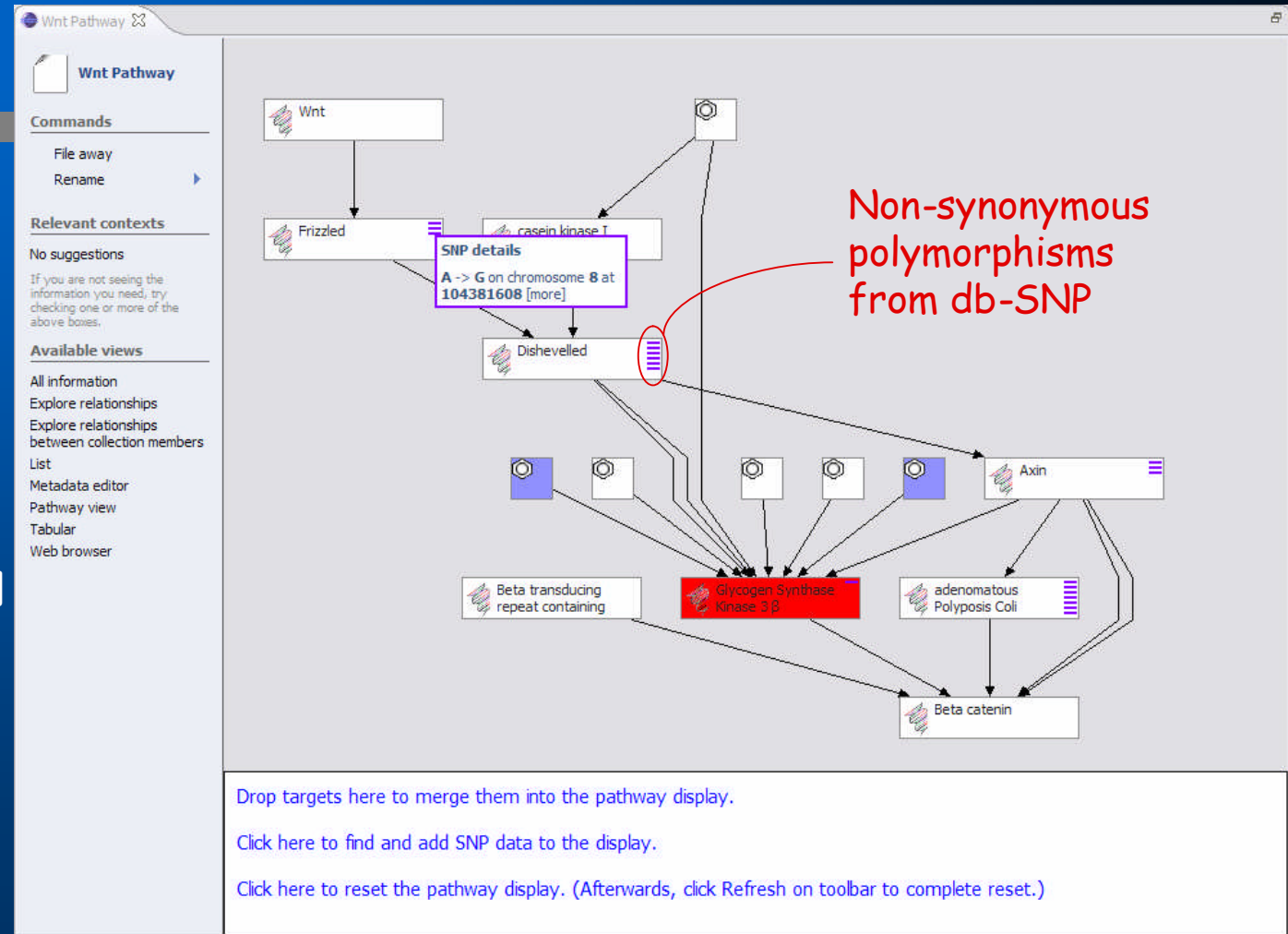


- Correspondence does not need to mean "same descriptive object", but may mean objects with identical references



# Pathway Polymorphisms

- Merge directly onto pathway graph
- Identify targets with lowest chance of genetic variance
- Predict parts of pathways with highest functional variability
- Map genetic influence to potential pathway elements
- Select mechanisms of action that are minimally impacted by polymorphisms



# Pathway Semantic Lens example

```
add { :predicateSet
      rdf:type graph:PredicateSet ;
      dc:title "BioPAX pathway arrows" ;
      hs:member    biopax:NEXT-STEP ;
      hs:member    :pointingTo ;
      hs:member ${
        rdf:type    vowl:RDFQueryLens ;
        vowl:sourceExistential    ?s ;
        vowl:targetExistential    ?t ;
        rdfs:label    "" ;
        vowl:existentials    @( ?s ?t ?type ) ;
        vowl:statement ${
          vowl:subject ?type ;
          vowl:predicate    biopax:LEFT ;
          vowl:object    ?s
        } ;
        vowl:statement ${
          vowl:subject ?type ;
          vowl:predicate    biopax:RIGHT ;
          vowl:object    ?t
        }
      }
    }
```

S emantic lenses  
are defined using  
RDF (or N3) as well !



# Microarray Data\* ala Semantic Web

*\*or any other kind of tabular data*

```
:diabetes-hepatocyte-dataset  
  rdf:type Is:MicroArrayExpt ;
```

```
  dc:title "GSK3beta Expression Study" ;  
  dc:date "4/15/04" ;  
  Is:experimentalist "David Brucker" ;  
  Is:targetSystem "mHep-R1 Hepatocytes" ;  
  Is:design :GSK3b_mus_Protocol ;
```

Any valid combination of  
qualia and quantities can  
be described for each  
Data Point

```
Is:valueTypes @( Is:GE_Expected_Ratio ) ;
```

```
Is:indivCell ${ rdf:type Is:GE_Cell; Is:probeHub gsk:CaseinK;  
  Is:conditionHub :GSK3b_RNAi_perturb; Is:GE_Expected_Ratio "0.909"; Is:GE_Variance "0.007" } ;
```

```
Is:indivCell ${ rdf:type Is:GE_Cell; Is:probeHub gsk:DVL;  
  Is:conditionHub :DBAP_perturb; Is:GE_Expected_Ratio "1.055"; Is:GE_Variance "0.007" } ;
```

```
Is:indivCell ${ rdf:type Is:GE_Cell; Is:probeHub gsk:Axin;  
  Is:conditionHub :SB216763_perturb; Is:GE_Expected_Ratio "0.881"; Is:GE_Variance "0.007" } ;
```

# Gene Expression Studies

- Sets of Genes and Conditions linked to each data cell via RDF properties
- Hierarchical Clustering
- Semantic links to each object

