The BioMANTA Ontology

Integrating Protein-Protein Interaction Data

InterOntology08 – Tokyo, Japan

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Project Overview

- Development of Semantic Interactome Ontology
- Infrastructure for Integration, Processing and Querying
- RDF and Inferencing on Scale-Out Architecture
- Output for Visualisation and Improve Data Quality through Network Analysis

The Domain is a Problem

- Genes. What are genes anyway? Do they even exist?
  - Unit of hereditary (1860s-1900s)
  - Locus (1910s)
  - Coding for a Protein (1940s)
  - Molecule (1950s)
  - Transcribed Code (1960s)
  - Open Reading Frame (1970s-1980s)
  - Annotated Entity (1990s-2000s)

“…the gene is […] neither discrete […] nor continuous […], nor does it have a location […], nor a clearcut function […], not even a constant sequence […] nor definite borderlines” – Falk (1986)

Other Problems

- Properties tied to Local or Global IDs
- Data formats
- Quality – missing, incomplete, wrong
- Project size, scope, scale
- Differing semantics and specialities
- Poor understanding or usage of model semantics

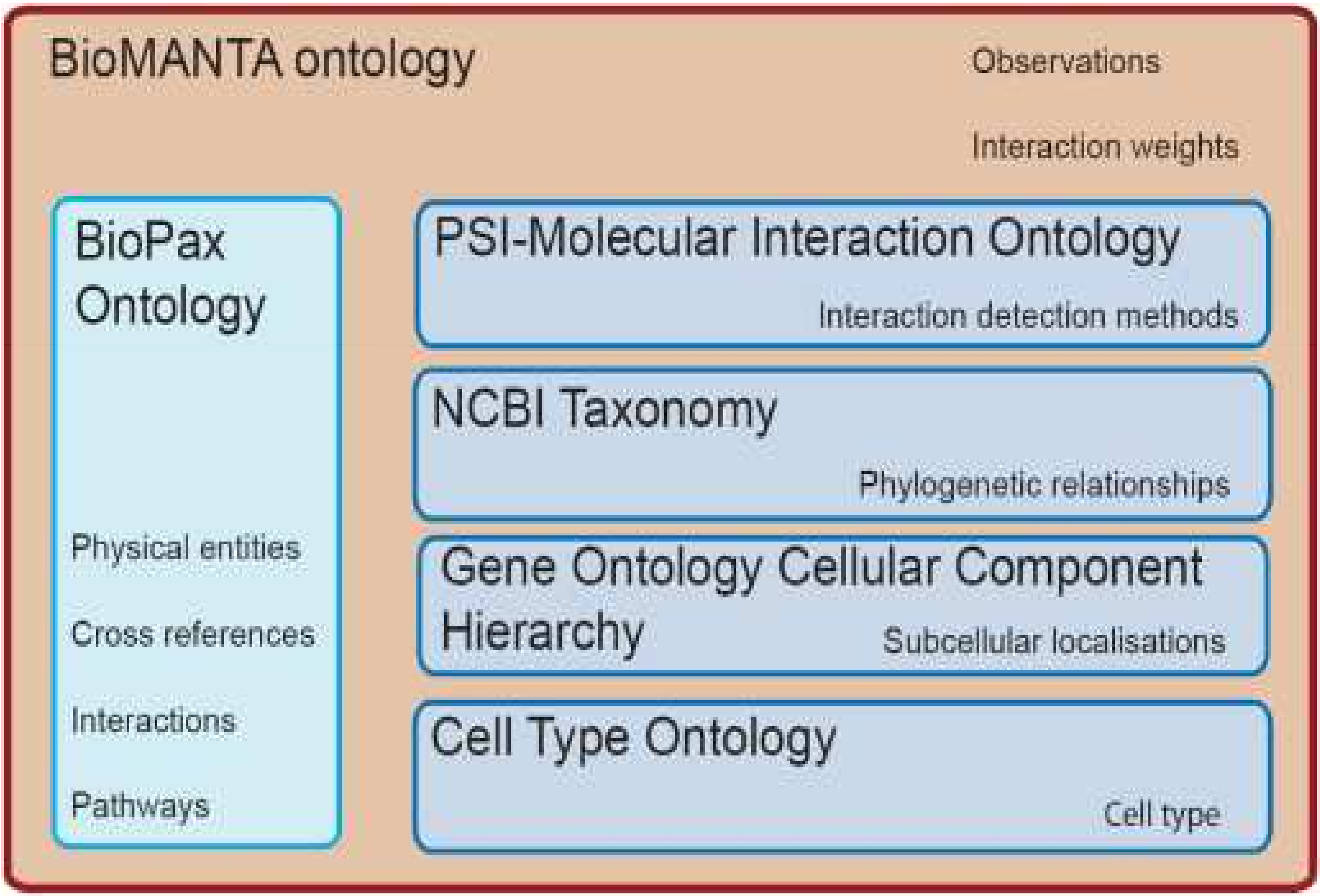
Some Questions

- What are we modelling? There is a record of an observation of an interaction in a given context about a protein.
- Do we need a new ontology for the domain? Not really.
- Why? We are integrating existing databases.
- We need to take the best bits from what we need to support our own in silico experiments.

