

Towards ubiquitous OWL computing: Simplifying programmatic authoring of and querying with OWL axioms

Hilmar Lapp, Jim Balhoff

National Evolutionary Synthesis Center (NESCent)
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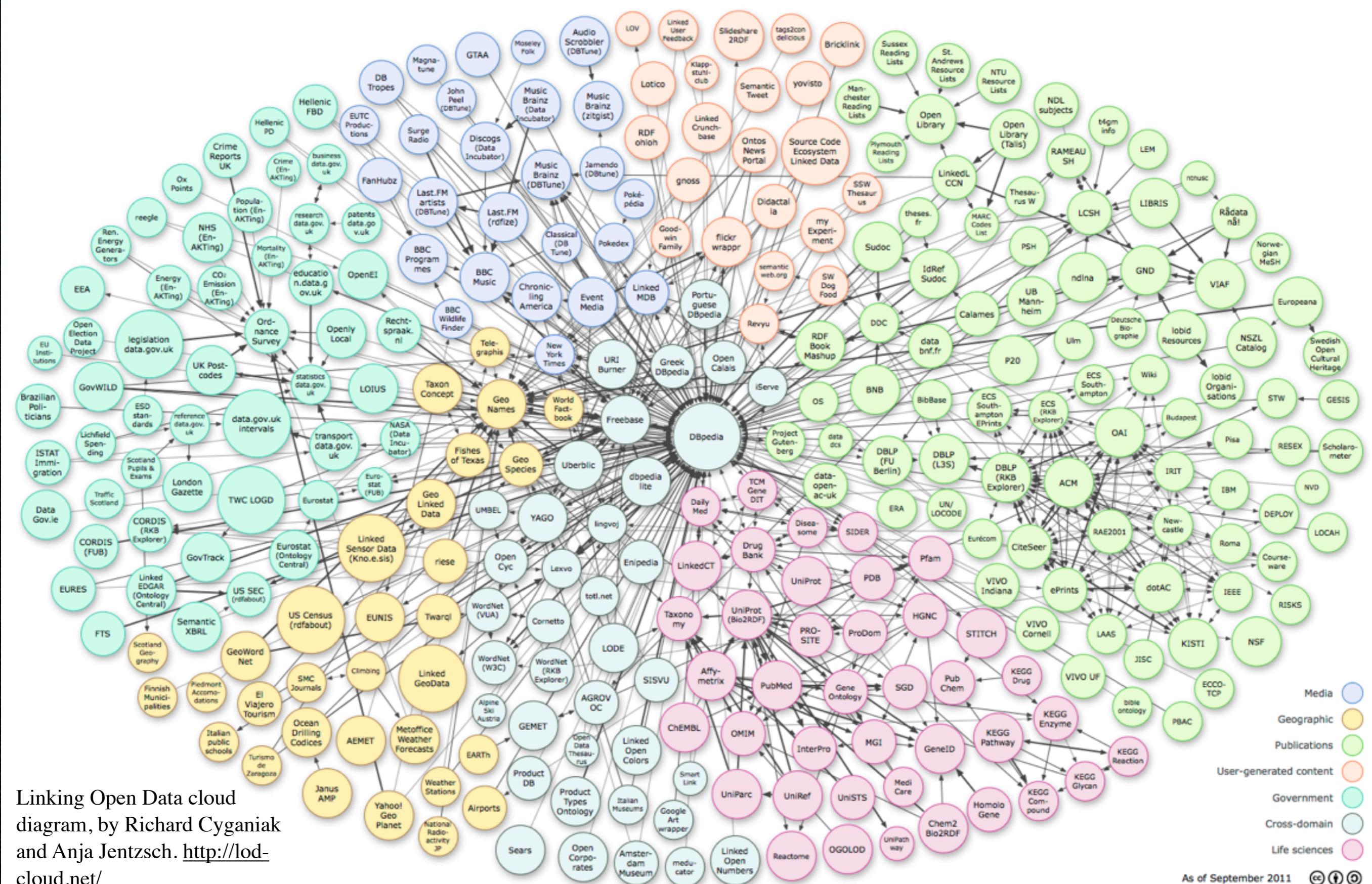
Did all the work:



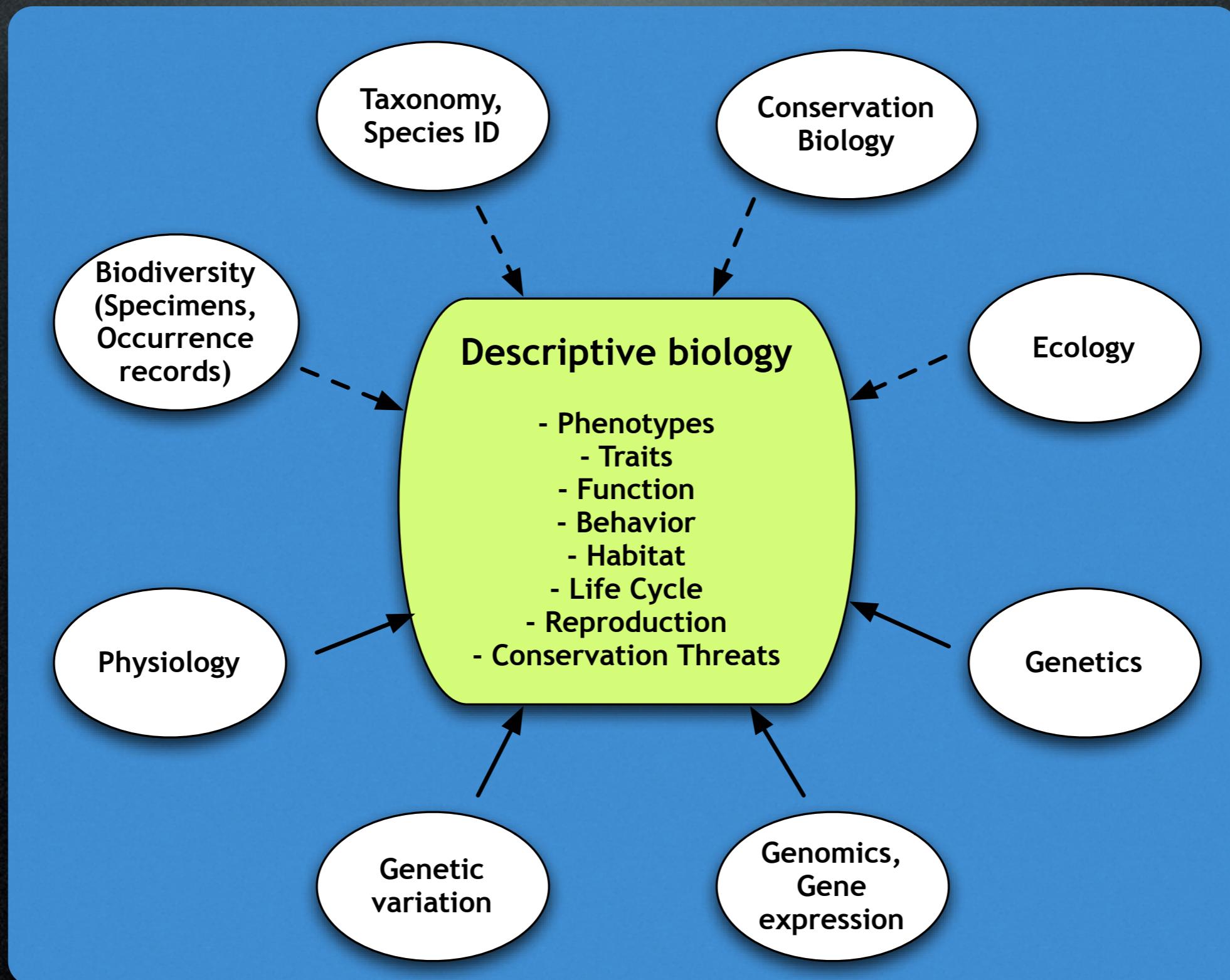
Jim Balhoff, Programmer extraordinaire

<http://github.com/balhoff>

