



ONSTR: Ontology for Newborn Screening Follow-up and Translational Research

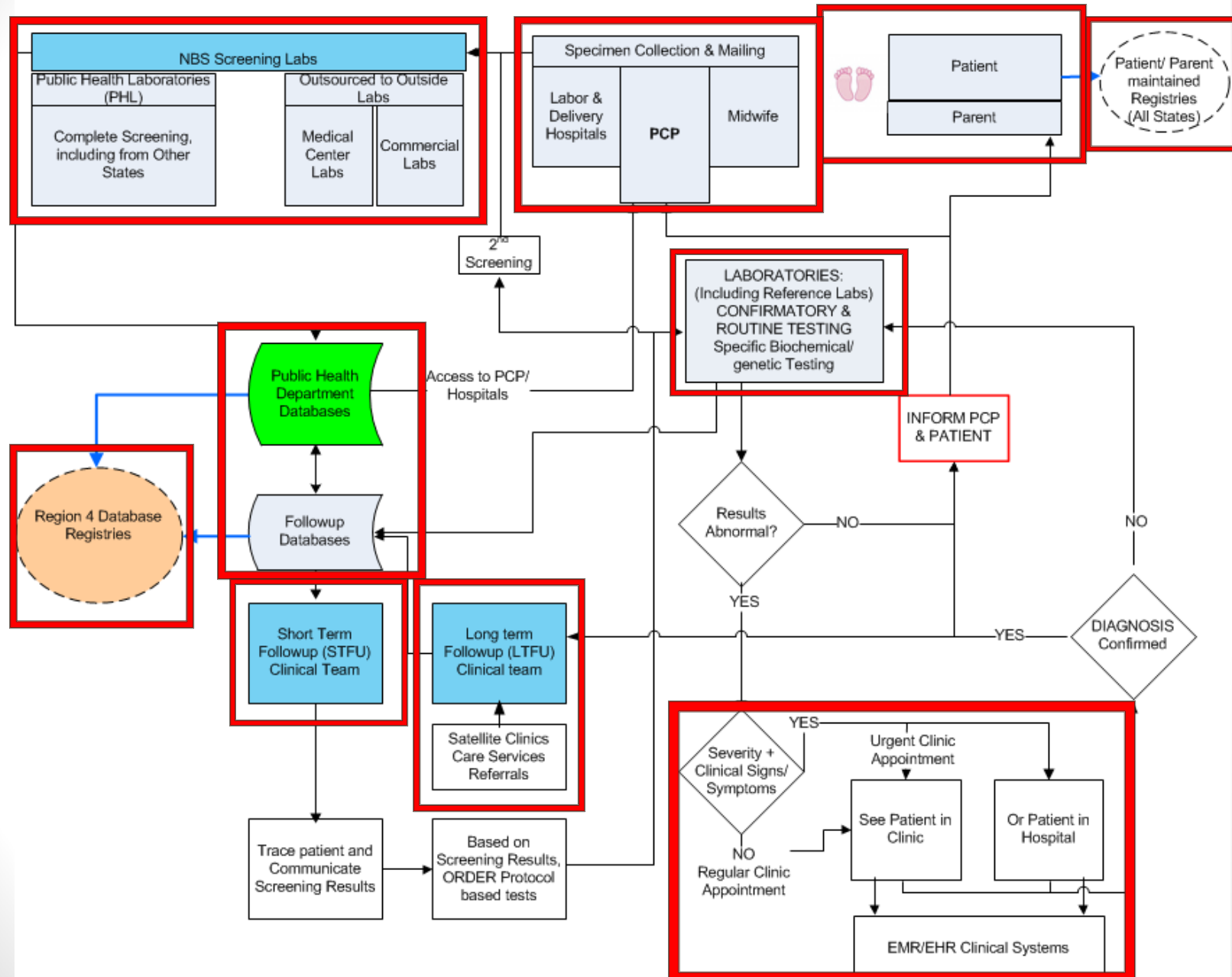
2013 Joint Meeting of the Newborn Screening and Genetic Testing Symposium
Thursday, May 9th
Atlanta

Prabhu Shankar MD, MS
Snežana Nikolić, MA,
Sivaram Arabandi, MD, MS
Shamakant Navathe
Kunal Malhotra
Rani H. Singh PhD, RD

Objective

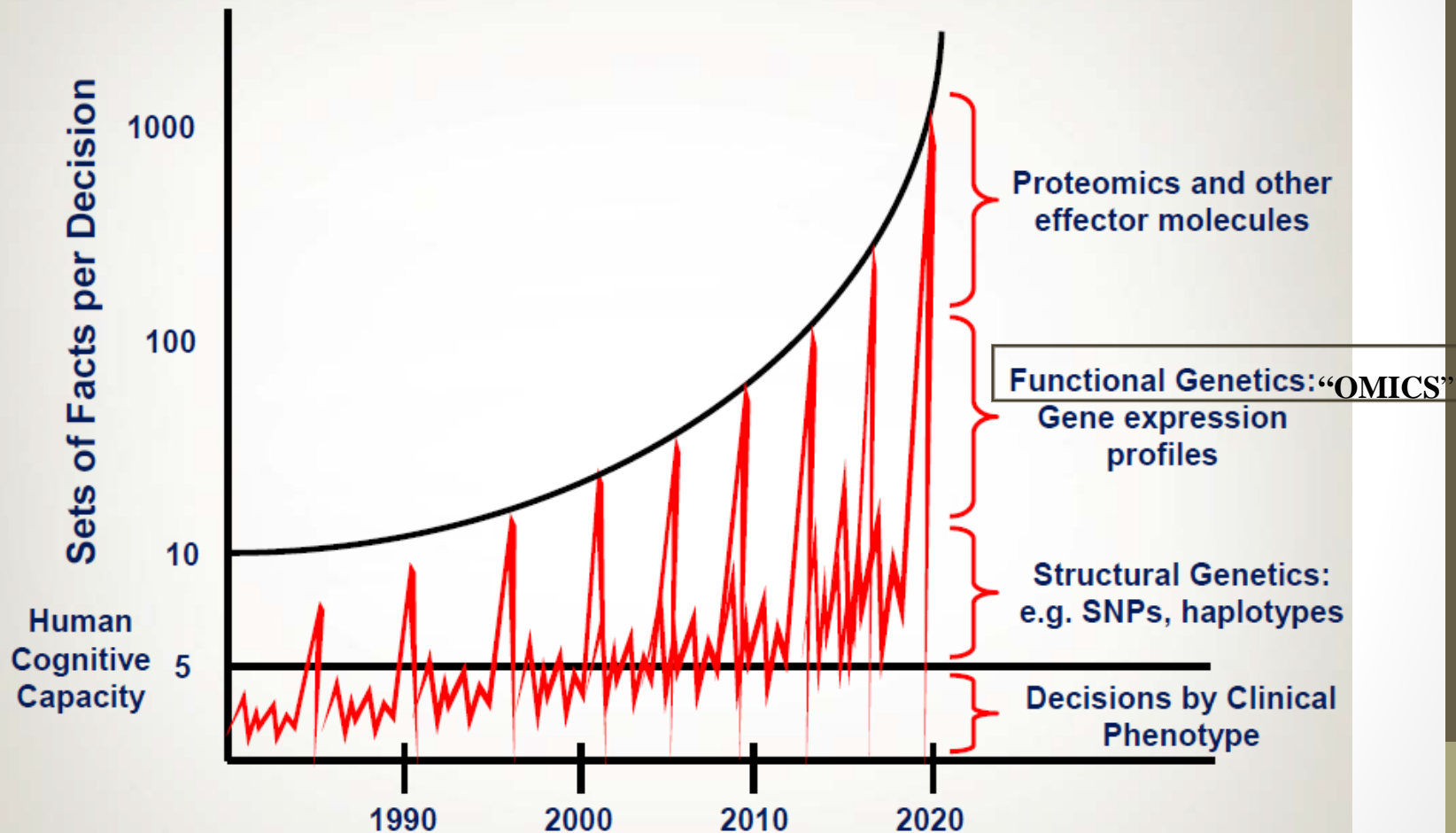
- **NBS and follow-up workflows and data complexity**
- **Ontology and Semantic Web technologies**
- **ONSTR**
- **Newborn Screening Follow-up Data Integration Collaborative (NBSDC)**
- **Semantic Web technology success stories in healthcare – if time permits!**

High Level View Of NBS and Follow-up System Workflow



External Computational Support!

