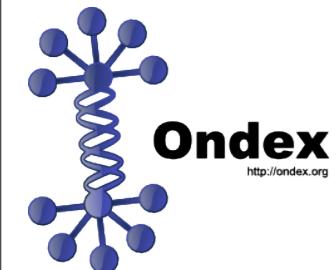


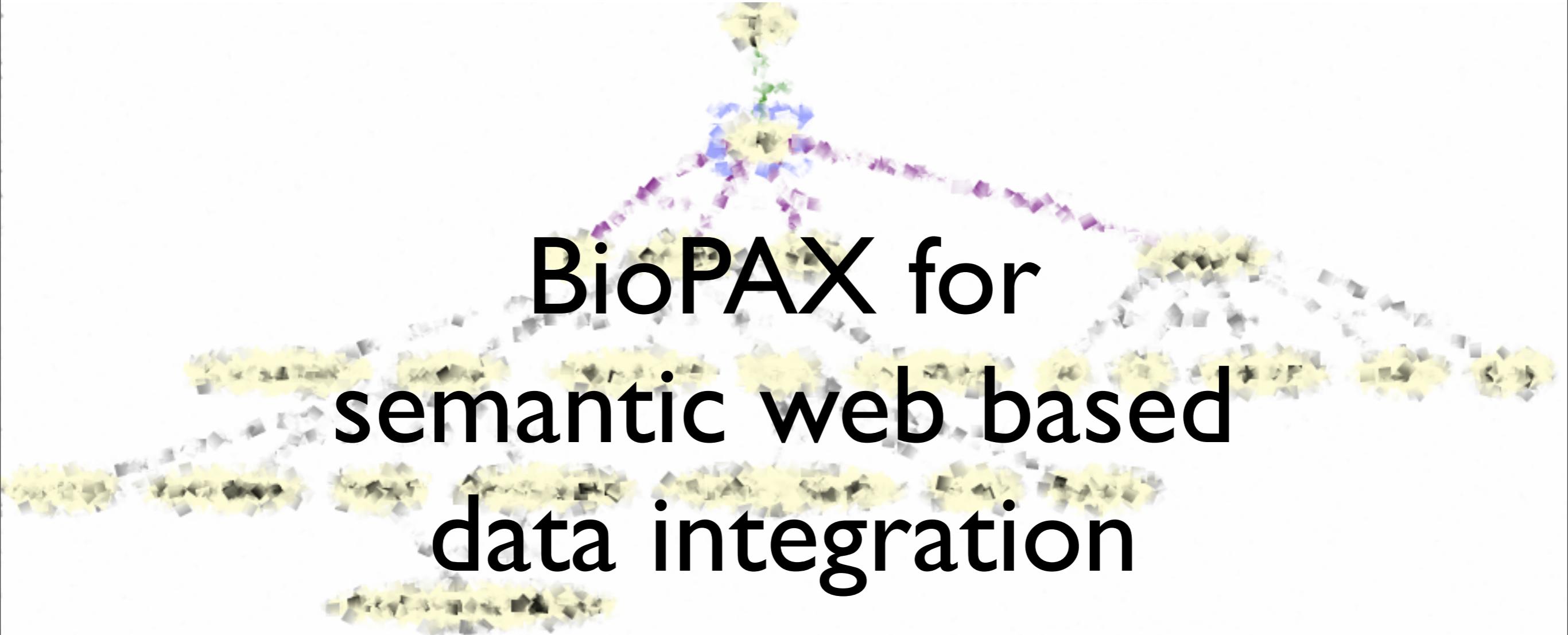
BioPAX for semantic web based data integration