RDF is a powerful data integrator



Ontologies allow integrating across descriptive biology



Translational bioinformatics

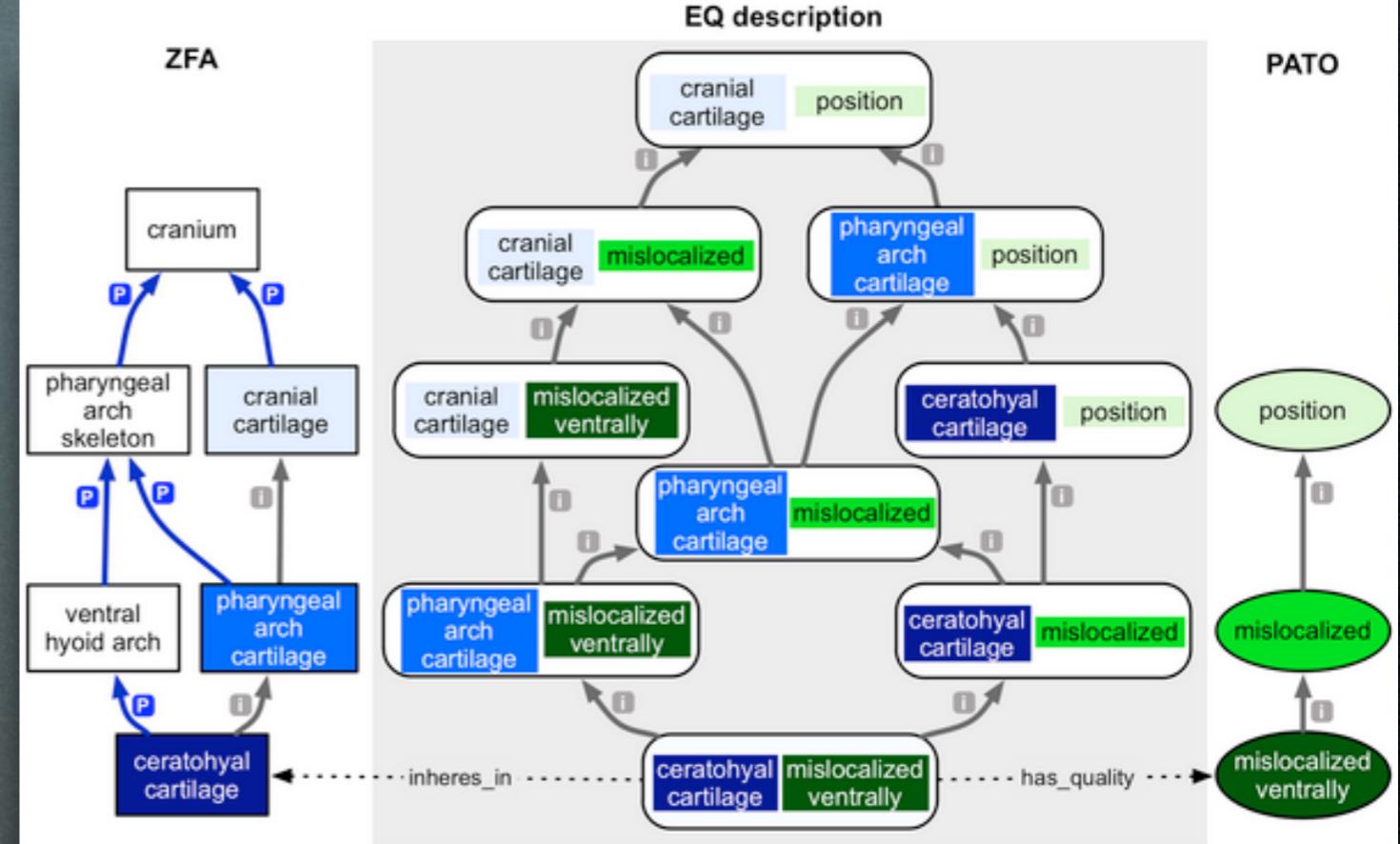
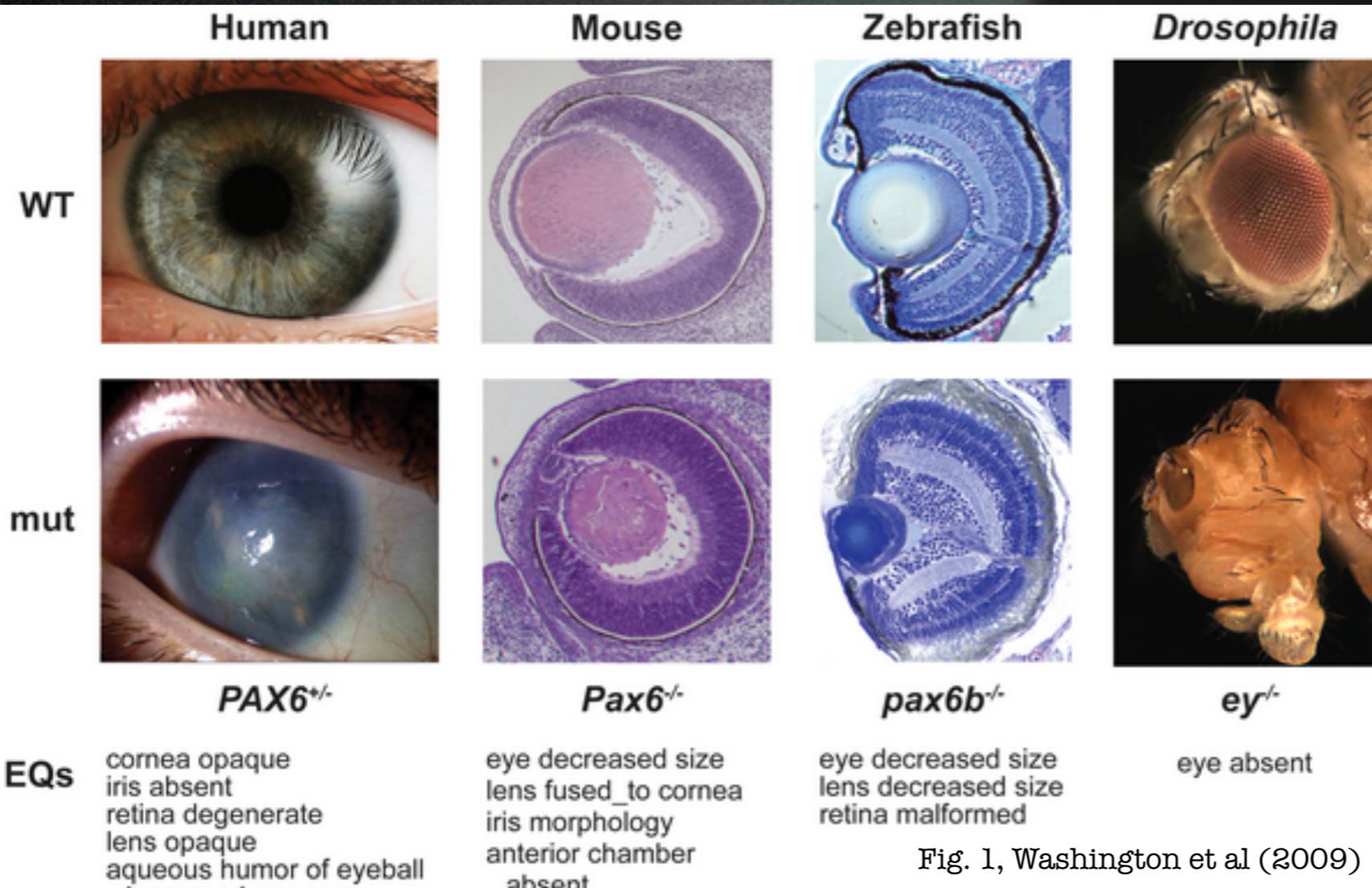