Central Challenge: Overwhelming Complexity

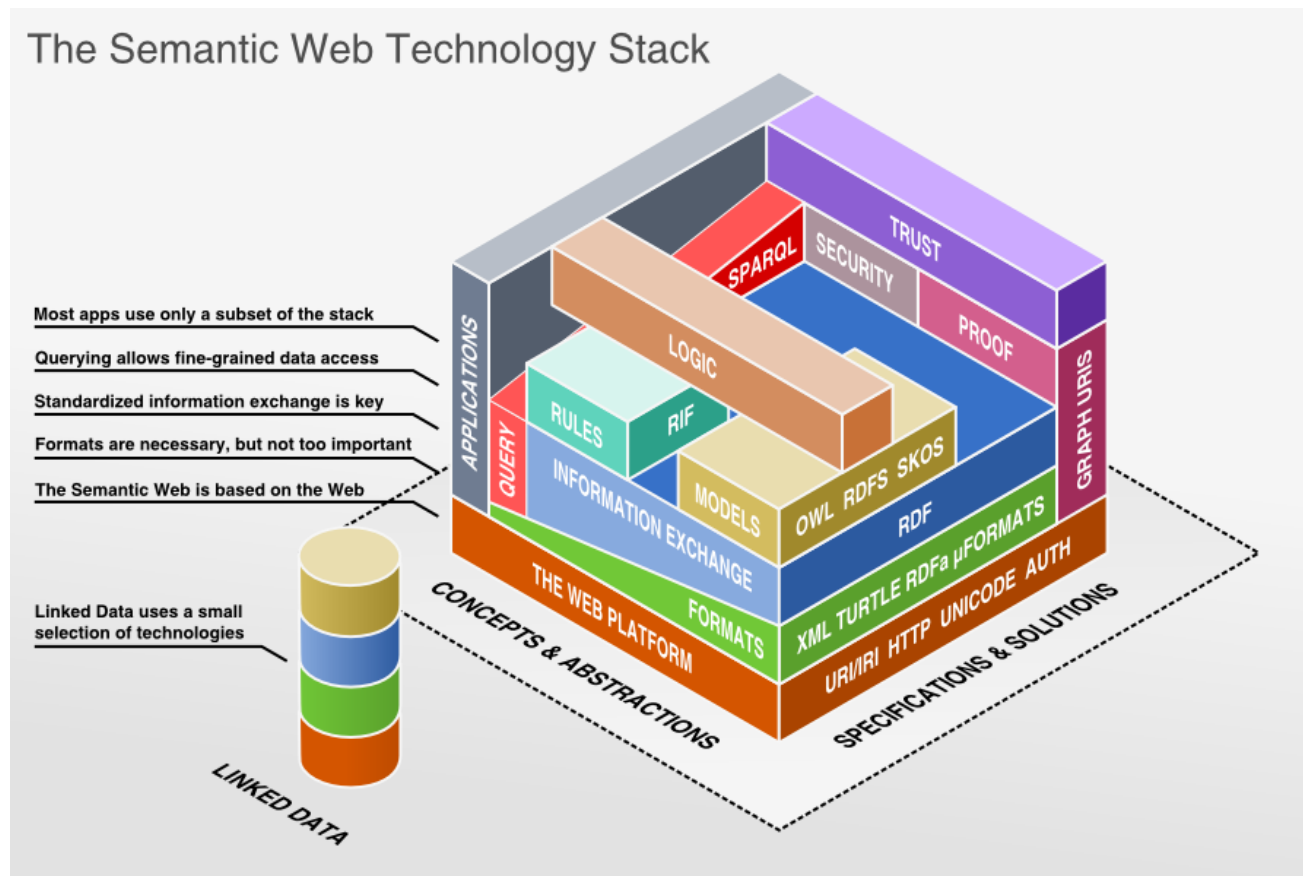


In Summary NBS Data is:

- **Geographically distributed** (data silos!)
- **Intersects clinical as well as many biomedical domains**, e.g., biochemistry, pathways, metabolomics, genomics, proteomics, pharmacogenomics
- **Various formats – structural, schematic and semantic variability**
- **Of rare diseases!**

Semantic Web Technologies

...technology stack to support a “Web of data”

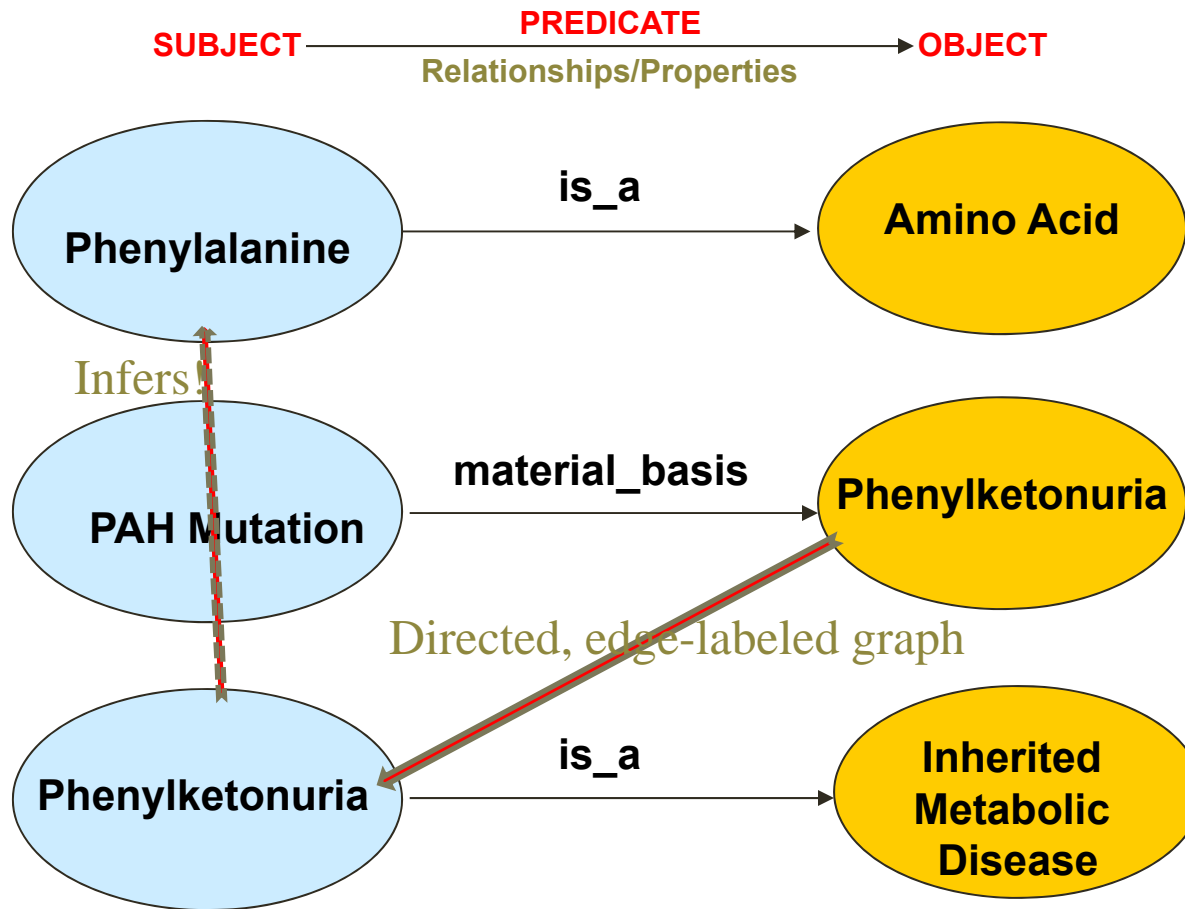


"The Semantic Web provides a common framework that allows data to be shared and reused across application, enterprise, and community boundaries." World Wide Web Consortium (W3C)



Triples:

Resource Description Framework (RDF)



Simple, Dynamic, Extensible, Interoperable

RDF Schema (RDFS), Web Ontology Language → 'Ontology'

What is ontology?