Andrea Splendiani
Biomathematics and Biostatistics Dept.
Rothamsted Research



CellML-SBGN-SBO-BioPAX-MIASE Workshop 2009, April 3-9 2009



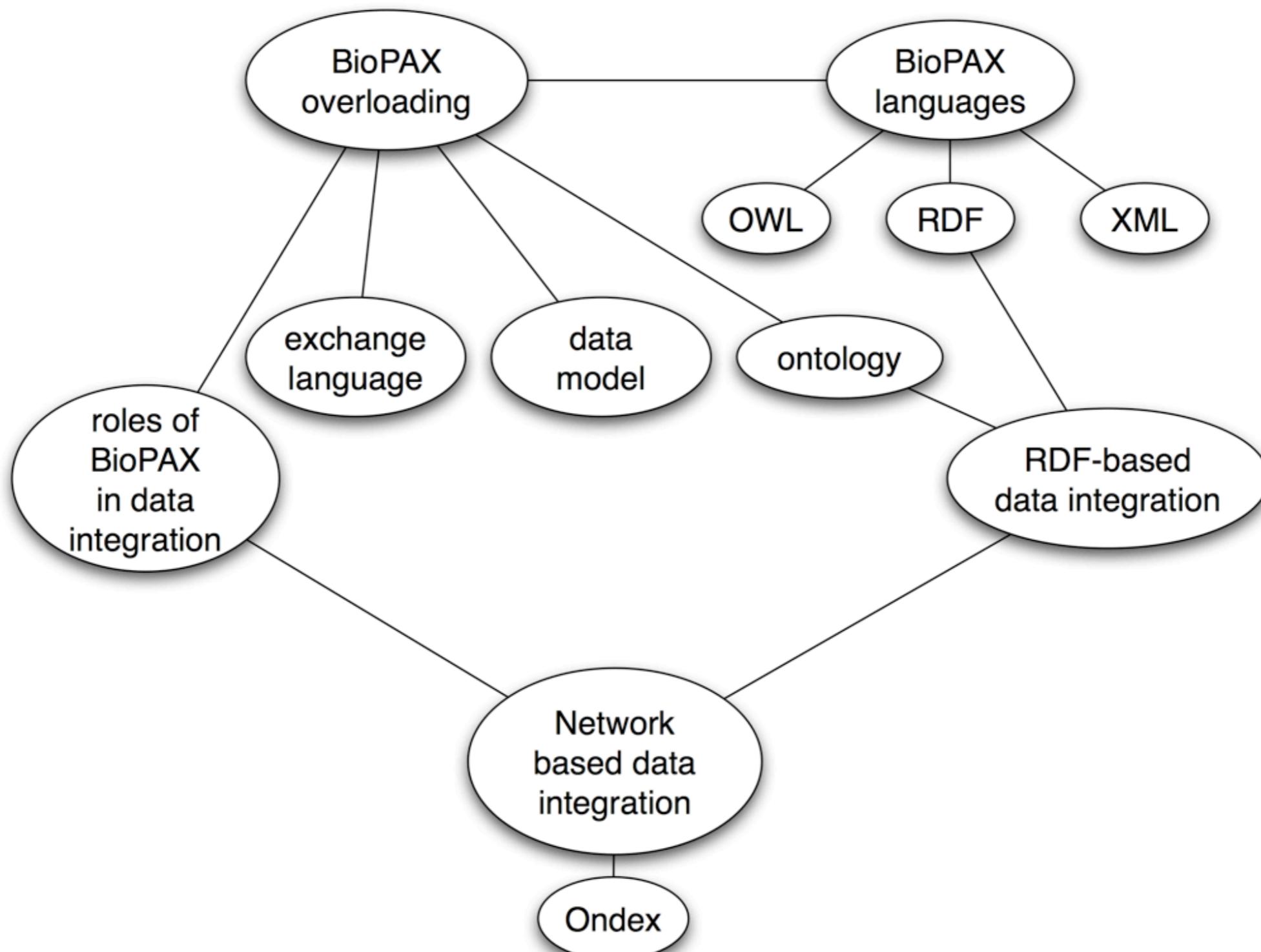


BioPAX for semantic web based data integration

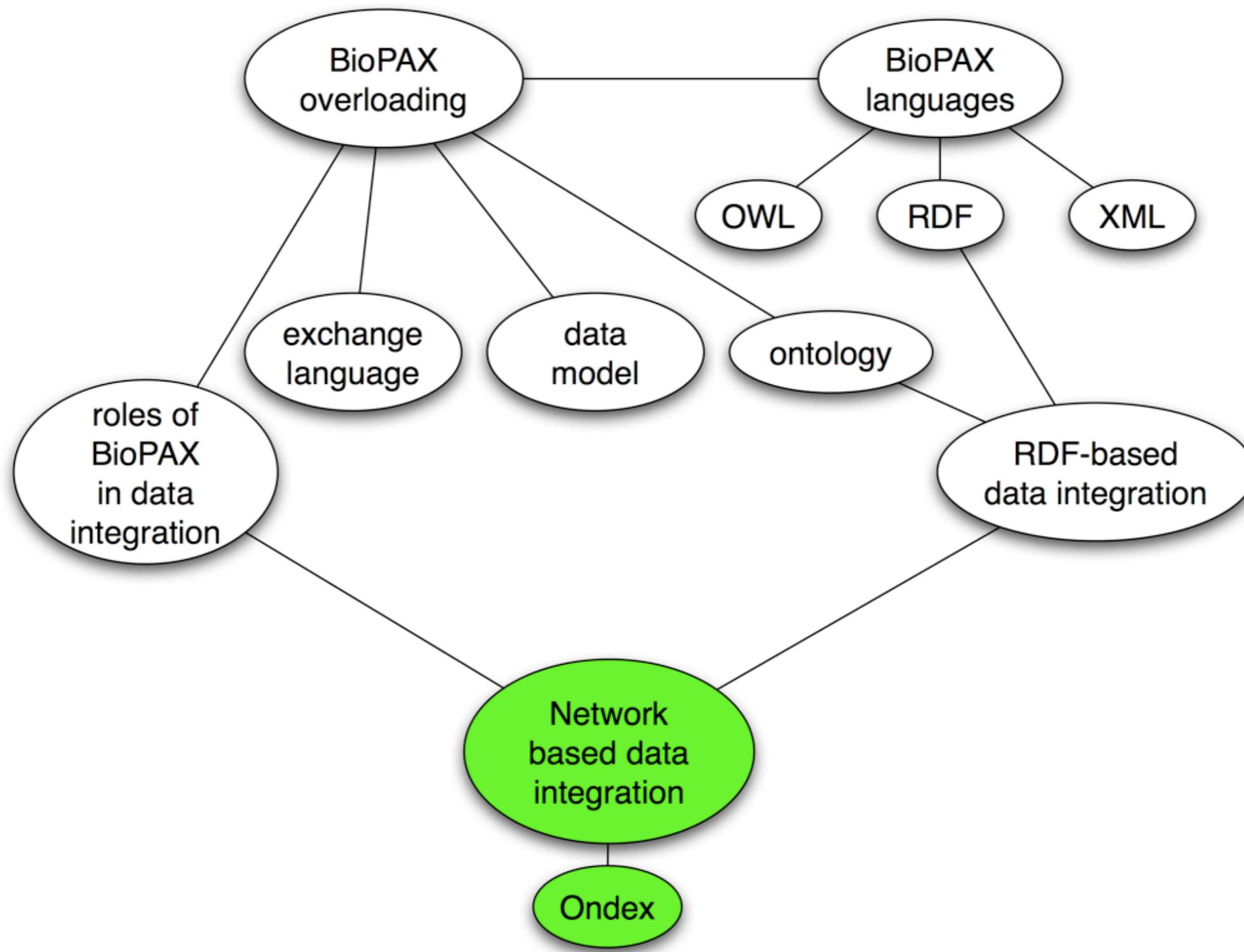
Andrea Splendiani

*Biomathematics and Biostatistics Dept.
Rothamsted Research*

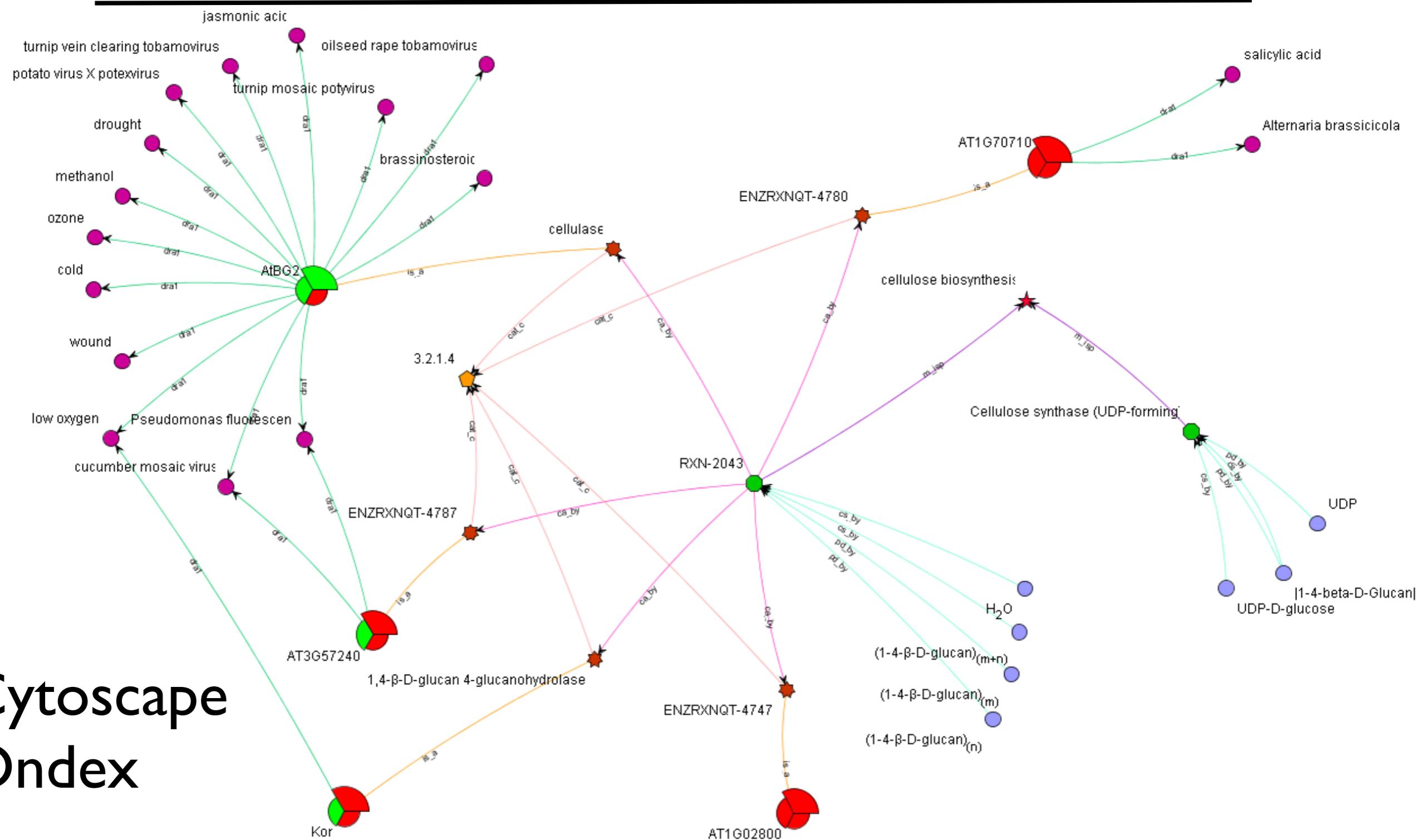
Outline



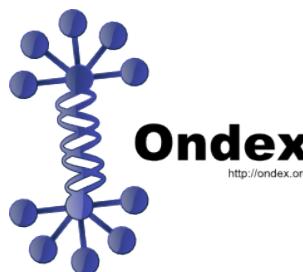
Outline



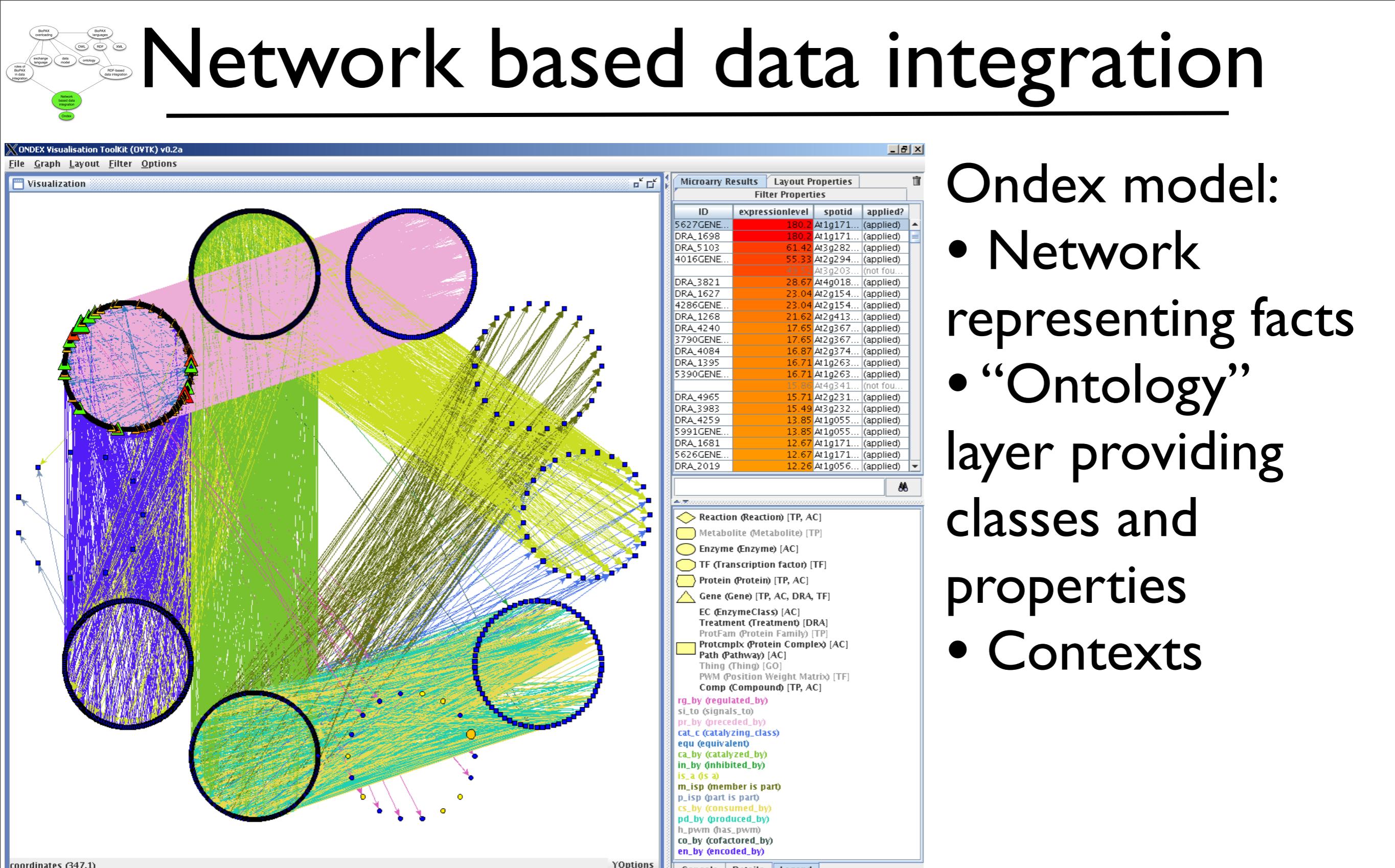
Network based data integration



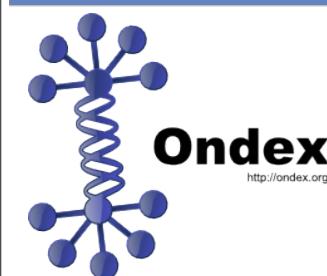
- Cytoscape
- Ondex



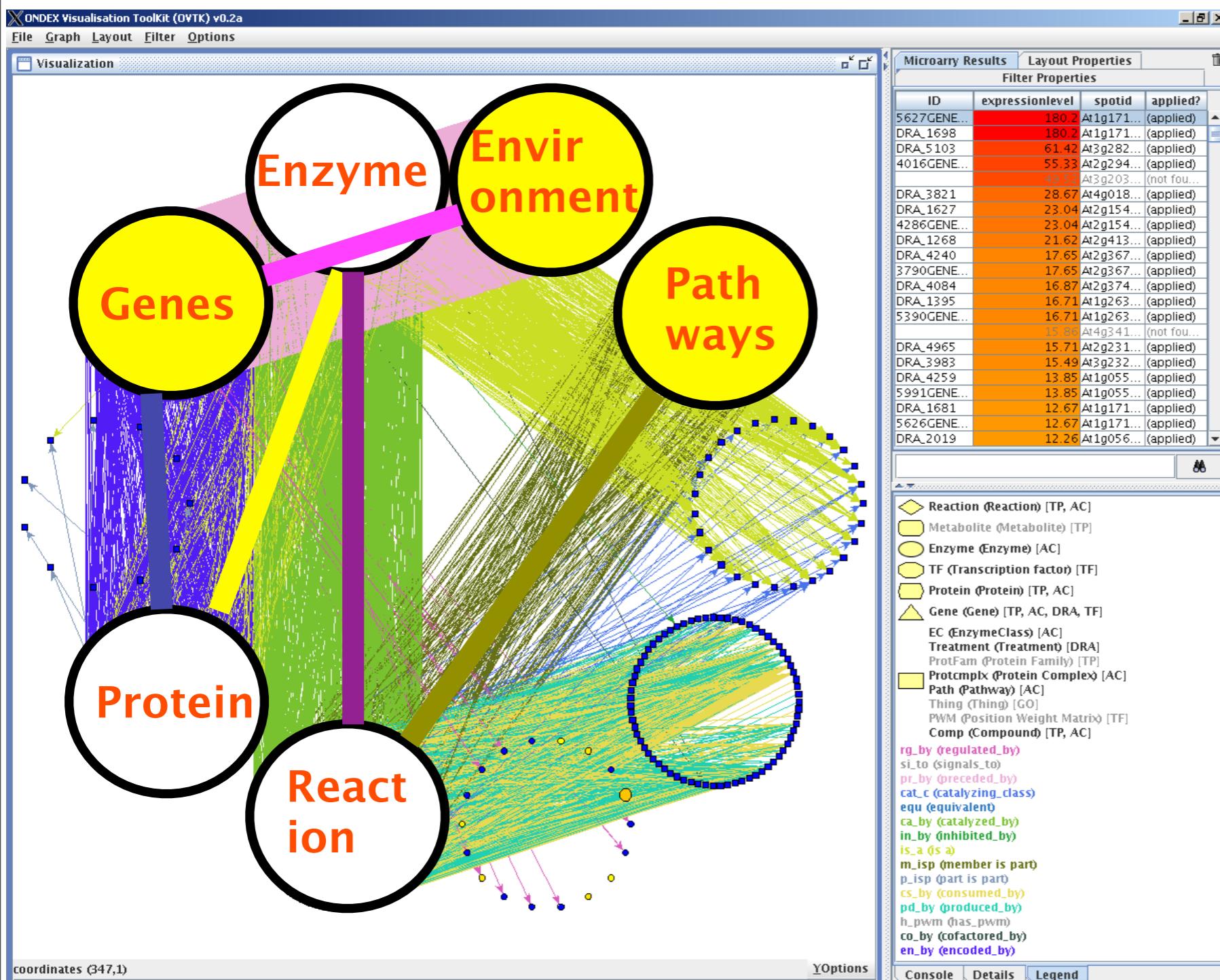
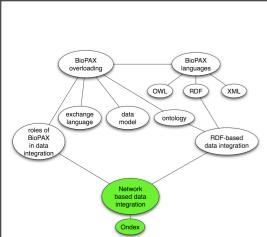
Network based data integration



- Ondex model:
- Network representing facts
 - “Ontology” layer providing classes and properties
 - Contexts



Network based data integration



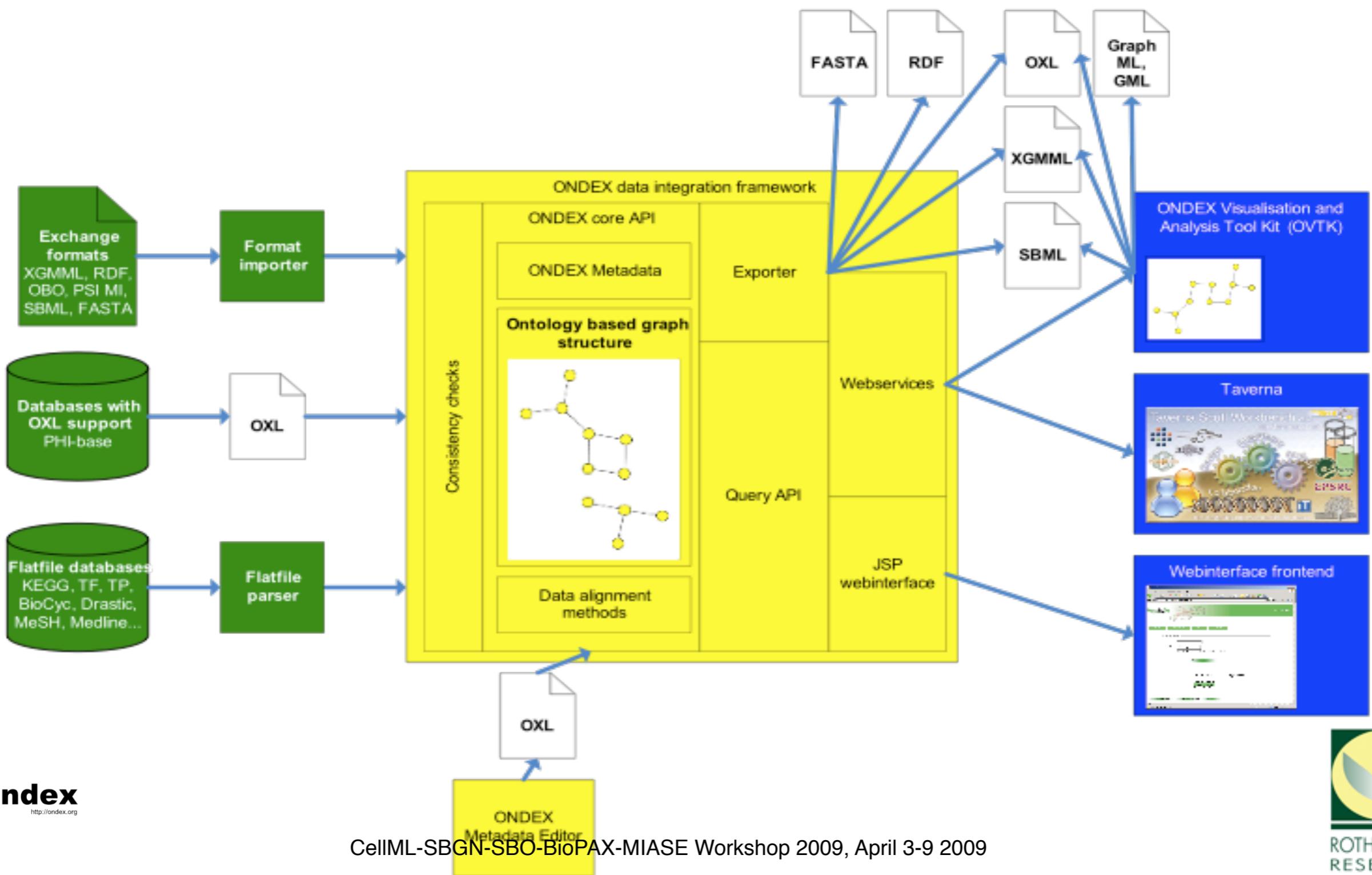
- ## Ondex
- Network representing facts
 - “Ontology” layer providing classes and properties
 - Contexts



Ondex

<http://ondex.org>

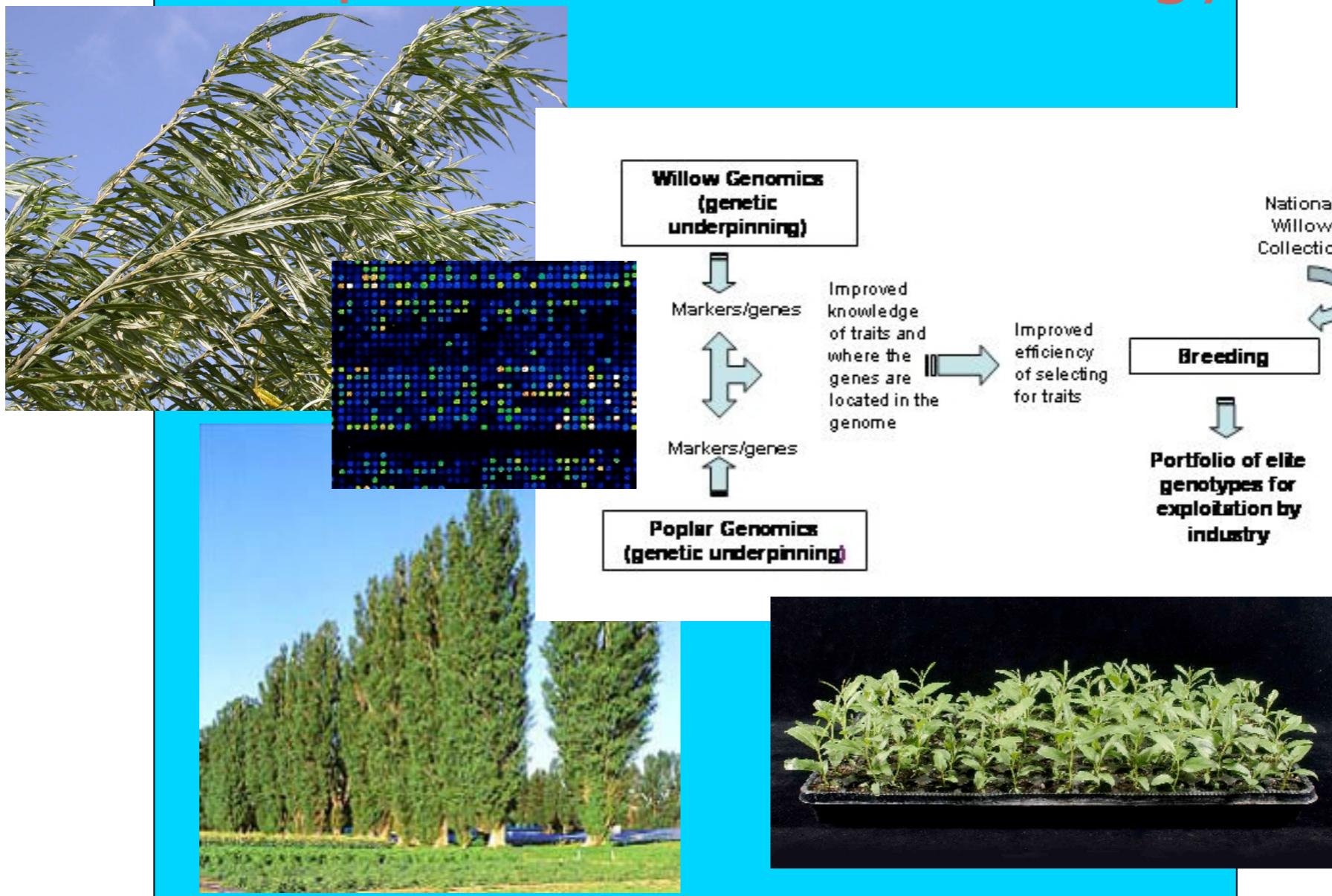
Network based data integration



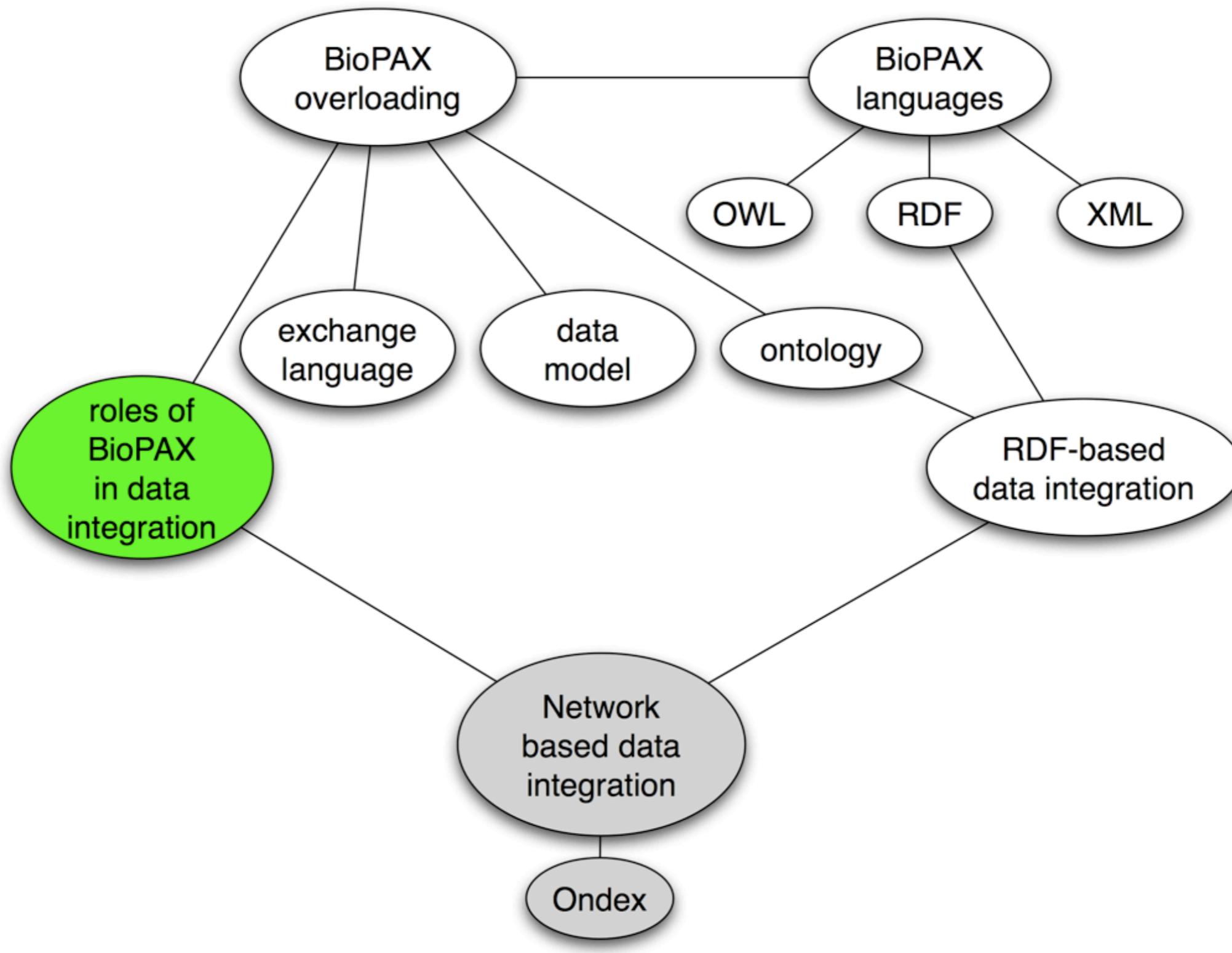
Network based data integration

What for ?

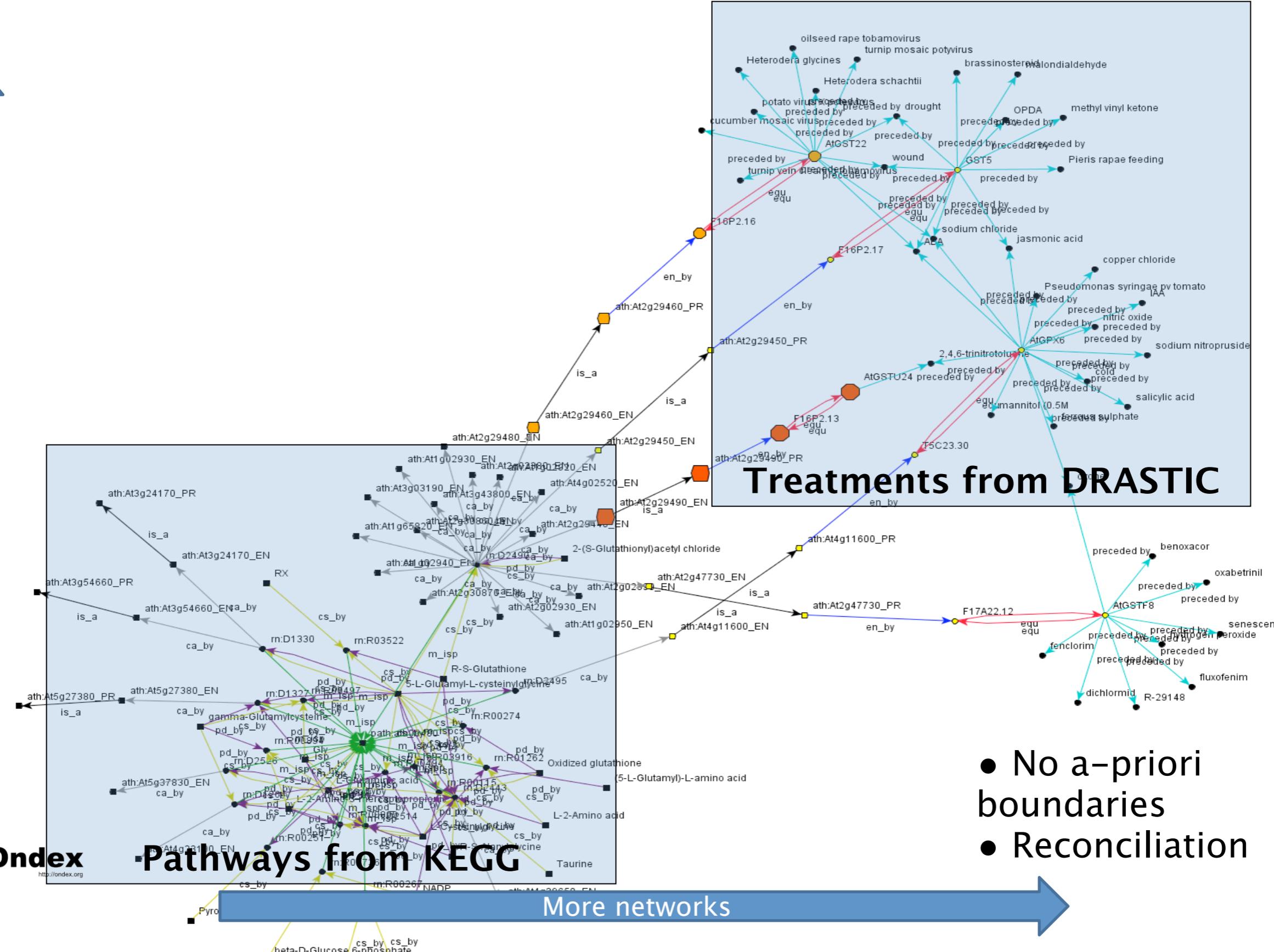
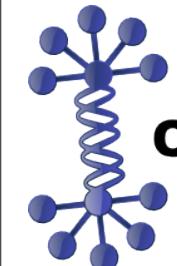
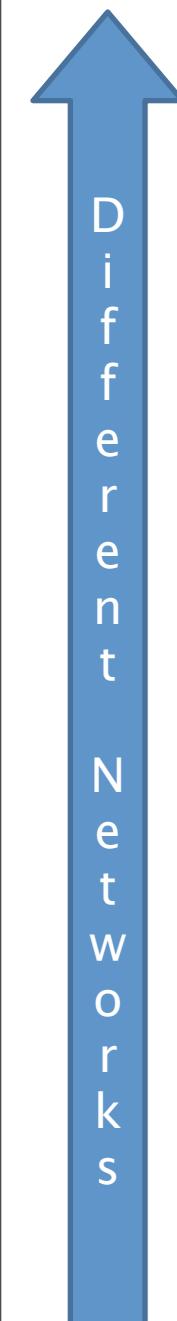
Bioenergy crop improvement
<http://www.biomass4energy.org>

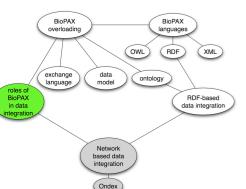


Outline



Network based data integration





Network based data integration

Extensional dimension: role of BioPAX



Search and visualize public biological pathway information. Single point of access. [\[more...\]](#)

Home | Filter | Stats | FAQ | Web Service | About

Send us your [feedback](#). Sign up for Pathway Commons [announcements](#).

