Adapting resources to the Semantic Web: Experience with Entrez Gene

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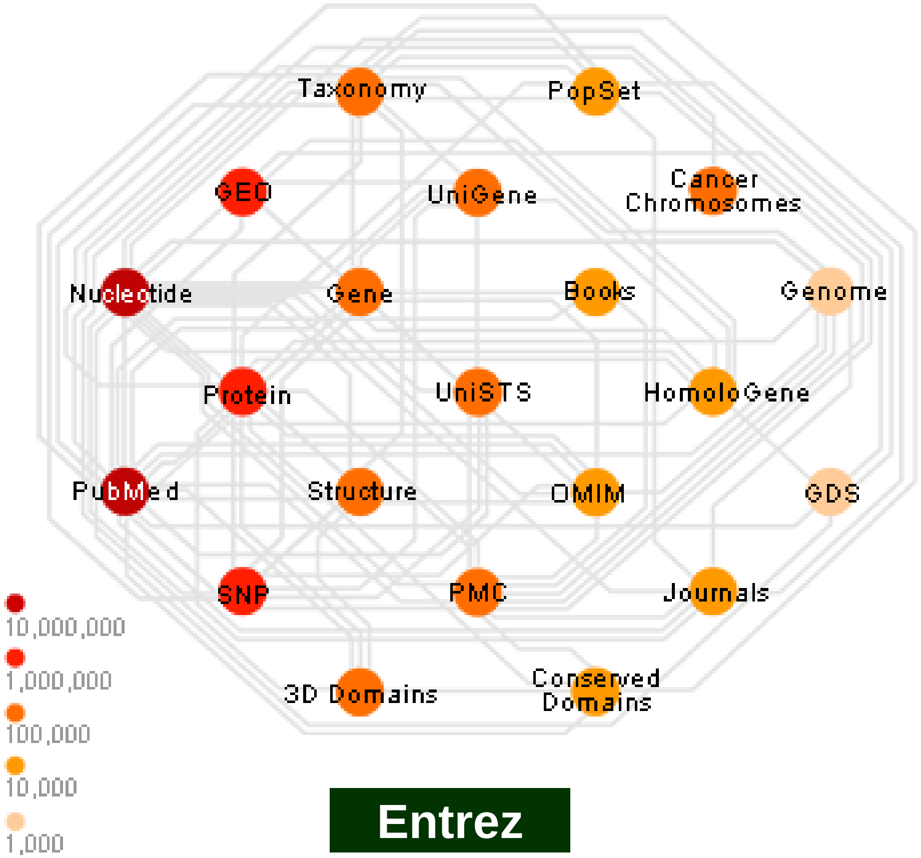
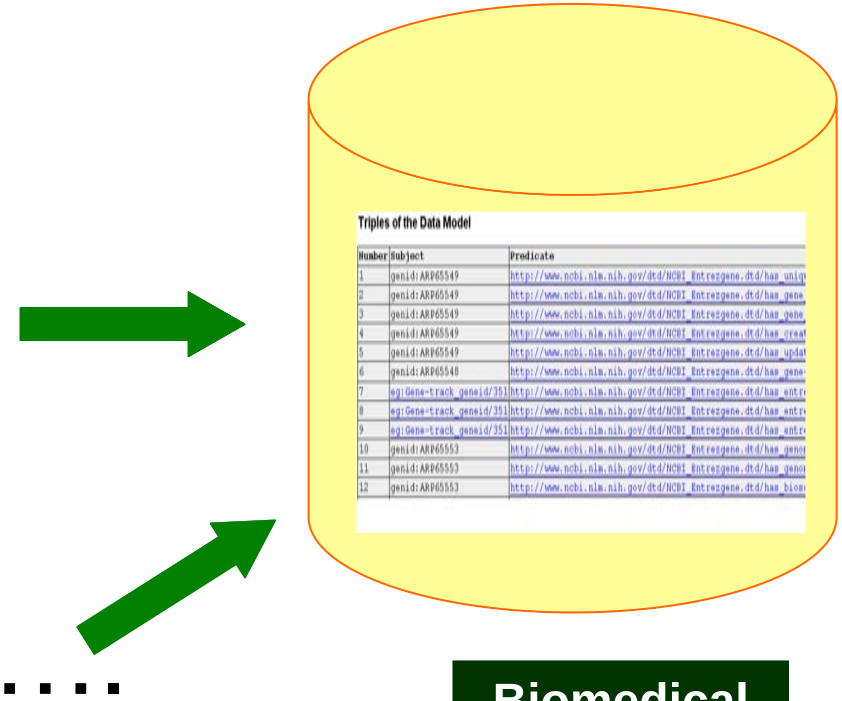
Outline