1. A branch of philosophy, studying categories and types of beings existing in the universe.

2. In Informatics, **explicit formal specifications** of the terms in the domain and relationships among them.

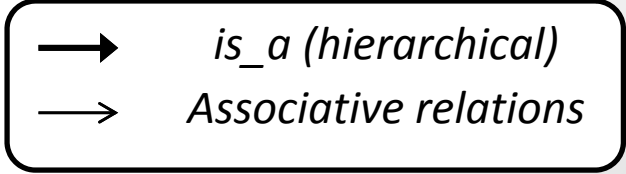
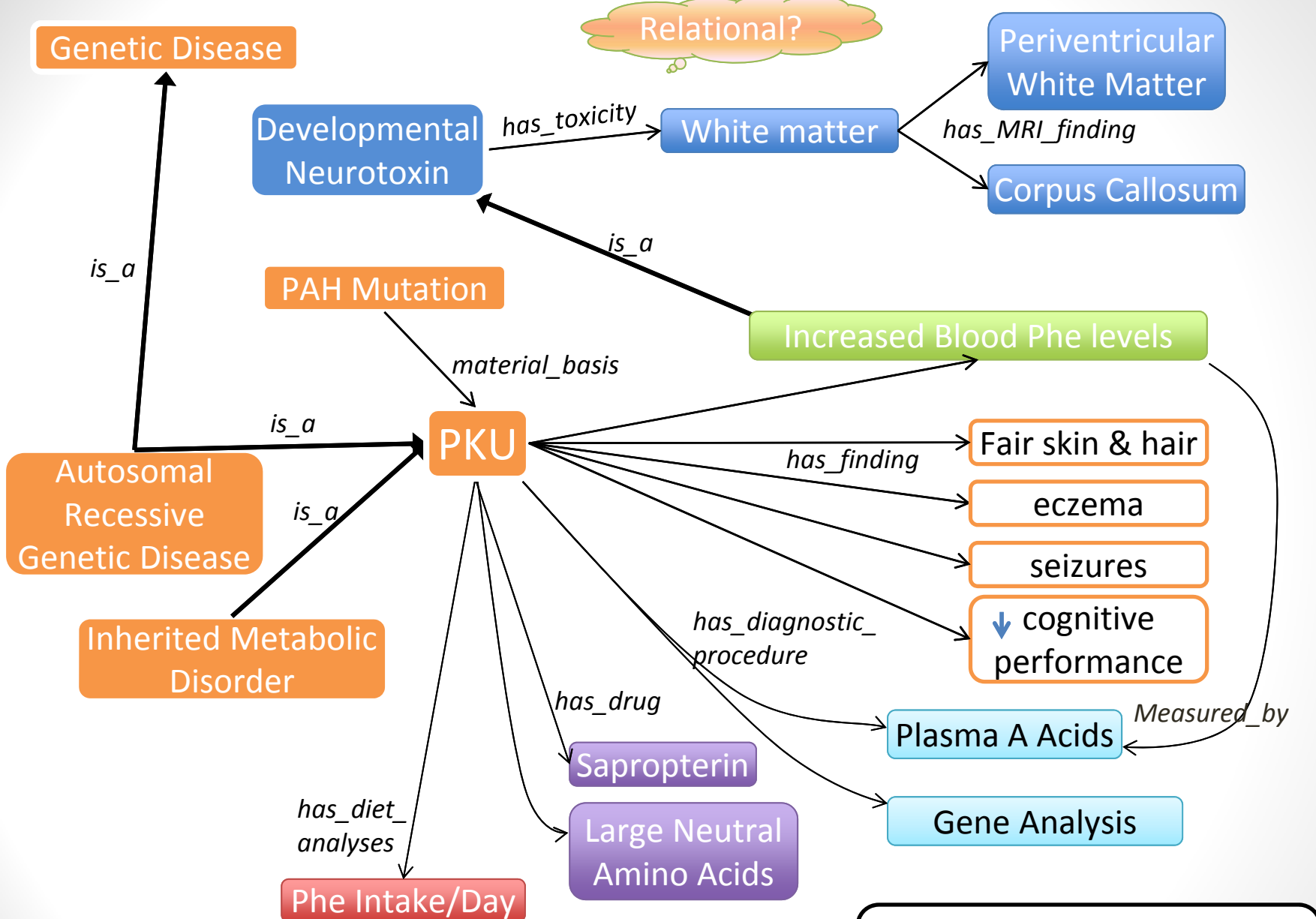
- Consensus based
- Associated with documentation and definitions
- Expressed in formal logic to support automated reasoning
- Interpretable by humans and computers

Semantic Methods and Characteristics

Deanna Pennington, LTER DataBits, Spring 2006

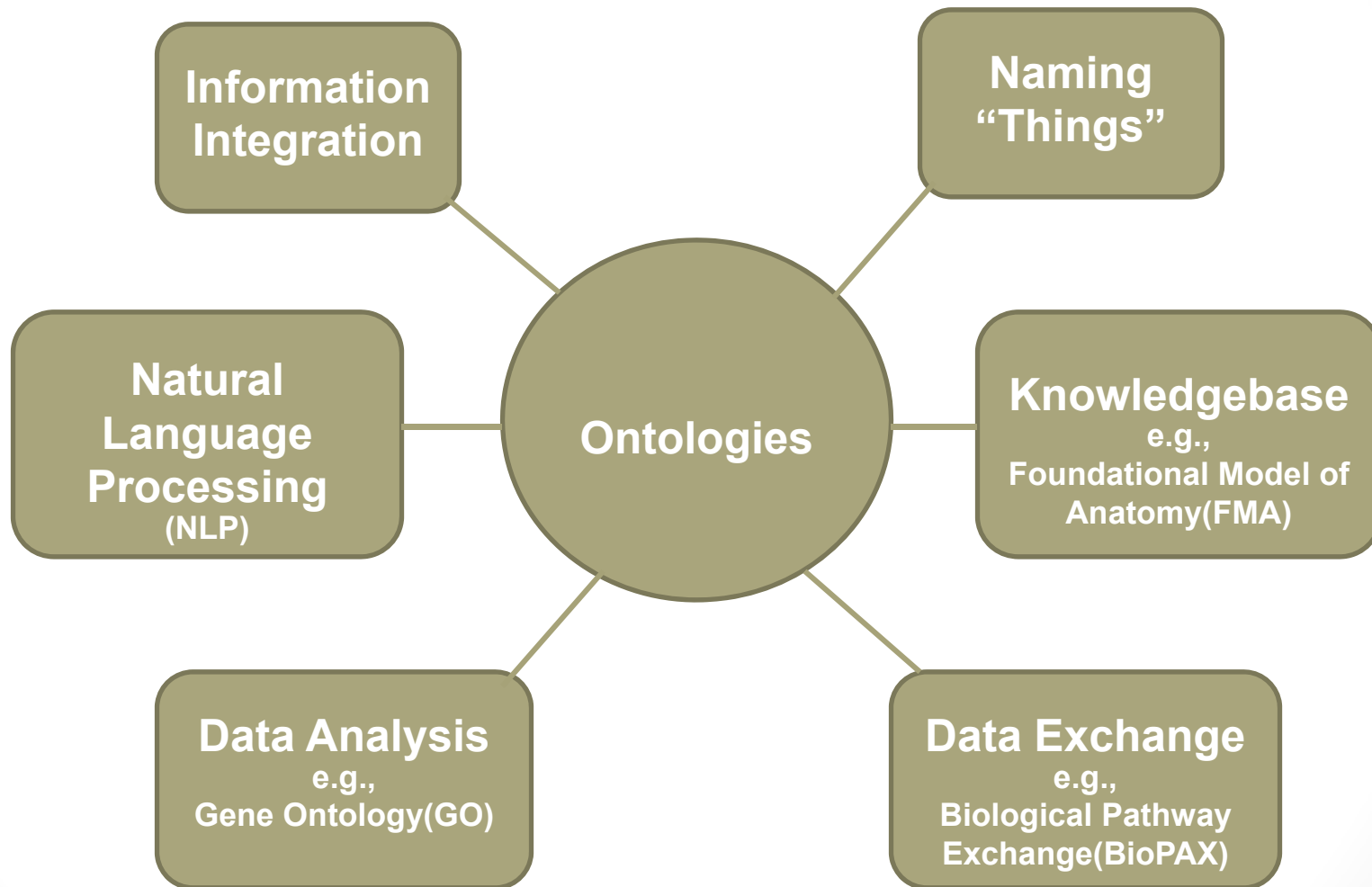
Method	Definition	Synonyms	Classification (isa)	Properties (has)	Other relations
Keywords					
Dictionary	X				
Controlled vocabulary	(X)	X			
Thesaurus	X	X			
Taxonomy	(X)	X	X Parrot is a bird	(X) Parrot has a beak	X
Ontology	X	X	X	X You can search by a term's properties	X

Relational?

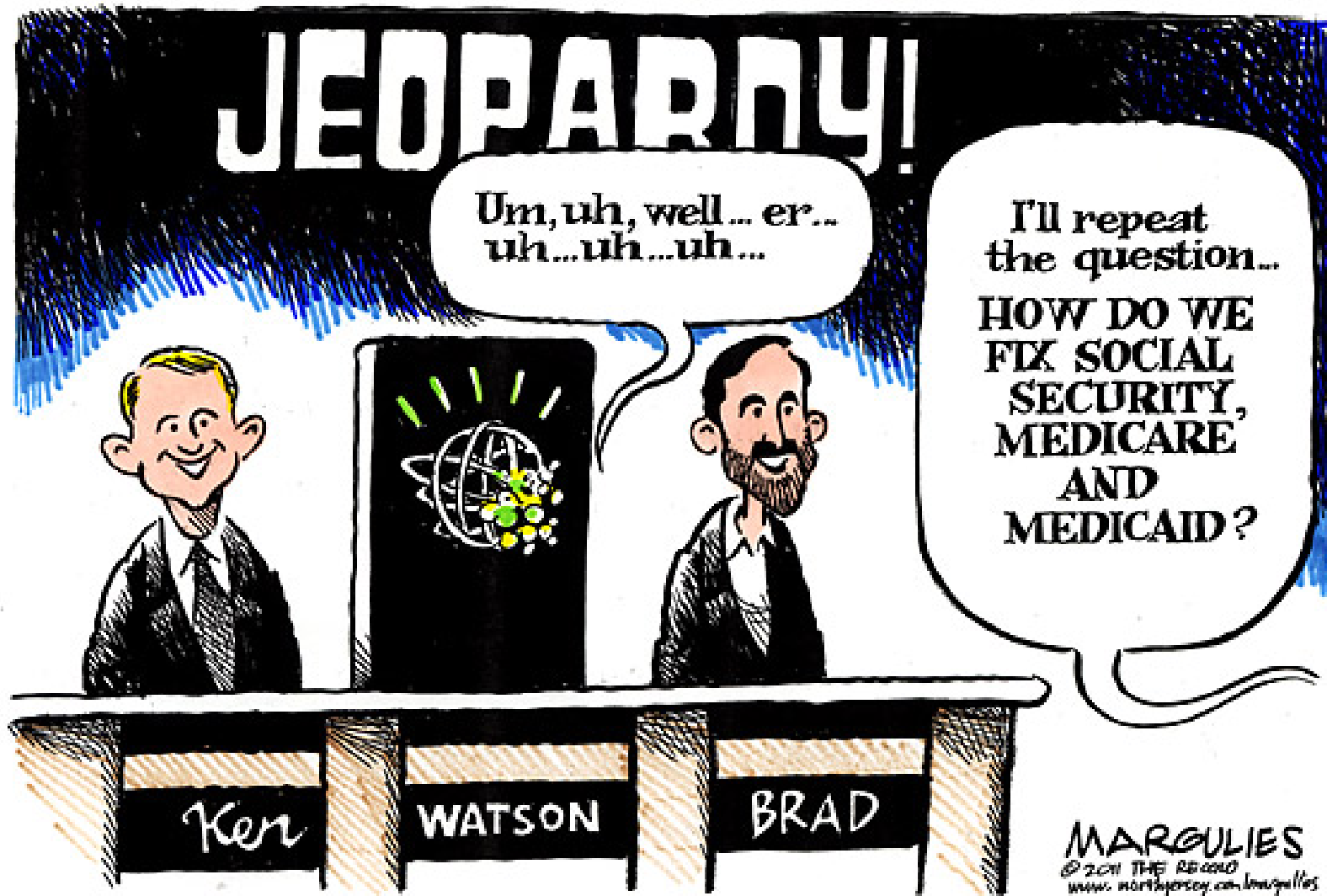


Schema-flexible!

