Ontology Views
An Update

A BISTI Collaborative RO1 with the National Center for Biomedical Ontology

James F. Brinkley, PI

Structural Informatics Group
University of Washington
Personnel

- Dan Suciu
- Linda Shapiro
- Marianne Shaw
- Todd Detwiler
- Joshua Franklin
- Onard Mejino

- Dan Cook
- John Gennari
- Max Neal
- Daniel Rubin
- Natasha Noy
- Mark Musen
Motivation

• Large number of application ontologies
• Need to link them together into the semantic web
• Reference ontologies as one way to do this
• But reference ontologies are (or will be) too large for practical use
• How can reference ontologies be made practical for applications, yet retain potential to link application ontologies?
Approach

• Application ontologies as views over one or more reference ontologies
• A view is a query that defines a formal transformation from one or more source ontologies to a target application ontology
Main advantage of views

• View query describes the specific operations used to create the application ontology
  – Therefore the connection to the source(s) are not lost
  – If the query can be made bidirectional (a mapping) then application ontologies can be related to each other via views
Secondary advantages

- View query can be re-run at any time as the reference ontology changes.
- The query is formal so can be manipulated by a GUI.
- Application ontology need not be materialized, so the update problem is not an issue (but there may be other reasons to materialize views).
Research Issues (aims)

1. How to define the view
2. How to implement the view query processor
3. How to graphically generate views

Driven by and evaluated in terms of use cases
Topics

- View definition language as SparQL extensions
- Expressiveness for use cases
- UW tools and demos
- Integration into BioPortal
- Current and planned work
Gleen regular path expression library
Todd Detwiler

{fma:Neuraxis gleen:OnPath ("([fma:regional_part]|[fma:constitutional_part])" ?part)}
vSparQL
Marianne Shaw, Todd Detwiler, Dan Suciu

- Subqueries
- Recursive Queries
- Skolem functions
vSparQL Subqueries

• Builds upon CONSTRUCT query

CONSTRUCT { ?subj ?prop ?obj }
FROM < ... >
WHERE { ?subj ?prop ?obj }

• Subqueries treated as data source
  • Named or unnamed data source

SELECT ...
FROM NAMED <subquery_name> [ 
  CONSTRUCT { ... }
  FROM < ... >
  WHERE { ... }
]
WHERE { GRAPH <subquery_name> { ... } }
Chaining Subqueries

SELECT ...
FROM NAMED <subquery_1> [
  CONSTRUCT { ... }
  FROM < ... >
  WHERE { ... }
]

FROM NAMED <subquery_2> [
  CONSTRUCT { ... }
  FROM < ... >
  WHERE { GRAPH <subquery_1> }
]

WHERE { GRAPH <subquery_2> { ... } }
vSparQL Recursive Subqueries

• Union of CONSTRUCT queries

SELECT ...
FROM NAMED <recursive_subq> [ 
    CONSTRUCT { ... }          # Base queries
    FROM < ... >
    WHERE { ... }
]

UNION          # Set union

CONSTRUCT { ... }      # Recursive queries
FROM NAMED <recursive_subq>
FROM < ... >
WHERE { GRAPH <recursive_subq> { ... } . 
    ...  
} ]
WHERE { GRAPH <recursive_subq> { ... } }
Skolem Functions

- \([[[<\text{skolem\_function\_url}>(\text{arg1}, \ldots )]]] \Rightarrow \langle \text{skolem\_function\_url}\rangle?\text{param1}=\text{arg1}&\text{param2}=\text{arg2}\)

- \([[[\text{fluid\_property}(<\text{blood\_in\_aorta}, \text{fluid\_pressure}>)]]) \Rightarrow \langle \text{fluid\_property}\rangle?\text{param1}=\text{blood\_in\_aorta}&\text{param2}=\text{fluid\_pressure}\)
Expressiveness in terms of three primary use cases

- Reorganization of RadLex
- Intelligent distributed queries
- Biosimulation model integration
Re-organization of RadLeX

Onard Mejino and Daniel Rubin

- Maryanne Martone, Jessica Turner, Beverly Collins
- RadLeX and the need to reorganize
- Neuroimaging as initial domain
- FMA as an organizing framework for the neuroanatomy component
Using FMA to reconcile different neuro terminologies

Onard Mejino

PROBLEM:

Correlate neuroanatomical imaging data using different annotation systems.