- Motivation
- Materials and Methods
- Results
- Issues and challenges

From supporting navigation to supporting knowledge processing



Entrez



Triples of the Data Model

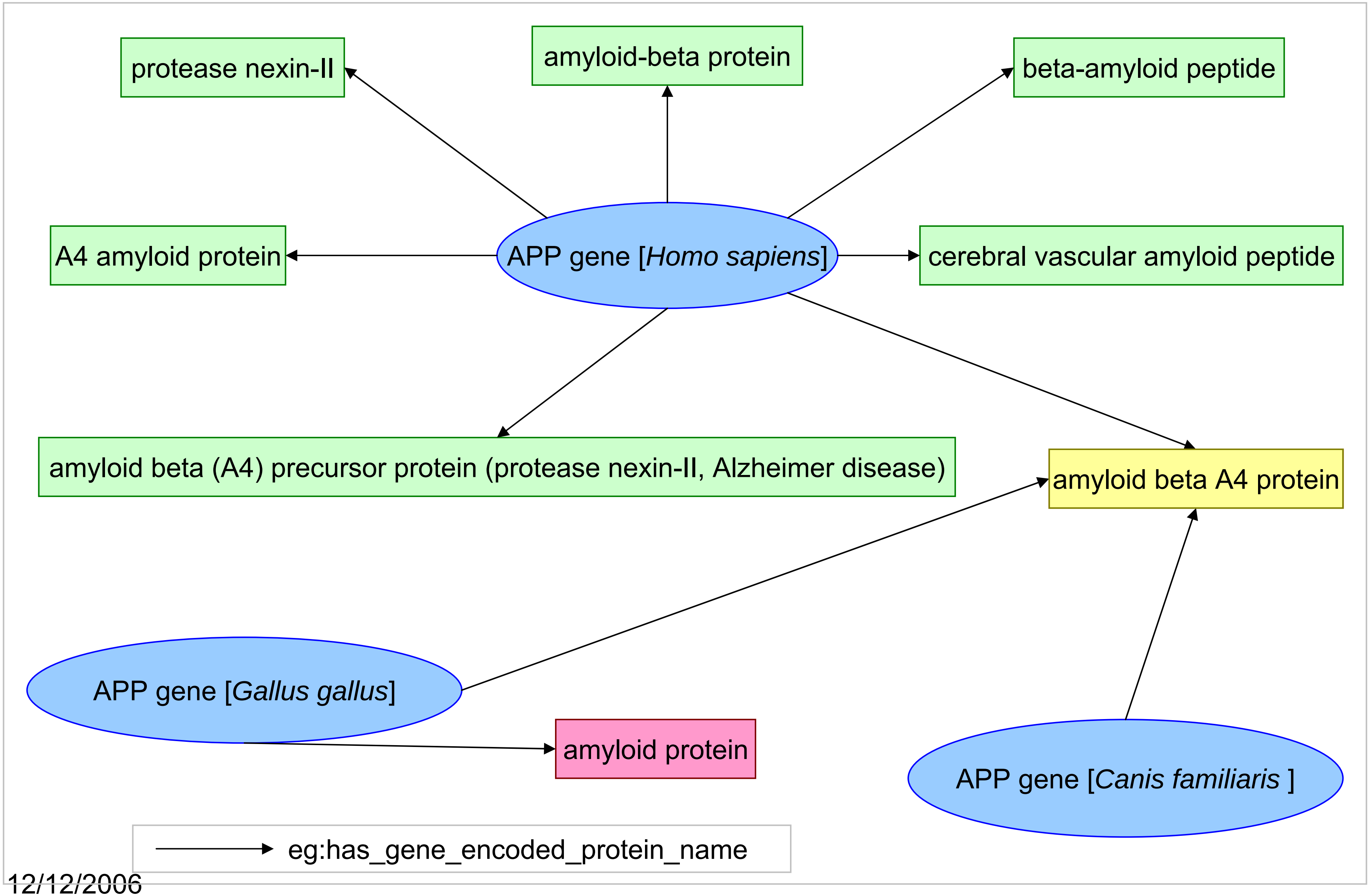
Number	Subject	Predicate
1	genid:ARP65549	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_uniq
2	genid:ARP65549	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_gene_
3	genid:ARP65549	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_gene_
4	genid:ARP65549	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_creat
5	genid:ARP65549	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_updat
6	genid:ARP65548	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_gene-
7	eg:Gene-track_geneid/351	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_entr
8	eg:Gene-track_geneid/351	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_entr
9	eg:Gene-track_geneid/351	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_entr
10	genid:ARP65553	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_genor
11	genid:ARP65553	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_genor
12	genid:ARP65553	http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd/has_bios