Search Pathway Commons:

To get started, enter a gene name, gene identifier or pathway name in the text box above. For example: [p53](#), [P38398](#) or [mTOR](#).

To restrict your search to specific data sources or specific organisms, update your [global filter settings](#).

Using Pathway Commons:

Biologists: Browse and search pathways across multiple valuable public pathway databases.

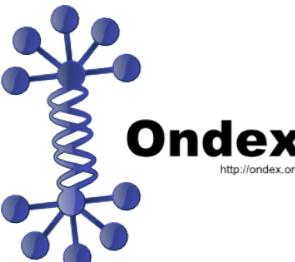
Computational biologists: Download an integrated set of pathways in BioPAX format for global analysis.

Software developers: Build software on top of Pathway Commons using our [web service API](#). Download and install the [cPath software](#) to create a local mirror.

Current Data Sources:

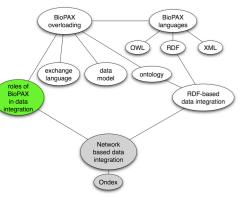
Pathway Commons currently contains the following data sources:

	Cancer Cell Map, Release: 1.0 [19-May-06] Browse
	HPRD [01-Sep-07] Browse
	HumanCyc, Release: 10.5 [18-Sep-06] Browse
	IntAct [14-Dec-07] Browse
	MINT [21-Dec-07] Browse
	NCI / Nature Pathway Interaction Database [28-Jan-08]



More networks

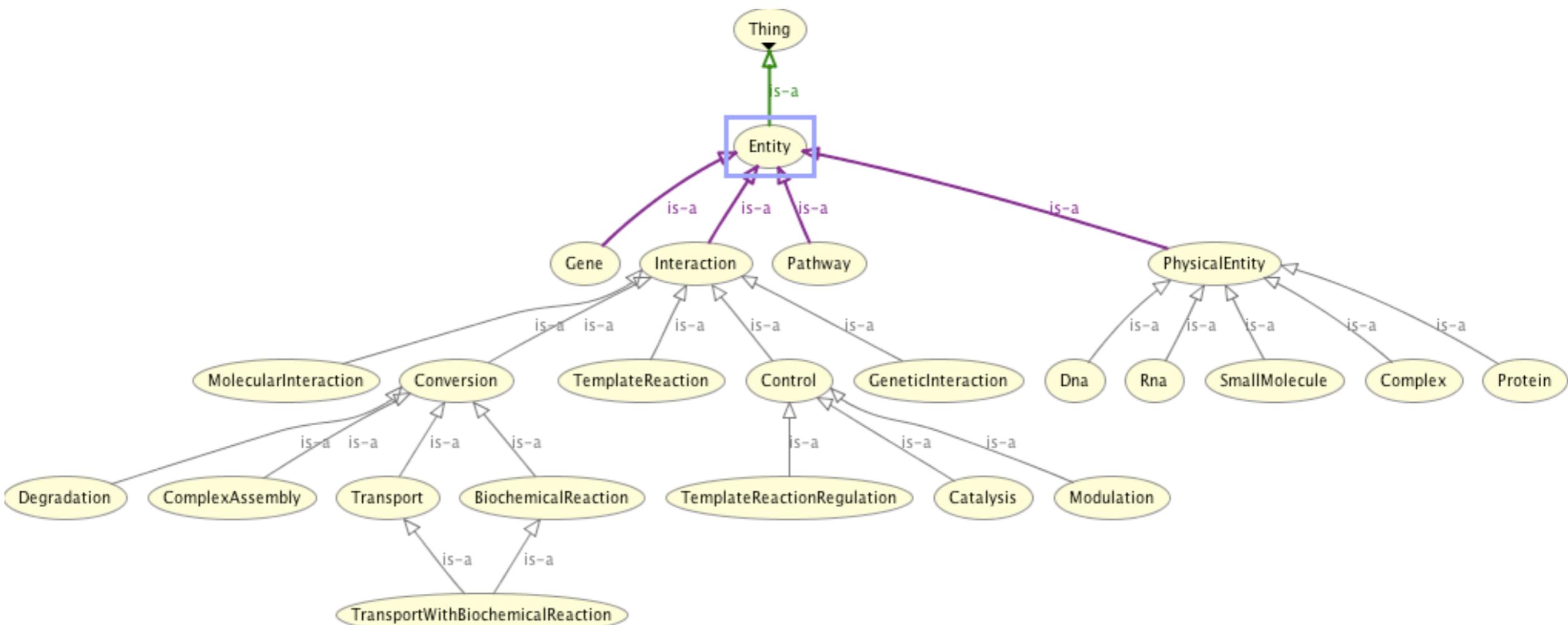




Network based data integration

Intensional dimension: role of BioPAX

Different Networks



Ondex
http://ondex.org

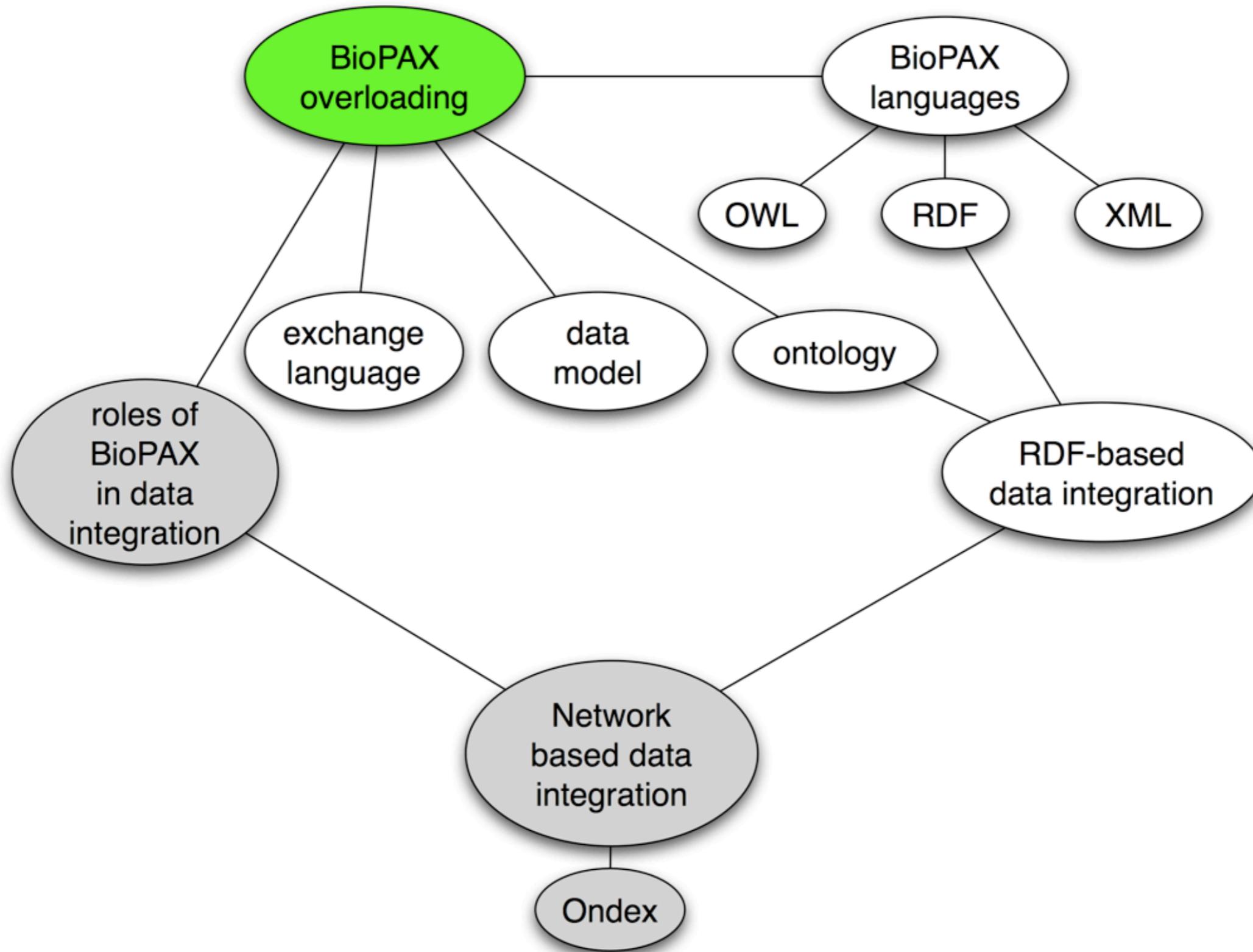
BioPAX as an ontology for the integration of heterogeneous networks

CellML-SBGN-SBO-BioPAX-MIASE Workshop 2009, April 3-9 2009

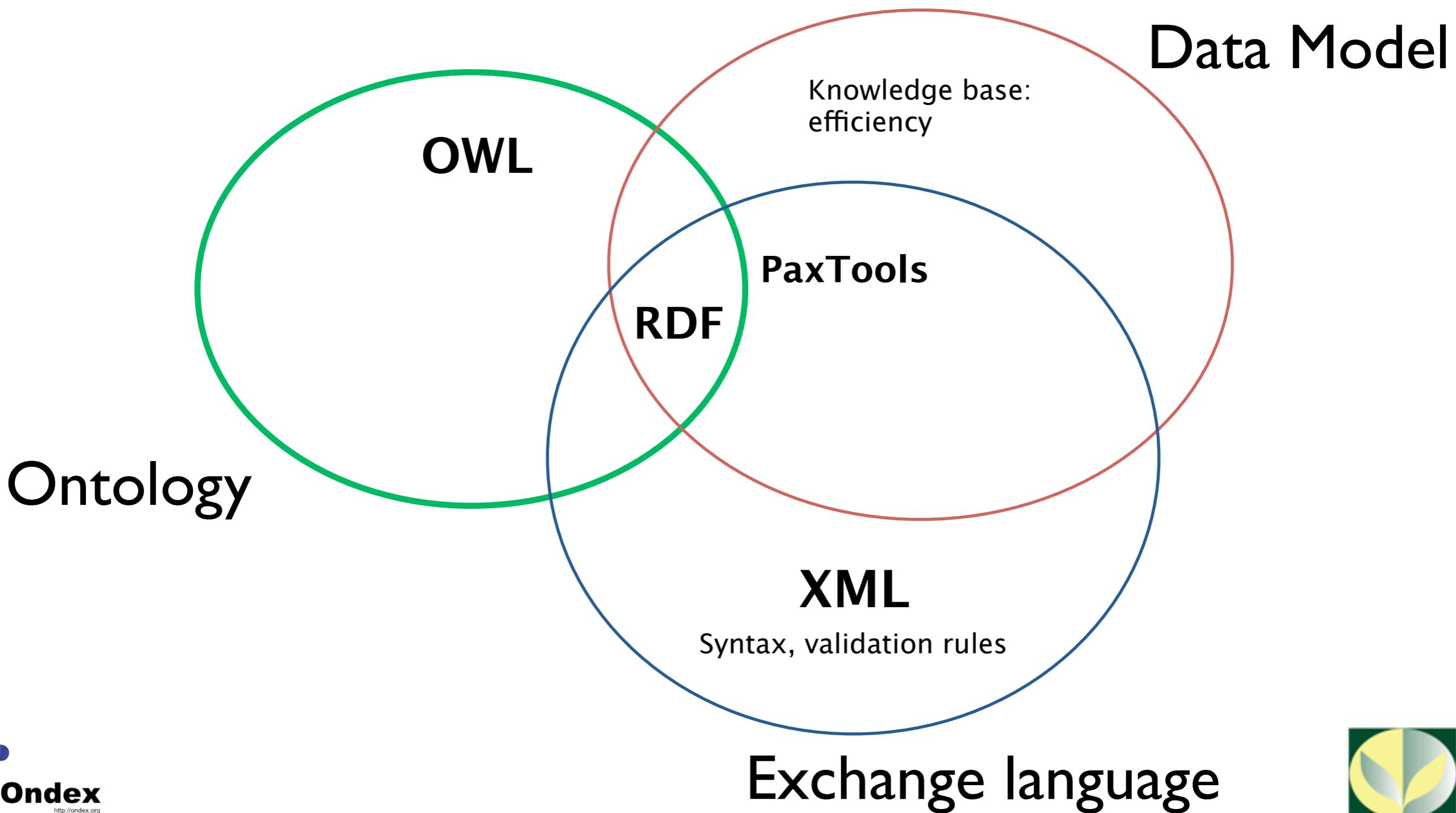
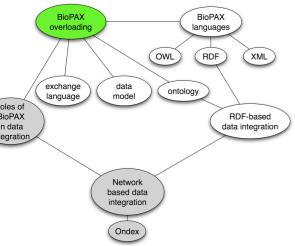


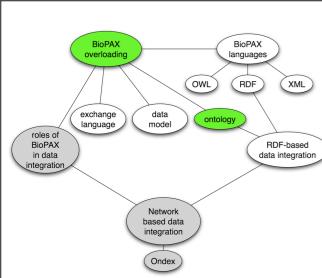
ROTHAMSTED
RESEARCH

Outline



BioPAX overloading





BioPAX overloading

ontology

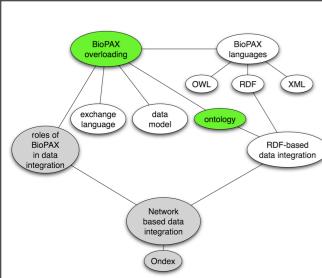


BioPAX is in part an
ontology of biological
networks

XML
Syntax, validation rules

Exchange language



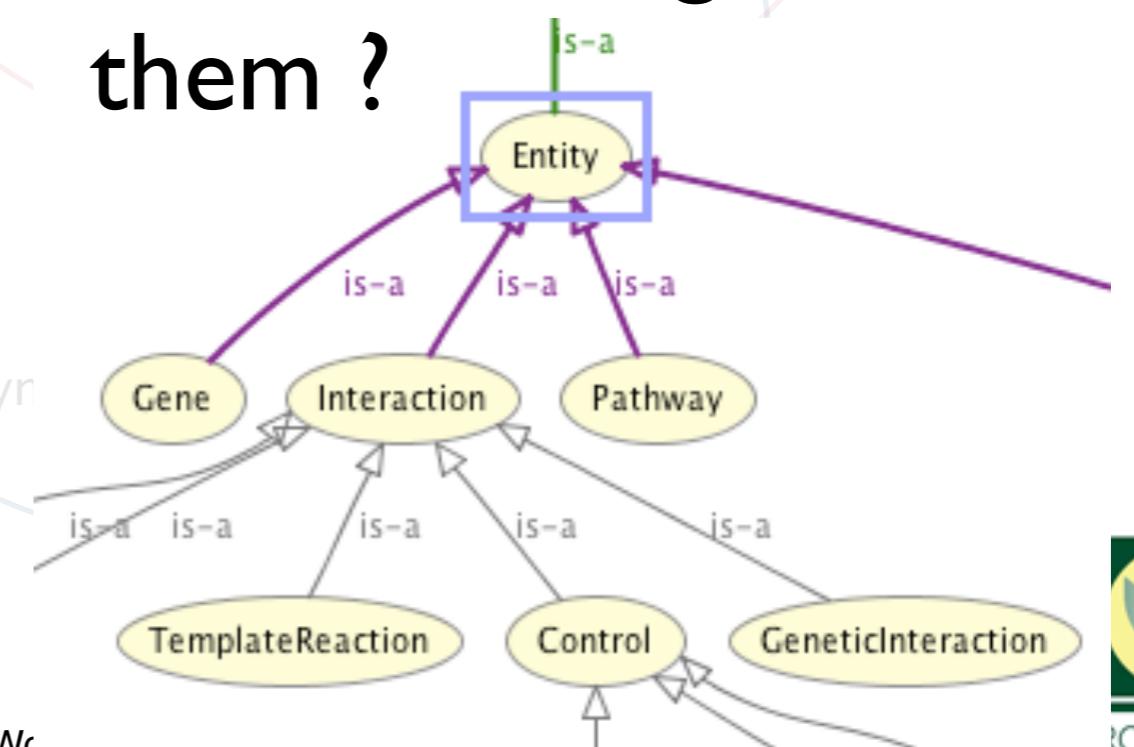


BioPAX overloading

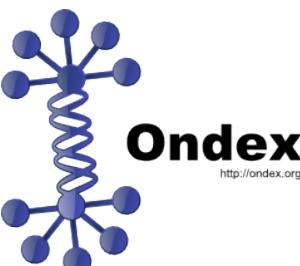
ontology

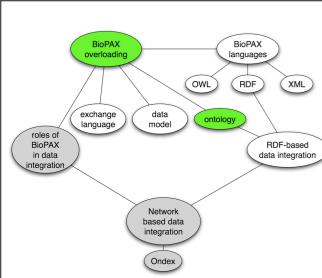


- Entities, Interactions, their types and relations
- What do a “control” and a “genetic interaction share” ?
- What distinguishes them ?