Ontology Applications



Natural Language Understanding!



http://sc6.blogspot.com/2011/02/cartoon-of-week_20.html

ONSTR: Ontology for Newborn Screening Follow-up and Translational Research

What is ONSTR?

An **application ontology** representing the processes, entities and knowledge in the Newborn Screening and follow-up system (Domain):

- Newborn screening Dried Blood Spot (NDBS) covering Inherited Metabolic Diseases (IMDs).
- Genetic basis of IMDs.
- Positive tested cases follow-up practice including: medical/clinical confirmatory testing (biochemical and molecular).
- Medical and nutritional treatment (dietary analysis monitoring)
- Outcomes, e.g., physical and cognitive growth and development evaluation.
- Research related to IMDs and NBS.

Why are we building ONSTR?

- To provide basis for **standardization of data** annotation in NBS domain.
- To provide **knowledge base** for integrating, aggregating and reasoning over data collected from different NBS sources.
- To **develop tools** for knowledge and data sharing to be used by greater IMD/NBS community.

Not Alone.....

Open Biomedical Ontologies (OBO) Foundry principles and framework.

RELATION TO TIME GRANULARITY	CONTINUANT		OCCURRENT		
	INDEPENDENT	DEPENDENT			
ORGAN AND ORGANISM	Organism (NCBI Taxonomy)	Anatomical Entity (FMA, CARO)	Organ Function (FMP, CPRO)	Phenotypic Quality (PaTO)	Biological Process (GO)
CELL AND CELLULAR COMPONENT	Cell (CL)	Cellular Component (FMA, GO)	Cellular Function (GO)		
MOLECULE	Molecule (ChEBI, SO, RnaO, PrO)		Molecular Function (GO)		Molecular Process (GO)

ONSTR building process

1. Use case Definition

‘of all the diagnosis confirmed patients who were new born screening positive, between 2005-2010, matching age and matching mutation (R408W), did good nutritional management VS Kuvan + Nutritional management had better outcome with regards to MRI White matter changes at five years?’.

2. Identification of key entities and relationships holding between these entities


Methodology:

- Top Down and Bottom Up
- Survey of relevant literature
- Identifying the common data elements (CDEs)
- Follow OBO Foundry best practices


Top Down and Bottom Up

Common Data Elements (CDEs)

317	Understanding about blood Phe monitoring demonstrated	yesno	1, Yes 2, No
Phenylketonuria			
318			
319	Data Label	Data Type	Choices
320	Plasma Amino Acids	dropdown	1, Not done 2, Abnormal 3, Normal 4, Non-diagnostic 5, Unknown
321	Urinary Pteridine Profile	dropdown	1, Not done 2, Abnormal 3, Normal 4, Unknown
322	Biopterin	text	
323	Pteridin	text	
324	Neopterin	text	
325	Red Blood Cell (RBC) Dihydropteridine reductase (DHPR) activity	text	
326	Genetic testing performed since last visit	radio	1, Yes 2, No 3, Unknown
327	If yes, genetic mutation detected	Drop down	1, Phenex-100 2, Phenex 3, Pro-----etc.
328	MEDICAL FOOD PRESCRIPTION		
329	Medical Food Prescribed	radio	1, Yes 2, No 3, Unknown
330	Name of the Medical Food prescribed	checkbox	1, p.R408W 2, IVS10-11G> 3, p.165T-----etc.
331	Intact (Natural) Protein Prescribed	radio	
332	Grams of Protein/day Prescribed from Intact (Natural) Protein	text/Nur	
333	Milligrams of Phe/day Prescribed from Intact (Natural) Protein	text/Nur	
334	Number of Phe exchanges/day	text/Nur	
335	Large neutral amino acids	radio	
336	Tyrosine supplementation	radio	
337	Pharmacological therapy (Kuvan)	radio	
338	Alternative pathway (PEG-PAL)	radio	
339	DIET ANALYSIS		
340	Type of Diet Record	radio	
341	Diet Analysis Results:		
342	Milligrams of Phe intake/day = mG/Day	text/Nur	
343	Milligrams of Tyrosine intake/day = mG/Day	text/Nur	
344	Grams of Protein intake from MEDICAL Foods/Day = G/Day	text/Nur	
345	Overall Total Protein intake/Day = G/Day	text/Nur	
346	Overall Total Energy intake/Day = G/Day	text/Nur	
347	DIET/PRESCRIPTION ADHERENCE AND COMPLIANCE		
348	Drinking Medical Food?	radio	
349	If yes, full or less than full	radio	
350	Consuming higher Phe than prescribed?	radio	
351	Consuming MEATS and DAIRY PRODUCTS?	radio	
352	Consuming MODIFIED LOW PROTEIN FOODS?	radio	



PKU Food Intake Record



Department of Human Genetics
404-778-8566

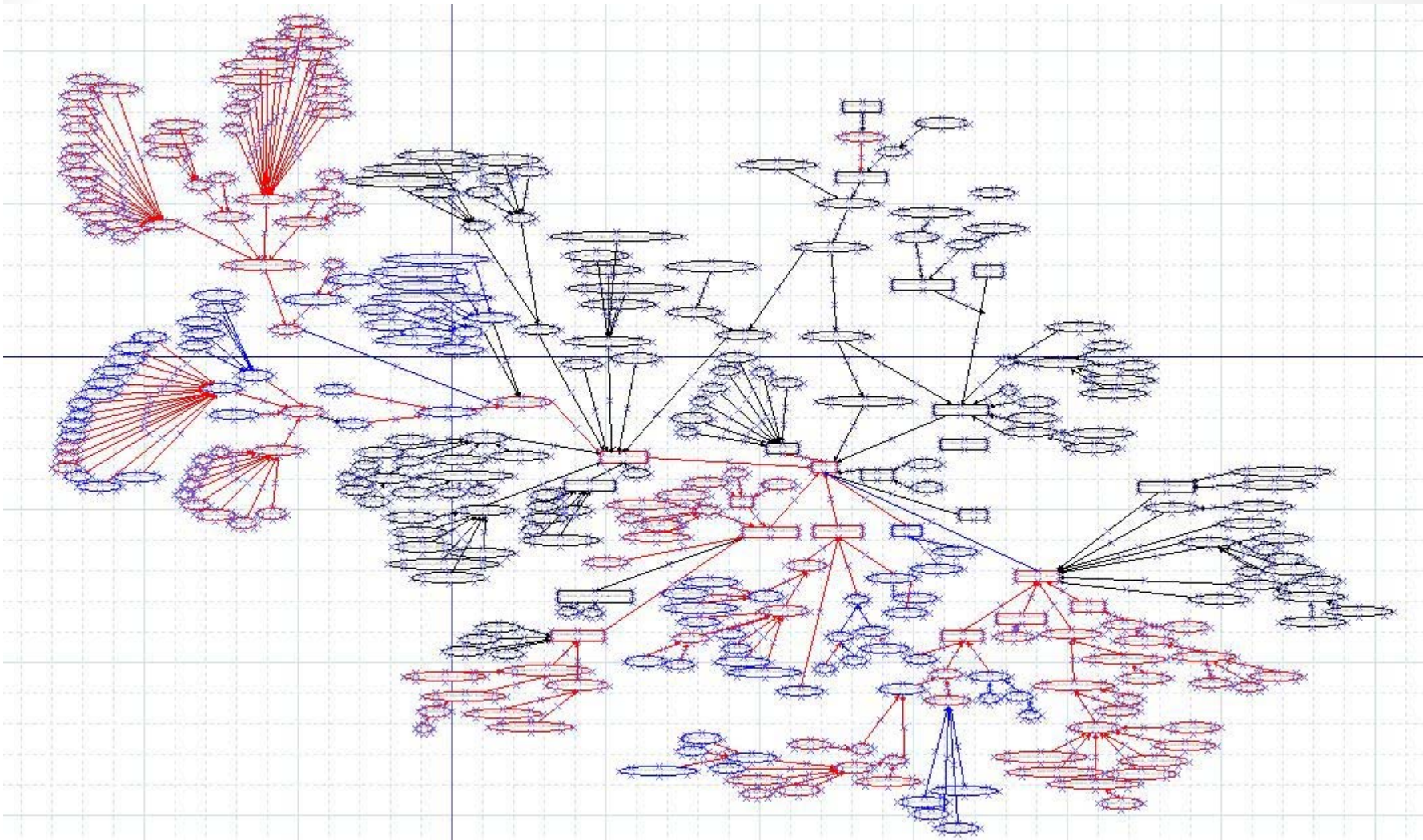
Date: 5/16/2011
 Name: _____ Date of Birth: _____
 Height: 32 in Weight: 27 lbs.
 Medications: _____
 Vitamins or Supplements: _____