Example:

Talairach:


Anatomical Automatic Labeling (AAL):

Temporal_Inferior_RIGHT

FreeSurfer (Query Atlas):

ctx-rh-inferiortemporal
ctx-rh-G_temporal_inferior

Neurolex (BIRNlex/NeuroNames):

Inferior temporal gyrus

NO ONE TO ONE MAPPING BETWEEN THE TALAIRACH LABEL AND OTHER SOURCES
Correlate different systems

Talairach:

FMA+
Brodman area 20 of right inferior temporal gyrus
Part_of
Gray matter of right inferior temporal gyrus
Right inferior temporal gyrus
Right temporal lobe

Part_of
Right Brodmann area 20

FreeSurfer
ctx-rh-inferiortemporal
ctx-rh-G_temporal_inferior

AAL Atlas
Temporal_Inferior_RIGHT

Neurolex
Inferior temporal gyrus
Temporal lobe
Brodmann area 20
Implementation in Protégé
neuroFMA as a view of enhanced FMA
NeuroFMA View
Marianne Shaw, Todd Detwiler

- All neural structures from the FMA
  - Attributes
  - Properties connecting them
- All types, superclasses, superproperties
NeuroFMA View Query

PREFIX fma: <http://sig.biostr.washington.edu/fma3.0#>
CONSTRUCT
{
}
FROM <http://sig.biostr.washington.edu/fma3.0>
# all parts recursively of neuraxis
FROM NAMED <top_pre_neuraxis_parts> [
  CONSTRUCT {temp: set temp: member ?part}
  FROM <http://sig.biostr.washington.edu/fma3.0>
  WHERE {fma: Neuraxis gleen: OnPath ("([fma: regional_part]| [fma: constitutional_part])*" ?part)}
]
FROM NAMED <pre_neuraxis_parts> [
  FROM NAMED <top_pre_neuraxis_parts>
  FROM <http://sig.biostr.washington.edu/fma3.0>
  WHERE {
    GRAPH <top_pre_neuraxis_parts> {?a ?b ?part} .
    OPTIONAL {?part rdf:type ?c}
  }
]
...
NeuroFMA Query Results

...<rdf:Description rdf:about="http://sig.biostr.washington.edu/fma3.0#Medullary_raphe_nuclear_complex">
  <fma:preferred_name rdf:resource="http://sig.biostr.washington.edu/fma3.0#Nucleus_raphe_obscurus"/>
  <fma:FMAID rdf:datatype="http://www.w3.org/2001/XMLSchema#string">68874</fma:FMAID>
  <fma:preferred_name rdf:resource="http://sig.biostr.washington.edu/su_incus_30067"/>
  <fma:preferred_name rdf:resource="http://sig.biostr.washington.edu/fma3.0#Nucleus_raphe_magnus"/>
  <rdfs:label xml:lang="en">Medullary raphe nuclear complex</rdfs:label>
  <fma:preferred_name rdf:resource="http://sig.biostr.washington.edu/fma3.0#Nucleus_raphe_pallidus"/>
</rdf:Description>
...

FMA
75,000 classes; 170 properties; >2 million relationships

NeuroFMA
2,300 classes; 40 properties; >70,000 relationships
Compare two methods

- vSparQL vs procedurally-generated
- Modified version of RDF-Sync
- All differences with triples containing blank nodes
  - Only syntactic
- When syntactic differences accounted for no differences were found
- => vSparQL is expressive enough to generate a complex view
Intelligent distributed queries over annotated data

Todd Detwiler, Joshua Franklin, Eider Moore, Dan Suciu et al
Data annotation

Middle part of the middle temporal gyrus
Title (a short phrase describing the query, max 200 chars):
What is the distribution of temporal lobe semantic errors for males?

Description (complete description of what the query does, max 400 chars):
Retrieve all male patients with a CSM error code = 2, semantic naming error, where the CSM stimulation site is located in the temporal lobe. For each of these patients return each stimulation site with any trial that has code 2. For each such site return the FMA name of the site, the patient-specific 3-D coordinates, and all trials with code 2.