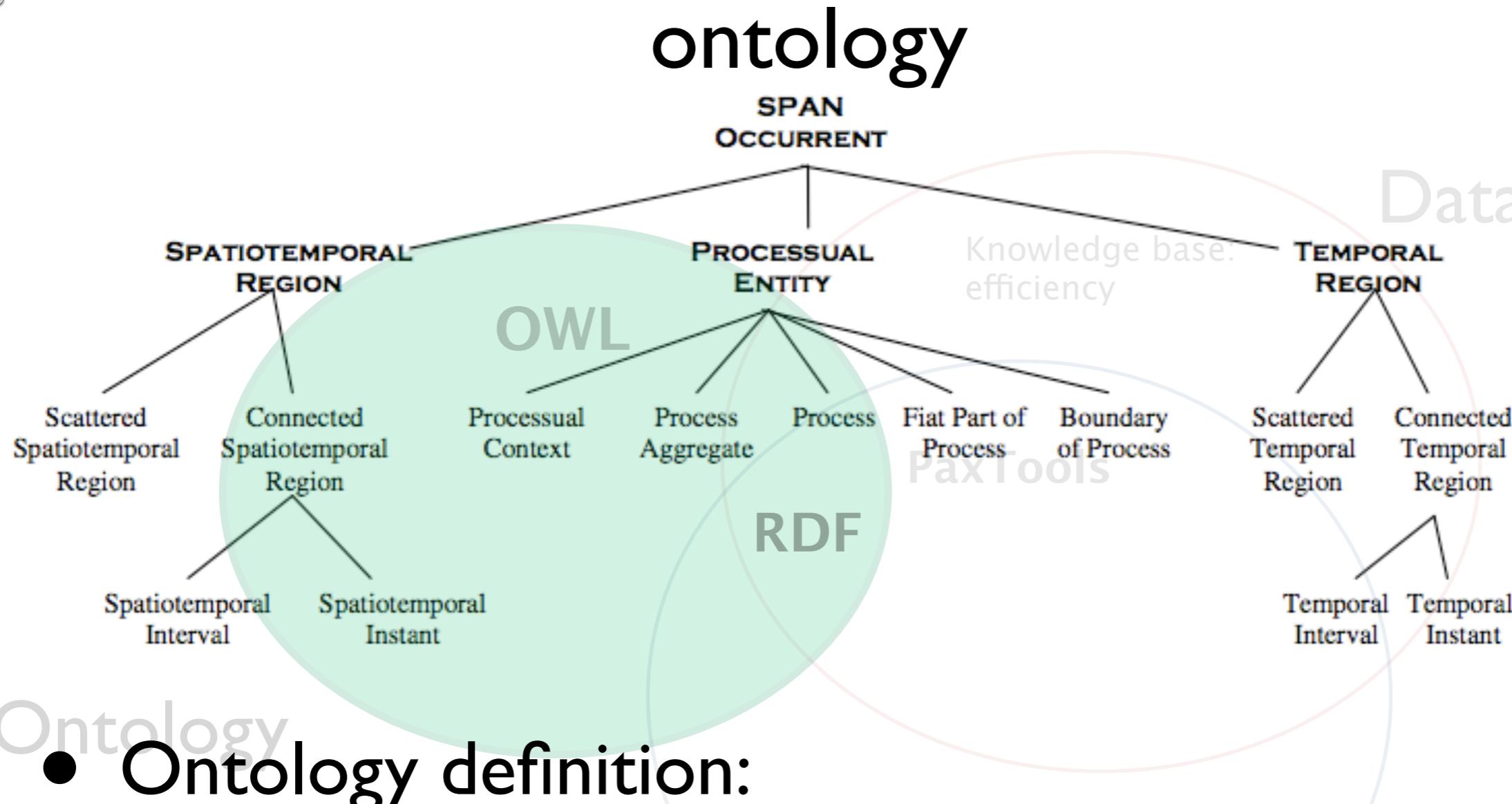


Ontology>>terminology!



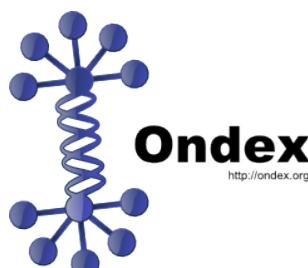


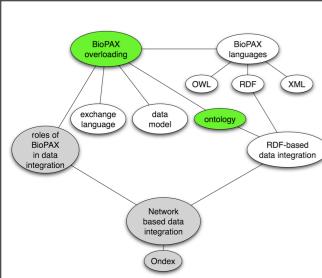
BioPAX overloading



- Ontology definition:

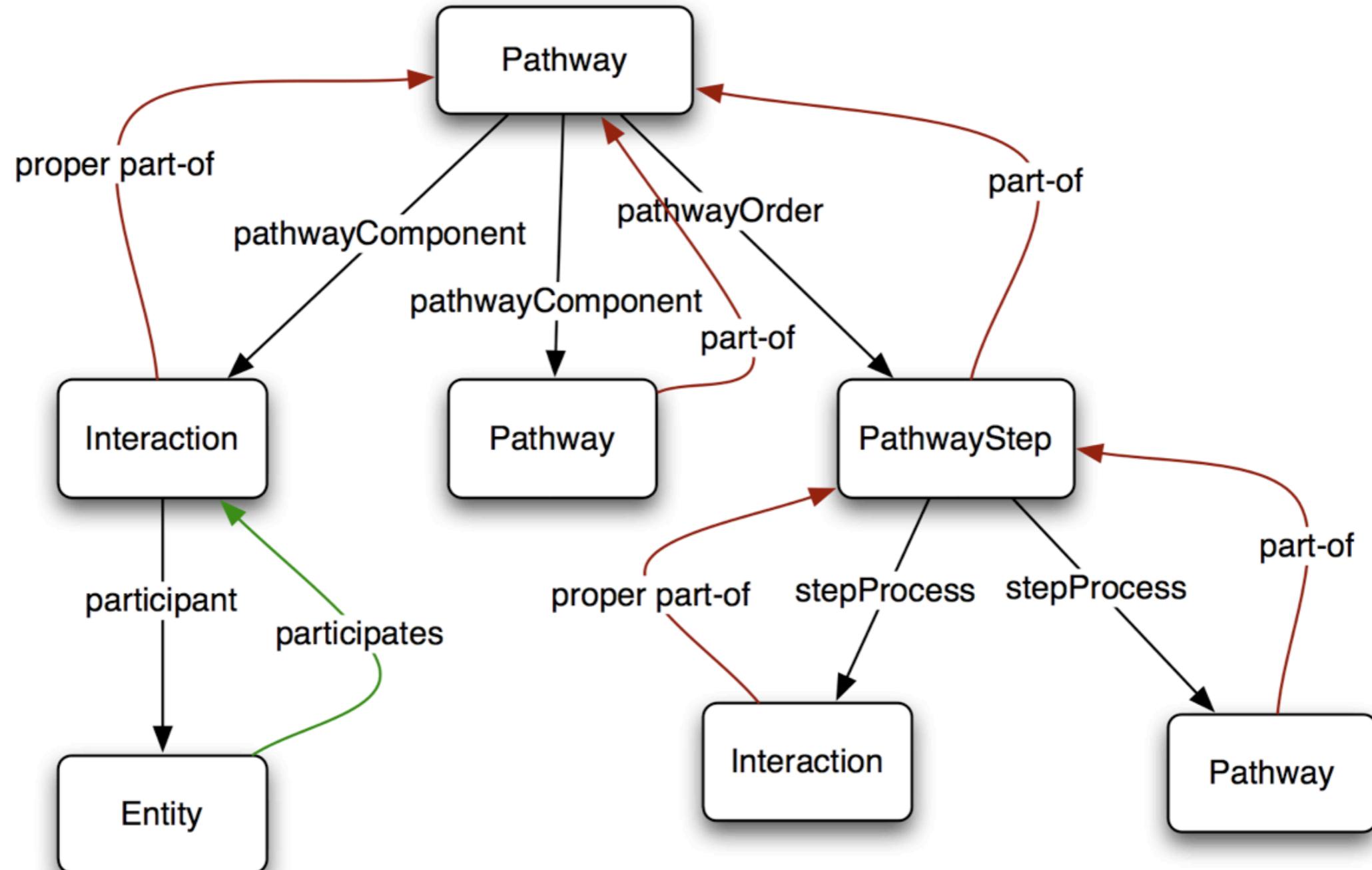
- An upper ontology as a reference.
- Well defined high-level information (e.g part of)



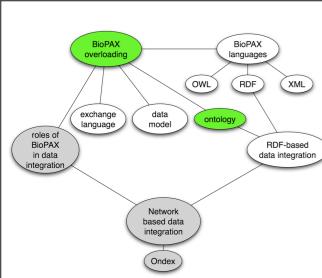


BioPAX overloading

ontology

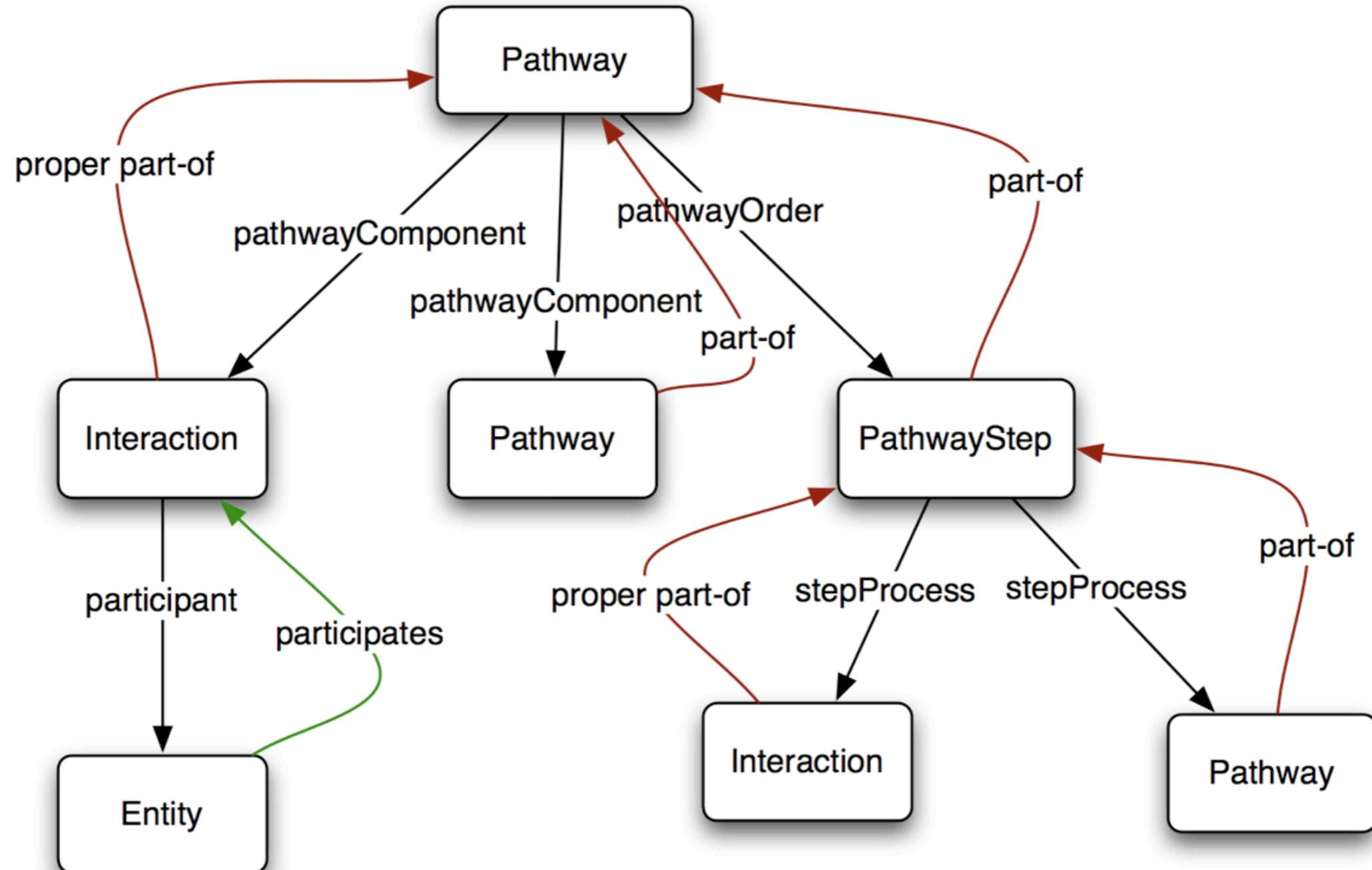


ex. query: find all protein participating in a pathway

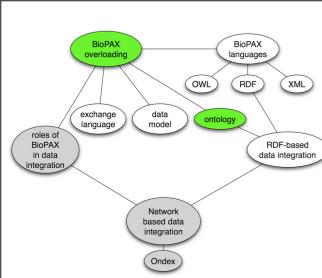


BioPAX overloading

ontology



ex. query: find all protein participating in a pathway

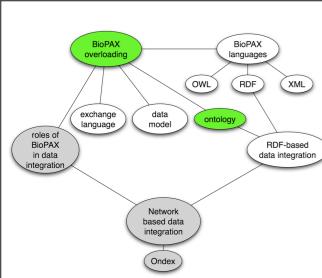


BioPAX overloading

part_of

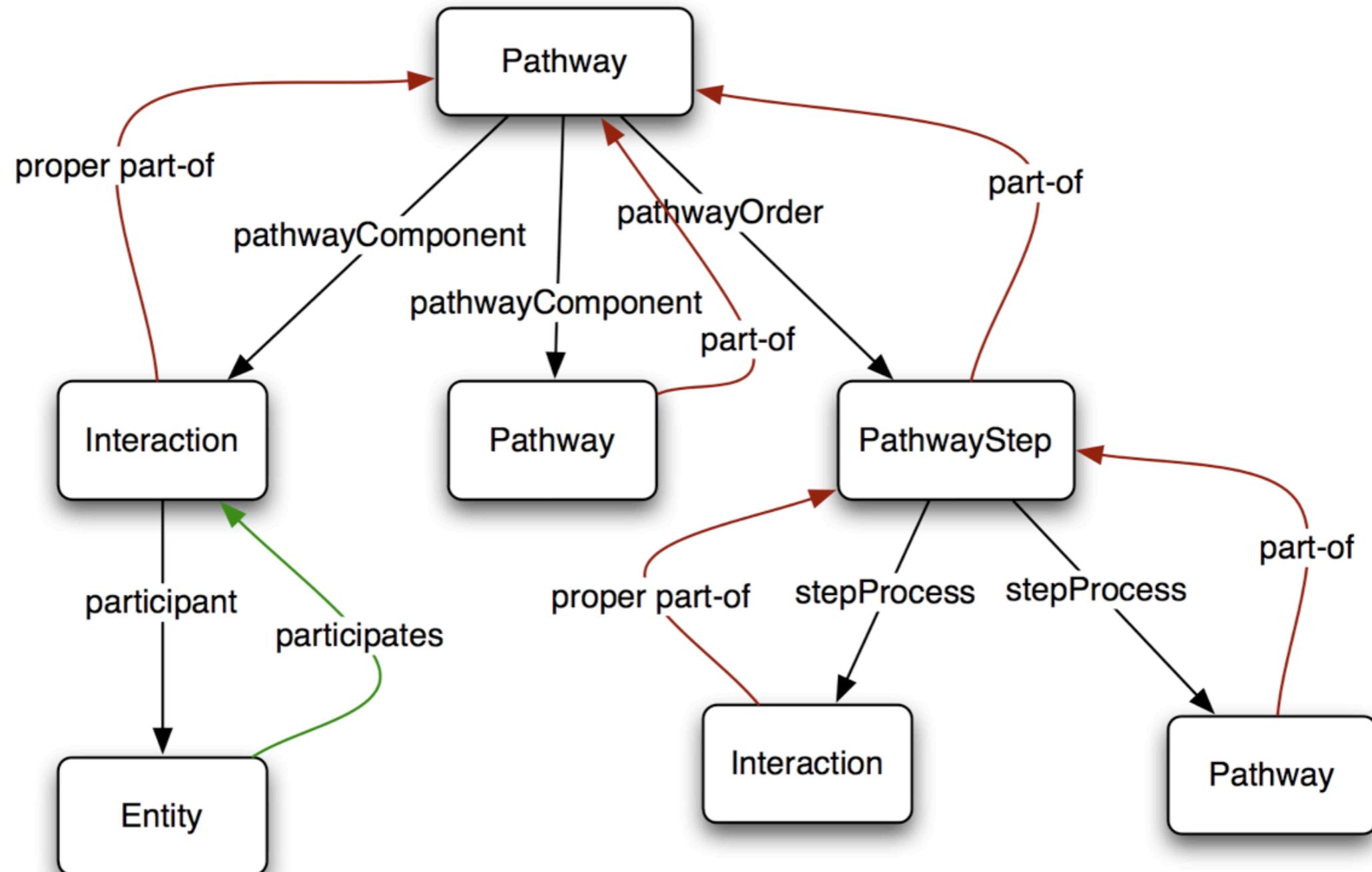
ID	OBO_REL:part_of
Name	part_of
Relation properties	[transitive] [reflexive] [anti-symmetric]
Definition	For continuants: C part_of C' if and only if: given any c that instantiates C at a time t, there is some c' such that c' instantiates C' at time t, and c *part_of* c' at t. For processes: P part_of P' if and only if: given any p that instantiates P at a time t, there is some p' such that p' instantiates P' at time t, and p *part_of* p' at t. (Here *part_of* is the instance-level part-relation.)
Comments	Parthood as a relation between instances: The primitive instance-level relation p part_of p1 is illustrated in assertions such as: this instance of rhodopsin mediated phototransduction part_of this instance of visual perception. This relation satisfies at least the following standard axioms of mereology: reflexivity (for all p, p part_of p); anti-symmetry (for all p, p1, if p part_of p1 and p1 part_of p then p and p1 are identical); and transitivity (for all p, p1, p2, if p part_of p1 and p1 part_of p2, then p part_of p2). Analogous axioms hold also for parthood as a relation between spatial regions. For parthood as a relation between continuants, these axioms need to be modified to take account of the incorporation of a temporal argument. Thus for example the axiom of transitivity for continuants will assert that if c part_of c1 at t and c1 part_of c2 at t, then also c part_of c2 at t. Parthood as a relation between classes: To define part_of as a relation between classes we again need to distinguish the two cases of continuants and processes, even though the explicit reference to instants of time now falls away. For continuants, we have C part_of C1 if and only if any instance of C at any time is an instance-level part of some instance of C1 at that time, as for example in: cell nucleus part_of cell.