Protocol Object

Condition Hub

Gene (Probe) Hub

GE Node

**All Properties**

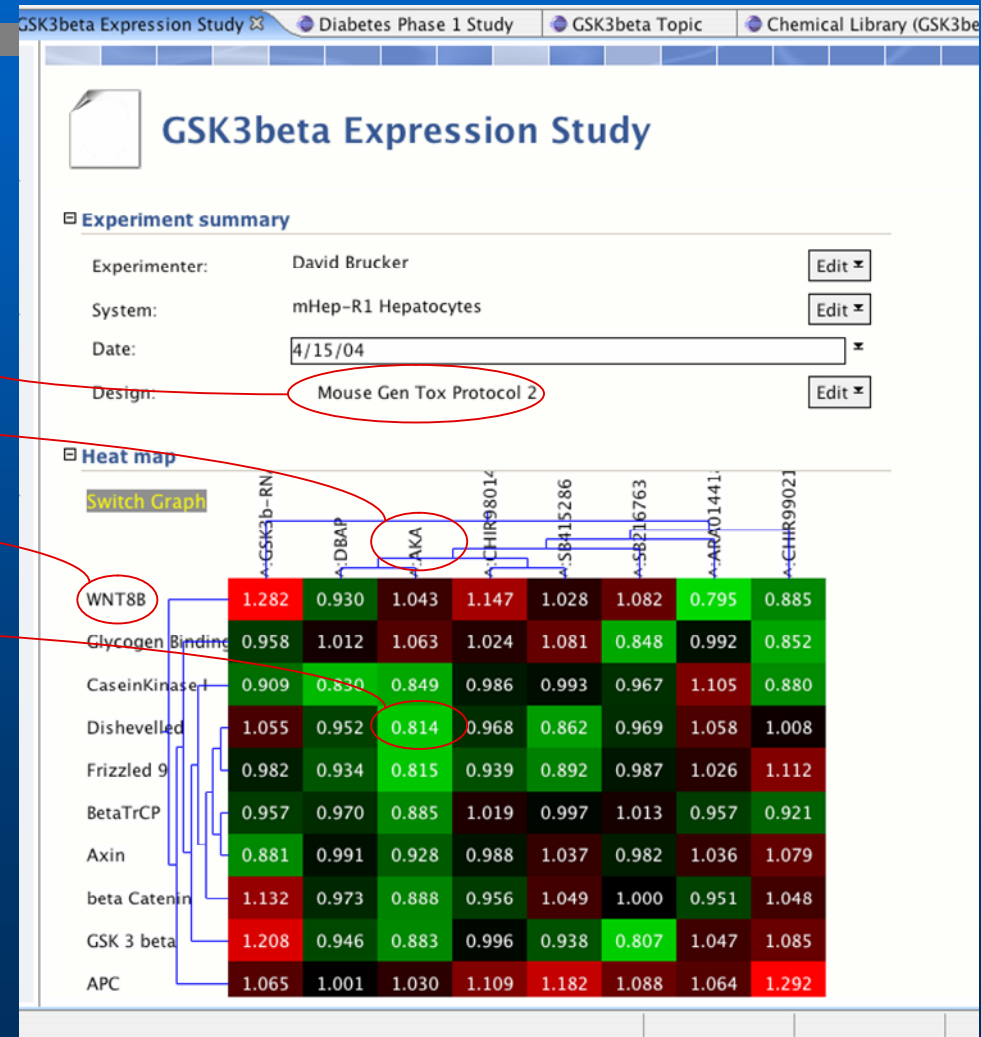
Condition: ^AKA

E[Ratio]: 0.814

Gene: Dishevelled

RDF Type: Expression Value

Var: 0.007



# Semantic Graphs

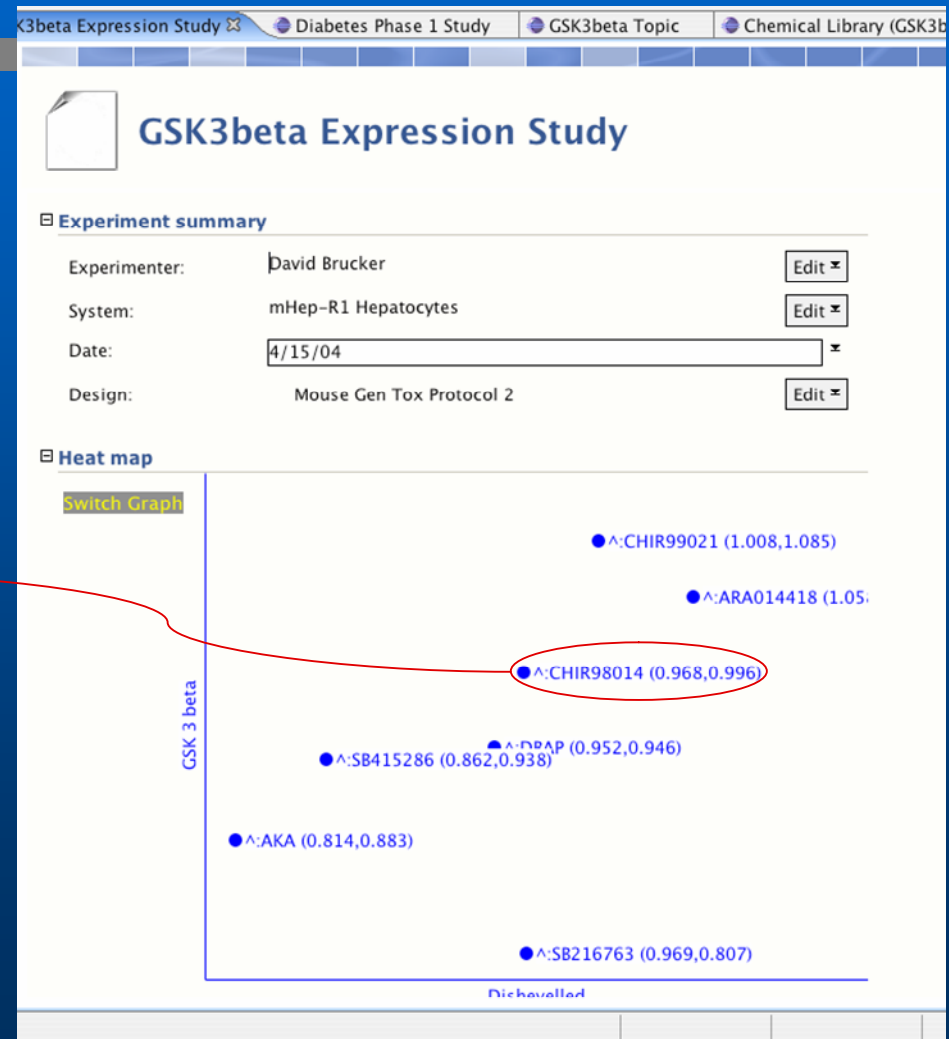
- The full set of probes or conditions is captured
- Data points can contain a wealth of semantic information

Each Data Point is a Semantic Hub

**^:CHIR98014**

**All Properties**

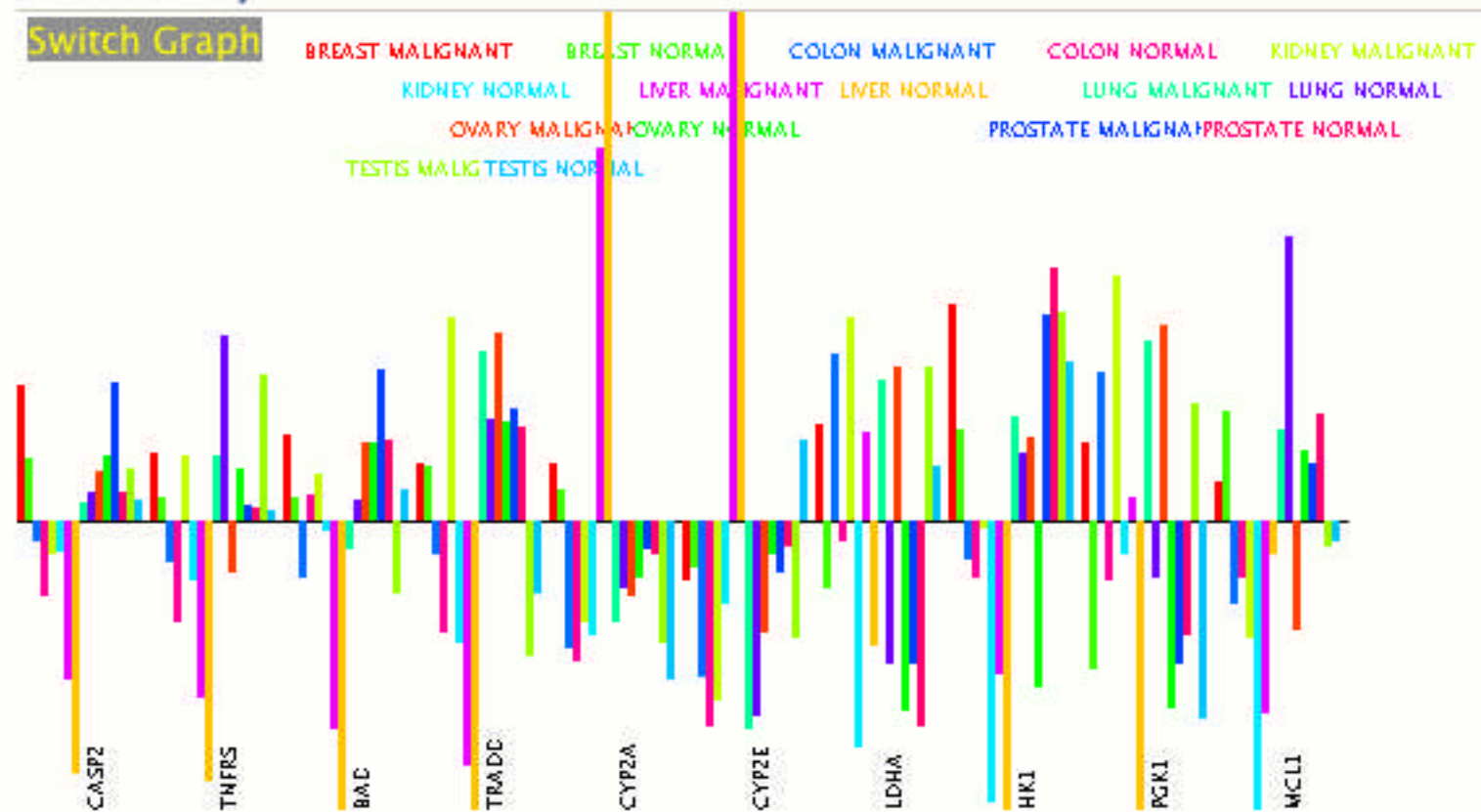
label:	^:CHIR98014
perturbed by:	CHIR98014
RDF Type:	Perturbation
treatment:	4.8ng/dl rosuvastatin 6 weeks



# Alternative Views

## ☐ Tissue Study

Switch Graph



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# Preclinical and Clinical Applications

- *in support of the Critical Path*

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# Critical Path

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## Support Innovation and Safety through-

- Capturing all information more carefully (semantically)
- Biomarkers, PGx, Pathways, drug profiling, etc.
- More Knowledge re-use
  - *Lessons Learned: Failures + Successes*
- Better coordination between groups
- Using better tools for Decision Making
- Paper trails
- Semantic Lenses

# Supporting Drug Safety


## *'Safety Lenses'*

- Semantic Lenses used to 'see' data in specific ways
- Can be "wrapped" around selected statistical tools
- Used by both reviewers and sponsors (different sets)
- View findings under different lenses depending on area of interest: hepatotoxicity vs. genotoxicity
- Aggregate other sources and findings (*knowledge*) in context with a particular project
- Support special "Alert-channels" by regulators for each different toxicity issue
- Align animal studies with clinical results
- Easy access to any new published and validated mechanisms of actions

# GeneLogic *GeneExpress* Data

- Additional relations and aspects can be defined additionally

Diseased  
Tissue

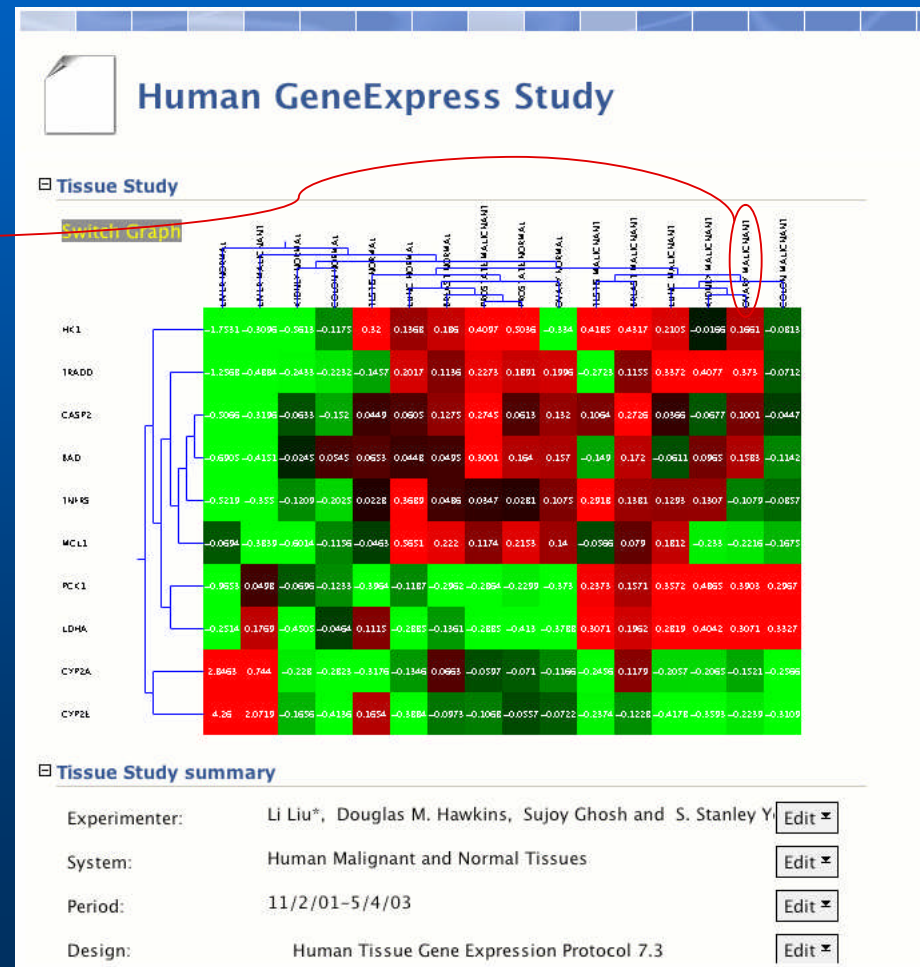


## OVARY MALIGNANT

All Properties

label:	OVARY MALIGNANT
normal form:	OVARY NORMAL
omim:	OVARIAN CANCER, EPITHELIAL
RDF Type:	Sample

Links to  
OMIM (RDF)






# Diseases Links

- All diseases linked dynamically to OMIM references

- OMIM is converted to RDF chunks, each queriable and annotatable.