XQuery (the actual XQuery itself):

```xml
<results>
{

let $code := ('2')
let $sex := ('M')
let $showtext := 'false'
let $color := 'Blue'
let $shape := 'BIG_SPHERE'

(.........................................................)
(: Reformulate CSM database for easier querying :)
let $csm_inverse :=
 dxq:csm("<csm_inverse>
{
for $p in $pw/patient
return
<patient>
{$p/pnum)
{$p/vid)
{$p/sex)
```
(: Find the parts of the temporal lobe then filter again such that only sites in the temporal lobe are kept :) 

let $wsdlURL := "http://xiphoid.biostr.washington.edu:8080/V SparQL_Service/wsdl/V SparQLService.wsdl" 
let $serviceName := "V SparQLService" 
let $methodName := "executeQuery" 

let $query := 
"PREFIX fma: <http://bioontology.org/projects/ontologies/fma/fmaOwlDIComponent_2_0#> 
PREFIX gleen: <java:edu washington sig gleen> 
PREFIX qv: <http://sig.biostr.washington.edu/query_view#> 

CONSTRUCT { fma:Temporal_lobe qv:hasPartName ?part_name. } 
FROM <http://bioontology.org/projects/ontologies/fma/fmaOwlFullComponent_2_0> 
WHERE 
{ 
  fma:Temporal_lobe gleen:OnPath 
}"

let $temporalLobeParts := dxq:xqueryWS($wsdlURL, $serviceName, $methodName, $query)/qv:hasPartName 

let $fma_filtered := 
<fma_filtered> 
{for $p in $sex_code_filtered/patient 
  where $p/surgery/stin/site/anatomical_name = $temporalLobeParts 
}"

<patient>
  <pnum>54</pnum>
  <viq>107</viq>
  <sex>M</sex>
  <age>25</age>
</patient>

<surgery>
  <stimsite>
    <ShowText>false</ShowText>
    <Color>Blue</Color>
    <Shape>BIG_SPHERE</Shape>
    <Size>1.75</Size>
    <type>Surgical</type>
    <site_label>21</site_label>
  </stimsite>
  <magnet_coordinates>
    <ant_coord>-19.2527</ant_coord>
    <sup_coord>-5.20435</sup_coord>
    <right_coord>66.8884</right_coord>
  </magnet_coordinates>
  <anatomical_name>Middle part of superior temporal gyrus</anatomical_name>
</surgery>

<trial>
  <trial_num>23</trial_num>
  <stimulated>Y</stimulated>
  <item>squirrel</item>
  <patient_response>"rat...um...squirrel"</patient_response>
  <trialcode>B</trialcode>
  <trialcode>2</trialcode>
  <trialcode>S</trialcode>
</trial>
Query

let $wsdiURL := "http://xiphoid.biostr.washington.edu:8080/VSparQL_Service/wsdl/VSparQLService.wsdl"
let $serviceName := "VSparQLService"
let $methodName := "executeQuery"

let $query :=
'PREFIX fma: <http://bioontology.org/projects/ontologies/fma/fmaOwlDILComponent_2_0#>
PREFIX qv:<http://sig.biostr.washington.edu/query_view#>

CONSTRUCT { fma:Frontal_lobe qv:hasPartName ?part_name. }
FROM <http://bioontology.org/projects/ontologies/fma/fmaOwlFullComponent_2_0>
WHERE
{
  fma:Frontal_lobe gleen:OnPath
  ((fma:regional_part||fma:constitutional_part)+"?part" .
  ?part gleen:OnPath ([fma:Preferred_name]@[fma:name]"?part_name") .
}

let $temporalLobeParts := dxq:xqueryWS($wsdiURL, $serviceName, $methodName, $query)//qv:hasPartName

let $fma_filtered :=
<fma_filtered>
{for $p in $sex_code_filtered/patient
  where $p/surgery/stimsite/anatomical_name = $temporalLobeParts
  return
  <patient>
    {$p/pnum}
    {$p/vig}
- <results>
  - <patients>
    <count>5</count>
    - <patient>
      <pnum>90</pnum>
      <viq/>
      <sex>F</sex>
      <age>49</age>
    - <surgery>
    - <stimsite>
      <ShowText>false</ShowText>
      <Color>Blue</Color>
      <Shape>BIG_SPHERE</Shape>
      <Size>1.75</Size>
      <type>Surgical</type>
      <site_label>2</site_label>
    - <magnet_coordinates>
      <ant_coord>-30.2406</ant_coord>
      <sup_coord>53.3675</sup_coord>
      <right_coord>24.744</right_coord>
    </magnet_coordinates>
    <anatomical_name>Dorsal part of precentral gyrus</anatomical_name>
  - <trial>
    <trial_num>200</trial_num>
    <stimulated>Y</stimulated>
    <item>leg</item>
    <patient_response>"foot" -- see trials # 56 & 136</patient_response>
    <trialcode>2</trialcode>
  </trial>
</results>
Biosimulation model integration