Biomedical Knowledge Repository

Relationships as first-class citizens

- Concentrate on the logical structure of data → named relationships
- Relationship-based complex query within a data resource
  - o K-hop path query with specified end-points
  - o Ranking of path query results using additional knowledge
- A formal model of relationships – currently a taxonomy

Integration *within* a resource


protease nexin-II
amyloid-beta protein
beta-amyloid peptide
A4 amyloid protein
APP gene [*Homo sapiens*]
cerebral vascular amyloid peptide
amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
amyloid beta A4 protein
APP gene [*Gallus gallus*]
amyloid protein
APP gene [*Canis familiaris*]
eg:has_gene_encoded_protein_name

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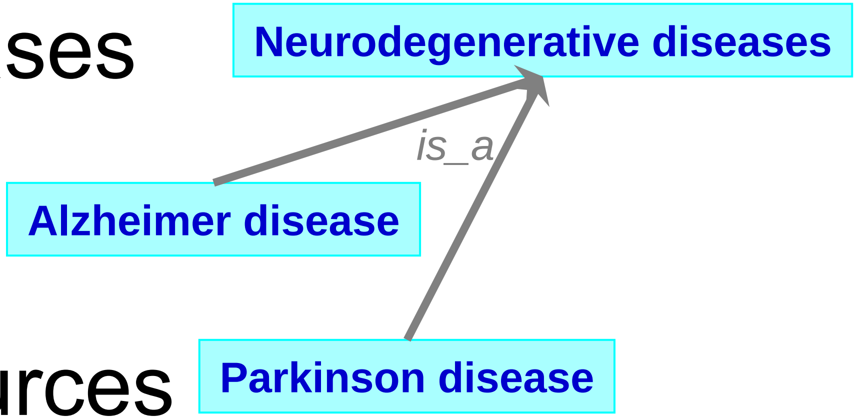
Integration *across* resources

- Transform additional resources into RDF
  - UMLS Metathesaurus
  - Other NCBI databases
  - Drug knowledge bases
  - …
- Integrate resources
  - Query across resources