Our Design

- Create or reuse dereferenceable URIs for names.
- Do not create another ID.
- The “thing” (protein, experiment, etc.) is a blank node.
- Global, local names and other properties are related to the blank node.
- Reusing existing terms where appropriate.
- It is a snapshot of the current data at a given time.
- Multiple versions of data and ontologies is expected.
- Instances of classes – for example Cell Type instances from Cell Type ontology (punning).

Ontology



BioMANTA ontology

Observations

Interaction weights

BioPax Ontology

Physical entities

Cross references

Interactions

Pathways

PSI-Molecular Interaction Ontology

Interaction detection methods

NCBI Taxonomy

Phylogenetic relationships

Gene Ontology Cellular Component Hierarchy

Subcellular localisations

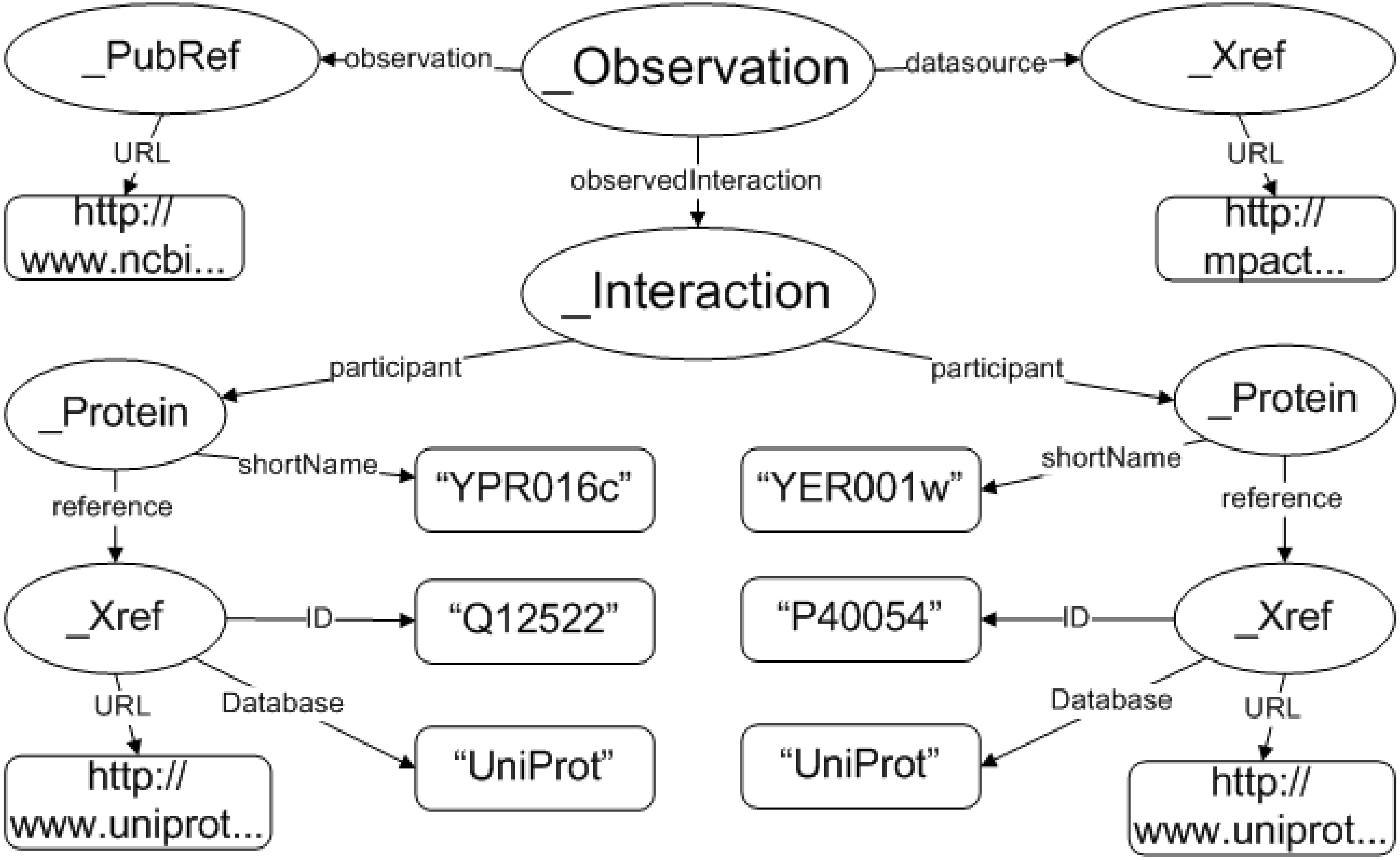
Cell Type Ontology

Cell type

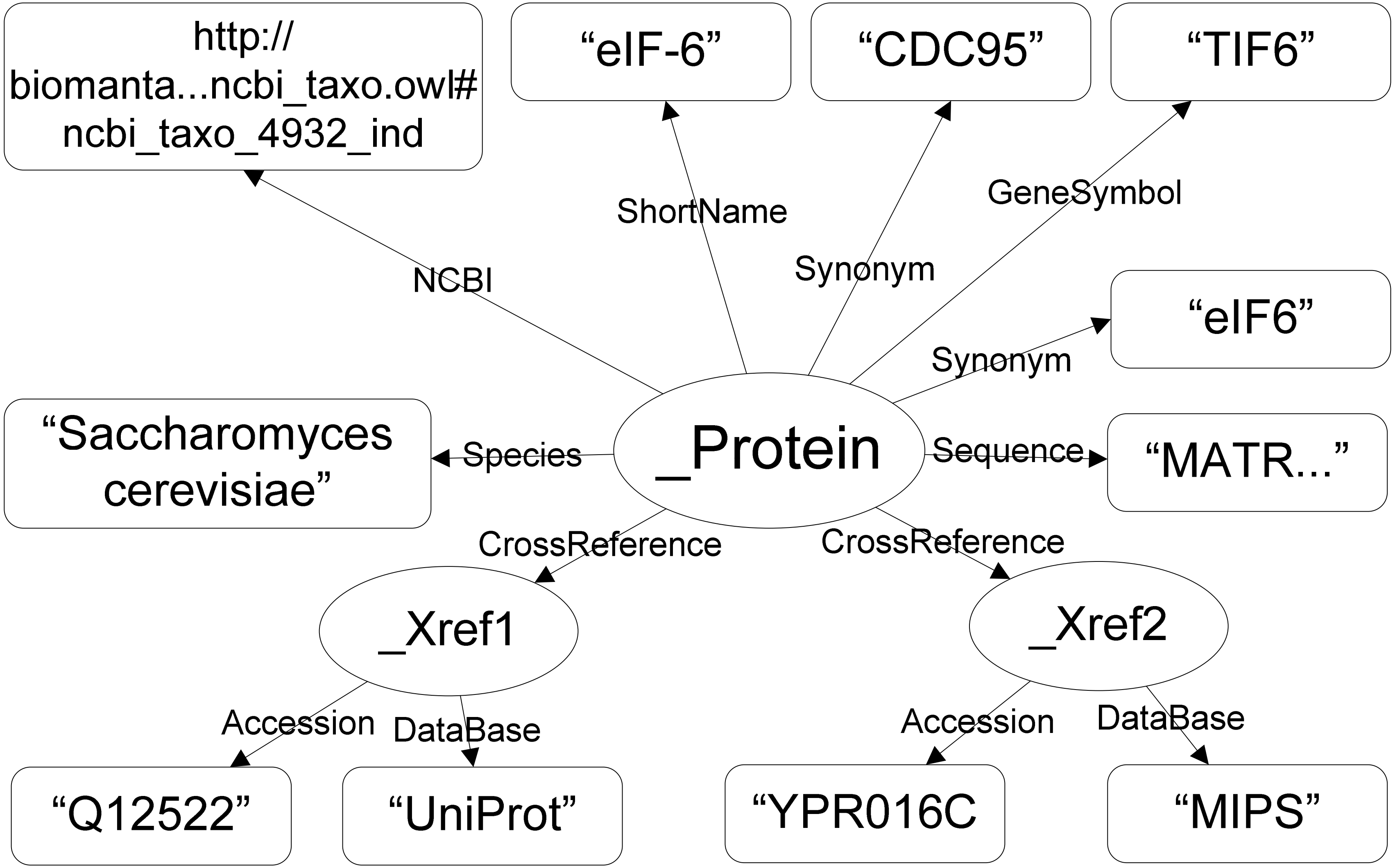
Examples of BioMANTA Extensions

- Experimental Observation ∩ Unspecified Observation ∩ Predicted Observation ∩ Inferred Observation = Ø
- sourceOfData – identity of 3rd party resource
- observedCellType – the cell type in which the experimental observation occurred.
- experimentalMethod – one type of evidence for a particular interaction.

An Overview of an Instance



A Protein


http://
biomanta...ncbi_taxo.owl#
ncbi_taxo_4932_ind
“eIF-6”
“CDC95”
“TIF6”
ShortName
GeneSymbol
NCBI
Synonym
“eIF6”
Synonym
“Saccharomyces cerevisiae”
Species
_Protein
Sequence
“MATR...”
CrossReference
CrossReference
_Xref1
_Xref2
Accession
DataBase
Accession
DataBase
“Q12522”
“UniProt”
“YPR016C”
“MIPS”

An Agile Process (Rip, Mix, Verify)

- People and interactions over process.
- Working ontologies over well documented ones.
- Collaboration over negotiation.
- Respond to change rather than follow a plan.
- This means:
  - Verify the output (interaction, PubMedID, Experimental method, etc).
  - Everything in RDF and OWL.
  - Feedback - find missing data or mistakes in the model.

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Links

Web Site

- http://biomanta.org/

Ontologies and other Results

- http://biomanta.org/downloads/

Sample Output

- http://biomanta.org/downloads/2008/yeast.zip

RDF Library for Scale-out (in development)

- http://jrdf.sf.net/