ex. query: find all protein participating in a pathway



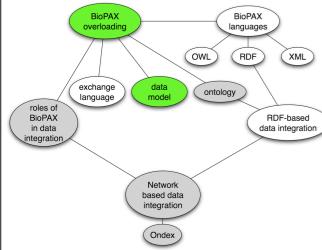
BioPAX overloading

ontology



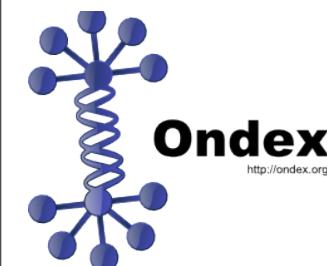
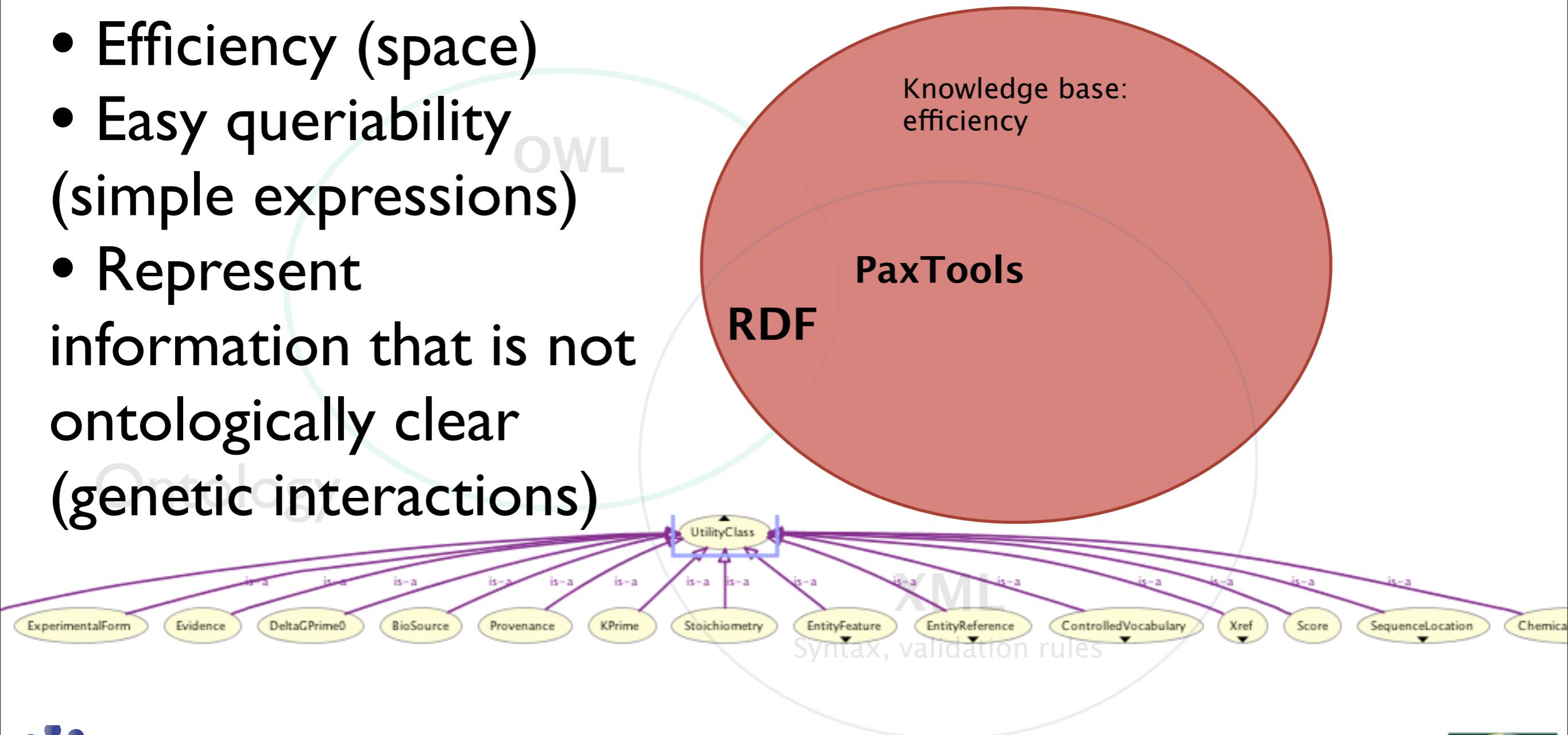
ex. query: find all protein participating in a pathway

BioPAX overloading



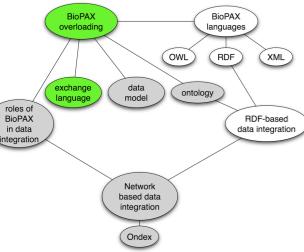
Data model

- Efficiency (space)
- Easy queriability (simple expressions)
- Represent information that is not ontologically clear (genetic interactions)



Exchange language

BioPAX overloading



Exchange language

Data Model

OWL

Knowledge base:
efficiency

PaxTools

RDF

XML

Syntax, validation rules

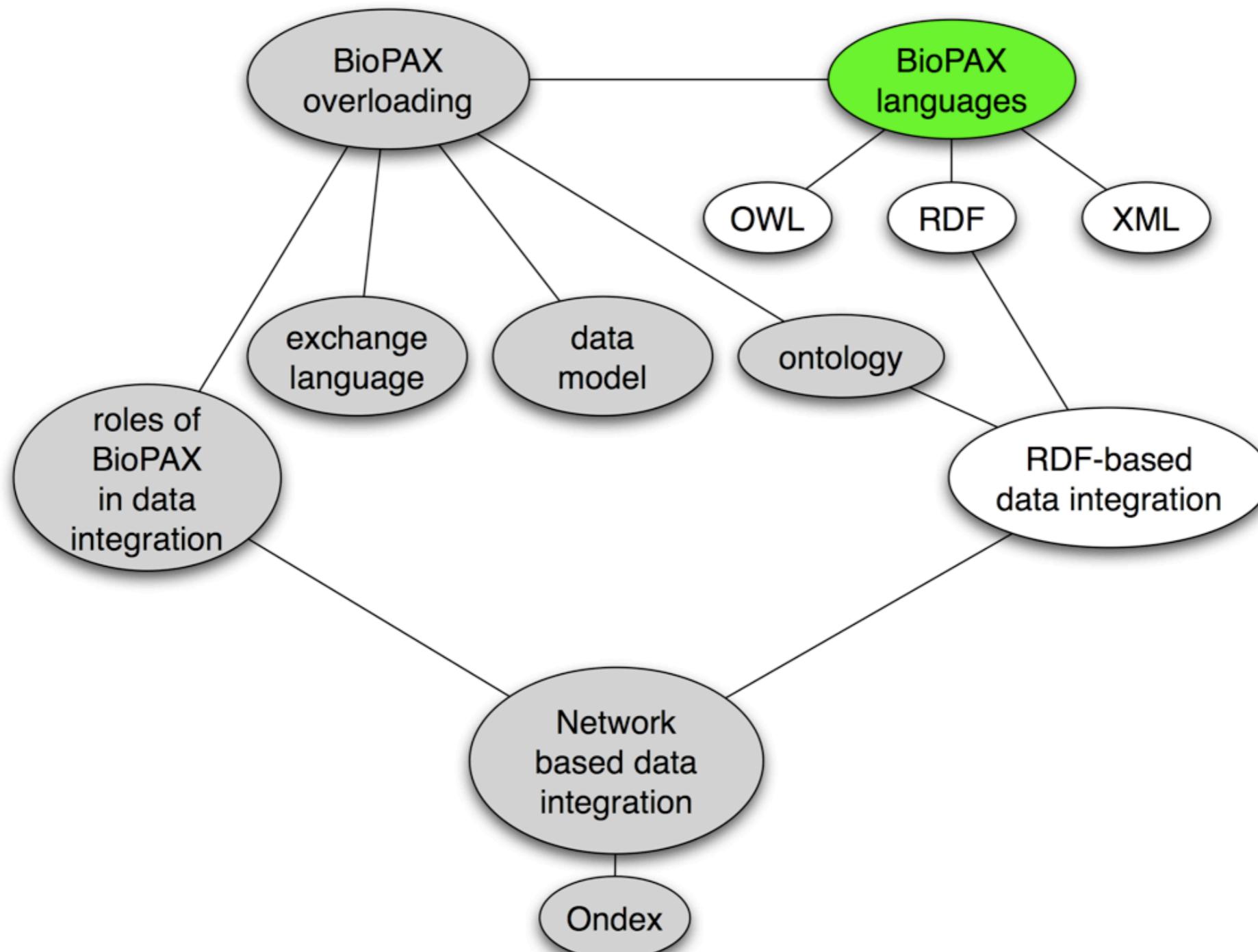
Exchange language

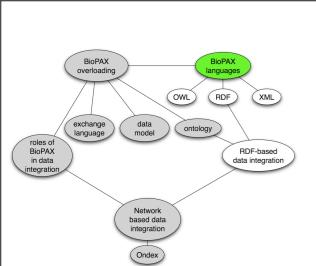
- “Correct unit of information”/ Validation.
- Necessity to be descriptive (an ontology is easily prescriptive!)



Ondex
<http://ondex.org>

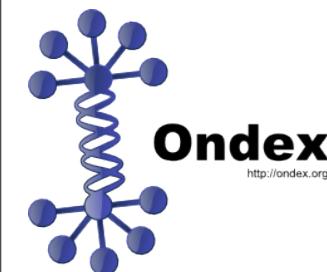
Outline

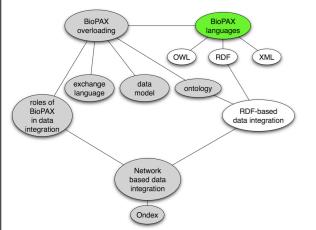




Languages in BioPAX

	Exchange	Data Model	Ontology
XML	Yes		
RDF	Yes	Yes	Yes
OWL			Yes





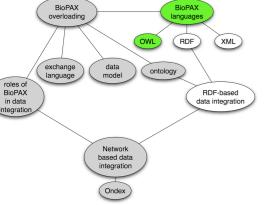
BioPAX overloading

Semantic Web metadata representation

	Exchange	Data Model	Ontology
XML	Yes		
RDF	Yes	Yes	Yes
OWL			Yes



BioPAX and OWL

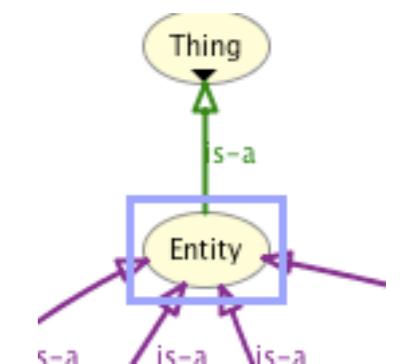
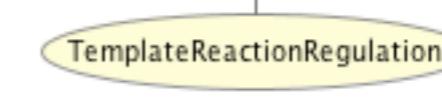
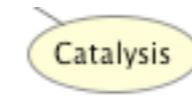
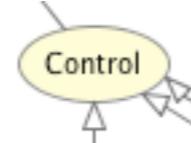
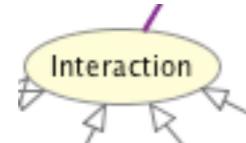
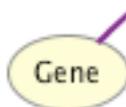
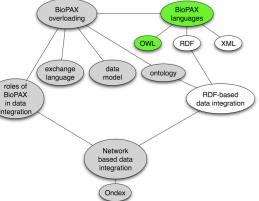


BioPAX, OWL, RDF

- BioPAX is represented in RDF
- BioPAX is serialized in XML
- The meaning of BioPAX is defined with terms defined in OWL (e.g.: disjoint class, necessary/sufficient restriction on properties,...)
- The use of OWL terms in BioPAX is restricted so that a pathway description is in OWL-DL.
- BioPAX doesn't make use of the expressivity provided by OWL-DL

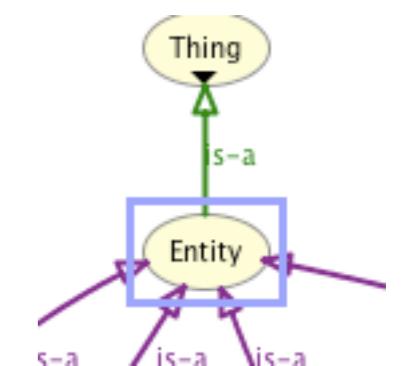
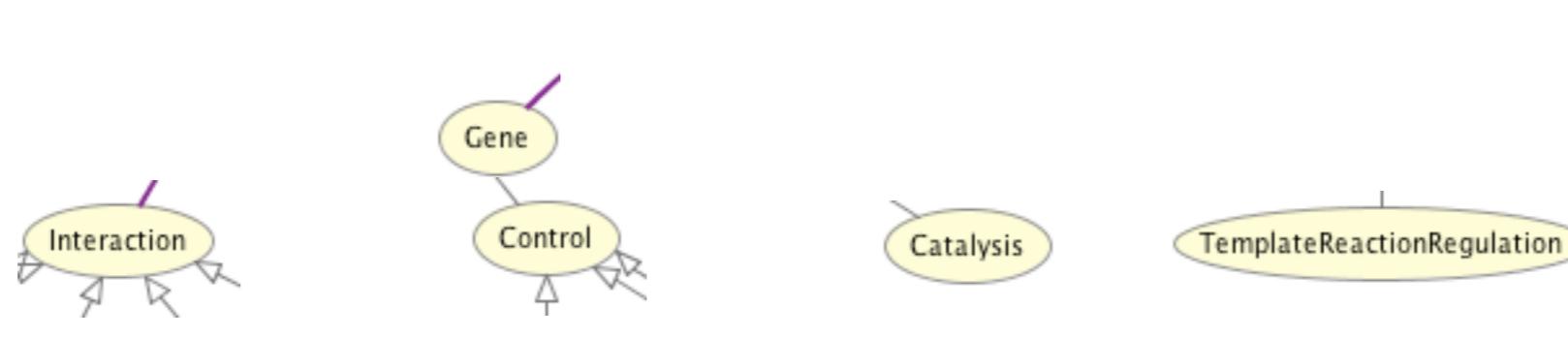
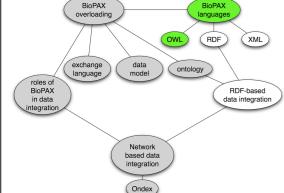
BioPAX and OWL

is biopax owl ?



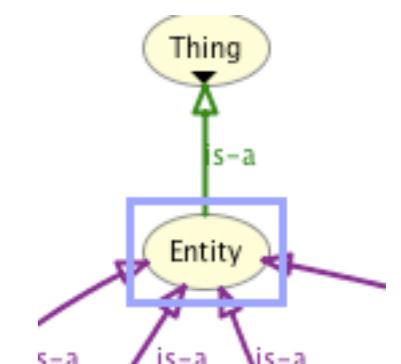
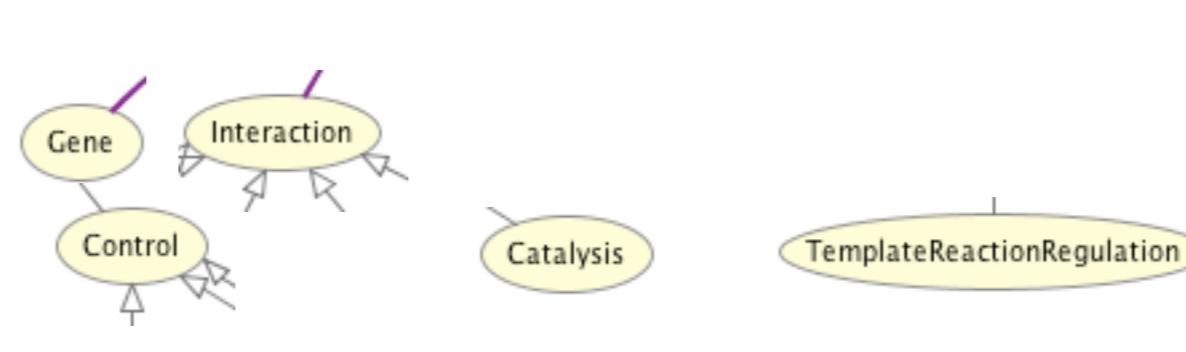
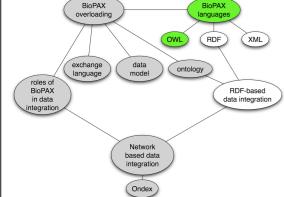
BioPAX and OWL

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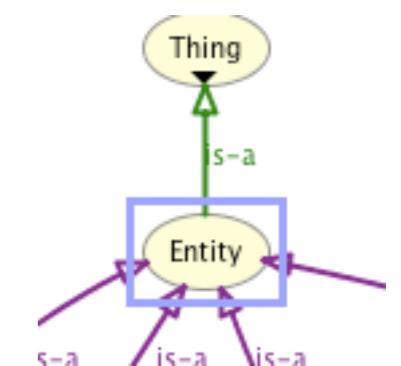
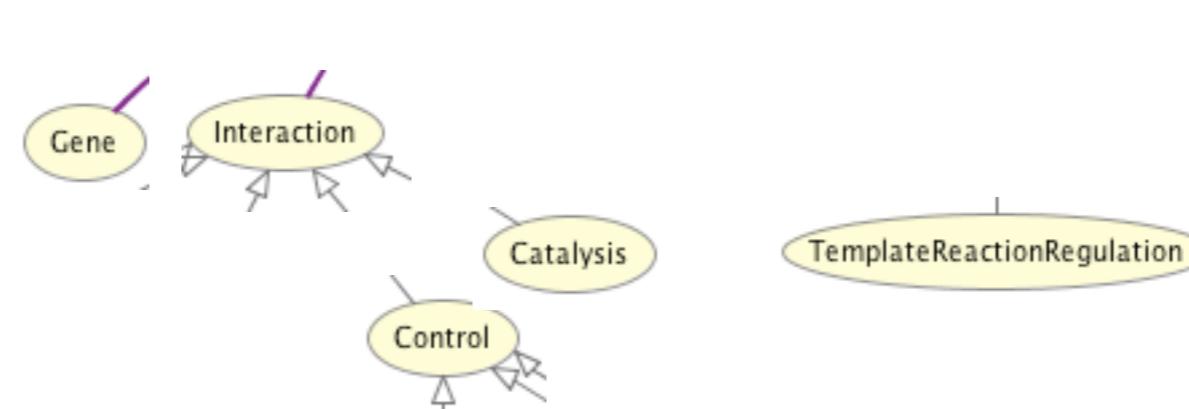
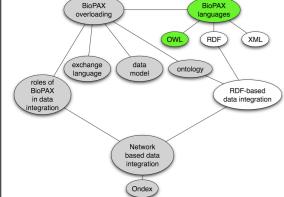
BioPAX and OWL

is biopax owl ?



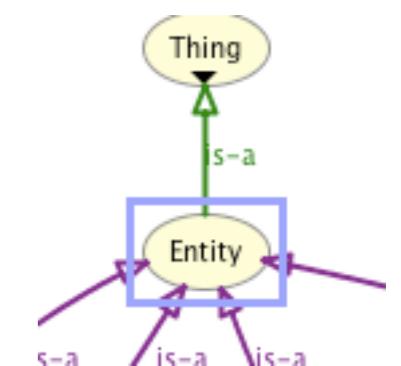
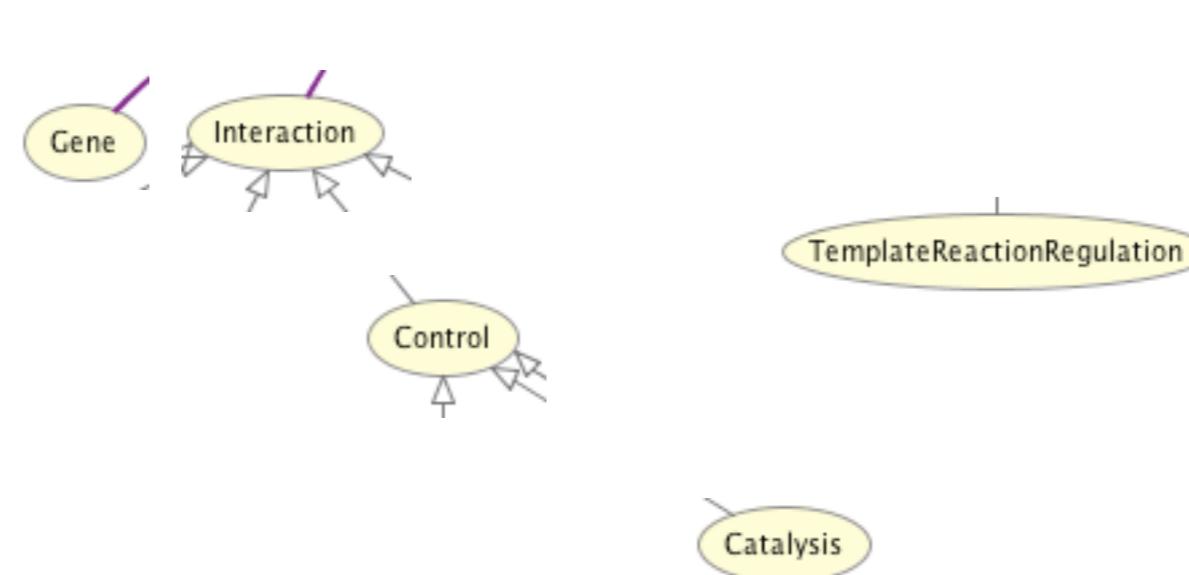
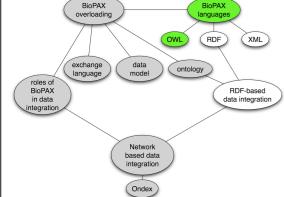
BioPAX and OWL

is biopax owl ?