Max Neal, Dan Cook, John Gennari
\[ \text{PacFOL.t} = (\text{Paco} - \text{PacFOL})/(0.0005\text{sec}) ; \]
\[ \text{Psa.e} = X_0 \times \log( ((Vsa-Vsa.o)/Do) + 1 ) ; \]
\[ \text{Psa.p} = X_0 \times \exp ( \tau_0 \times (Vsa-Vsa.o) ) + \text{Kp} \times Vsa \]
\[ \text{Psa} = F_{vano} \times \text{Psa.a} + (1 - F_{vano}) \times \text{Psa.p} ; \]
\[ \text{Psa} = 0.5 \times \text{Psa.a} + 0.5 \times \text{Psa.p} ; \]
\[ \text{Psap} = Vsa.p / Cmap - \text{Pz} \times (1/(\exp(Vsap/Vx_8) - 1)) ; \]
\[ \text{Pso} = \text{Vsc} / Csc - \text{Pz} \times (1/(\exp(Vsc/Vx_8) - 1)) ; \]
\[ \text{Rev} = -\text{Xv}\times \log ( (\text{Vmax.ev/\text{Vuv}) - 0.99) ) ; \]
\[ \text{Pve} = \text{if} ( (\text{Vpe} > \text{Vo}) \text{D2} + \text{K2} \times \exp (\text{Vo}/\text{Vmin.ve}) + \text{K1} \times (\text{V}) \text{else D2} + \text{K2} \times \exp (\text{Vpe}/\text{Vmin.ve}) - \text{Fx1} / (\text{ex}) \]
\[ \text{Pscc} = \text{Pve} + \text{Ppec} ; \]

\[ \text{Flows:} \]
\[ \text{Forb} = (\text{Pace.p} - \text{Pucc}) \times \text{Rcrb} ; \]
\[ \text{Fsp} = (\text{Psap} - \text{Pscc}) / \text{Rsp} ; \]
\[ \text{Fsa} = (\text{Pso} - \text{Psa}) / \text{Rsa} ; \]
\[ \text{Fsr} = (\text{Psar} - \text{Psap}) / \text{Rsr} ; \]
\[ \text{Fve} = (\text{Pve} - \text{Pscc}) / \text{Rve} ; \]

\[ \text{RA} \]
\[ \text{Era} = (\text{Emax.r.a} - \text{Emin.r.a}) \times \text{yra} + \text{Emin.r.a} ; \]
\[ \text{Vrvar} = (1 - \text{yra}) \times (\text{Vr.var} - \text{Vr.arr}) + \text{Vrarr} ; \]

\[ \text{RV} \]
\[ \text{Erv} = (\text{Emax.r.v} - \text{Emin.r.v}) \times \text{yrv} + \text{Emin.r.v} ; \]
\[ \text{Vrvar} = (1 - \text{yrv}) \times (\text{Vr.var} - \text{Vr.arr}) + \text{Vrarr} ; \]

\[ da = a0a \times (1 - \exp(-a1a^2)) \]
\[ da = a0a \times (1 - \exp(-a1b^2)) \]
\[ db = a0b \times (1 - \exp(-a2b^2)) \]
\[ db = a0b \times (1 - \exp(-a2c^2)) \]
\[ dc = a0c \times (1 - \exp(-a3b^2)) \]
\[ dc = a0c \times (1 - \exp(-a3c^2)) \]
\[ dd = a0d \times (1 - \exp(-a4b^2)) \]
\[ dd = a0d \times (1 - \exp(-a4c^2)) \]
\[ dd = a0d \times (1 - \exp(-a4d^2)) \]
\[ + a5d \times \exp(ucf \times ((\text{E}-a6a)/a7a)^2) ; \]
- real ELV(t) mmHg/ml; // Elastance of left ventricle
- real VrestLV(t) ml; // Rest volume of left ventricle
- real VLV(t) ml; // Volume of left ventricle
- realState EDVLV(t) ml; // End-diastolic volume of left ventricle
- real ERV(t) mmHg/ml; // Elastance of right ventricle
- real VrestRV(t) ml; // Rest volume of right ventricle
- real VRV(t) ml; // Volume of right ventricle
- realState EDVRV(t) ml; // End-diastolic volume of right ventricle
- // systemic
- real Paorta(t) mmHg; // Transmural pressure in aorta
- real PSysVeins(t) mmHg; // Transmural pressure in systemic veins
- real PLV(t) mmHg; // Transmural pressure in left ventricle
- real PLA(t) mmHg; // Transmural pressure in left atrium
- real VrestLA(t) ml; // Rest volume of left atrium