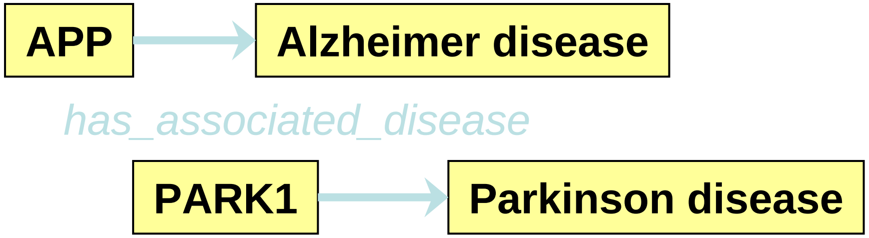


Neurodegenerative diseases

is_a

Alzheimer disease

Parkinson disease



APP

Alzheimer disease

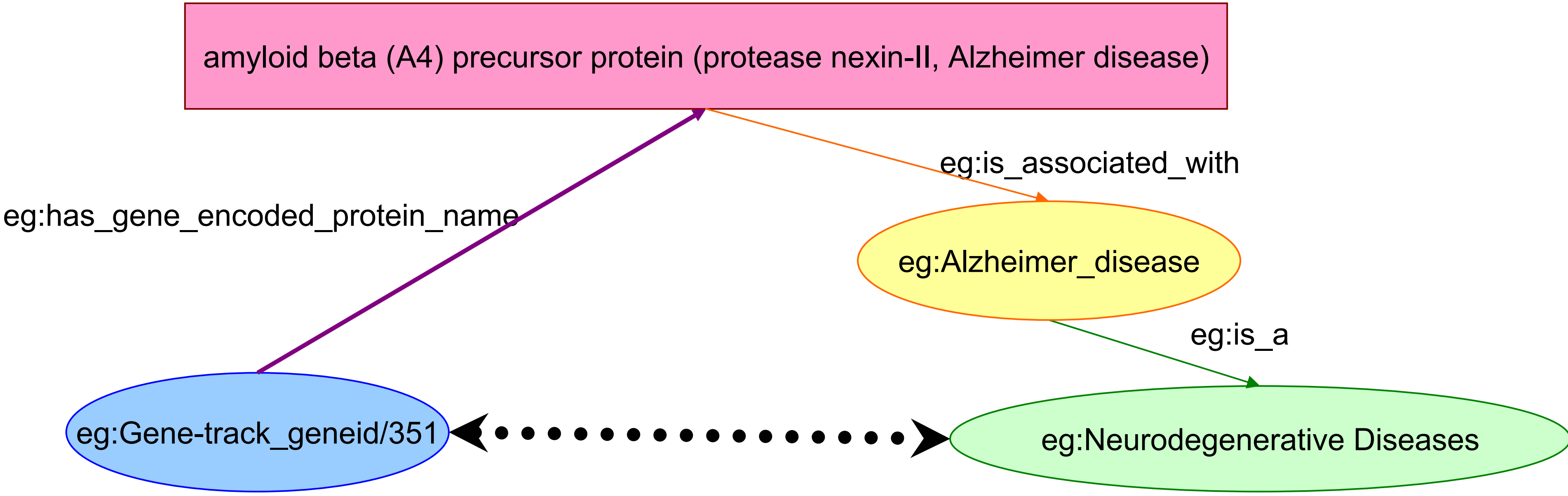
has_associated_disease

PARK1

Parkinson disease

Inference

- Rules are objects that allow inference from RDF data [Alexander, N. et. al., Oracle]
- Oracle 10g allows the creation of rulebase based on RDFS (RDF Schema)


amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
eg:is_associated_with
eg:has_gene_encoded_protein_name
eg:Alzheimer_disease
eg:is_a
eg:Gene-track_geneid/351
eg:Neurodegenerative Diseases

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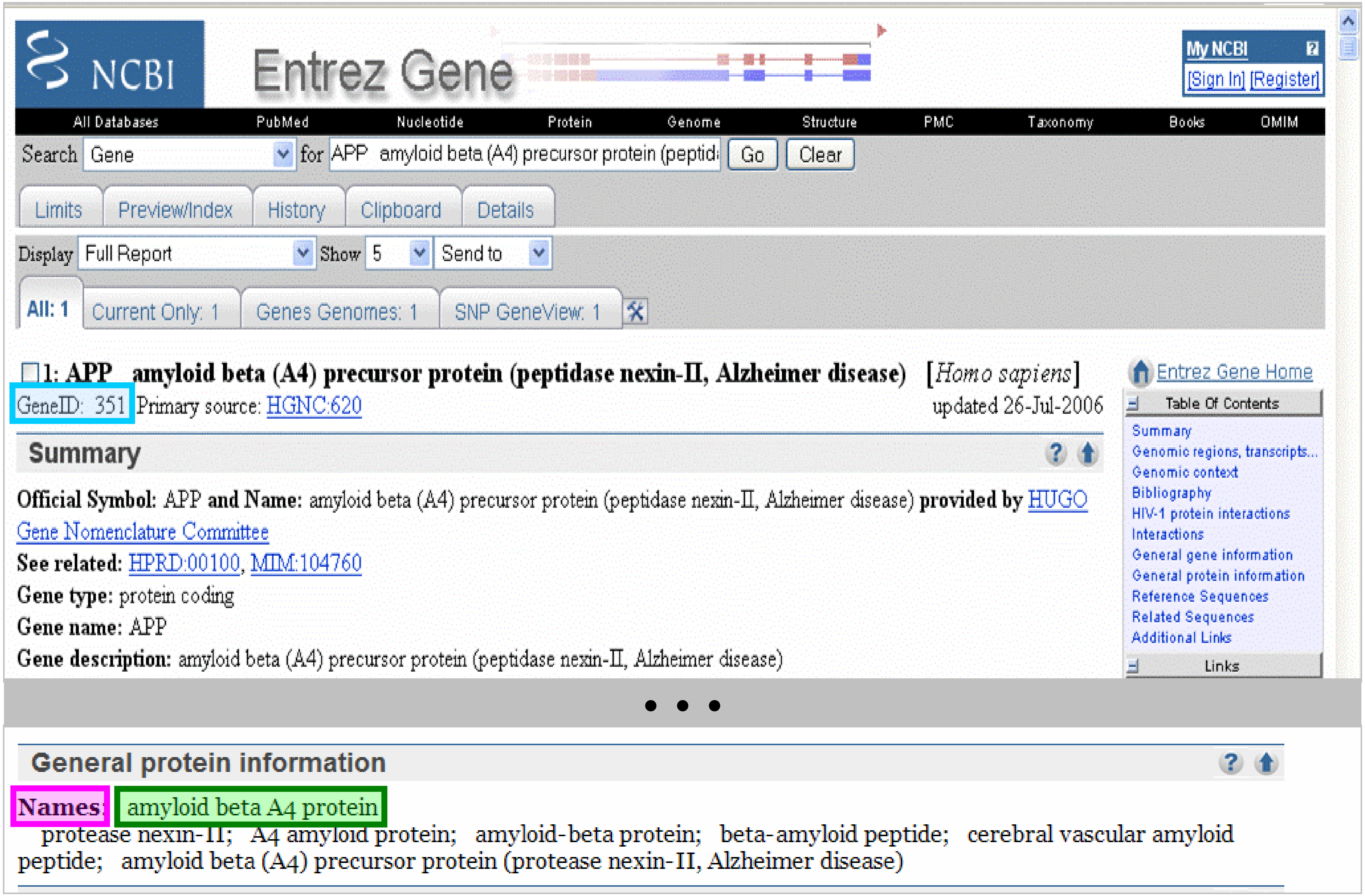
Entrez Gene Structure