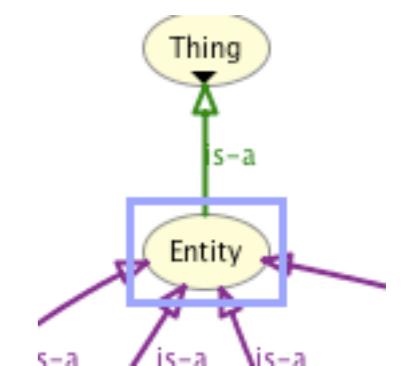
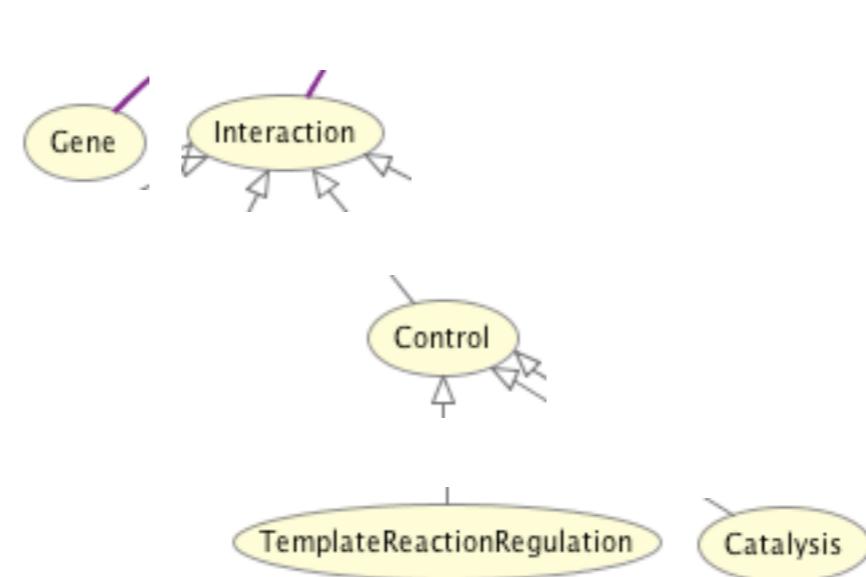
BioPAX and OWL

is biopax owl ?



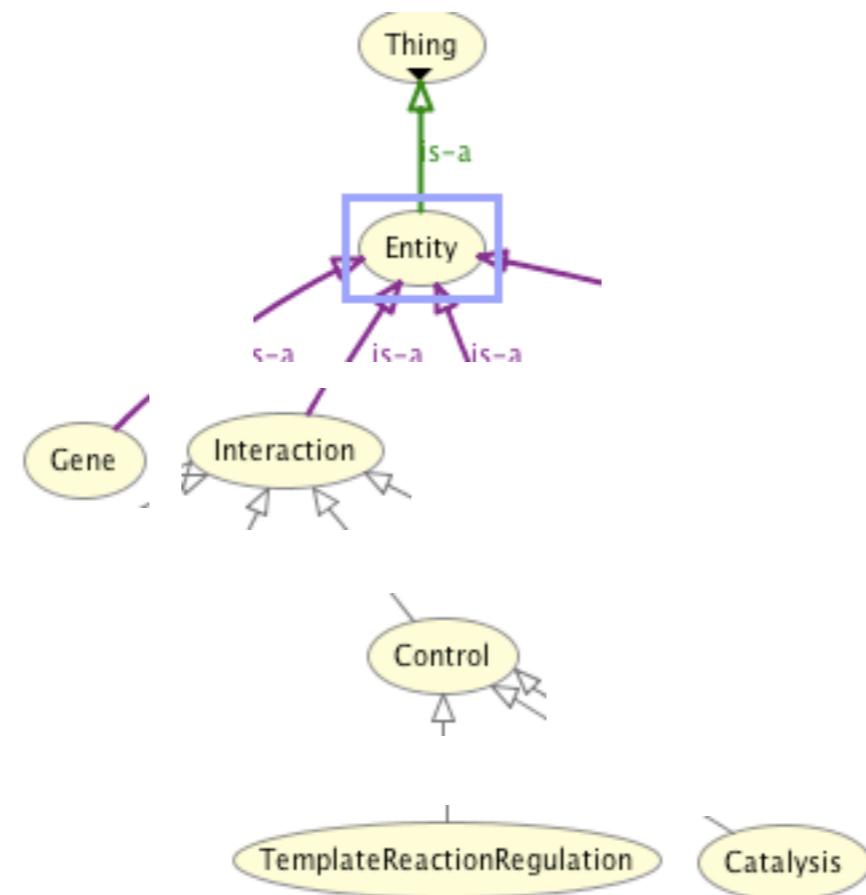
BioPAX and OWL

is biopax owl ?



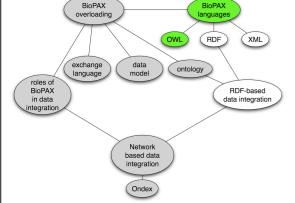
BioPAX and OWL

is biopax owl ?



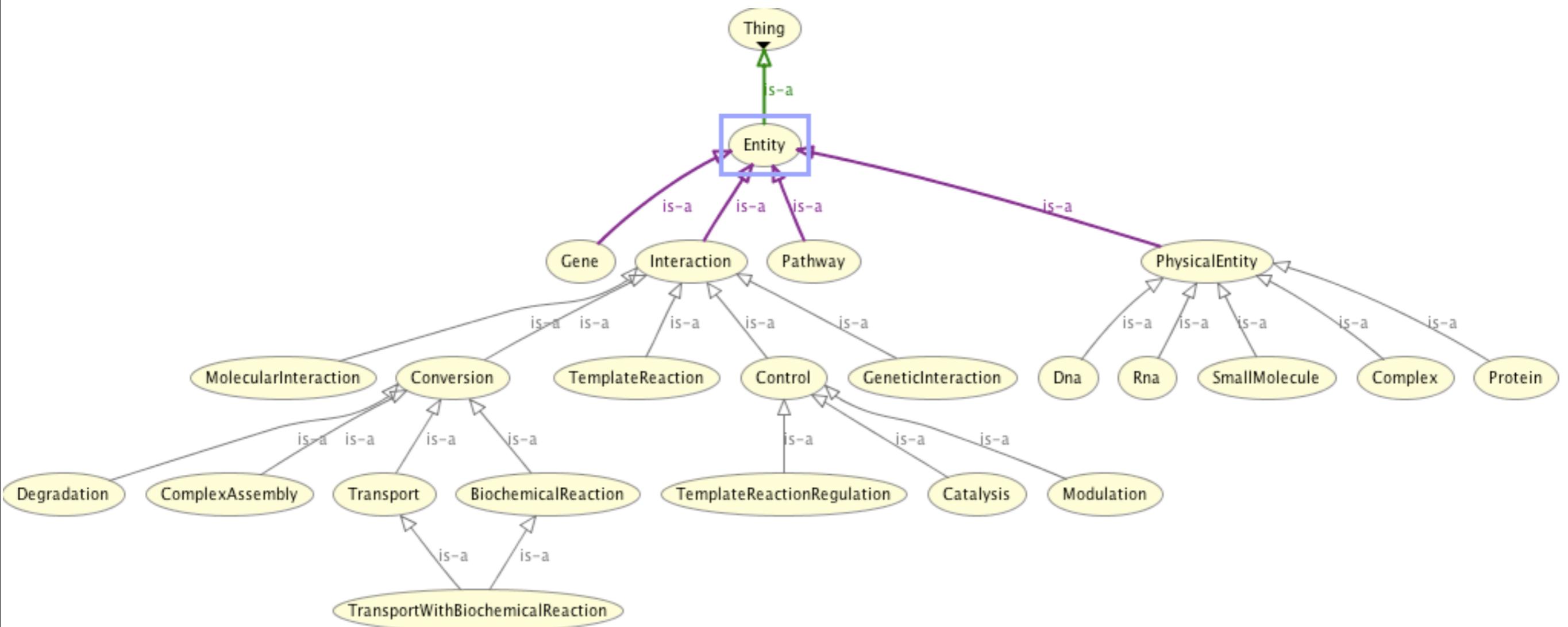
BioPAX and OWL

is biopax owl ?

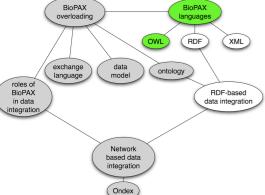


BioPAX and OWL

is biopax owl ?



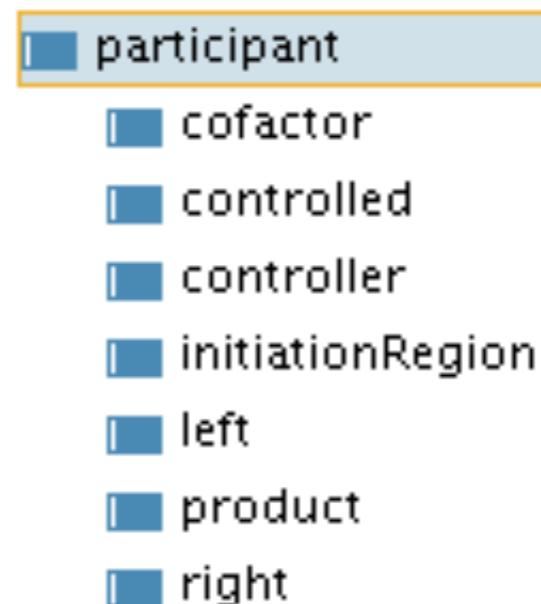
BioPAX and OWL



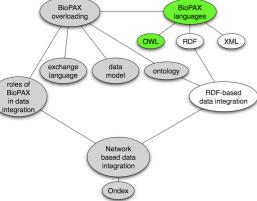
“participant” in BioPAX

```
<bp:biochemicalReaction rdf:ID="_2_H202_____02____2_H20">
  <bp:LEFT rdf:resource="#H202_peroxisomal_matrix_" />
  <bp:RIGHT rdf:resource="#H20_peroxisomal_matrix_" />
  <bp:RIGHT rdf:resource="#Oxygen_peroxisomal_matrix_" />
  <bp:EC-NUMBER rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
    1.11.1.6
  </bp:EC-NUMBER>
  <bp:NAME rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
    2 H202 => O2 + 2 H20
  </bp:NAME>
  ...

```

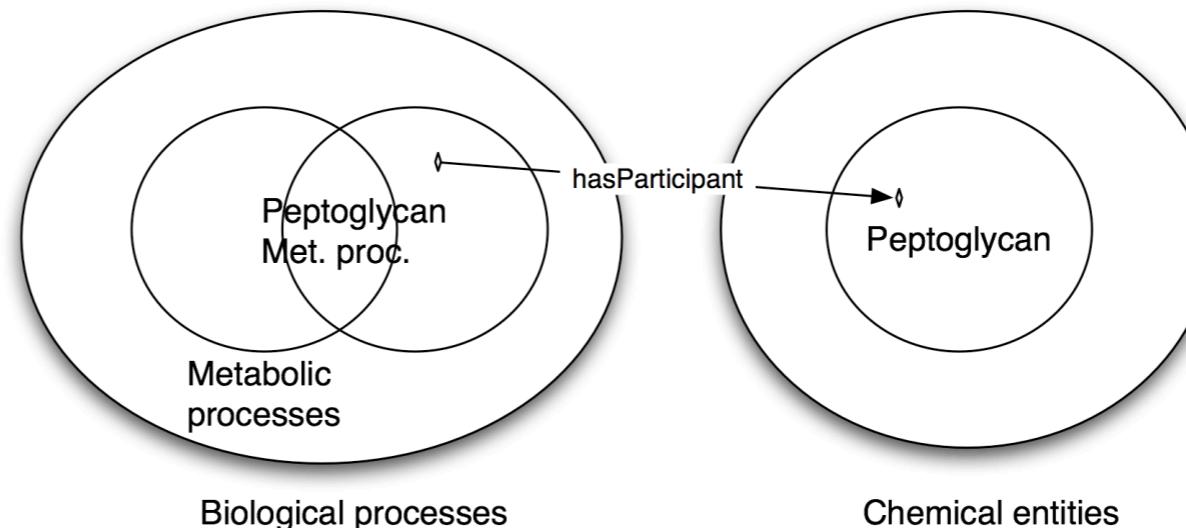


BioPAX and OWL

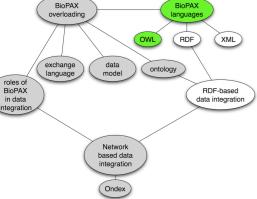


“participant” in OBO-OWL

```
<owl:Class rdf:about="http://purl.org/obo/owl/GO#GO_0000270"> Peptidoglycan  
metabolic process  
...  
<owl:equivalentClass>  
<owl:Class>  
<owl:intersectionOf rdf:parseType="Collection">  
<owl:Class rdf:about="http://purl.org/obo/owl/GO#GO_0008152"/>  
<owl:Restriction> Metabolic process  
<owl:onProperty>  
<owl:ObjectProperty rdf:about=  
"http://purl.org/obo/owl/OBO_REL#OBO_REL_has_participant"/>  
</owl:onProperty>  
<owl:someValuesFrom rdf:resource=  
"http://purl.org/obo/owl/CHEBI#CHEBI_8005"/> Peptidoglycan  
</owl:Restriction>  
</owl:intersectionOf>  
</owl:Class>  
</owl:equivalentClass>  
</owl:Class>
```



BioPAX and OWL



“participant” in RO

`has_participant`

ID	OBO_REL:has_participant
Name	has_participant
Relation properties	
inverse_of	OBO_REL:participates_in <small>(instance level)</small>
Definition	P has_participant C if and only if: given any process p that instantiates P there is some continuant c, and some time t, such that: c instantiates C at t and c participates in p at t
Comments	Has_participant is a primitive instance-level relation between a process, a continuant, and a time at which the continuant participates in some way in the process. The relation obtains, for example, when this particular process of oxygen exchange across this particular alveolar membrane has_participant this particular sample of hemoglobin at this particular time.
Sub-relation Of	OBO_REL:relationship

BioPAX and OWL

Properties and descriptions in BioPAX

The screenshot shows the Ondex Class Editor interface. On the left is the Subclass Explorer, which lists various classes under the project 'biopax-level3-latest'. In the center is the 'CLASS EDITOR for Stoichiometry (instance of owl:Class)'. It displays the following properties for the 'Stoichiometry' class:

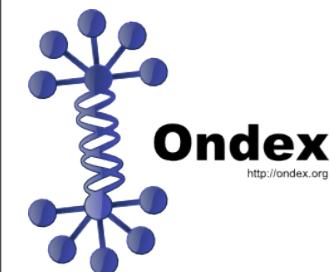
Property	Value
rdfs:comment	Definition: Stoichiometric coefficient of a interaction or complex. Note that this class has no right properties.
physicalEntity	(single PhysicalEntity) (cardinality 1)
stoichiometricCoefficient	(single float) (cardinality 1)
comment	(multiple string)

At the bottom of the editor, the 'Stoichiometry' class is selected. To the right is the 'PROPERTY BROWSER' window, which shows the properties of the 'physicalEntity' class. The 'Object properties' section includes:

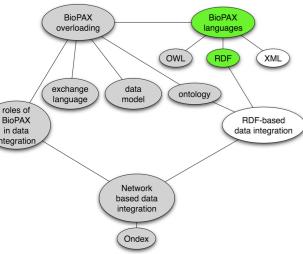
- experimentalFormEntity
- feature
- featureLocation
- Region
- inScore
- inType
- intensityReference
- feature
- physicalEntity
- ionType
- re

The 'Domain' and 'Range' fields for the 'physicalEntity' property are set to 'Stoichiometry' and 'PhysicalEntity' respectively.