## OVARIAN CANCER, EPITHELIAL

Contains A Reference To

The genetic epidemiology of early-onset epithelial ovarian cancer: a population-based study. OPCML at 11q25 is epigenetically inactivated and has tumor-suppressor function in epithelial ovarian cancer. Definition and refinement of a region of loss of heterozygosity at 11q23.3-q24.3 in epithelial ovarian cancer associated with poor prognosis.

Edit

OMIM record summary

DC Title: OVARIAN CANCER, EPITHELIAL

Edit

Alternate Title And Symbols: EPITHELIAL OVARIAN CAN

Edit

Description: A number sign (#) is used with this entry because genetic or epigenetic

Edit

Date Created: 12/27/1999

Edit

Date Last Modified: 4/14/2005

Edit

Mode Of Inheritance: Mutation

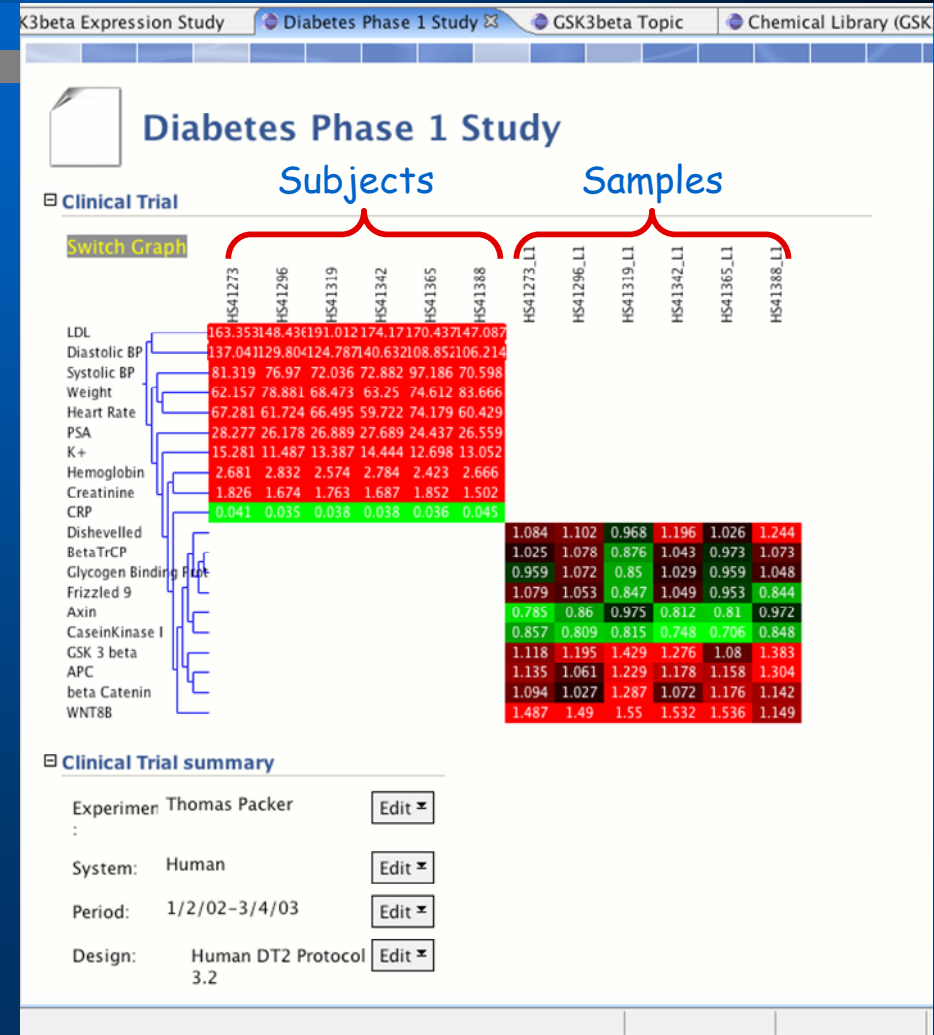
Edit

Mode Of Inheritance Of The Phenotype: Autosomal loci or phenot

Edit

# Clinical Trials

- Combine Clinical Observations with other measurements (e.g., gene expression) Clinical Obs
- Semantic links between samples and subjects Expression Data
- Semantically defined Clinical protocols



# Clinical Trials

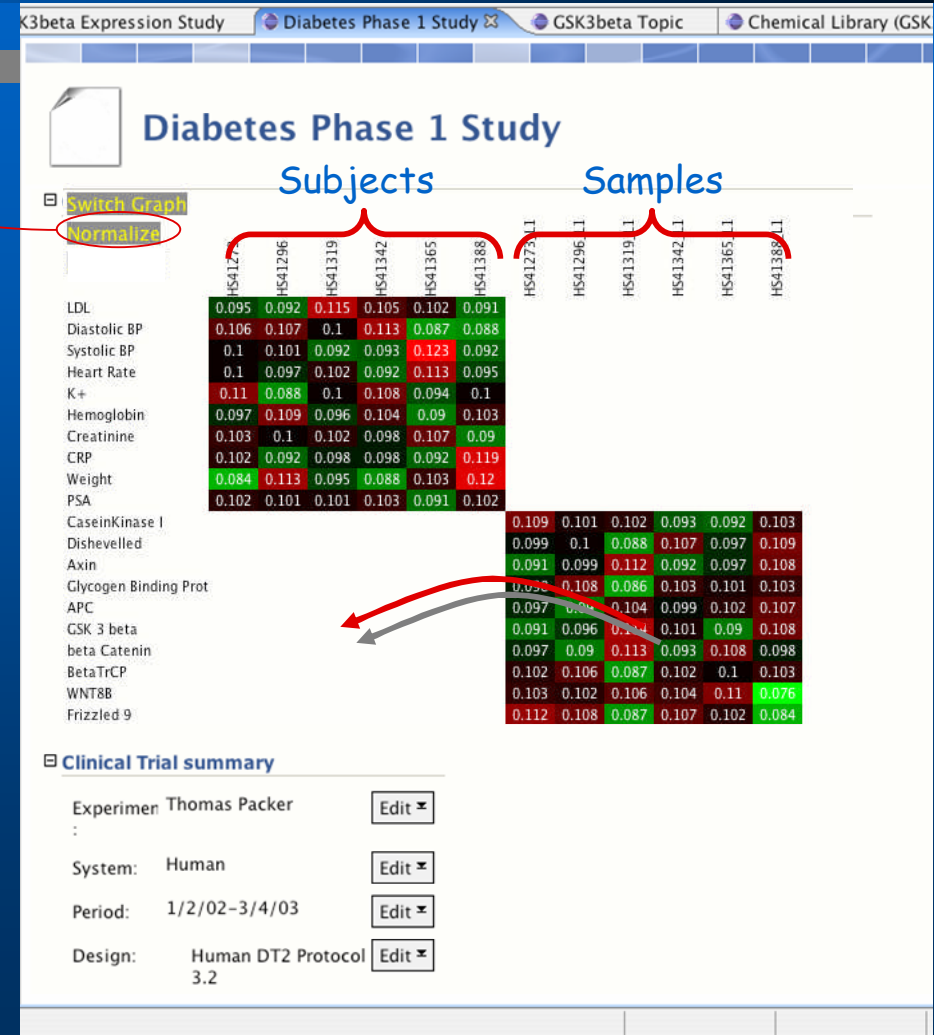
- Values can be normalized across all measurables (rows)

- Samples can be aligned to their subjects using RDF rules

Normalize

Clinical Obs

Expression Data



# Clinical Trials

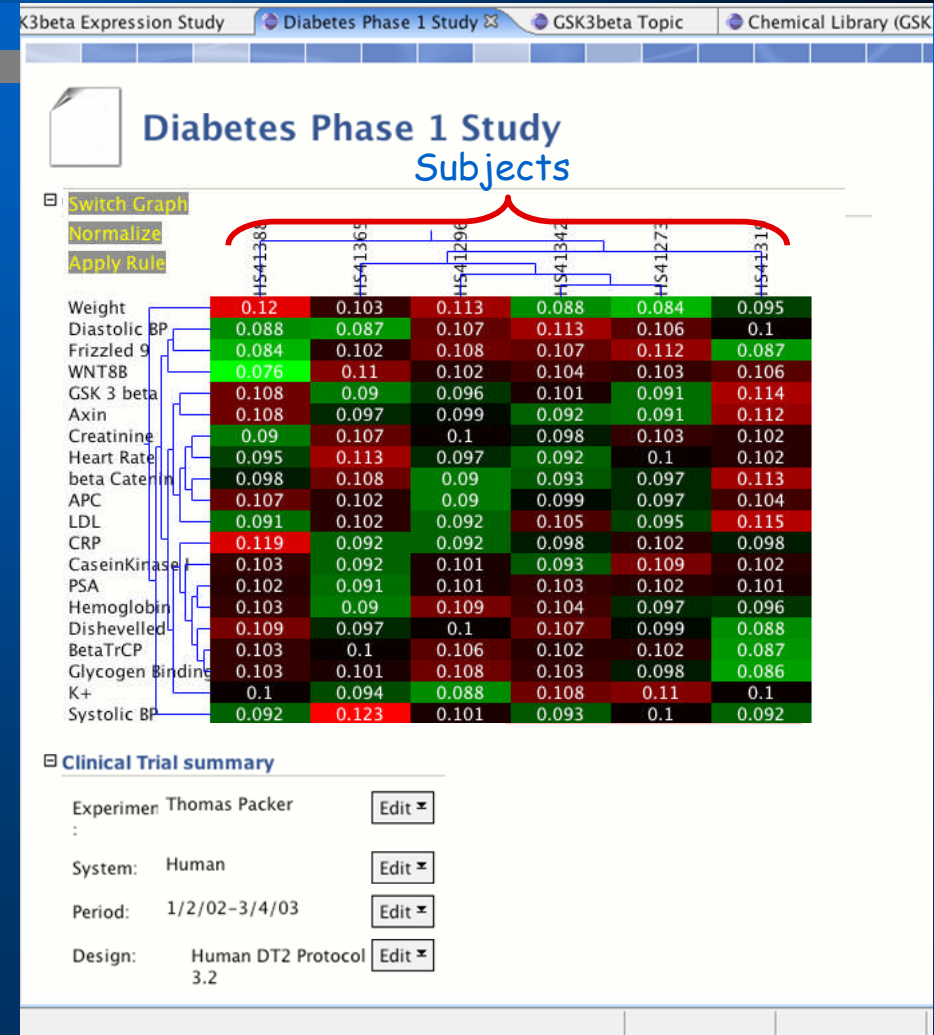
- Values can be normalized across all measurables (rows)

- Samples can be aligned to their subjects using RDF rules

- Clustering can now be done over all measureables (rows)

Clinical Obs

Expression Data



# CDISC and the Semantic Web

- Reduce the need to write data parsers to any CDISC XML Schema
- Make use of ontologies and terminologies directly using RDF
- Easier inclusion of Genomic data
- Use Semantic Lenses for Reviewers
- Easier acceptance by industry with their current technologies

QuickTime™ and a  
TIFF (LZW) decompressor  
are needed to see this picture.