Formula Prescription: *(Please include the name and amount of each ingredient used to make your Formula.)*
Ingredients: PERIFLEX JUNIOR PKU **Amount:** 82.5g

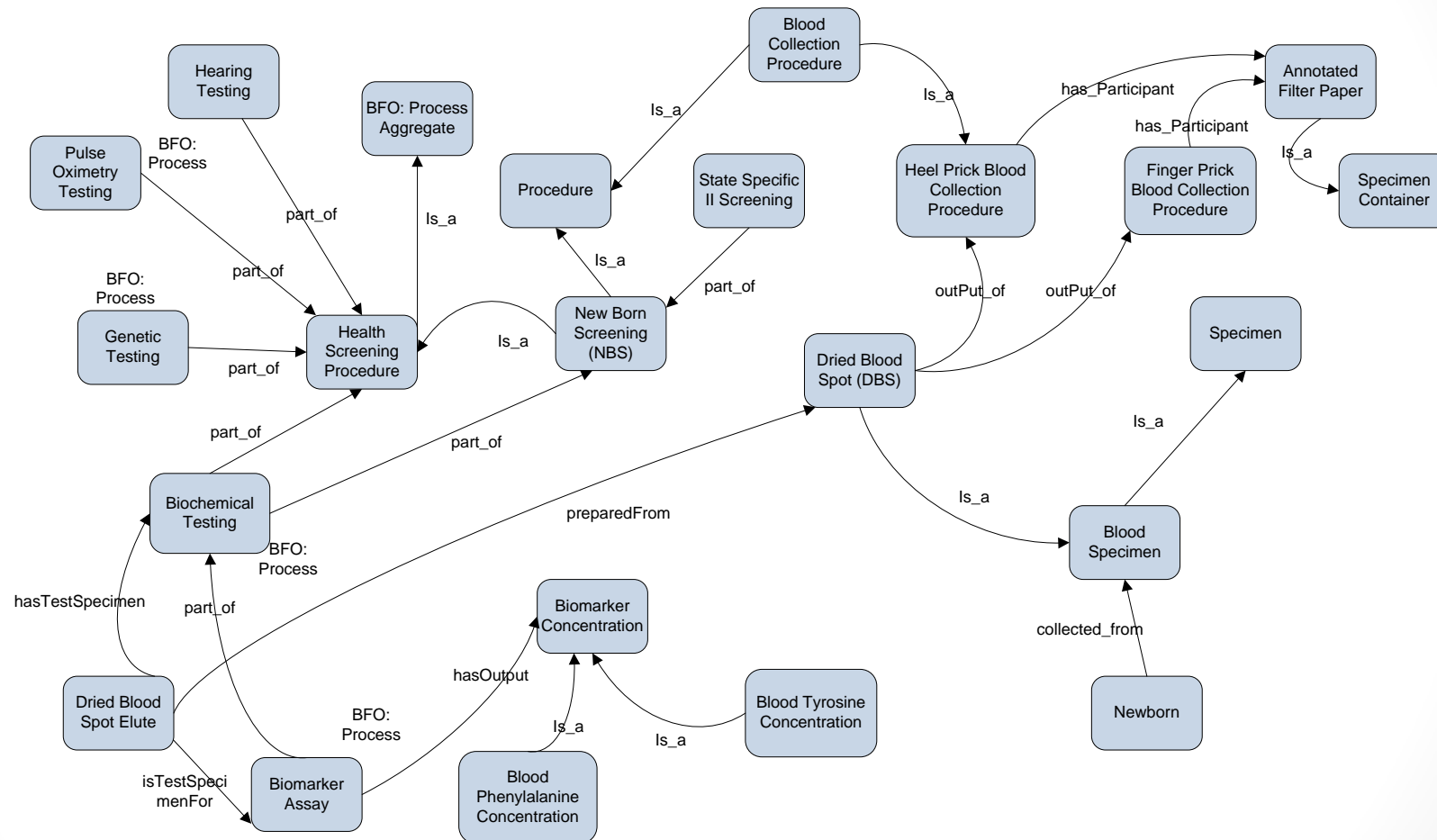
Volume Mixed: 12 oz. Volume Consumed: 11 oz. # of servings: 3

* Meal	Food/Beverage Item	Amount of Food Eaten	Phe (mg)	** Exchanges	Comments
D	Walmart brand honey nut cereals	5g	25	1.67	
L	banana	47g	17	1.13	
L	yogurt	1 tube (64g)	102	6.8	
L	green beans	35g	23.5	1.56	
L	Smarties	1 package	0	0	
T		82g	4	0.22	

All Common Data Elements (CDEs)



Modeling with Relations



ONSTR building process contd.

3. Ontology coding

- ONSTR is formally encoded as a RDF/XML serialization of OWL2 (W3C semantic Web standards)

4. Ontology integration

- Mappings between ONSTR and other relevant ontologies/vocabularies (Future work).

5. Ontology evaluation

- In progress, concomitant with ONSTR development.

6. Ontology documentation

- Available on the ONSTR project page:
<http://code.google.com/p/onstr/source/docs>)

ONSTR Statistics

Total number of classes: 1842

ONSTR native classes: 1100

Imported classes: 742

BioPortal

<http://bioportal.bioontology.org/ontologies/49978>
National Center for Biomedical Ontology (NCBO), Stanford University



Ontology for Newborn Screening Follow-up and Translational Research - Summary | NCBO BioPortal - Mozilla Firefox

bioportal.bioontology.org/ontologies/3137

BioPortal Browse Search Mappings Recommender Annotator Resource Index Projects Sign In Help Feedback

Ontology for Newborn Screening Follow-up and Translational Research

Summary

Details

ONTOLOGY ID	3137
ACRONYM	ONSTR
VISIBILITY	Public
BIOPORTAL PURL	http://purl.bioontology.org/ontology/ONSTR
STATUS	
FORMAT	OWL
CATEGORIES	Biological Process Human Phenotype Health Development Dysfunction
GROUPS	
CONTACT	Rani Singh, Prabhu Shankar, Snezana Nikolic, snez.sn@gmail.com
HOME PAGE	
PUBLICATIONS PAGE	
DOCUMENTATION PAGE	http://onstr.googlecode.com/svn/docs/
DESCRIPTION	Ontology for Newborn Screening Follow-up and Translational Research (ONSTR) is an application ontology covering the domain of newborn screening, follow-up and translational research pertaining to patients diagnosed with inheritable and congenital diseases mainly identified through newborn dried blood spot screening. ONSTR uses the Basic Formal Ontology v2 (BFO2, v2012-07-20) as top-level ontology and extends the classes imported from OBO Foundry ontologies and candidate ontologies. For latest release notes please see: http://onstr.googlecode.com/svn/tags/currentRelease/2013-03-20/

Metrics

NUMBER OF CLASSES:	1842
NUMBER OF INDIVIDUALS:	0
NUMBER OF PROPERTIES:	107
MAXIMUM DEPTH:	35
MAXIMUM NUMBER OF SIBLINGS:	32
AVERAGE NUMBER OF SIBLINGS:	13
CLASSES WITH A SINGLE SUBCLASS:	306
CLASSES WITH MORE THAN 25 SUBCLASSES:	2
CLASSES WITH NO DEFINITION:	177