□ 1: **APP amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)** [*Homo sapiens*]

GeneID: 351 Primary source: HGNC:620

updated 26-Jul-2006

Summary

Official Symbol: APP **and Name:** amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease) **provided by** HUGO Gene Nomenclature Committee

See related: HPRD:00100, MIM:104760

Gene type: protein coding

Gene name: APP

Gene description: amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)

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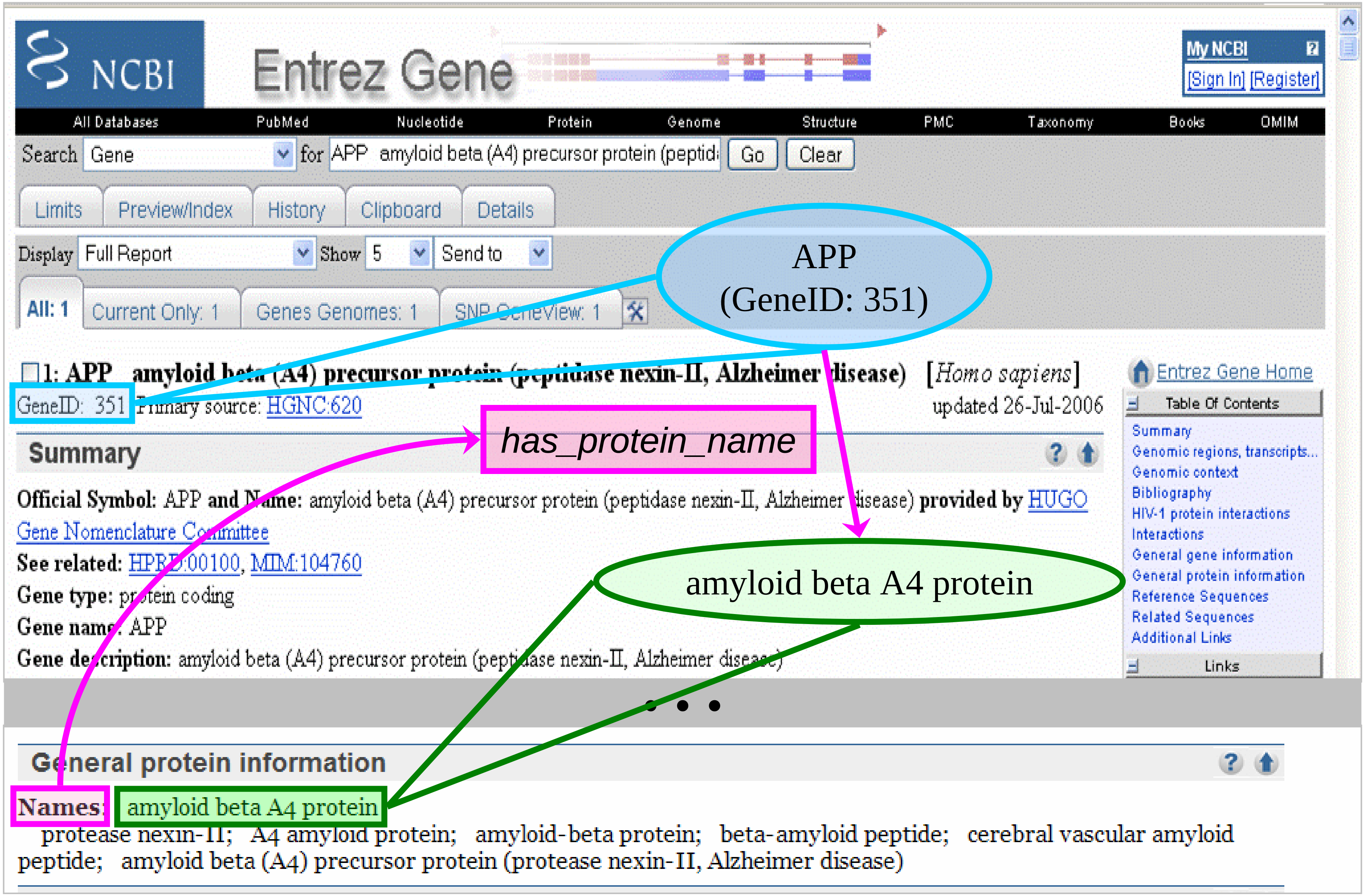
General protein information