# Merging Clinical Evidence with Interpretation and Models

- **Semantic linking to the Narrative**
  - Observations
  - Genomics
  - Biomarkers
  - PK/PD
  - Statistical Reasoning and Inference
- **Justifications**
  - Efficacy
  - Toxicity
  - Mechanism of Action
- **Built into Application Submission**
- **Use of Semantic Lenses by reviewers to compare all evidence**

# How to get there?

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- Current Standards into SW format (OWL and RDF)
  - CDISC, RCRIM, MEDRA, UMLS, ICD10
- Use secure-web as infrastructure
- Semantic wrappers for Relational Databases (W3C, Oracle)
- Using SW to define and apply *policies* through rule-based semantics

# Vendor Adoption

## RDF in Oracle Spatial



**Nicole Alexander**, Xavier Lopez,  
Siva Ravada, Susie Stephens &  
Jack Wang

**Oracle Corporation**

October 27 – 28, 2004

ORACLE

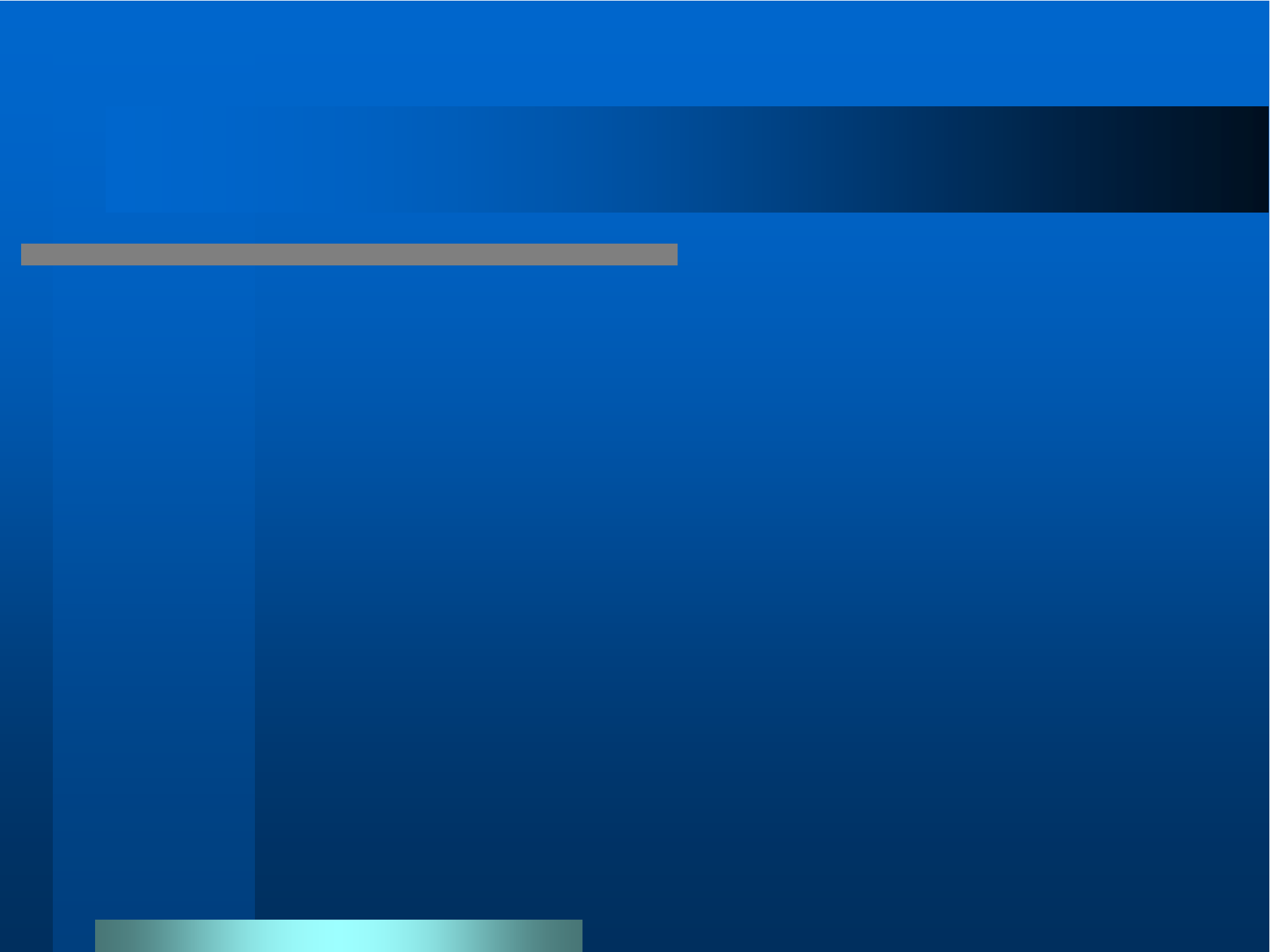


# SW Public Domain Tools

- Haystack - <http://haystack.lcs.mit.edu>
- RDB-RDF-Access -
  - <http://www.w3.org/2004/04/30-RDF-RDB-access/>
  - <http://www.w3.org/2004/10/04-pharmaFederate/>
- XML-->RDF - <http://www.w3.org/2005/02/13-KEGG/>
- Protégé - <http://protege.stanford.edu/>
- SESAME - <http://www.openrdf.org/>
- JENA - <http://www.hpl.hp.com/semweb/jena2.htm>
- SWOOP - <http://www.mindswap.org/2004/SWOOP/>

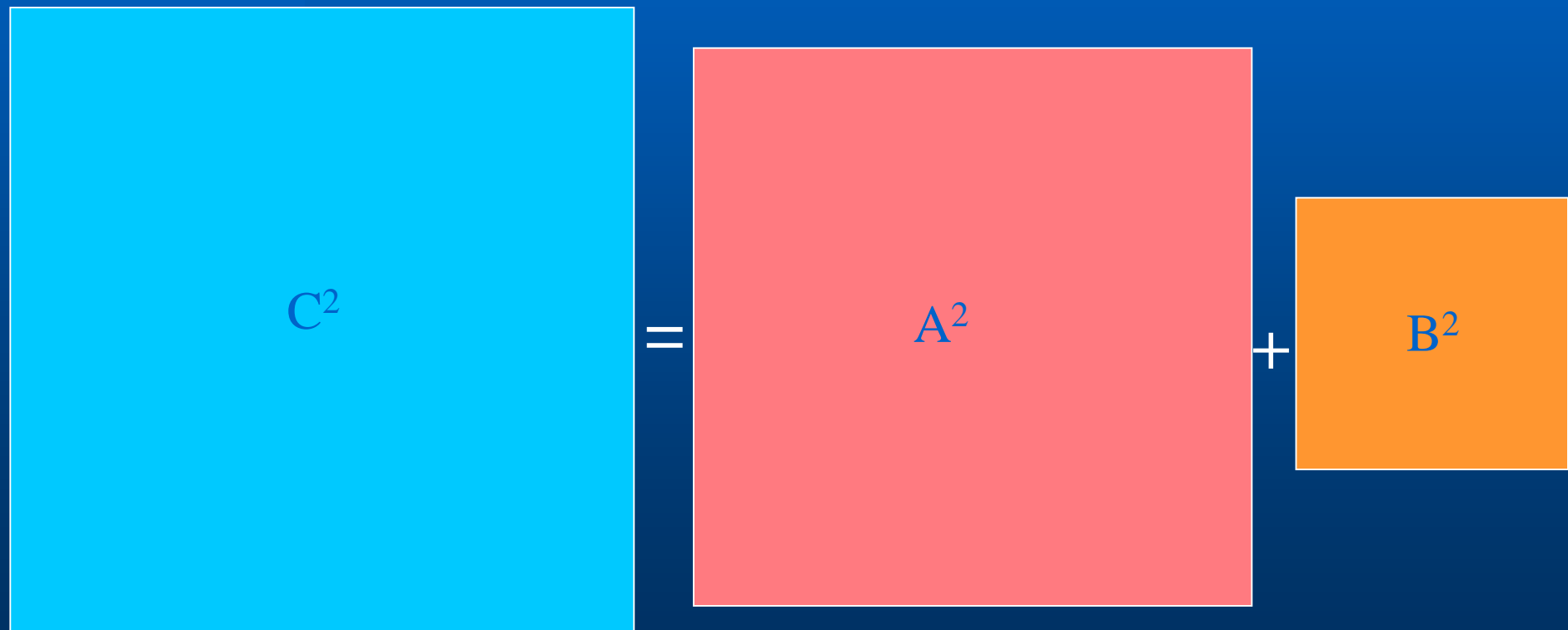
# Thank You

- **Healthcare and Life Sciences Interest Group (HCLSIG)**
  - Tonya Hongsermeier, co-chair Partners Healthcare
  - Eric Neumann, co-chair Clinical Semantics Group
- **Eric Miller, Semantic Web Lead**
- **<http://www.w3.org/2005/04/swls>**
- **<http://www.w3.org/sw>**