Reviews

Add your review

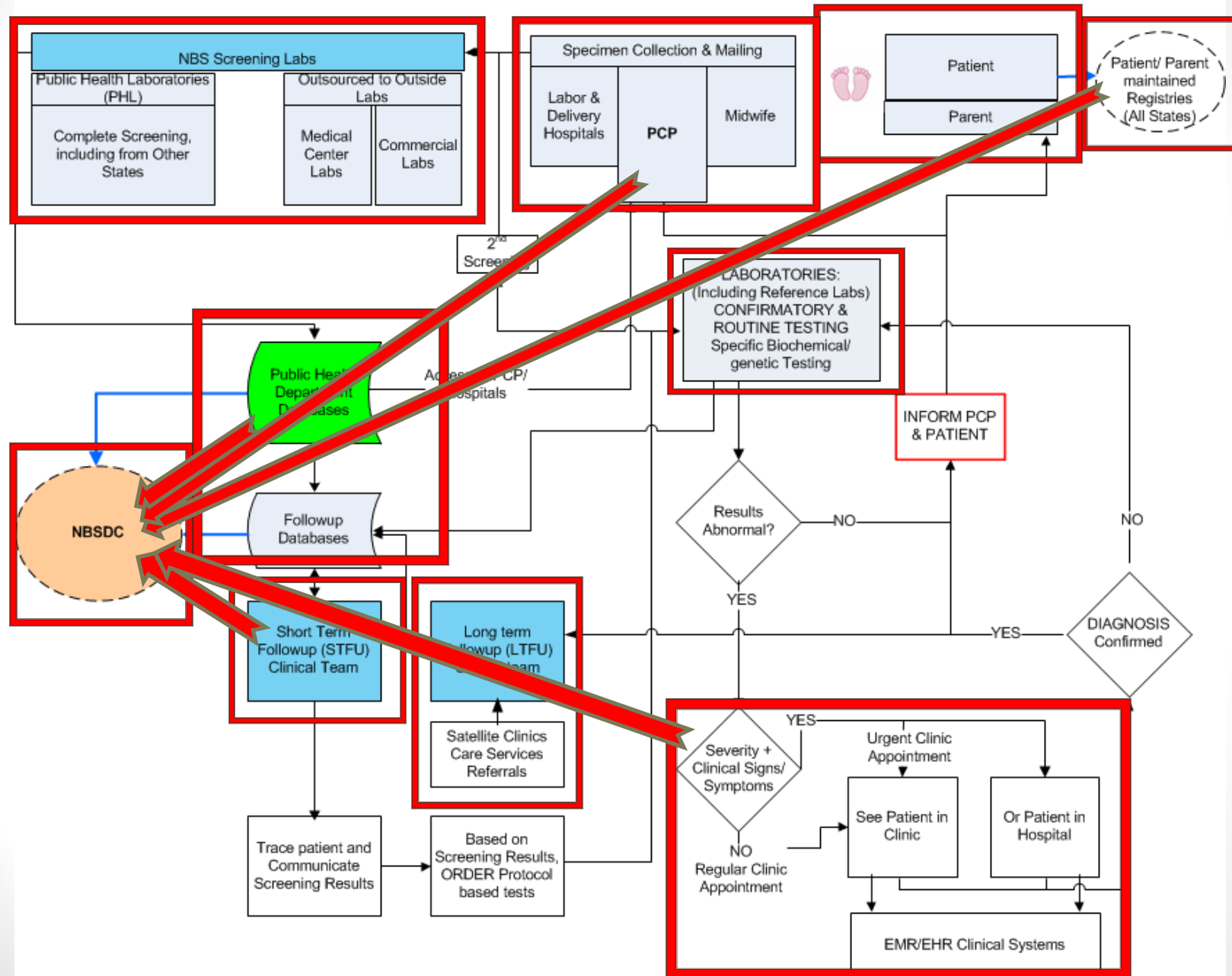
No reviews available.

Versions

VERSION	RELEASE DATE	UPLOAD DATE	DOWNLOADS
0.2	03/20/2013	03/22/2013	Ontology
0.1	08/30/2012	08/30/2012	Ontology
2012-09-17	09/17/2012	09/14/2012	Ontology

Desktop 5:03 PM

Newborn Screening Follow-up Data Integration Collaborative (NBSDC)



Acknowledgements:

Funded by:

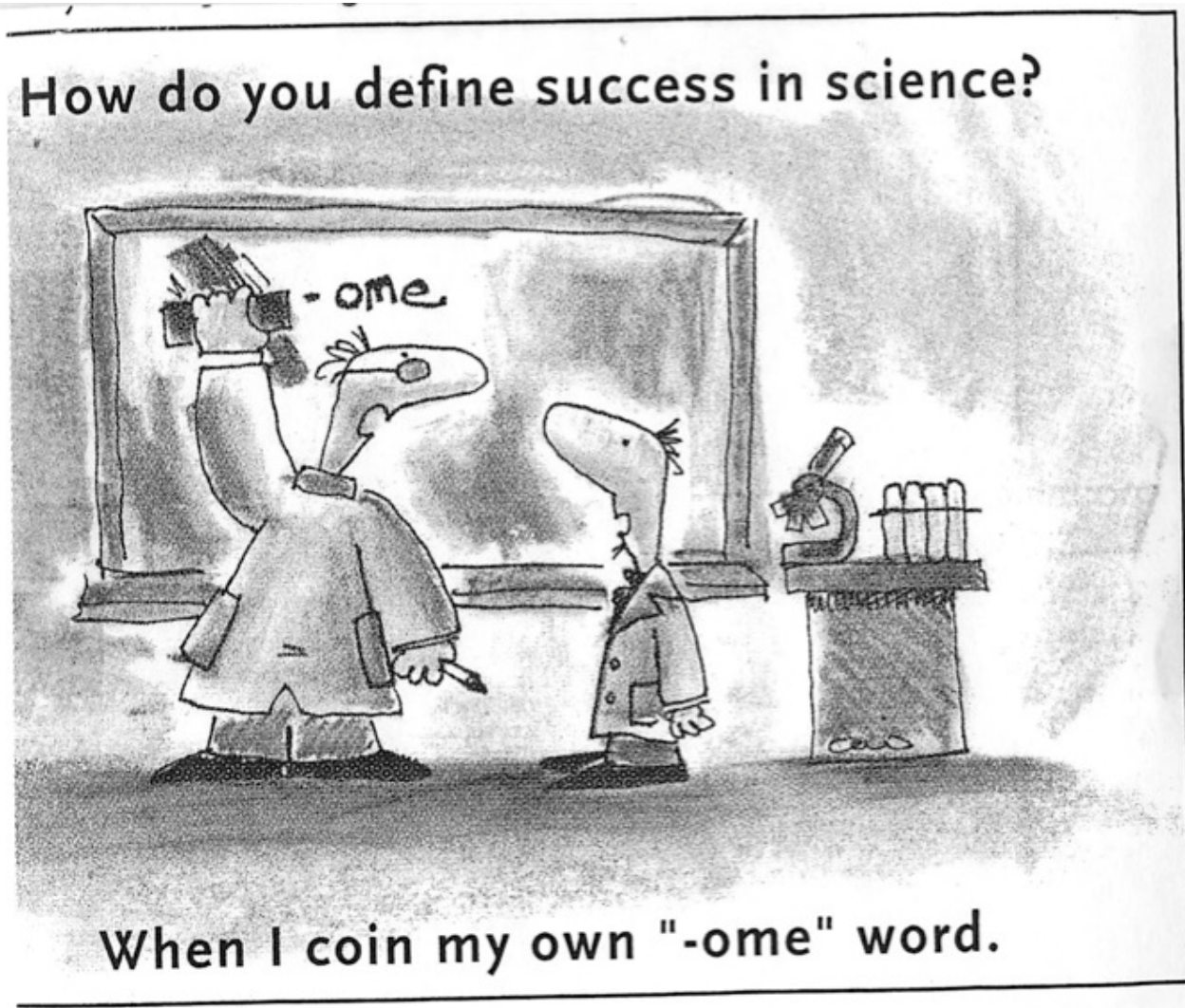
- **2009-10 HSI Seed Grant, a Clinical Outcomes Research and Public Health (CORPH) Pilot Grants Program, jointly supported by Georgia Tech and Children's Healthcare of Atlanta and**
- **The Southeast NBS & Genetics Collaborative (SERC) Grant from the Maternal and Child Health Bureau, HRSA Grant U22MC10979.**

Special thanks to:

- **Dr. Barry Smith, National Center for Ontological Research (NCOR), University @ Buffalo, Buffalo.**

Thank You

Questions: PRSHANK@emory.edu



Semantic technologies in action....

Cross-Species Biomarkers Reducing Animal Testing



The screenshot displays the Sentient Knowledge Explorer interface. On the left, there are navigation panels for 'My Queries' and 'Browse iPool'. The main area shows a network diagram of metabolic pathways, including 'tryptophan metabolic pathway', 'fatty acid metabolic pathway', and 'arachidonic acid metabolic pathway'. A search window is open, showing search results for '1.14.1. metabolic disease'. Below the diagram, there is a table of '53 instances of Enzyme' with columns for EC number, Gene ID, Gene Name, Gene Symbol, Probe ID, Source, UnGene ID, Metabolite, Protein, and Tissue Type. A small image of a dog is visible in the bottom right corner of the interface.

IMO Name	Creator
LiverKidney_Biopsy1_0001.imo	egombocz A
LiverKidney_Biopsy1_0001.imo	egombocz A
Plasma_enro_levels1.imo	egombocz A
PROJ_1EFE_ProInsulin.imo	egombocz P
PROJ_3405Kidney.imo	egombocz P
PROJ_ALS_Immunoblot_PNAS02907-1.imo	egombocz P
PROJ_ALS_Immunoblot_PNAS02907-2.imo	egombocz P
PROJ_AS_xray4.imo	egombocz P
PROJ_bcr293-1[1].imo	egombocz E
PROJ_bmbm_gei0001.imo	egombocz E
REB_RBM_pseudoDatafile3_RBM.imo	egombocz H
REB_RBM_pseudoDatafile4_RBM.imo	egombocz H

Result: Semantic integration (large animals to small animals to cell culture) to discover cross-species biomarkers applicable to human adverse events and diseases

Courtesy: Erich Gombocz, VP & CSO, IO Informatics, Inc.

Semantic technologies in action....