Names: amyloid beta A4 protein

protease nexin-II; A4 amyloid protein; amyloid-beta protein; beta-amyloid peptide; cerebral vascular amyloid peptide; amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)

Entrez Gene Structure



Search Gene for APP amyloid beta (A4) precursor protein (peptid

Display Full Report Show 5 Send to

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APP
(GeneID: 351)

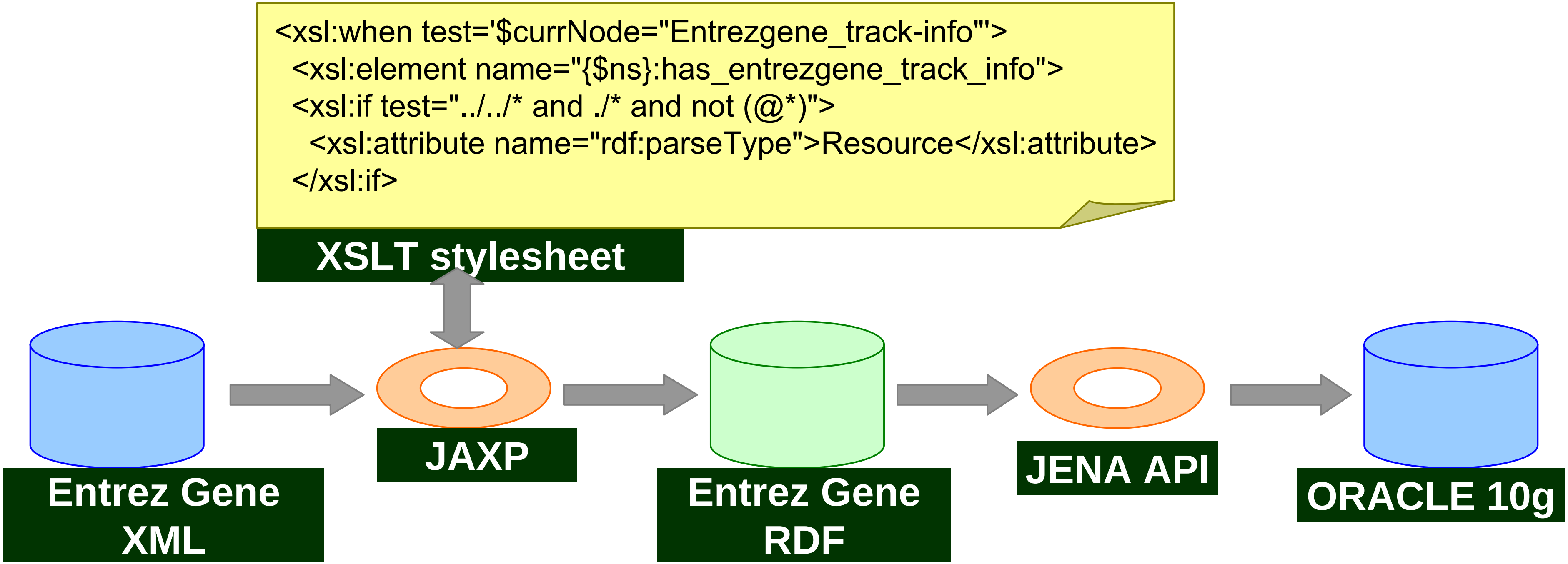
has_protein_name

amyloid beta A4 protein

RDF Conversion Approach

- Preserve or enhance the information in native Entrez Gene
- Element tags to named relationships
  - 133 element tags (*attributes* considered as separate tags)
  - 105 named relationships
- Incorporate the notion of RDF containers to group logically similar values
- RDF model enables complex queries not possible on current repository

Implementation



```
<xsl:when test='$currNode="Entrezgene_track-info"'>
  <xsl:element name="{$ns}:has_entrezgene_track_info">
  <xsl:if test="../../* and ./* and not (@*)">
    <xsl:attribute name="rdf:parseType">Resource</xsl:attribute>
  </xsl:if>
```

- Modular - Separates application code from transformation framework
- Extensible – Specific stylesheets may be used to for each of the Entrez databases
- Flexible – Changes in application logic or transformation logic are separate