### PLV

#### Physical entity annotation
- Blood_in_left_ventricle (FMA)

#### Physical property annotation
- Fluid_pressure (OPB)

#### Human-readable definition
- [not specified]

#### Physical dependency annotation
- [not specified]
FMA-OPB View: More than one source ontology

Todd Detwiler
FMA-OPB Query

PREFIX fma:<http://sig.biostr.washington.edu/fma3.0#>  
PREFIX opb:<http://sig.biostr.washington.edu/OPB-01.owl#>  
PREFIX annot_view:<http://sig.biostr.washington.edu/annot_v1.0#>  

CONSTRUCT 
{  
  [[annot_view:annotation(?pob,?property)]] rdf:type rdf:Statement.  
  [[annot_view:annotation(?pob,?property)]] rdf:subject ?pob .  
  [[annot_view:annotation(?pob,?property)]] rdf:predicate opb:hasProperty.  
  [[annot_view:annotation(?pob,?property)]] rdf:object ?property . 
}  
FROM NAMED <http://sig.biostr.washington.edu/fma3.0>  
FROM NAMED <http://sig.biostr.washington.edu/-detwiler/OntViews/OPB/OPB-01.owl>  
WHERE  
{  
  GRAPH <http://sig.biostr.washington.edu/fma3.0>  
  {  
  }  
  GRAPH <http://sig.biostr.washington.edu/-detwiler/OntViews/OPB/OPB-01.owl>  
  {  
    ?property opb:Physical_domain_class opb:Fluid_domain .  
  }  
}
FMA-OPB View (graphical example)
RELEASED OR DEPLOYED TOOLS at UW

Todd Detwiler
Gleen Regular Path Library

Structural Informatics Group

GLEAN: Regular Paths for ARQ SparQL

Contents:
- Regular Paths in SparQL
- ARQ Property Functions
- OnPath Function
- Subgraph Function
- Comparing OnPath and Subgraph
- Web Demo
- Download and Install
- Changes
- Known Issues
- Future Work
- Contact
- Acknowledgements
VSparQL Demo Client

VSparQL Demo

Enter SparQL Query:

```sparql
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX owl: <http://www.w3.org/2002/07/owl#>

PREFIX nei: <http://nciob.nci.nih.gov/xml/owl/EVS/Thesaurus.owl#>
SELECT ?a ?prop ?c
FROM <http://nciob.nci.nih.gov/xml/owl/EVS/Thesaurus.owl>
WHERE
{
    ?a nei:Preferred_Name "Heart" .
    ?a rdfs:subClassOf ?b .
    ?b owl:someValuesFrom ?c .
}
```

Submit Query

Sample Queries:

Sample Query 1: (Get the existential property restrictions for the class Heart)

```sparql
PREFIX nei: <http://nciob.nci.nih.gov/xml/owl/EVS/Thesaurus.owl#>
SELECT ?a ?prop ?c
FROM <http://nciob.nci.nih.gov/xml/owl/EVS/Thesaurus.owl>
WHERE
{
    ?a nei:Preferred_Name "Heart" .
    ?a rdfs:subClassOf ?b .
    ?b owl:someValuesFrom ?c .
}
```
Integrating views in BioPortal

Natasha Noy
Csongor Nyulas
Stanford
BioPortal Metadata

- BioPortal infrastructure and functions are supported by metadata
  - Ontology details
  - Mappings
  - Notes, reviews
  - Views
- Ontologies are used describe metadata and instances of ontology classes are used to store metadata
Metadata as ontology instances