# A Point of View

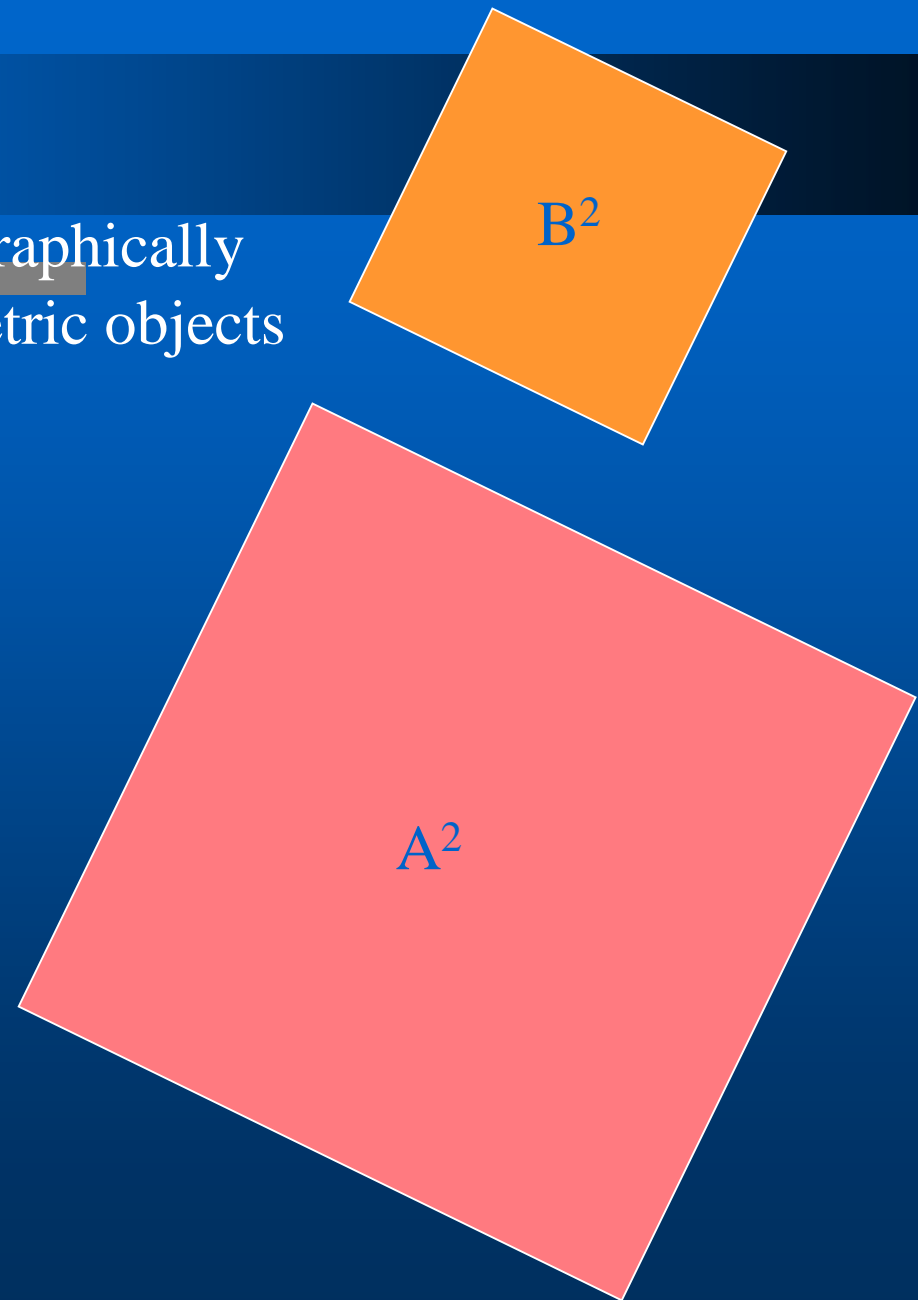
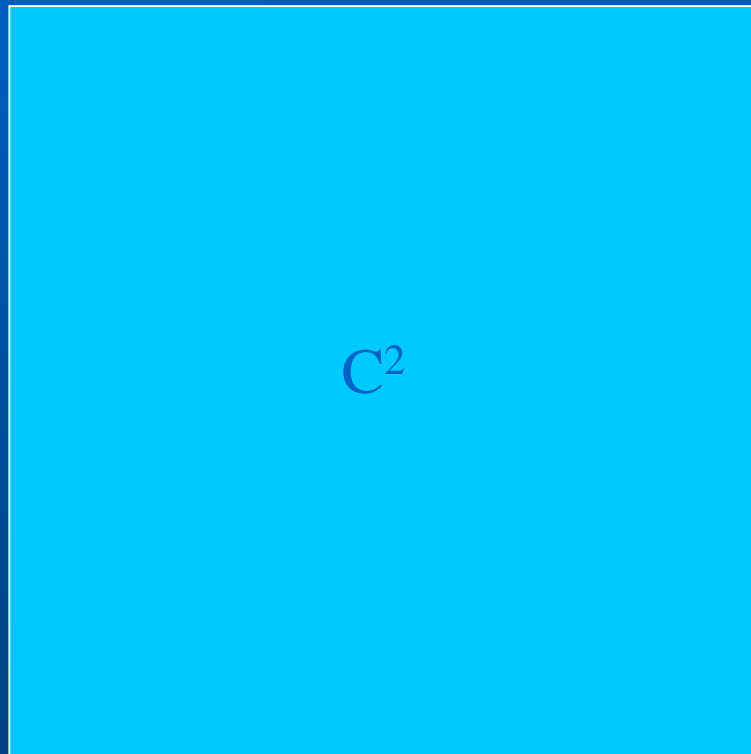
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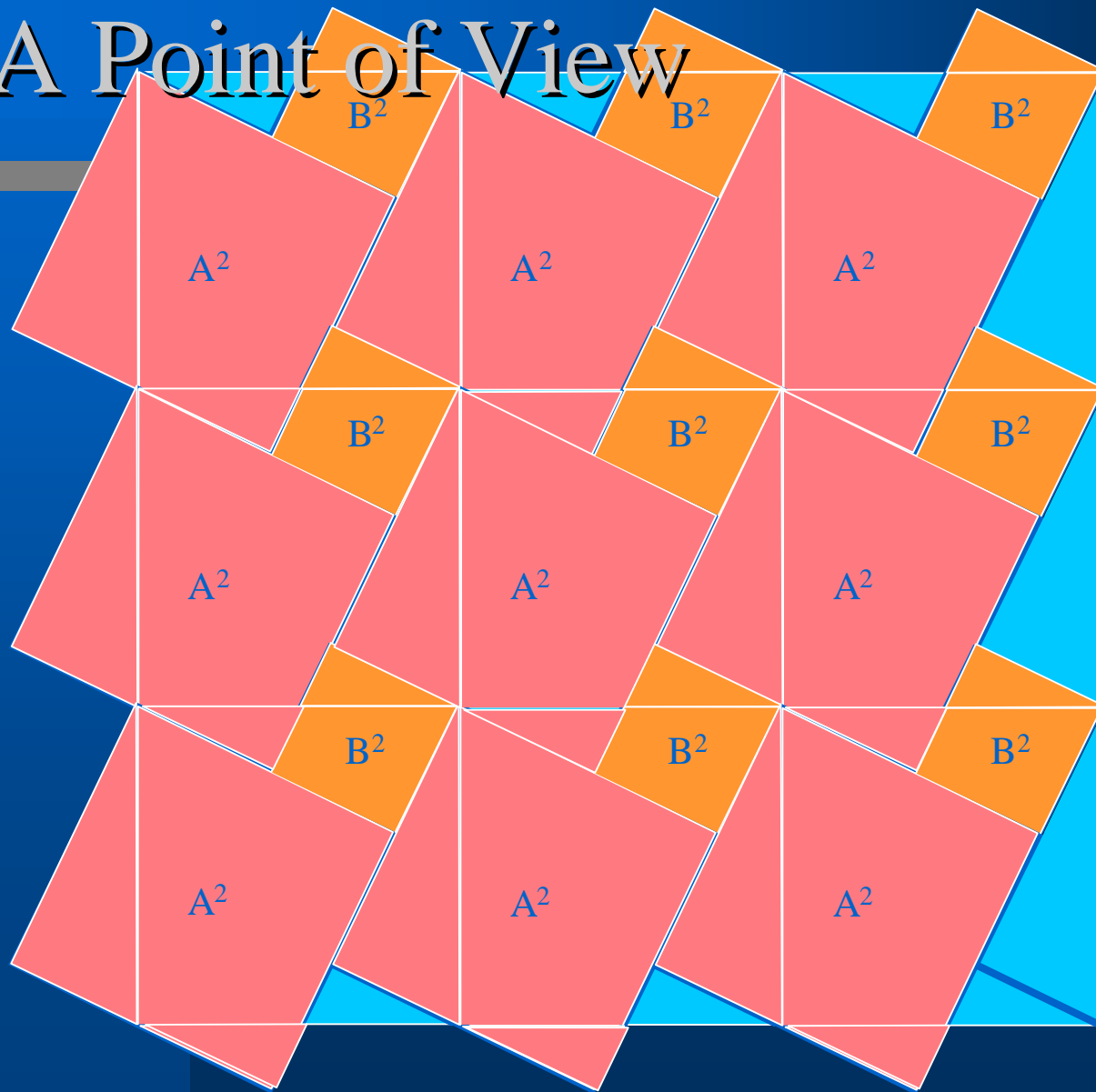
# A Point of View

Goal:

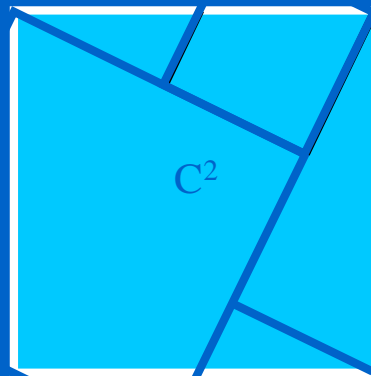
Prove Pythagoras' Theorem graphically  
without rearranging any geometric objects