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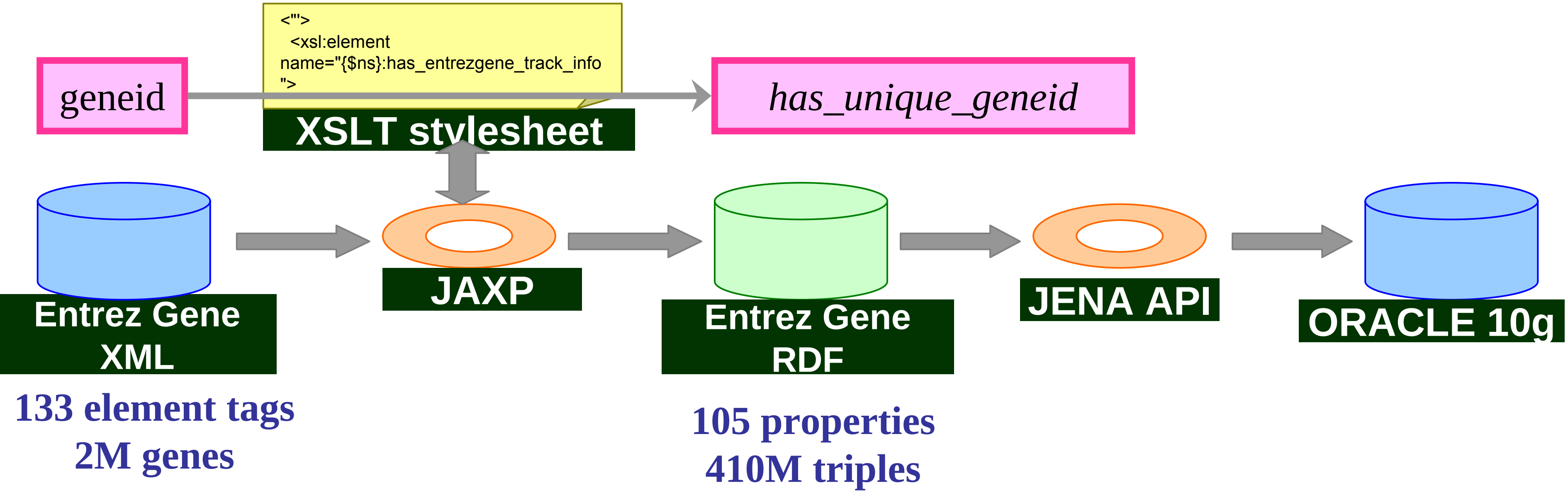
Results



geneid

```
<"'>
  <xsl:element
name="{$ns}:has_entrezgene_track_info
">
```

XSLT stylesheet

has_unique_geneid

Entrez Gene XML

133 element tags
2M genes

JAXP

Entrez Gene RDF

105 properties
410M triples

JENA API

ORACLE 10g

- 1 Record (geneid = 351) → 16,180 RDF triples
- Identified 3 candidate RDF containers → *Protein names, Gene reference synonyms, Organism reference synonyms*
- 50 GB Entrez Gene XML file → 39 GB RDF file
- Curation: Removed null literals and literals with leading space

