

Large Life Science Datasets with SPARQL or Prolog



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You work in the life sciences:

How do you use AllegroGraph?



This talk

- AllegroGraph in a few slides
- Using the Science Commons datasets
- Gruff: A rich client for data exploration, prolog and sparql
- AGWebview: a webbrowser
- Some observations of Science Commons dataset users
- Prolog or SPARQL



Graphs, triples, triple-store?

createTripleStore("seminar.db")

addTriple	(Person1	first-name Steve)
addTriple	(Person1	isa Organizer)
addTriple	(Person1	age 52)
addTriple	(Person2	first-name Jans)
addTriple	(Person2	isa Psychologist)
addTriple	(Person2	age 50)
addTriple	(Person3	<pre>first-name Craig)</pre>
addTriple	(Person3	isa SalesPerson)
addTriple	(Person3	age 32)

addTriple (Person1 colleague-of Person2)
addTriple (Person1 colleague-of Person3)
addTriple (Person3 neighbor-of Person1)
addTriple (Person3 neighbor-of Person2)

addTriple (Person1 likes Pizza)





And now you can query in Prolog or Sparql

(select (?xname ?yname)

- (q ?x colleague-of ?y)
- (q ?y neighbor-of ?x)
- (q ?x first-name ?xname)
- (q ?y first-name ?yname))

```
SELECT ?xname ?yname WHERE {
    ?x ex:colleague-of ?y .
    ?y ex:neighbor-of ?x .
    ?x ex:first-name ?xname .
    ?y ex:first-name ?yname . }
```



AllegroGraph

- Scalable and persistent Triple (Quad) Store
 - Load and query over Billions of RDF triples
 - The only fast reasoner that doesn't need materializing
- Compliant with standards
 - RDF, RDFS, OWL, SPARQL, Named Graphs, ISO Prolog, OWL-lite reasoning
- RDFS++ Reasoning
 - All of RDFS + owl:sameAs, owl:transitiveProperty, owl:inverseOf, owl:hasValue
- Full text indexing
- Spatial, Temporal and Social







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Harnessing the Semantic Web to Answer Scientific Questions:

A Health Care and Life Sciences Interest Group demo

Alan Ruttenberg, Science Commons



Accelerating the Scientific Research Cycle



Looking for Alzheimer Disease targets

Signal transduction pathways are considered to be rich in "druggable" targets - proteins that might respond to chemical therapy

CA1 Pyramidal Neurons are known to be particularly damaged in Alzheimer's disease.

Casting a wide net, can we find candidate genes known to be involved in signal transduction and active in Pyramidal Neurons?



A SPARQL query spanning 4 sources

prefix go: <http://purl.org/obo/owl/GO#> prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> prefix owl: <http://www.w3.org/2002/07/owl#> prefix mesh: <http://purl.org/commons/record/mesh/> prefix sc: <http://purl.org/science/owl/sciencecommons/> Mesh: Pyramidal Neurons prefix ro: <http://www.obofoundry.org/ro/ro.owl#> select ?genename ?processname where graph <http://purl.org/commons/hcls/pubmesh> ?paper ?p mesh:D017966 . 4 ?article sc:identified by pmid ?paper. **Pubmed: Journal Articles** ?gene sc:describes gene or gene product mentioned by ?article. graph <http://purl.org/commons/hcls/goa> { ?protein rdfs:subČlassOf ?res. ?res owl:onProperty ro:has function. ?res owl:someValuesFrom ?res2. ?res2 owl:onProperty ro:realized as. ?res2 owl:someValuesFrom ?process. Entrez Gene: Genes graph <http://purl.org/commons/hcls/20070416/classrelations> {{?process <http://purl.org/obo/owl/obo#part_of> go:GO_0007166} union {?process rdfs:subClassOf go:GO 0007166 }} ?protein rdfs:subClassOf ?parent. ?parent owl:equivalentClass ?res3. ?res3 owl:hasValue ?gene. GO: Signal Transduction graph <http://purl.org/commons/hcls/gene> { ?gene rdfs:label ?genename } graph <http://purl.org/commons/hcls/20070416> { ?process rdfs:label ?processname} Inference`required



AllegroGraph and NC dataset

• Loading 100,000,000 triples, including text indexing for rdf:comment and rdfs:label

- Loading	1:30:23
- Indexing:	15:19
- Total time:	1:45:43



Demo

- Gruff and NC
- AGWebview and NC



Some Observations



Issue [1] - Graphs

In which Graph(s) are my triples?

- Researchers are forced to partition the data through graphs (the fourth argument of a triple) at load time
- Researchers are forced to remember which graph knows about what predicates (or risk severe performance penalties)
- AllegroGraph supports <u>federation</u>: you can partition your data through graphs in one db, or you can have your data in different dbs on different machines...