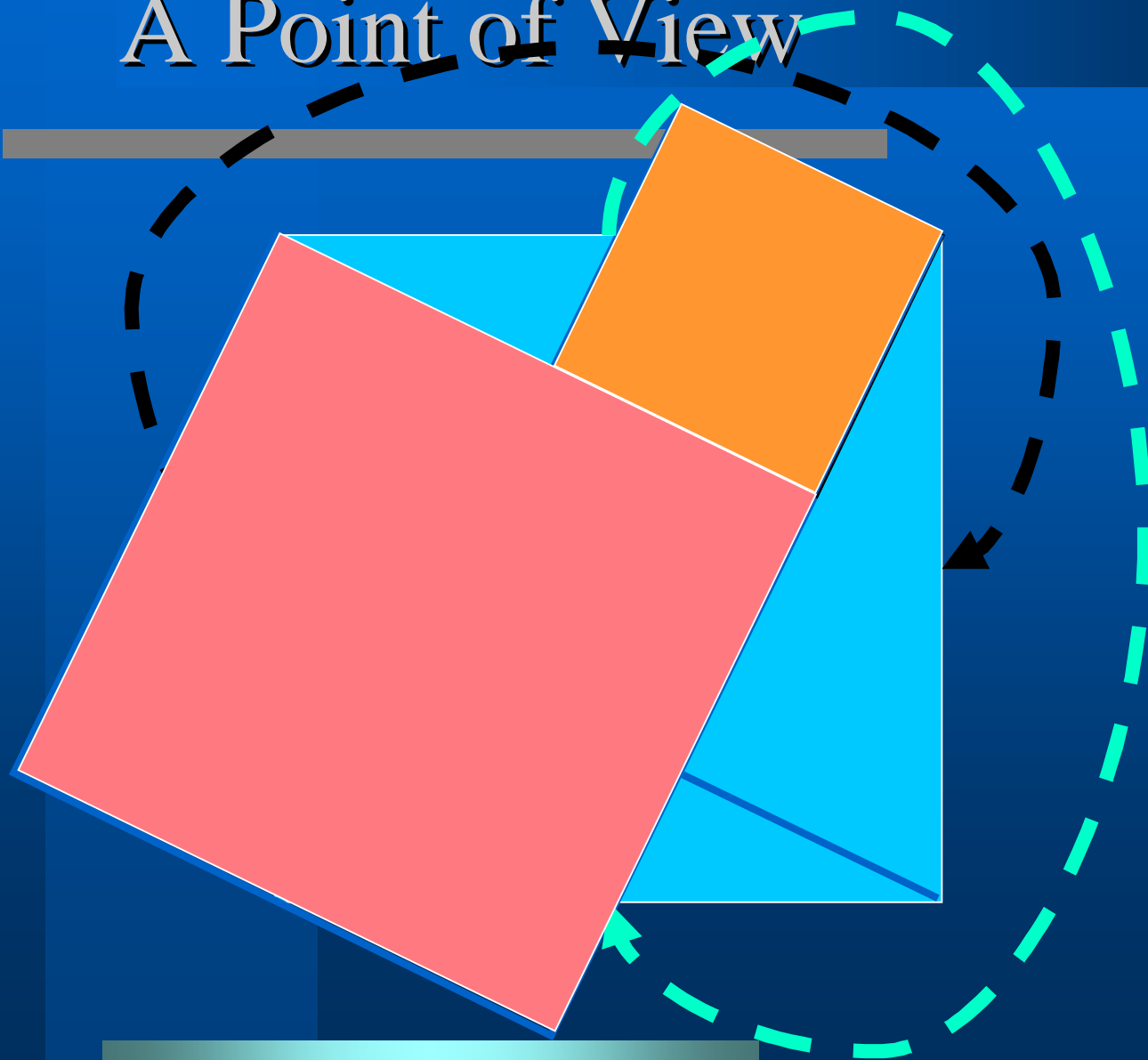
# A Point of View



# A Point of View

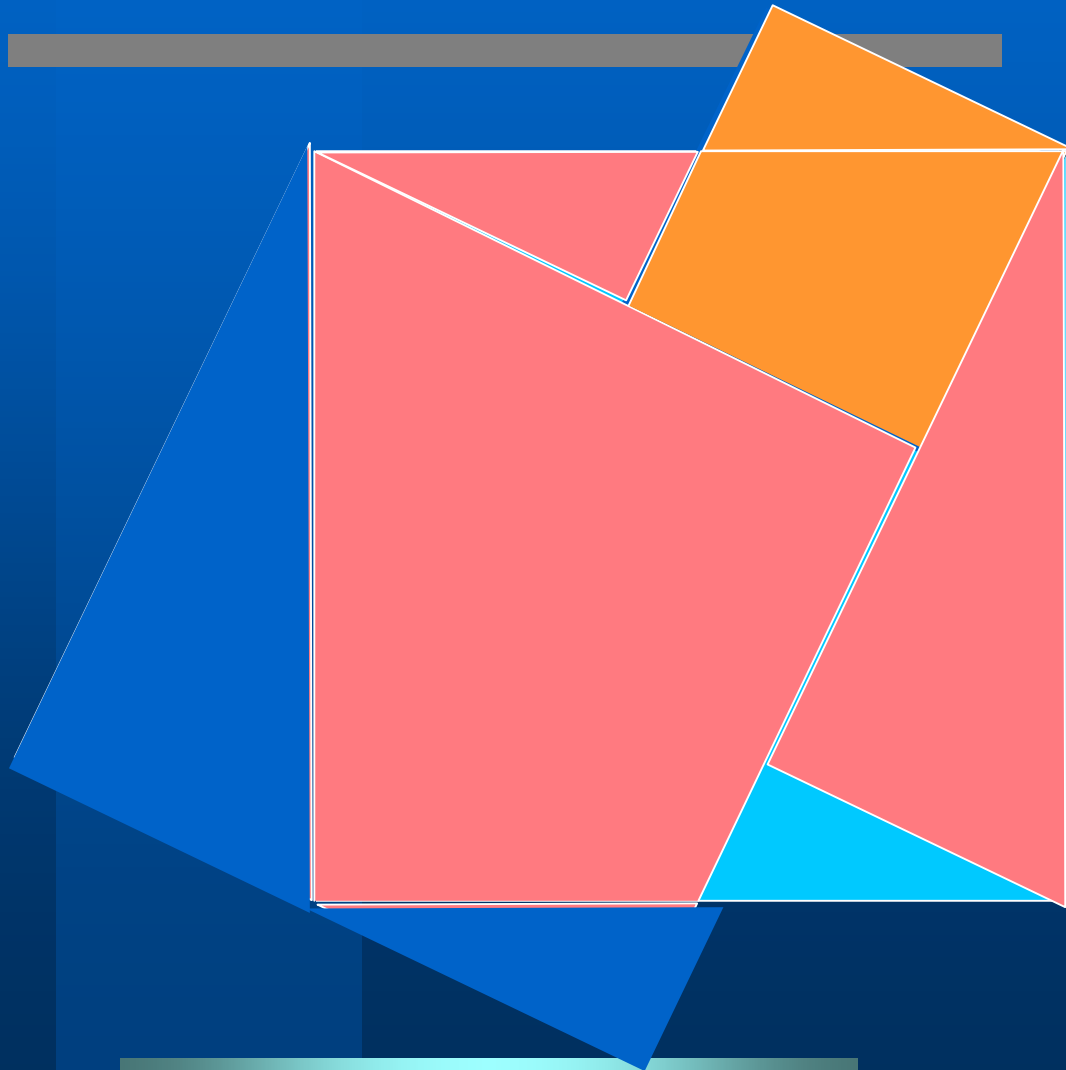


# A Point of View

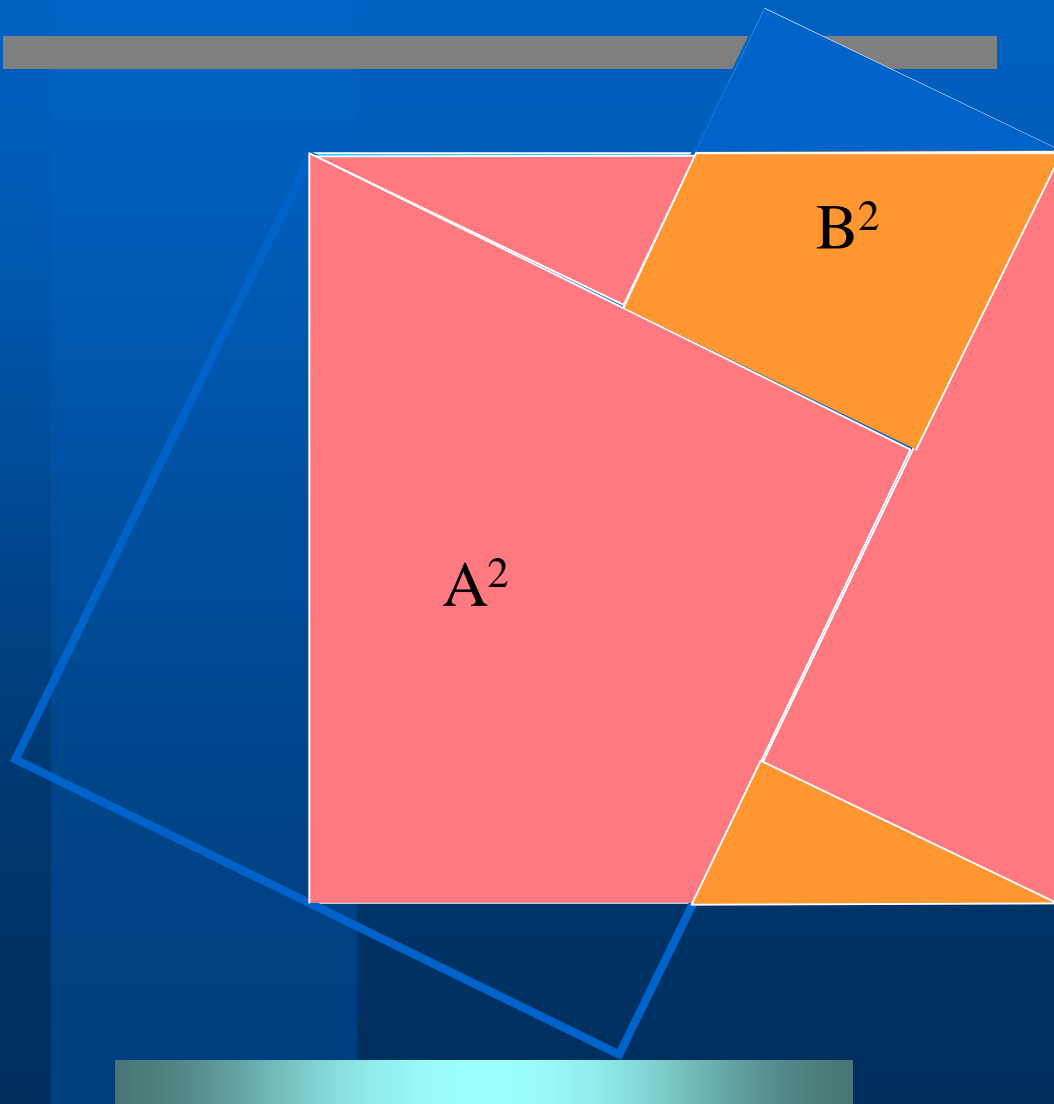




# A Point of View



# A Point of View



# Chemical Libraries

- Lists of Compounds and progressed Chemical Entities

- All Chem properties semantically defined

- Target and assay information associated

Compound Objects

Known Targets

Studies applied to

K3beta Expression Study | Diabetes Phase 1 Study | GSK3beta Topic | Chemical Library (GSK3beta)