OWL: properties are axioms, open world assumption



BioPAX and RDF



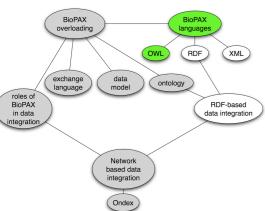
BioPAX in RDF

- BioPAX is essentially relying on RDF (RDFS)
- It is using OWL for “documentation” purposes
- It uses a subset of RDF that is compliant with OWL

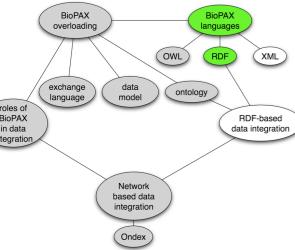
BioPAX and OWL

biopax and OWL

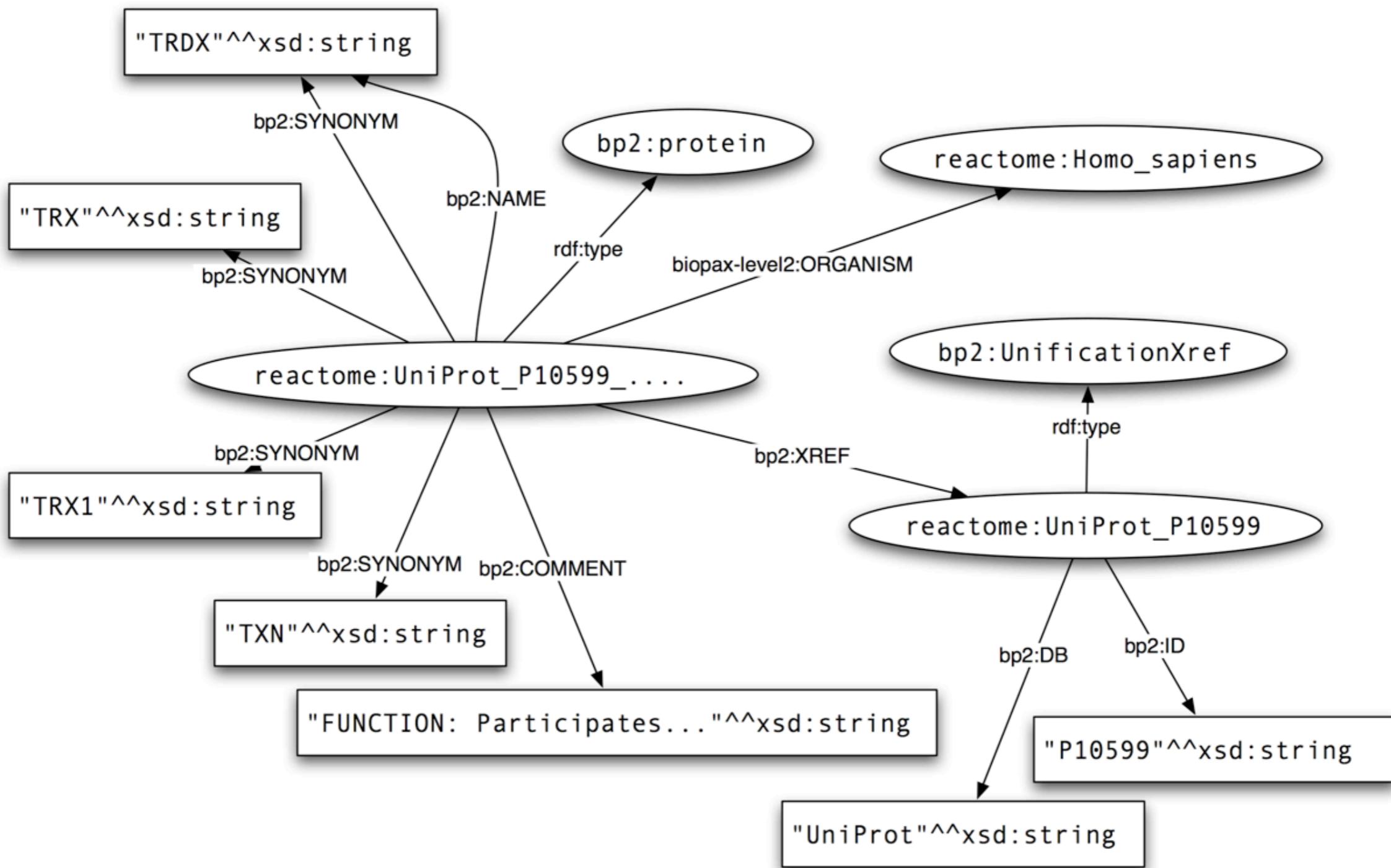
- In principle it is possible to automatically classify entities or to discover that some class is equivalent to (or a subclass of) a biopax class
- In practice, types are usually known a-priori... given the number of classes involved, if they can be well described, classification may be unnecessary



BioPAX in RDF



Facts in RDF



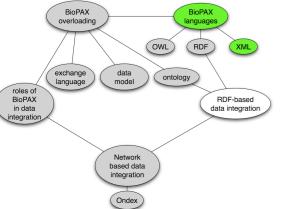
BioPAX in RDF

Syntaxes: RDF/XML

```
<biopax-level2:protein
rdf:about="#UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sulphy
yl_protein__SASP_>
<biopax-level2:COMMENT rdf:datatype="xsd:string">
  FUNCTION: Participates ...
</biopax-level2:COMMENT>
<biopax-level2:SYNONYMS rdf:datatype="xsd:string">TRDX</biopax-level2:SYNONYMS>
<biopax-level2:SYNONYMS rdf:datatype="xsd:string">TRX</biopax-level2:SYNONYMS>
<biopax-level2:NAME rdf:datatype="xsd:string">TRX</biopax-level2:NAME>
<biopax-level2:SYNONYMS rdf:datatype="xsd:string">TRX1</biopax-level2:SYNONYMS>
<biopax-level2:SYNONYMS rdf:datatype="xsd:string">TXN</biopax-level2:SYNONYMS>
<biopax-level2:ORGANISM rdf:resource="#Homo_sapiens"/>
<biopax-level2:DATA-SOURCE rdf:resource="#ReactomeDataSource"/>
<biopax-level2:XREF rdf:resource="#UniProt_P10599"/>
</biopax-level2:protein>

<biopax-level2:unificationXref rdf:about="#UniProt_P10599">
  <biopax-level2:ID rdf:datatype="xsd:string">P10599</biopax-level2:ID>
  <biopax-level2:DB rdf:datatype="xsd:string">UniProt</biopax-level2:DB>
</biopax-level2:unificationXref>
```

BioPAX in RDF

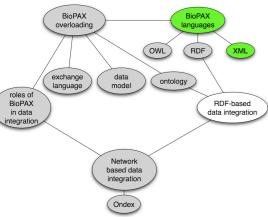


Syntaxes: Turtle

```
:UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sul
    rdf:type biopax-level2:protein ;
biopax-level2:COMMENT "FUNCTION: ... ."^^xsd:string ;
biopax-level2:SYNONYMS "TRDX"^^xsd:string ,
                      "TRX"^^xsd:string ;
biopax-level2:NAME "TRX"^^xsd:string ;
biopax-level2:SYNONYMS "TRX1"^^xsd:string ,
                      "TXN"^^xsd:string ;
biopax-level2:ORGANISM :Homo_sapiens ;
biopax-level2:DATA-SOURCE :ReactomeDataSource ;
biopax-level2:XREF :UniProt_P10599 .

:UniProt_P10599 rdf:type biopax-level2:unificationXref ;
                biopax-level2:ID "P10599"^^xsd:string ;
                biopax-level2:DB "UniProt"^^xsd:string .
```

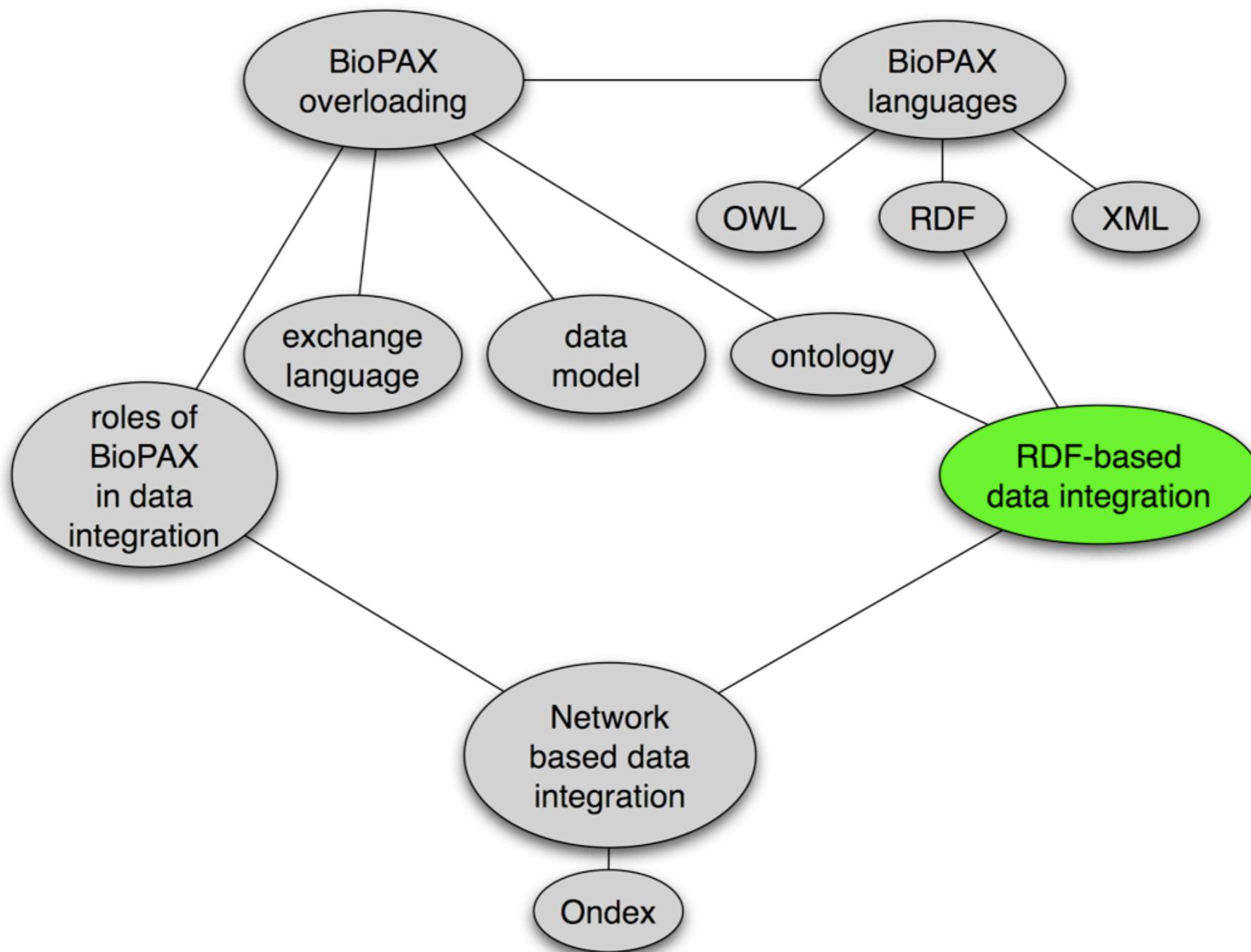
BioPAX in RDF

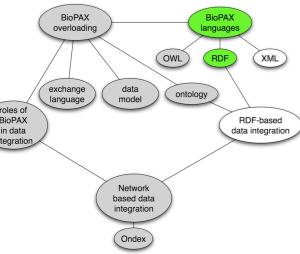


Syntaxes: OWL/XML

```
<ClassAssertion>
  <OWLClass URI="<&biopax-level2;protein"/>
  <Individual URI="<&biopax;UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sulphydryl_protein__SASP"/>
</ClassAssertion>
...
<ObjectProperty URI="<&biopax-level2;ORGANISM"/>
  <Individual URI="<&biopax;UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sulphydryl_protein__SASP"/>
  <Individual URI="<&biopax;Homo_sapiens"/>
</ObjectPropertyAssertion>
<ObjectPropertyAssertion>
<ObjectProperty URI="<&biopax-level2;XREF"/>
  <Individual URI="<&biopax;UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sulphydryl_protein__SASP"/>
  <Individual URI="<&biopax;UniProt_P10599"/>
</ObjectPropertyAssertion>
<DataPropertyAssertion>
<DataProperty URI="<&biopax-level2;COMMENT"/>
  <Individual URI="<&biopax;UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sulphydryl_protein__SASP"/>
  <Constant datatypeURI="<&xsd:string">FUNCTION: ...</Constant>
</DataPropertyAssertion>
<DataPropertyAssertion>
<DataProperty URI="<&biopax-level2;NAME"/>
  <Individual URI="<&biopax;UniProt_P10599_Thioredoxin_ATL_derived_factor__ADF__Surface_associated_sulphydryl_protein__SASP"/>
  <Constant datatypeURI="<&xsd:string">TRX</Constant>
</DataPropertyAssertion>
...
<ClassAssertion>
  <OWLClass URI="<&biopax-level2;unificationXref"/>
  <Individual URI="<&biopax;UniProt_P10599"/>
</ClassAssertion>
<DataPropertyAssertion>
  <DataProperty URI="<&biopax-level2;DB"/>
  <Individual URI="<&biopax;UniProt_P10599"/>
  <Constant datatypeURI="<&xsd:string">UniProt</Constant>
</DataPropertyAssertion>
<DataPropertyAssertion>
  <DataProperty URI="<&biopax-level2;ID"/>
  <Individual URI="<&biopax;UniProt_P10599"/>
  <Constant datatypeURI="<&xsd:string">P10599</Constant>
</DataPropertyAssertion>
```