Combination Treatment Effectiveness in Prostate Cancer



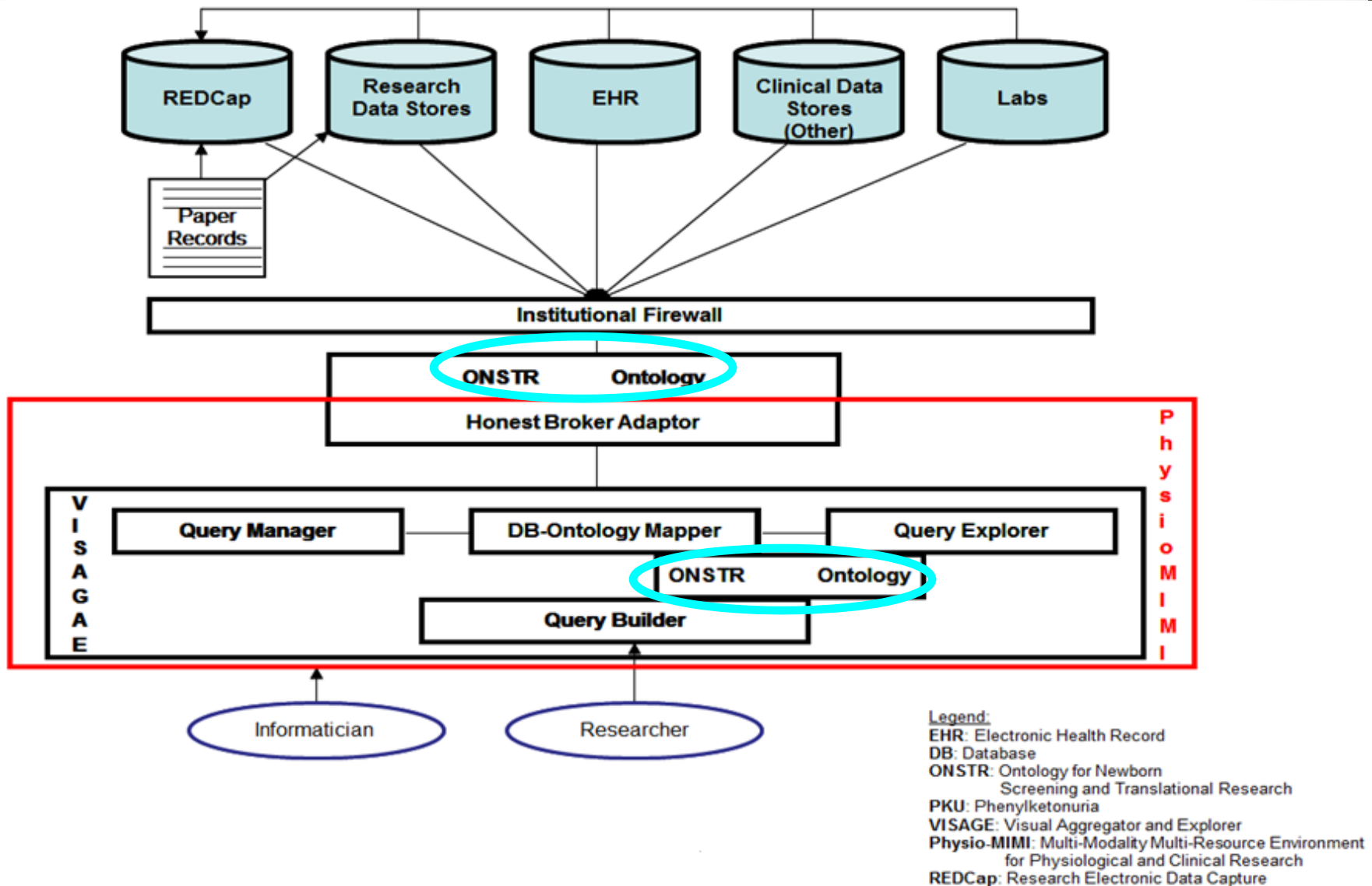
VANCOUVER PROSTATE CENTRE
A UBC & VGH Centre of Excellence

The screenshot displays a complex semantic web application interface. On the left, a sidebar shows a hierarchical menu with categories like 'ComparisonID', 'GeneSymbol', and 'FoldChange'. The main area features a network diagram with nodes representing genes and their interactions. Below the diagram, a table lists search results for 'Treatment effects, strong down-regulated genes [multi-platform]'. The table includes columns for ComparisonID, GeneSymbol, FoldChange, and Gene_Description. The results show various comparisons such as AR_siRNA_RvsNegR, LORvsLOE, and NegRvsLOR, with associated gene symbols like PLA2G2A, SERPIN1, and MSMB. The interface also includes a search bar, navigation tabs, and a footer with copyright information.

ComparisonID	GeneSymbol	FoldChange	Gene_Description
AR_siRNA_RvsNegR	PLA2G2A	-19.5934561994912	Phospholipase A2- membrane associated precursor secretory phospholipase A2) (NPS-PLA2). [Source:U
LORvsLOE	PLA2G2A	-19.5934561994912	Phospholipase A2- membrane associated precursor secretory phospholipase A2) (NPS-PLA2). [Source:U
AR_siRNA_EvsNegE	SERPINI1	-13.8921693717385	Neuroserpin precursor (Serpin I1) (Protease inhibit
LORvsLOE	SERPINI1	-13.8921693717385	Neuroserpin precursor (Serpin I1) (Protease inhibit
NHT8to9vsNHT0	C4orf18	-13.3050313075417	TCPD2512. [Source:Uniprot/SPTREMBL;Acc:Q6UJWH
NHT5to6vsNHT0	C4orf18	-13.3050313075417	TCPD2512. [Source:Uniprot/SPTREMBL;Acc:Q6UJWH
AR_siRNA_EvsNegE	C4orf18	-13.3050313075417	TCPD2512. [Source:Uniprot/SPTREMBL;Acc:Q6UJWH
AR_siRNA_RvsNegR	C4orf18	-13.3050313075417	TCPD2512. [Source:Uniprot/SPTREMBL;Acc:Q6UJWH
LORvsLOE	C4orf18	-13.3050313075417	TCPD2512. [Source:Uniprot/SPTREMBL;Acc:Q6UJWH
AlvsNHT0	MSMB	-12.6863047591418	Beta-microseminoprotein precursor (Prostate secr (Immunoglobulin-binding factor) (IGBF) (PN44). [Sou
NegRvsLOR	MSMB	-12.6863047591418	Beta-microseminoprotein precursor (Prostate secr (Immunoglobulin-binding factor) (IGBF) (PN44). [Sou
AR_siRNA_RvsNegR	MSMB	-12.6863047591418	Beta-microseminoprotein precursor (Prostate secr (Immunoglobulin-binding factor) (IGBF) (PN44). [Sou
AlvsNHT0	MSMB	-12.3925399110126	Beta-microseminoprotein precursor (Prostate secr (Immunoglobulin-binding factor) (IGBF) (PN44). [Sou
NegRvsLOR	MSMB	-12.3925399110126	Beta-microseminoprotein precursor (Prostate secr (Immunoglobulin-binding factor) (IGBF) (PN44). [Sou
AR_siRNA_RvsNegR	MSMB	-12.3925399110126	Beta-microseminoprotein precursor (Prostate secr (Immunoglobulin-binding factor) (IGBF) (PN44). [Sou

Result: effectiveness comparison of different combination treatments based on multi-platform genomic and proteomic marker profiles and patient match

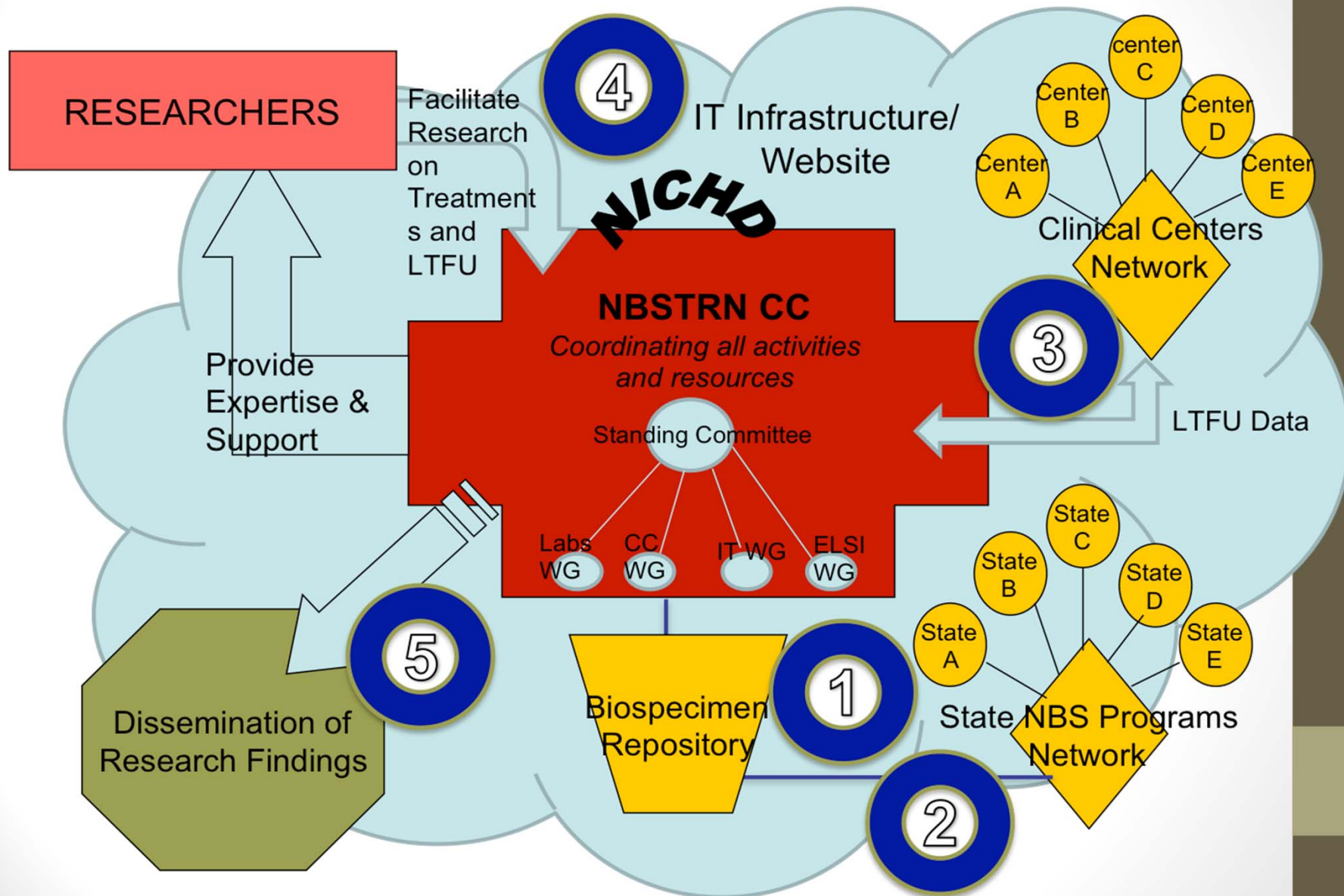
Tools already being developed...