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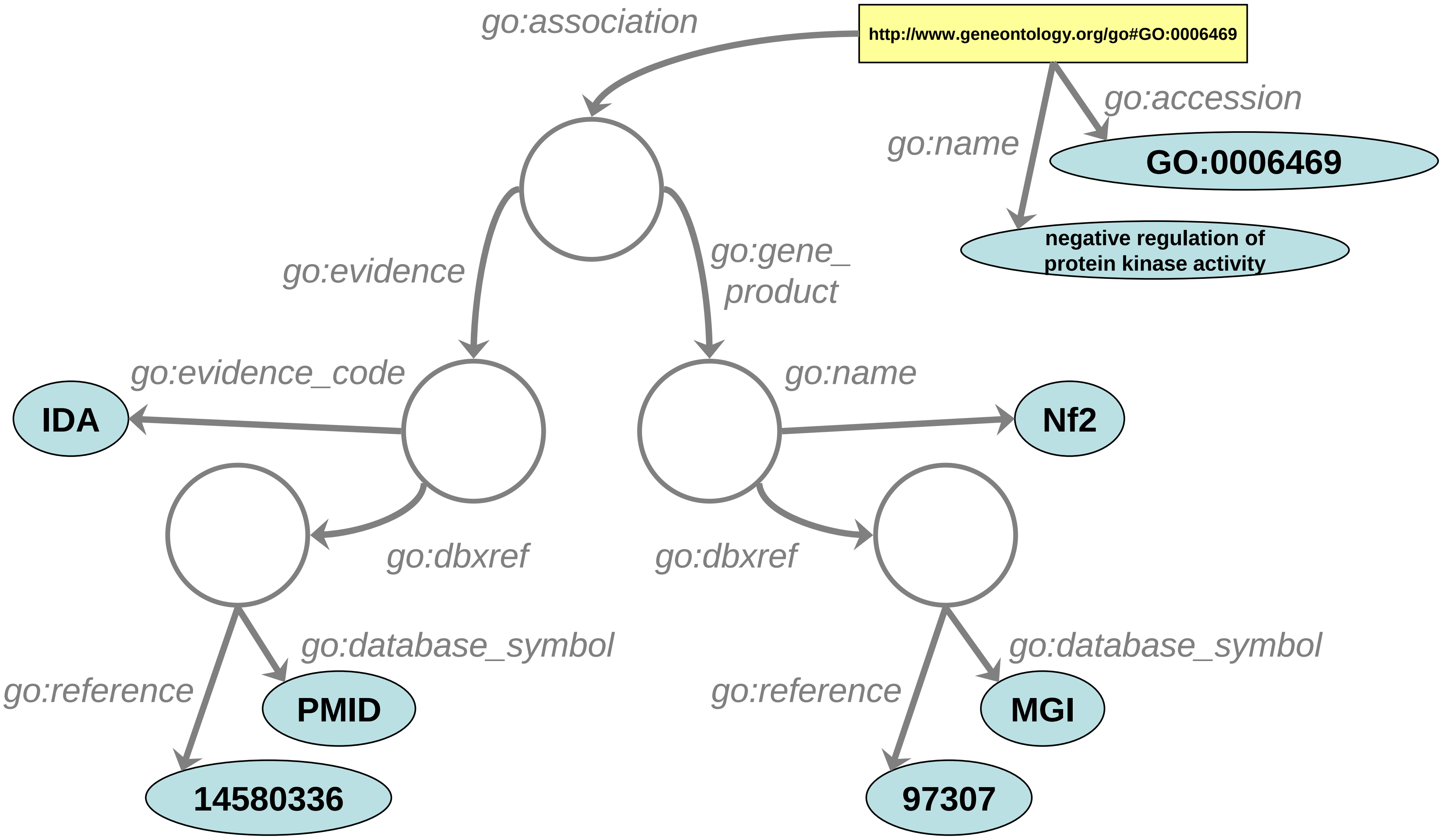
Separation of Data and Metadata - ongoing

- A gene record contains both:
  - Metadata: *date of creation*, *status*, *update date*
  - Data: *biological source organism*, *sequence intervals*
- Enable efficient query processing – two level filtering on resources
- Difficulty: context for metadata or data?

Issues and Challenges

- Blank nodes chain length?

RDF Blank nodes (Gene Ontology RDF)



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Issues and Challenges

- Blank nodes chain length?
- Reconcile overlapping element tags in multiple data sources
- Nesting structure, bi-directionality of relations and, circularity need to be solved
- Relationships name should evolve with community participation

Issues and Challenges – Unique Identifier

- Identifier for biological entities is an issue of debate in the community
- Issues:
  - o Can be dereferenced or not
  - o Persistent or transient identifiers
- For now, we use the Entrez Gene DTD as the namespace

  http://www.ncbi.nlm.nih.gov/dtd/NCBI_Entrezgene.dtd
- The possible candidates include:
  - o LSID: Life Sciences Identifier
  - o URI: NLM through UMLS and Entrez Gene

Further Information at:

http://esw.w3.org/topic/HCLSIG_BioRDF_Subgroup/Tasks/Entrez_Gene_to_RDF

Thank You

Bioinformatics Apps & Ontologies

- GlycO: A domain ontology for glycan structures, glycan functions and enzymes (embodying knowledge of the structure and metabolisms of glycans)
  - Contains 600+ classes and 100+ properties – describe structural features of glycans; unique population strategy
  - URL: http://lsdis.cs.uga.edu/projects/glycomics/glyco
- ProPreO: a comprehensive process Ontology modeling experimental proteomics
  - Contains 330 classes, 40,000+ instances
  - Models three phases of experimental proteomics* – Separation techniques, Mass Spectrometry and, Data analysis; URL: http://lsdis.cs.uga.edu/projects/glycomics/propreo
- Automatic semantic annotation of high throughput experimental data **(in progress)**
- Semantic Web Process with WSDL-S for semantic annotations of Web Services

  – http://lsdis.cs.uga.edu/projects/glycomics/glyco/GlycOdoc2/

More information at

- http://lsdis.cs.uga.edu/projects/glycomics