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prefix go: <http://purl.org/obo/owl/GO#> prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> prefix owl: <http://www.w3.org/2002/07/owl#> prefix mesh: <http://purl.org/commons/record/mesh/> prefix sc: <http://purl.org/science/owl/sciencecommons/> Mesh: Pyramidal Neurons prefix ro: <http://www.obofoundry.org/ro/ro.owl#> select ?genename ?processname where graph <http://purl.org/commons/hcls/pubmesh> ?paper ?p mesh:D017966 . 4 ?article sc:identified by pmid ?paper. **Pubmed: Journal Articles** ?gene sc:describes gene or gene product mentioned by ?article. graph <http://purl.org/commons/hcls/goa> { ?protein rdfs:subČlassOf ?res. ?res owl:onProperty ro:has function. ?res owl:someValuesFrom ?res2. ?res2 owl:onProperty ro:realized as. ?res2 owl:someValuesFrom ?process. Entrez Gene: Genes graph <http://purl.org/commons/hcls/20070416/classrelations> {{?process <http://purl.org/obo/owl/obo#part_of> go:GO_0007166} union {?process rdfs:subClassOf go:GO 0007166 }} ?protein rdfs:subClassOf ?parent. ?parent owl:equivalentClass ?res3. ?res3 owl:hasValue ?gene. GO: Signal Transduction graph <http://purl.org/commons/hcls/gene> { ?gene rdfs:label ?genename } graph <http://purl.org/commons/hcls/20070416> { ?process rdfs:label ?processname} Inference`required



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Issue [2] – Materializing is pain

An amazing 3.4 M subclass relationships, sometimes to 10 levels deep,

- Reasoning without materialization is painfully slow
- But: Materializing takes hours
- Multiplies the number of triples
- Any serious change to the ontology forces re-materialize
- AllegroGraph we do not need to <u>materialize</u>
- We optimize Prolog queries
 - Statistics based
 - Predicates are indexed on the fly
 - Industry Leading LUBM results *without* materializing



Issue [3] - Numbers

Range queries on numbers and dates is slow if data doesn't fit in memory

- Find every subject S for measurement M where the certainty values are between 0.7 and 0.9
- Millions of numbers in NeuroCommons datasets
- In lab data more numbers than symbols
- In AllegroGraph numbers are *not* in string table but natively encoded. We support nearly all XML Schema data types.



Issue [4] - Abstractions

 Interesting SPARQL Queries are usually far too long because SPARQL doesn't support Abstractions

- AllegroGraph supports full Prolog and Prolog functors
- Franz is considering Common Logic as a more user friendly, and more declarative way to do queries and rules



SPARQL or Prolog

- 70 % of our users use SPARQL only
 - It is the standard QL, good descriptions on the web, quickly growing community that can help.., many SPARQL end points
- 30 % use Prolog
 - Not limited to two arguments
 - Range queries are naturally encoded
 - Use rules and build layer of abstractions
 - Has already query optimizer
 - Statistics based, indices on the fly
 - No need for static materializing
 - Reasoner integrated
 - Will be important in the future if rule-ML or Common Logic take off





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SPARQL Query



Graph View Table View

select ?x ?p ?o where

{ ?x rdfs:subClassOf <http://purl.org/science/owl/sciencecommons/synthetic_plasmid> .
 ?x ?p ?o . }

Enter a SPARQL SELECT query to the left and press the Do Query button. All known namespace abbreviations will be in effect.

Click a node cell (for a subject or object) to visit that resource or literal in the table view AND add the node to the graph view, connecting it to other nodes by the current predicates. Shift-click a node cell to ONLY add the node to the graph. Control-click a node cell to ONLY visit the resource in the table view. Control-click a IRI to visit it in your web browser. Control-click a predicate

Add to Visual Graph from Results

Query Results

<u>C</u>reate Visual Graph from Results

?x	?p	?0	
pGEX-2T-NM	Is described in	11685242	^
pGEX-2T-NM	Label	pGEX-2T-NM	-
pGEX-2T-NM	Sub Class Of	Synthetic plasmid	
pGEX-2T-NM	Carries sequence described by	851752	
pGEX-2T-NM	Availability described by	Pgvec1?f=c&attag=b&cmd=findpl&identifier=1127	
pGEX-4T3-p85beta-SH3	Is described in	7592789	
pGEX-4T3-p85beta-SH3	Label	pGEX-4T3-p85beta-SH3	
pGEX-4T3-p85beta-SH3	Sub Class Of	Synthetic plasmid	
pGEX-4T3-p85beta-SH3	Carries sequence described by	18708	
pGEX-4T3-p85beta-SH3	Availability described by	Pgvec1?f=c&attag=b&cmd=findpl&identifier=1394	
pGEM cWht14 (CT#692)	Is described in	11239392	
pGEM cWht14 (CT#692)	Label	pGEM cWnt14 (CT#692)	
pGEM cWht14 (CT#692)	Sub Class Of	Synthetic plasmid	
pGEM cWht14 (CT#692)	Carries sequence described by	395829	
pGEM cWht14 (CT#692)	Availability described by	Pgvec1?f=c&attag=b&cmd=findpl&identifier=13947	
pGEM cAgg (CT#689)	Is described in	11239392	~
2			P

Explicit Nodes from Query		Explicit Predicates from Query	
Synthetic plasmid	^	Sub Class Of	^
	~		Y

Type or paste a SPARQL query here, then press Do Query.

_ & X

~



Gruff - An AllegroGraph Browser

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pAd-Track HA PGC-1 alpha

Property	Value Click the righthand column to visit that resource in the table view AND add the triple to the graph view. Shift-click the righthand column to ONLY add the node to the graph. Control-click to ONL visit the resource in the table. Control-shift-click a uRL to visit it in your web browser. Shift-click the left column to add every node under that predicate to the visual graph. Control-click the column to toggle whether that predicate is a current predicate. Right-click anywhere to go back. The spacebar acts like a left click.		
Availability described by	Pgvec1?f=c&attag=b&cmd=findpl&identifier=14427		
Carries sequence described by	19017		
Is described in	16753578		
Label	pAd-Track HA PGC-1 alpha		
Sub Class Of	Synthetic plasmid		

http://purl.org/science/owl/sciencecommons/synthetic_plasmid

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Show All Triples

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