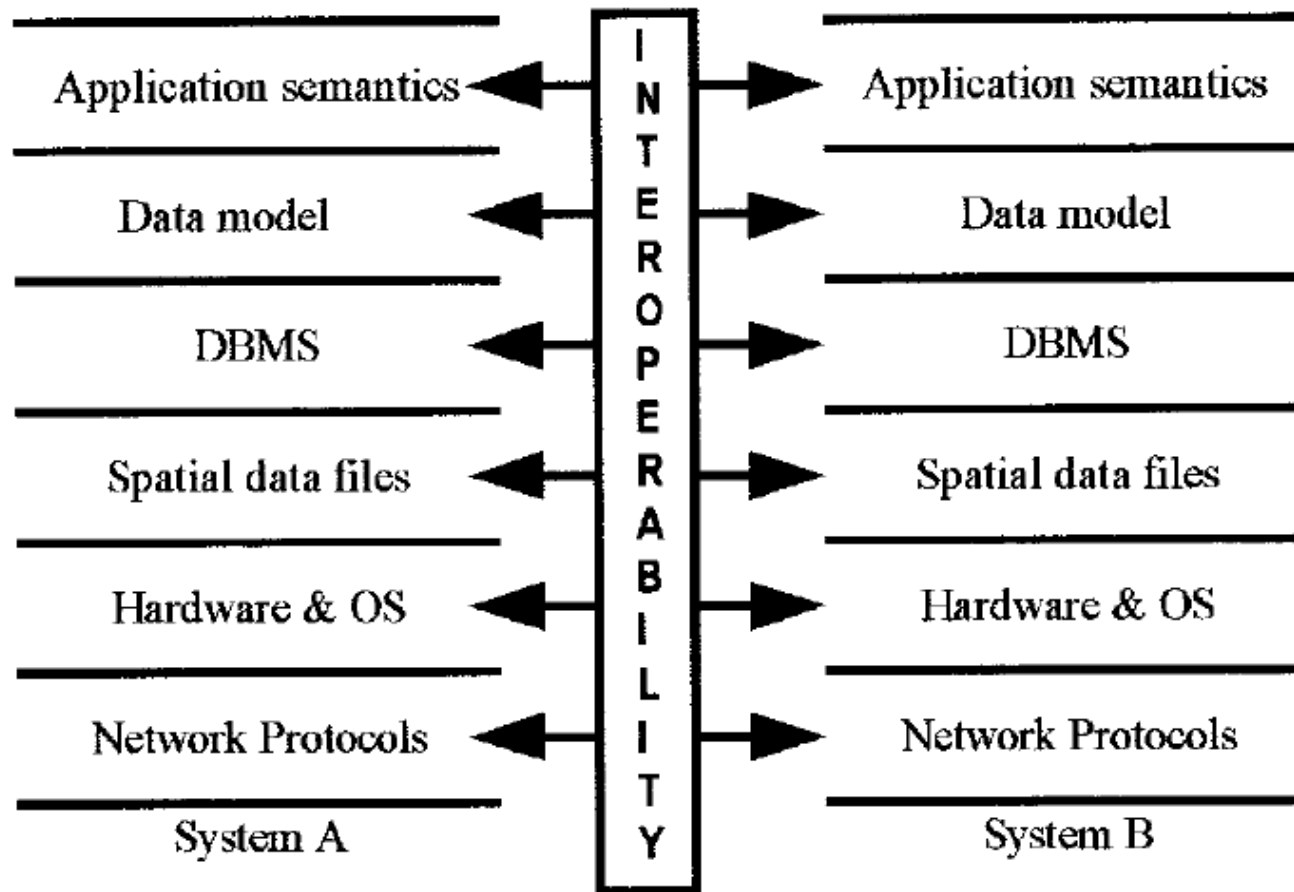
Challenges

- **Time consuming**
- **Domain knowledge, Multi-disciplinary**
- **Computing Capacity to process Graphs**
- **Skilled personnel**
- **Funding**
- **Issues with data sharing**
 - **Buy in**
 - **Policy**
 - **HIPAA**

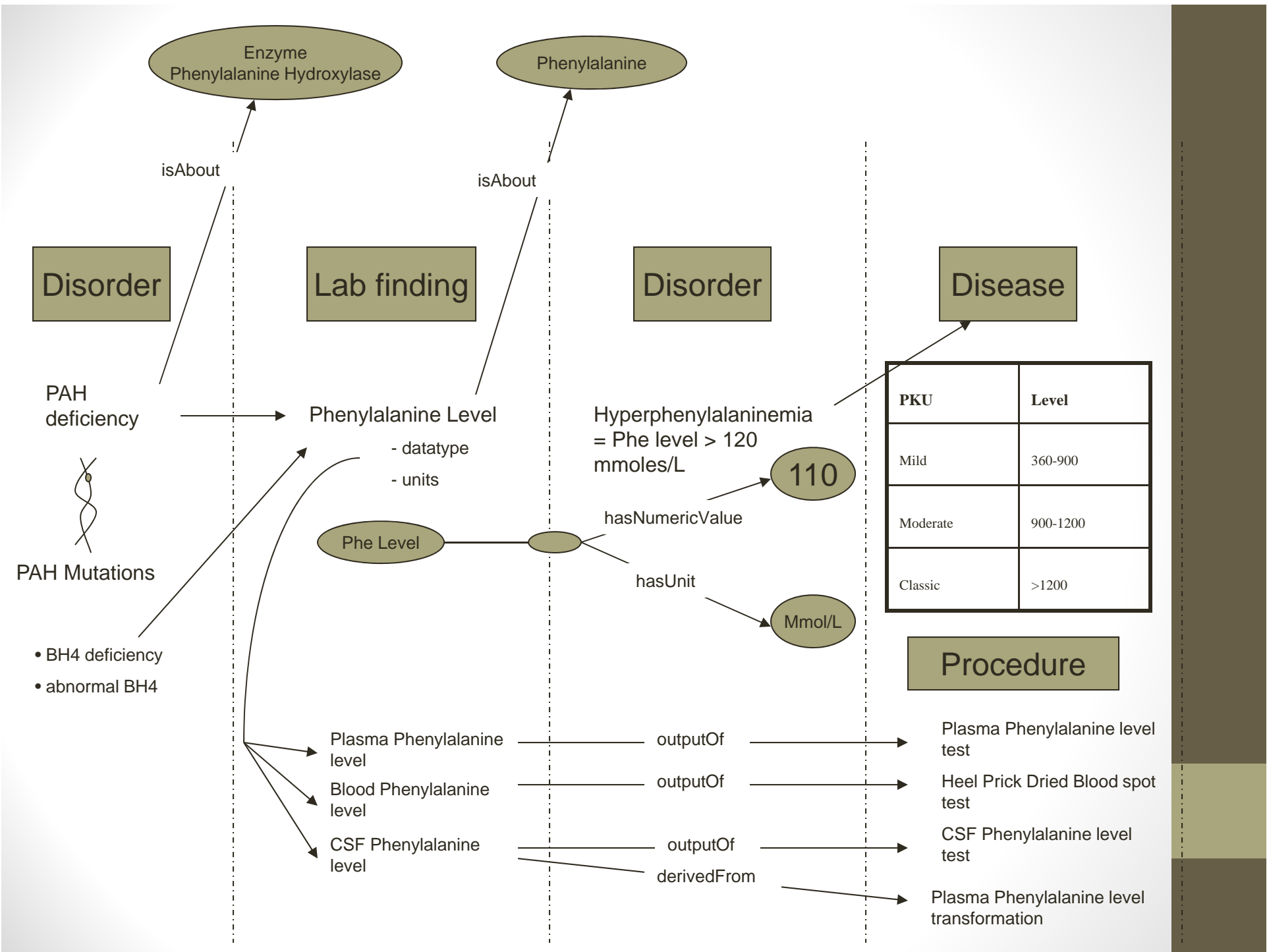
NBSTRN



Interoperability



Levels of interoperability.



Big Picture