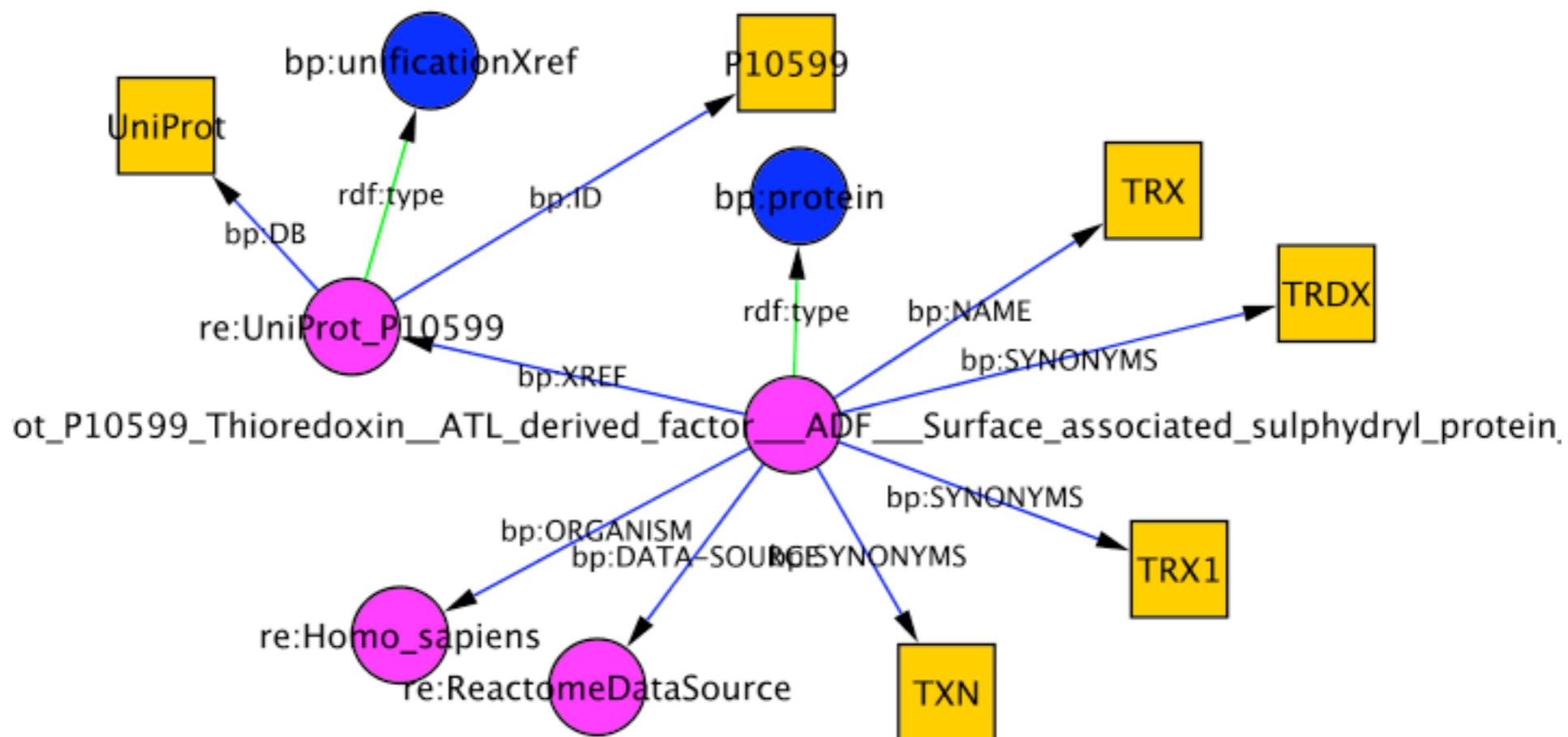
Outline





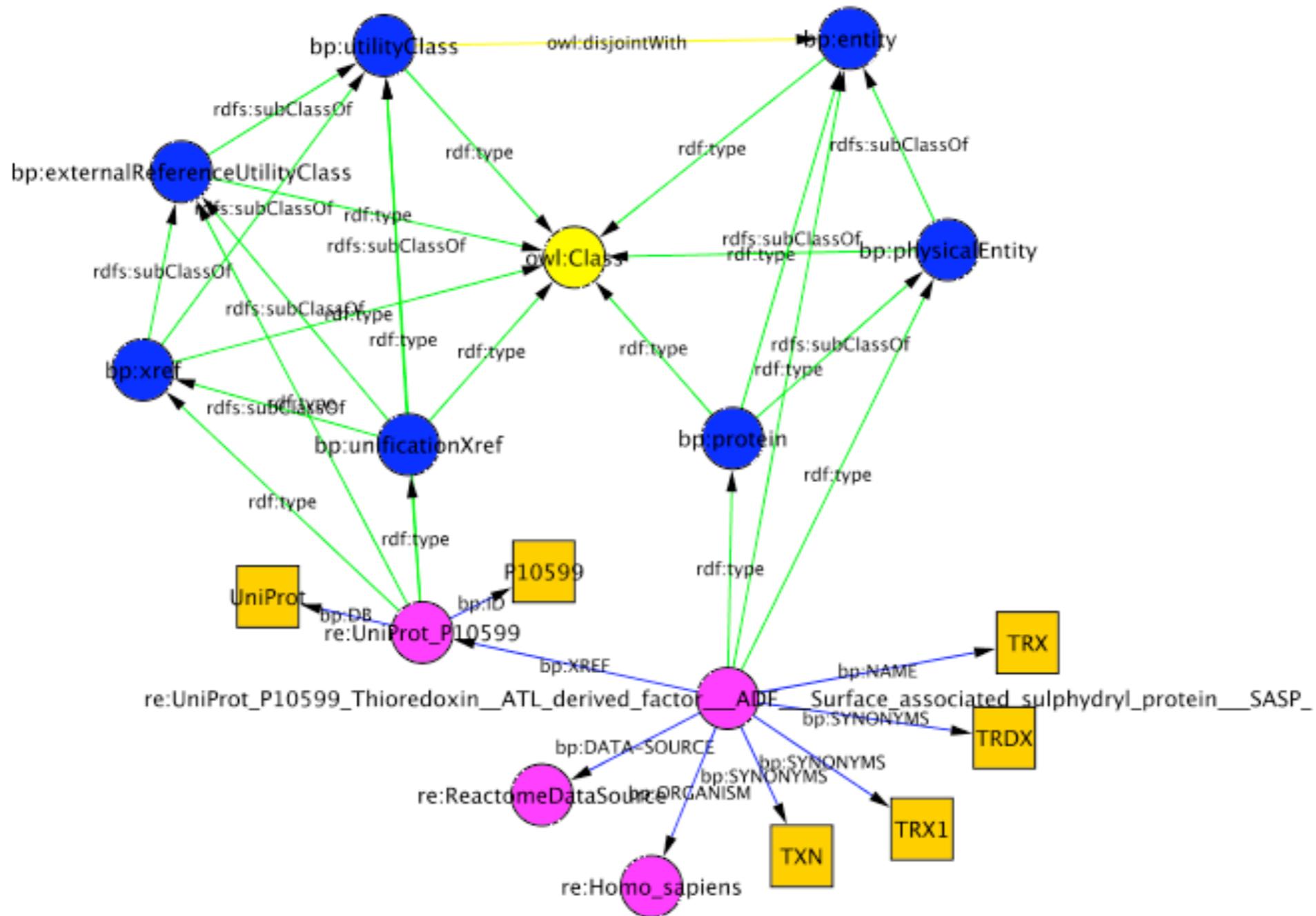
BioPAX in RDF

Facts in RDF



BioPAX in RDF

Meta-meta-view



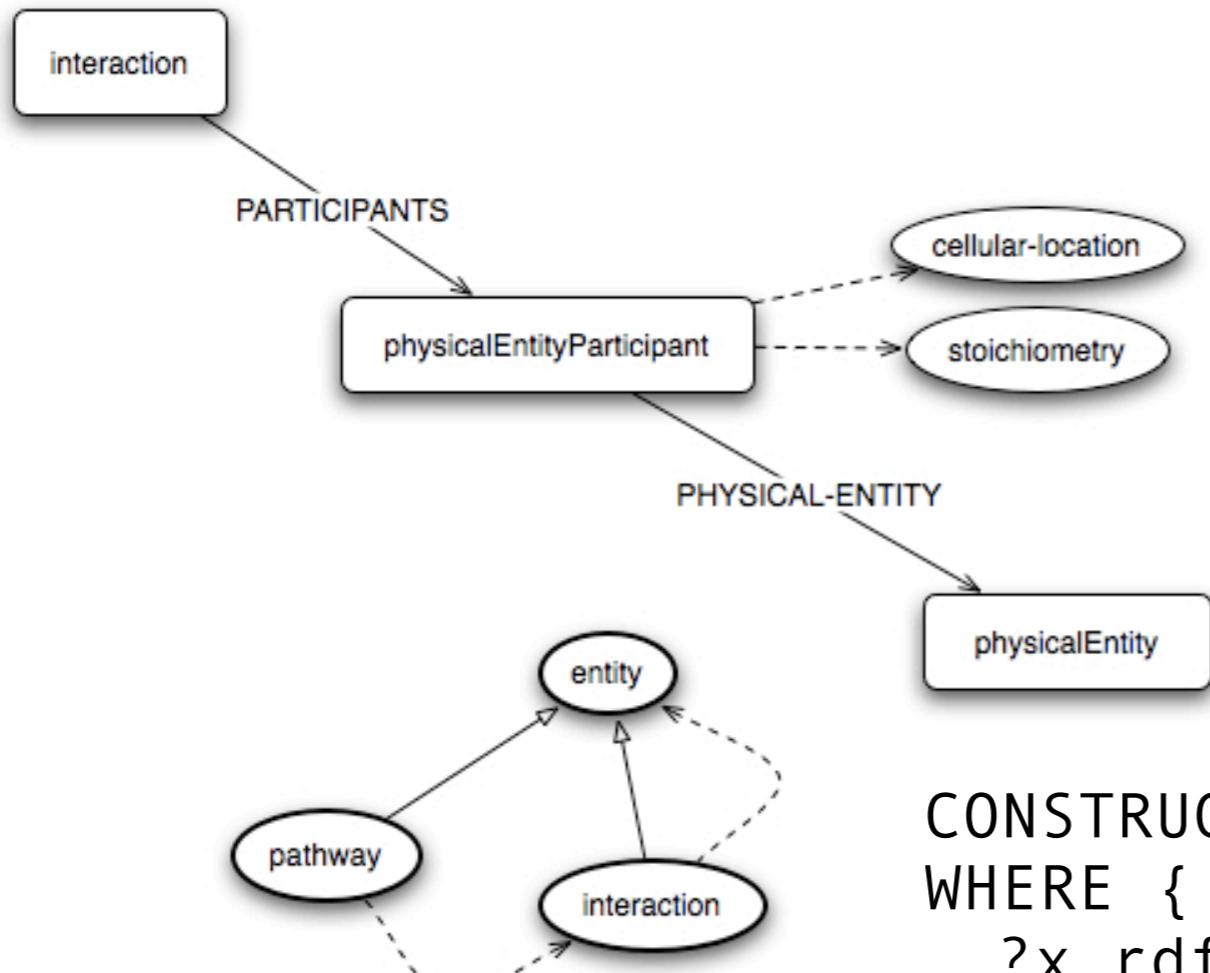
BioPAX in RDF

Unification Xrefs

```
CONSTRUCT ?x owl:sameAs ?y
WHERE {
    ?x bp:unificationXrefs ?x1 .
    ?y bp:unificationXrefs ?y1 .
    ?x1 bp:ID ?i .
    ?x1 bp:version ?v .
    ?y1 bp:ID ?i .
    ?y1 bp:version ?v
}
```

BioPAX in RDF

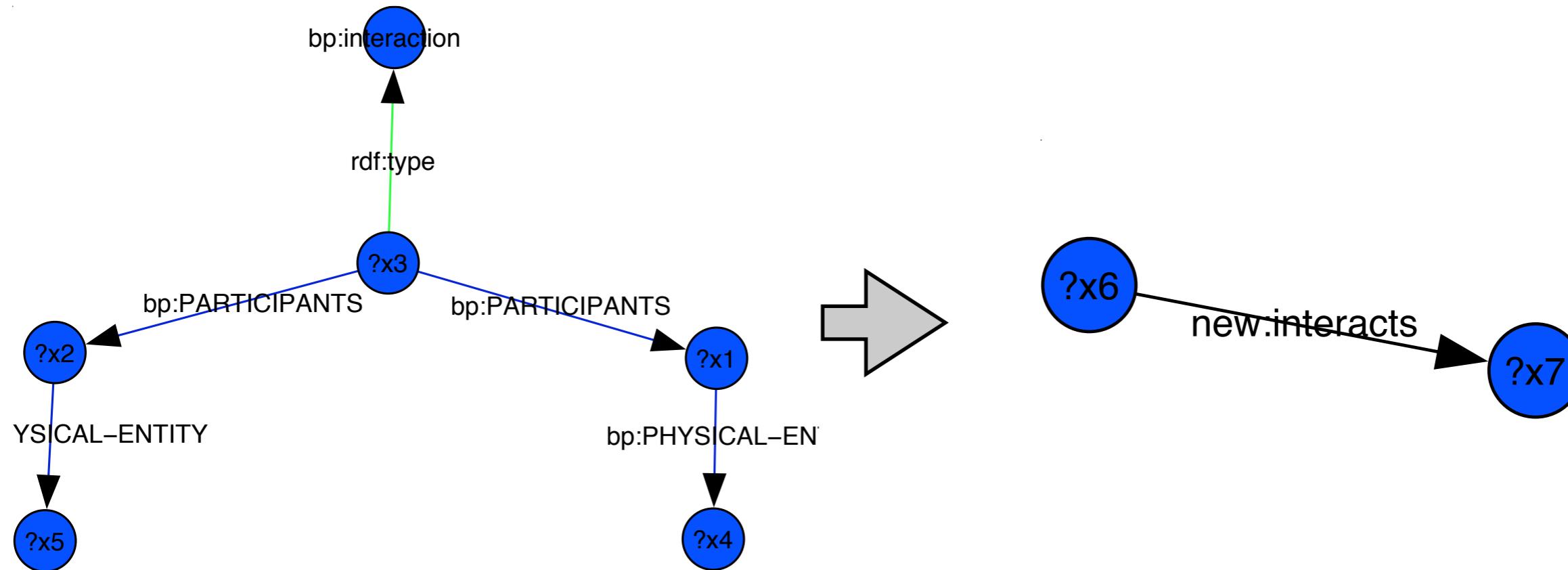
PEPs (level2)



```
CONSTRUCT ?interactor new:dirInt ?p
WHERE {
    ?x rdf:type bp:interaction .
    ?x bp:PARTICIPANTS ?px .
    ?px bp:PHYSICAL-ENTITY ?p
}
```

BioPAX in RDF

Interactions

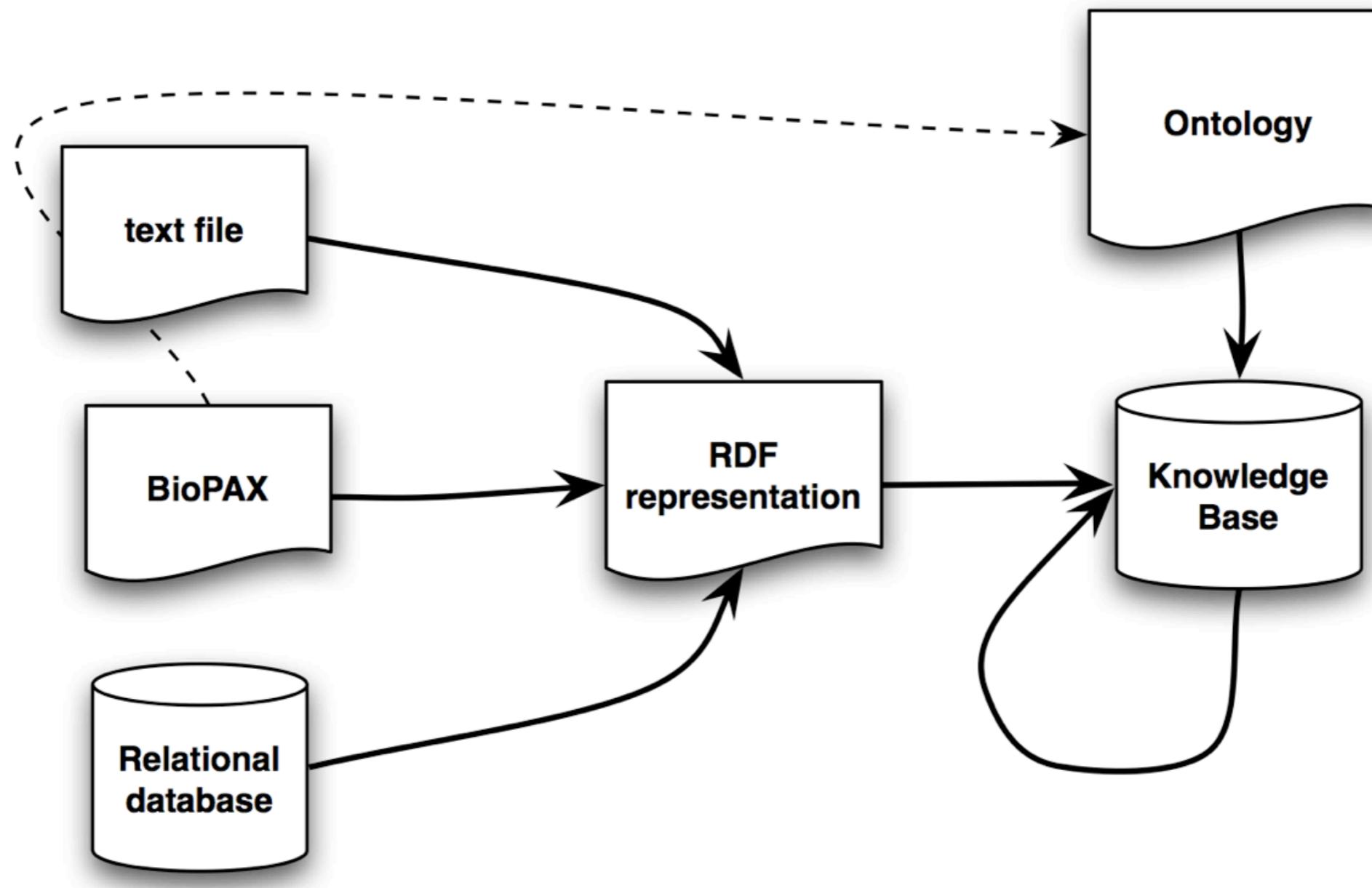


[Direct-interaction:
(?interactor new:dirInt ?p)
<-
(?x rdf:type bp:interaction)
(?x bp:PARTICIPANTS ?px)
(?px bp:PHYSICAL-ENTITY ?p)]

[Define-interaction:
(?pe1 new:interacts ?pe2)
<-
(?x rdf:type bp:interaction)
(?x new:dirInt ?pe1)
(?x new:dirInt ?pe2)]

BioPAX in RDF

Integration of BioPAX and other data sources



BioPAX in RDF

Relational declarative approach

Chemical

ID	Int
CASNumber	VARCHAR
Name	VARCHAR
ChebiID	Int

```
# Table Chemical
map:chemical a d2rq:ClassMap;
d2rq:dataStorage map:database;
d2rq:bNodesIdColumns "Chemical.ID";
d2rq:class biopax-level2:smallMolecule;
.

map:NAME a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:chemical;
d2rq:property biopax-level2:NAME;
d2rq:pattern "@@Chemical.Name@@";
d2rq:datatype xsd:string;

map:Chemical_ID a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:chemical;
d2rq:property phibase:CASNumber;
d2rq:pattern "@@Chemical.CASNumber@@";
d2rq:datatype xsd:string;

.

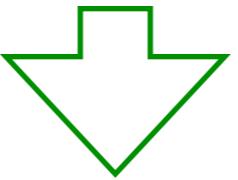
map:interaction_interaction_id a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:chemical;
d2rq:property rdf:type;
d2rq:pattern "http://purl.org/obo/owl/CHEBI#CHEBI\_@@Chemical.ChebiID@@";
```

Details from **D2RQ** mapping file

BioPAX in RDF

Direct mapping of tables to RDF

CAS reg. Number	Chemical name	CHEBI ID
17804-35-2	Benomyl	3015
36734-19-7	Iprodione	28909
65277-42-1	Cis-Ketoconazole	47519



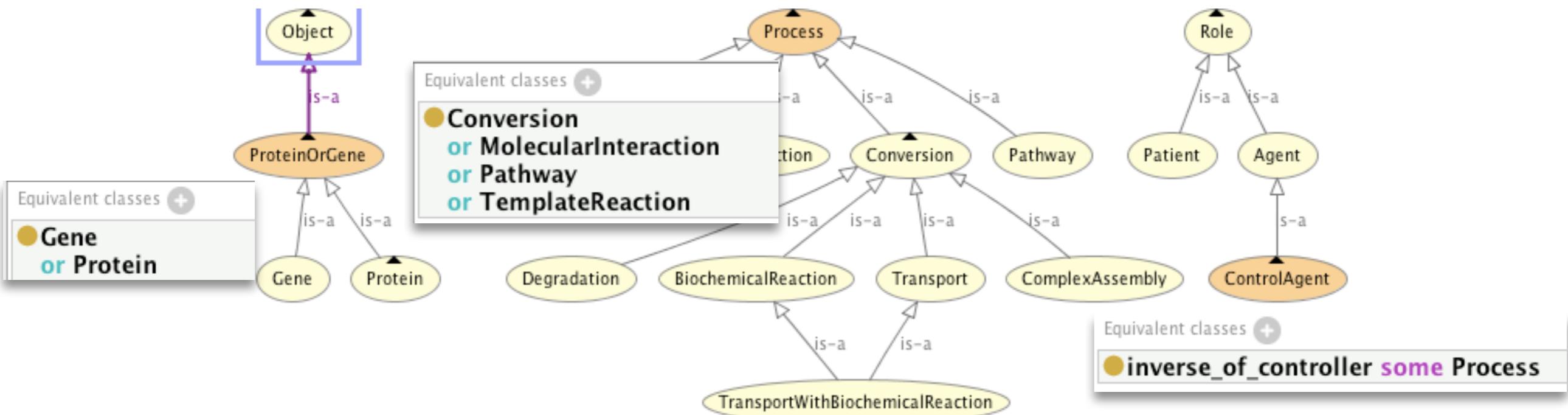
```
:ID1 rdf:type chebi:CHEBI_3015 ;
:CHEBI_3015 a biopax-level2:smallMolecule .
    biopax-level2:NAME "Benomyl"^^xsd:string .
    phibase:casNumber "17804-35-2" .

:ID2 rdf:type chebi:CHEBI_28909 ;
:CHEBI_3015 a biopax-level2:smallMolecule .
    biopax-level2:NAME "Iprodione"^^xsd:string .
    phibase:casNumber "36734-19-7" .

:ID3 rdf:type chebi:CHEBI_47519 ;
:CHEBI_3015 a biopax-level2:smallMolecule .
    biopax-level2:NAME "Cis-Ketoconazole"^^xsd:string .
    phibase:casNumber "65227-42-1" .
```

BioPAX in RDF

Ontologies as interpretation



Concepts in biopax can be used in different ontologies to provide interpretations of facts

BioPAX in RDF

BioPAX and Semantic Web based data integration

- BioPAX: concepts to describe pathways (entities, properties, abstraction(RDFS))
- RDF: (graph based) data model
- RDF declarative processing of information (sparql, rules)
- Constraint checking can be implemented as an additional layer

Re-composing BioPAX

Problems with pathway data integration

- Identity (beyond chemicals, states, generics, reactions)
- Representation dishomogeneity
- Non-explicitely encoded knowledge

Re-composing BioPAX

Problems with pathway data integration

```
<bp:catalysis
rdf:ID="protein_tyrosine_kinase_activity_of_GP_VI_phosphorylated_Fc_Epsilon_R1_gamma_Collagen_IV
__Syk_complex__plasma_membrane_>
<bp:CONTROLLER rdf:resource=
"#GP_VI_phosphorylated_Fc_Epsilon_R1_gamma_Collagen_IV__Syk_complex__plasma_membrane_" />
<bp:CONTROLLED rdf:resource="#Syk-mediated_phosphorylation_of_Phospholipase_C_gamma_2" />
<bp:DIRECTION rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
PHYSIOL-LEFT-TO-RIGHT</bp:DIRECTION>
<bp:CONTROL-TYPE rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
ACTIVATION</bp:CONTROL-TYPE>
</bp:catalysis>

<bp:biochemicalReaction rdf:ID="Syk-mediated_phosphorylation_of_Phospholipase_C_gamma_2">
<bp:LEFT rdf:resource="#Phospholipase_C_gamma_2__plasma_membrane_" />
<bp:RIGHT rdf:resource="#Phosphorylated_phospholipase_C_gamma_2__plasma_membrane_" />
</bp:biochemicalReaction>
```

Re-composing BioPAX

Problems with pathway data integration

```
<bp:catalysis rdf:ID="kinase_activity_of_PIP3_Phosphorylated_PKB_complex_plasma_membrane">
  <bp:CONTROLLER rdf:resource="#PIP3_Phosphorylated_PKB_complex_plasma_membrane" />
  <bp:CONTROLLED rdf:resource="#Phosphorylation_of_PDE3B" />
  <bp:DIRECTION rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
    PHYSIOL-LEFT-TO-RIGHT</bp:DIRECTION>
  <bp:CONTROL-TYPE rdf:datatype="http://www.w3.org/2001/XMLSchema#string">ACTIVATION
  </bp:CONTROL-TYPE>
</bp:catalysis>

<bp:biochemicalReaction rdf:ID="Phosphorylation_of_PDE3B">
  <bp:LEFT rdf:resource="#PDE3B_cytosol" />
  <bp:LEFT rdf:resource="#ATP_cytosol" />
  <bp:RIGHT rdf:resource="#ADP_cytosol" />
  <bp:RIGHT rdf:resource="#Phosphorylated_PDE3B_cytosol" />
</bp:biochemicalReaction>

<bp:biochemicalReaction rdf:ID="Syk-mediated_phosphorylation_of_Phospholipase_C_gamma_2">
  <bp:LEFT rdf:resource="#Phospholipase_C_gamma_2_plasma_membrane" />
  <bp:RIGHT rdf:resource="#Phosphorylated_phospholipase_C_gamma_2_plasma_membrane" />
</bp:biochemicalReaction>
```

Conclusions

- Pathways as part of a broader set of biological information that can be represented as networks.
- BioPAX addresses distinct requirements, sometimes conflicting.
- Facts expressed in BioPAX can be seen as RDF. This is a good basis for network based data integration.
- Ontologies provide interpretations of these data.

Acknowledgments

BioPAX Working group

BioPAX-OBO

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