## Chemical Library (GSK3beta)

Chemical Library

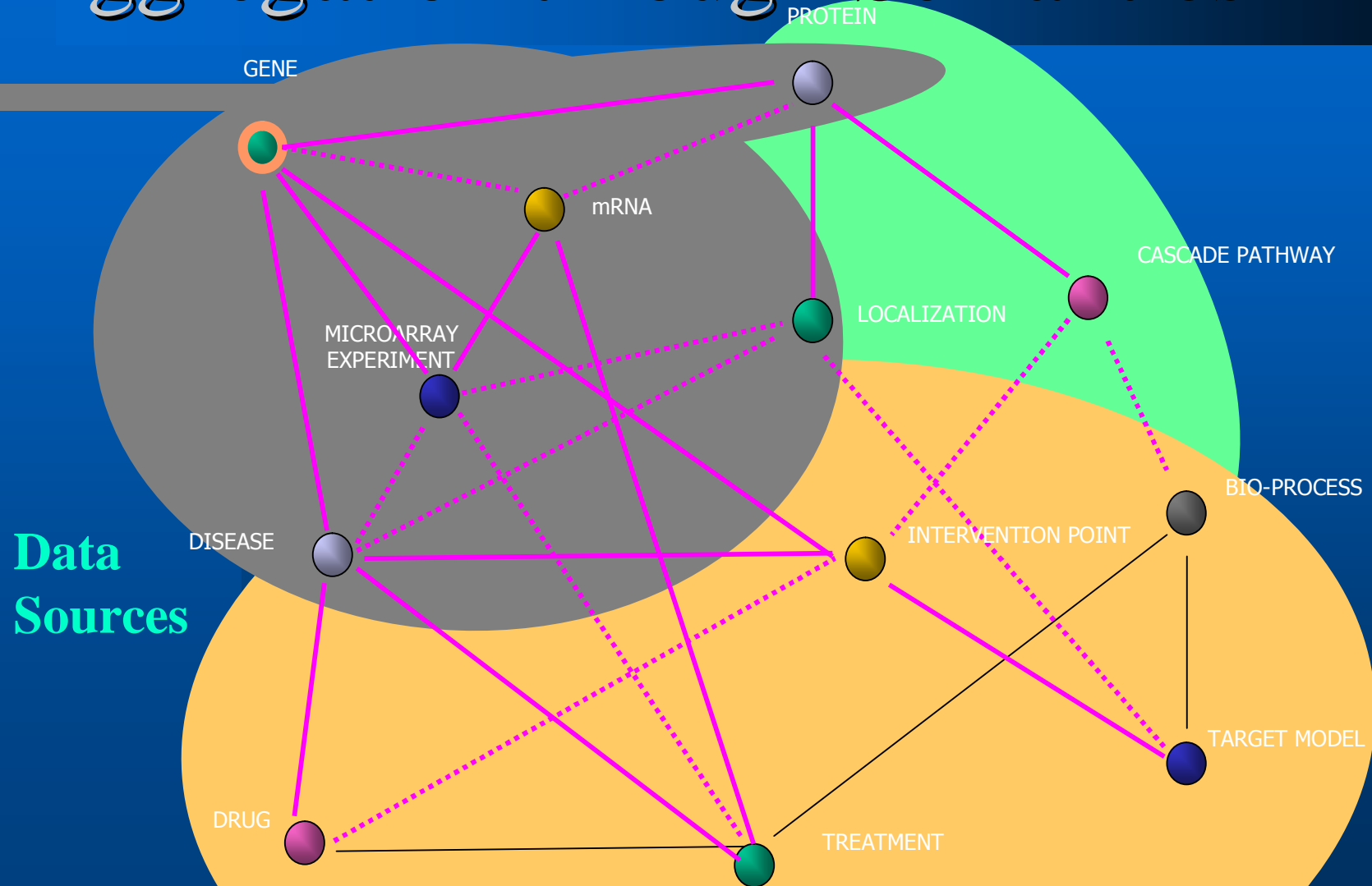
Title	ID	chemical structure	mol ...	ic50	CLog P
OTDZT	2323	C16H14N2OS2	314.4	--	3.8
SB216763	176158	C19H12Cl2N2O2	371.21	34 nM	4.514
SB415286	176159	C16H10ClN3O5	359.7	78 nM	1.799
TDZD-8	46329	C10H10N2SO2	222.3	2 uM	5.4
alpha-4-Dibromoac...	7454	C8H6Br2O	277.9	0.5 mM	3.248
azakenpaullone	48832	C15H10BrN3O	328.2	18 nM	5.4
bis-7-indolym...	74811	No items in list	412.48	--	4.1
kenpaullone	3820	C16H11BrN2O	327.17	23nM	2.4

Library summary

label:	Chemical Library (GSK3beta)	Edit
Library ID:	cl-326	Edit
Owner:	Frank Schlossen	Edit
created date:	4/11/02	Edit
licensed from:	Chiron Inc.	Edit
Targets:	CaseinKinase I GSK-3beta	Edit
used in:	GSK3beta Expression Study	Edit

All Properties

# Aggregation through Semantics



# Toxicogenomics

- Gene responses to administered drugs
- Drug Dosing can be associated with trends



## 2 Big Topics in Clinical Trials

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- **Safety**

- More Conclusive (making a better case)
- Earlier Prediction (reduce costs)

- **Efficacy**

- Clearly identify value to market
- Better business planning

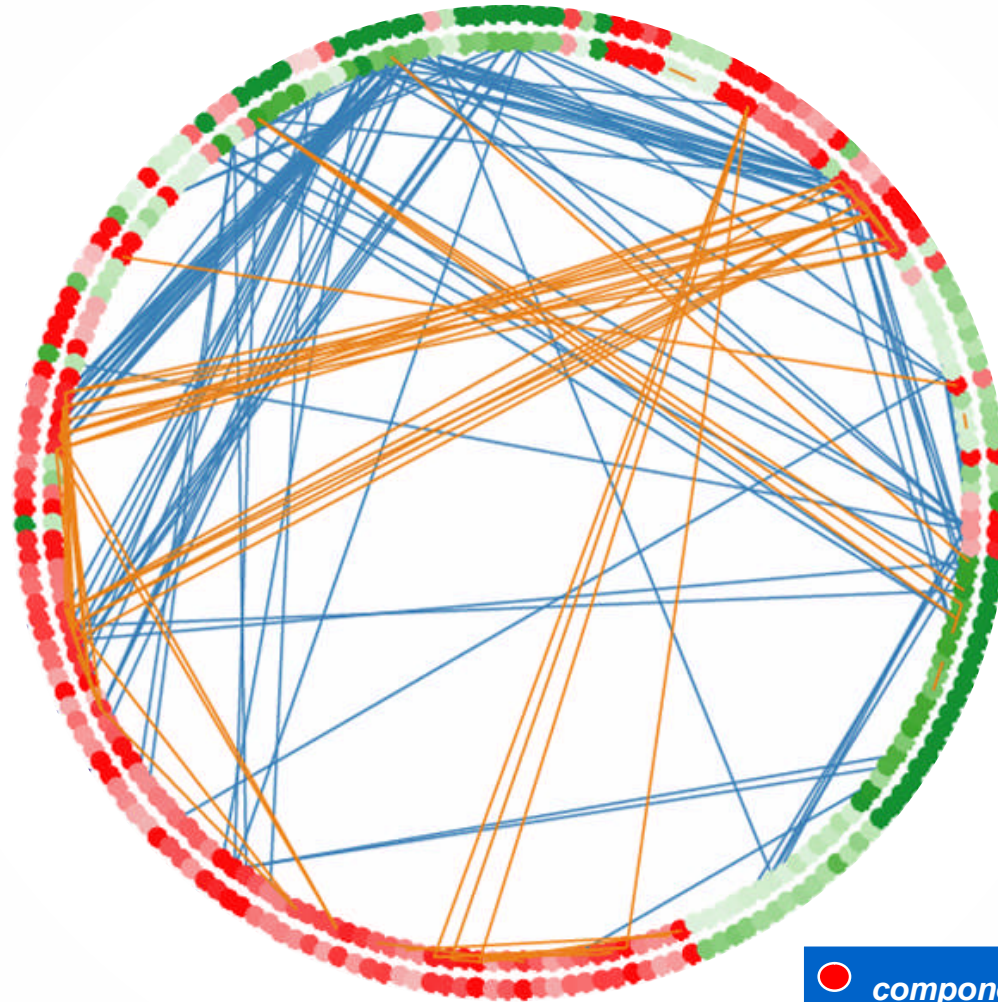
# What's the Path to get there?

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- **Optimal Trial Designs**
  - Using knowledge for recruitment
  - Judicious Choice of Biomarkers
  - Bayesian enablers
- **Better information utilization**
  - Animal-Human Cross studies
  - Compiled Tox-response knowledge
  - Just-in-Time use of external information

# Correlation Network

- *Cross Species Comparison: Human vs. Animal Metabolites*



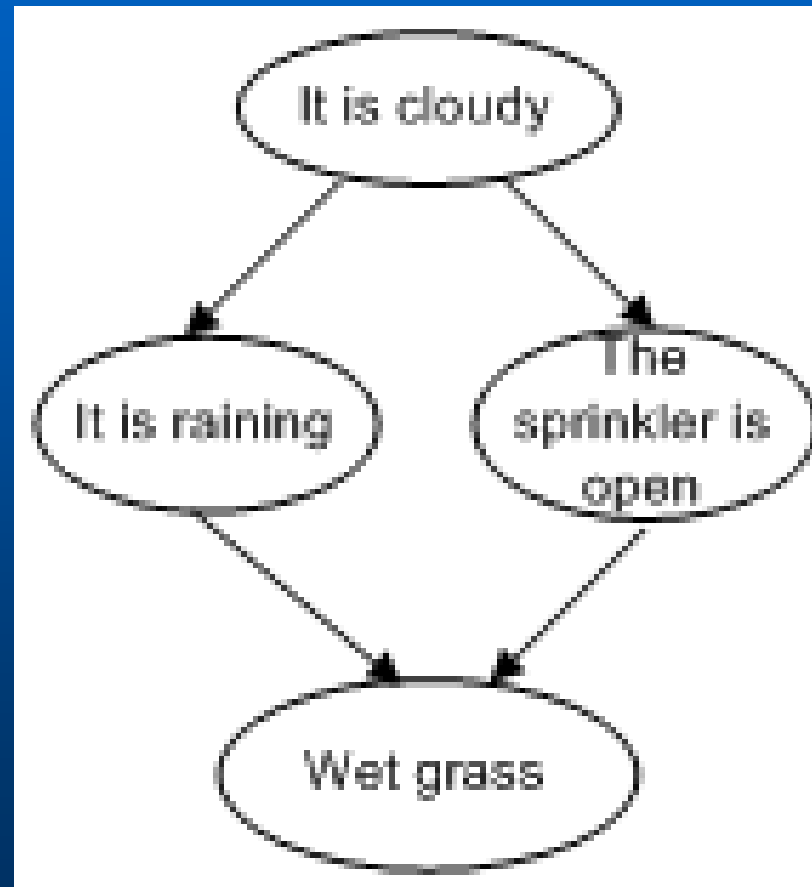
inner circle = affected **humans** vs. unaffected **humans**  
outer circle = affected **animals** vs. unaffected **animals**

● component higher in disease  
● component lower in disease



# Bayesian Networks

- Captures Causality
- Usually a DAG
- Defines Conditional Independence
- Useful for Intervention Analysis