BioPortal Metadata Ontology
(including the imports: OMV, changes, mappings)

- Class OMV:Ontology
- Class Review
- Class mappings:One_to_one_mapping

owl:imports

BioPortal Metadata Knowledge Base

- FMA, v.1.0
  Instance of OMV:Ontology

- FMA, v.2.0
  Instance of OMV:Ontology

Review
Ontology: FMA
Text: Key enabler in bioinformatics

A regular ontology in BioPortal (administered by BioPortal developers)

not visible directly to BioPortal users (accessed only through the API that processes metadata)
Requirements for representing views

• Each view is itself an ontology and can have metadata, be explorable, etc.
• A view is defined on a specific version of an ontology
• There is a notion of a "virtual view" (cf. "virtual ontology"): for example, a view of Liver-related concepts in FMA created for a particular purpose
  – each virtual view has at least one version, but can have several
  – a virtual view has metadata attached to it (name, contact, etc.)
  – each version of the view also has its own metadata (inherited from ontology metadata, but with additional fields)
• Must be able to represent views on views
• Must be able to represent views that include more than one ontology
How it will all look in BioPortal
Next Steps in Integrating Views in BioPortal

• Finish implementing the complete set of REST services
• Implement a user interface for displaying views and their metadata
• Enable community features, such as commenting on views
• Linking concepts in views to the corresponding concepts in the “master” ontology (right now, a view is independent from the ontology)
Current and Planned work

• Additional features in vSparQL
• Optimization
• Non-materialized views
• Query manager
• Graphical view generation
• Intermediate Language
• Other use cases
Title
Liver View

Description
Liver sub-ontology from FMA

Query
```
?inputSub apf:assign fma:Liver.

{?super apf:assign fma:Organ.} UNION {?super apf:assign fma:Cardinal_organ_part.}
```

WHERE
{ GRAPH <visible_liver_parts>
{ (?x ?y ?z)UNION {?z apf:assign fma:Liver.}
{?inputSub apf:assign ?z.} UNION {?inputSub apf:assign (?inputSub "rdfs:subClassOf" ?inputObj) glen:Subgraph}
}
}

Query Results
```
<rdf:RDF
xmlns:fma="http://sig.biostr.washington.edu/fma3.0#"
xmlns:glen="java:edu.washington.sig.gleen."
xmlns:rdfs="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
xmlns:apf="java:com.hp.hpl.jena.query.pfunction.library."
xmlns:rdfs="http://www.w3.org/2000/01/rdf-schema#">
<rdf:Description rdf:about="http://sig.biostr.washington.edu/fma3.0#Mucosa_of_
<rdfs:subClassOf rdf:resource="http://sig.biostr.washington.edu/fma3.0#Mucos
</rdf:Description>
<rdf:Description rdf:about="http://sig.biostr.washington.edu/fma3.0#Organ">
```
Graphical view generation
Intermediate Language

• Higher-level functionality
  – Can be mapped to vSPARQL queries

• Operations
  – Extract
    • edges, nodes, tree
  – Union
  – Copy
  – Delete / Add
    • edges, nodes, tree
  – Merge / split nodes
  – Cleanup
Other potential use cases

- Ontology of cardiovascular system (OCV) for Cardiovascular Imaging Informatics (CVII)
- Ontology of head and neck lymphatic system for radiation treatment planning
- Ontology of musculoskeletal system in support of Human Phenotype Ontology
- Mammalian Anatomy Ontology as resource for different species ontologies
- Ontology of skeletal system for computational biomechanics of bone and orthopedic devices
- Latin only (Terminologia Anatomica) terminology for head and neck anatomy
- Ontology of genito-urinary system for micturition control studies
- Minimum Information for Biological and Biomedical Investigations
- Ontology of Clinical Research (OCRE)

More…..
Conclusions

• A query-based approach to deriving application ontologies from reference ontologies
• Appears to be expressive enough
• Needs to be made faster and easier to use
• Large number of potential applications
Bioportal Challenges/Questions

- Search: should views be searchable just like other ontologies? (if yes, the same concept may appear in multiple views and will be returned multiple times in the search)
- Mapping: should users be allowed to map concepts from the views? If yes, should these mappings propagate to the source ontology?
- Notes: When users comment on a concept on a view, should that note be seen in the source ontology?