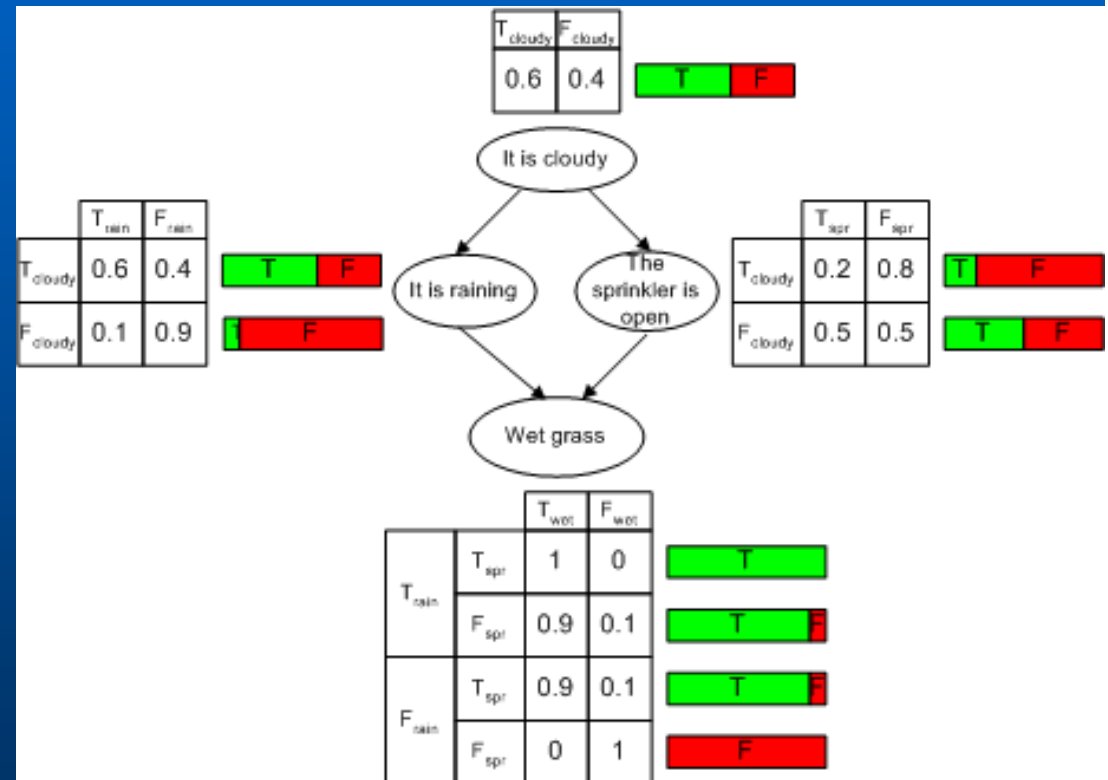
# Bayesian Networks

## Building Conditional Prob Tables

A path  $p$  between two variables  $X$  and  $Y$  is **d-separated** by a set of nodes  $Z$  iff

1.  $p$  contains a *chain*  $i \rightarrow m \rightarrow j$  or a *fork*  $i \leftarrow m \rightarrow j$  such that  $m$  is in  $Z$ , or
2.  $p$  does not contain a collider  $i \rightarrow m \leftarrow j$  such that  $m$  or any of its descendents are in  $Z$ .

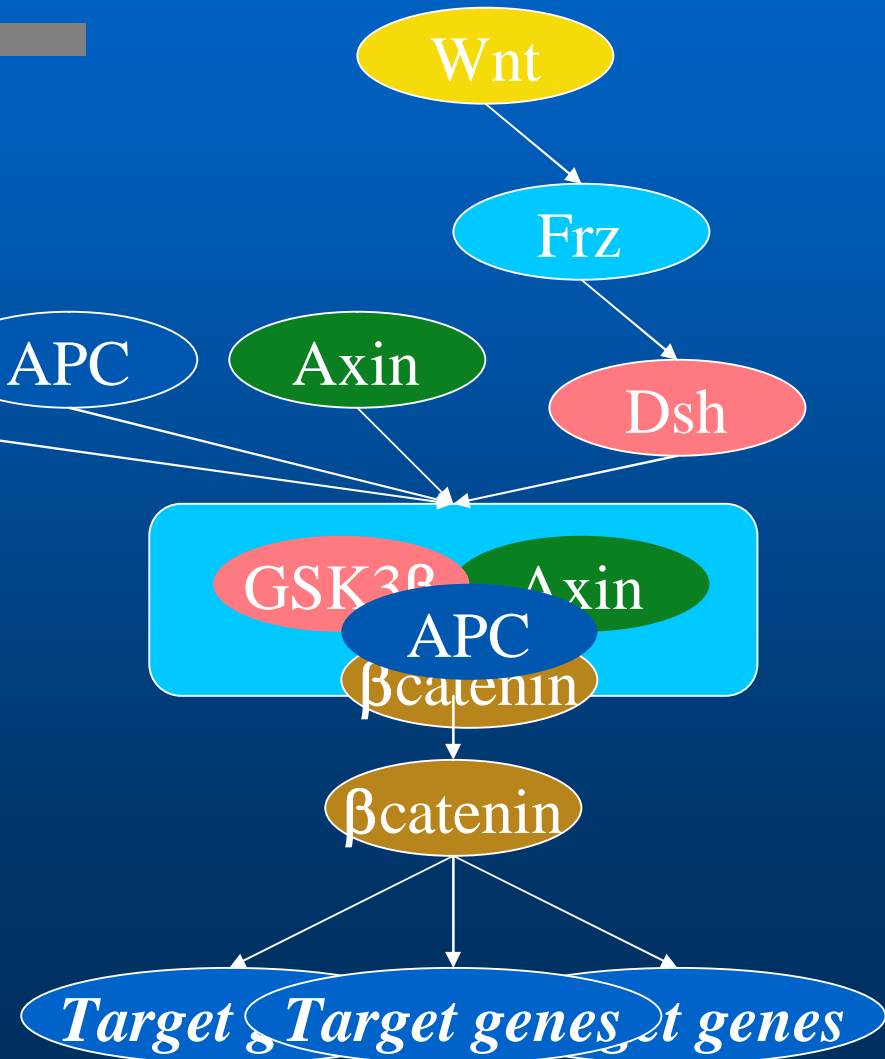
A set  $Z$  is said to **d-separate**  $X$  from  $Y$  iff  $Z$  blocks every path between  $X$  and  $Y$ .



# Causal Flow in Pathways

Each step is d-separated

⇒ Pathways can be  
inferred from analyses  
of d-separation



# SB Impact on Informatics

- How to re-organize data and information around these
  - Experiments that generate multiple kinds of data (BG)
  - Heterogeneous info sources (DBs, literature)
  - Use of Pathway knowledge
  - Handling analyzed info for interpretation
- Proposing and encoding models and hypotheses
  - Data format (syntax) standards will not work
  - Need to code “Statements” - more like linguistics
- The need for a higher form of information service:  
*Semantics*

# Handling High-Throughput Data

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## Unsupervised

- Cluster Analysis
- PCA
- Self-Organizing Maps

## Supervised

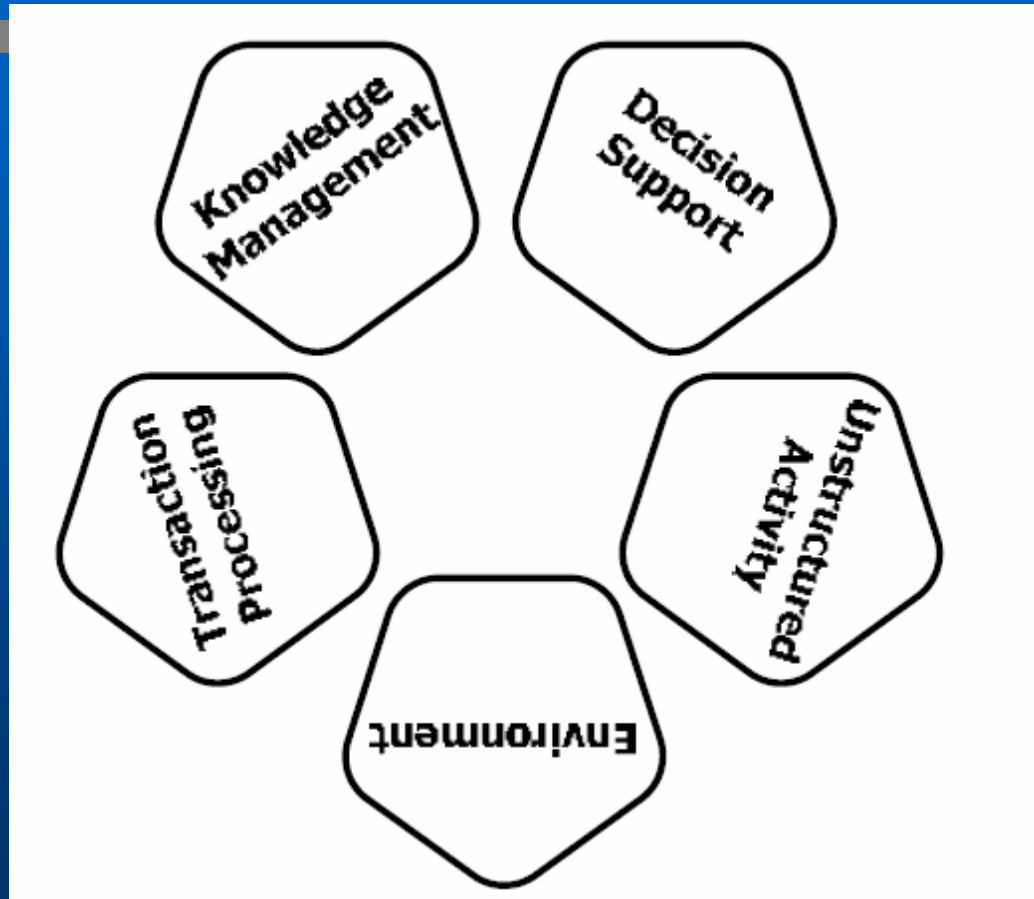
- Support Vector Machines (incl. NN)
- Bayesian Networks

# Five Areas of Semantic Applications

**Ontologies and  
Semantic Consistency**

**EAI (Enterprise  
Application Integration),  
Service Oriented  
Architectures**

Where 35% to 65% of budgets for integration and interoperation are spent because a large percentage of those systems have semantic mismatches as their basis. .



**Information  
Consolidation and ETL  
QC**

**Content Management  
and Emails**

Individual interaction of employees that affect tasks, resulting in transactions that are currently well captured and structured..

**Enterprise Mapping and CRM**

Supply chain and our demand chain, through which we are currently connected with e-commerce and B2B.