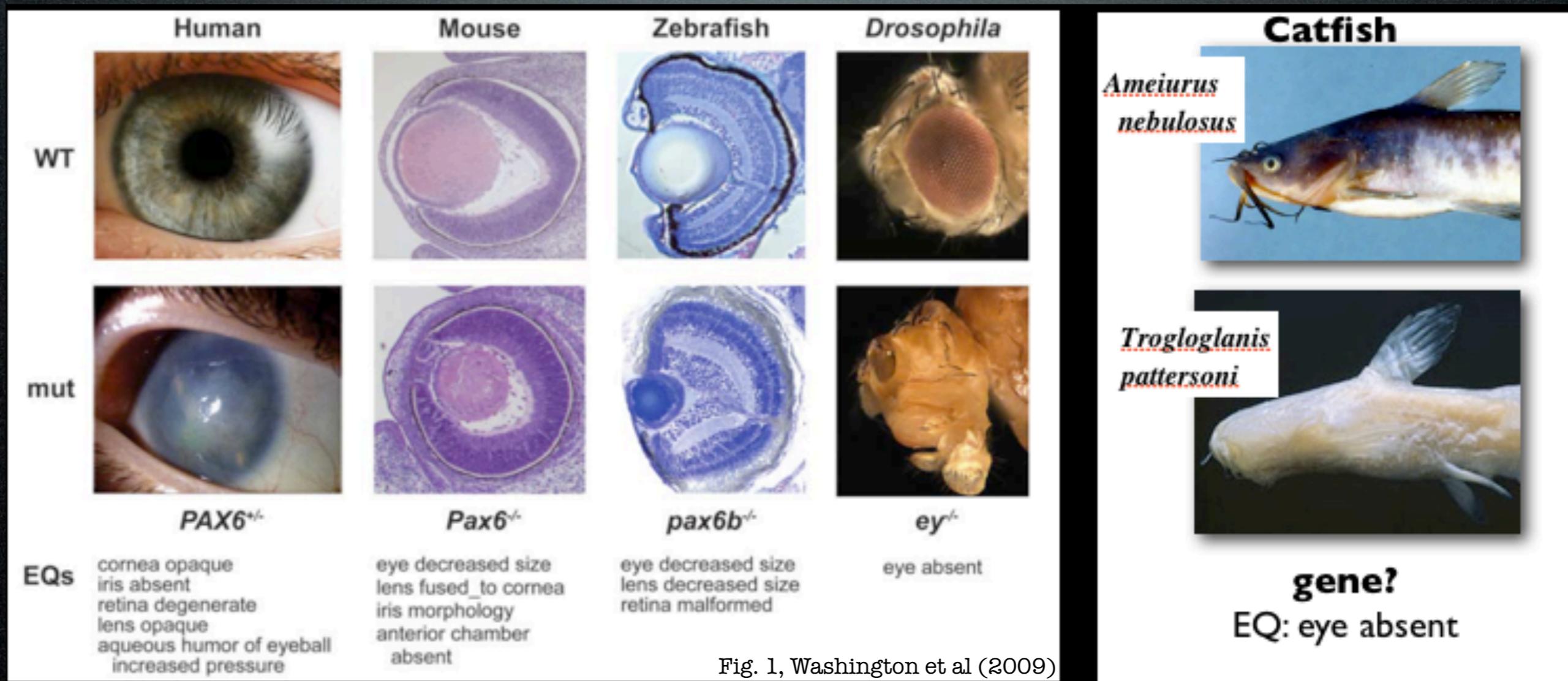
Fig. 3, Washington et al (2009)



Model organism
->
Human

Fig. 1, Washington et al (2009)

Translational biodiversity informatics



Model organism genes -> Evolutionary diversity
by semantic similarity of phenotypes

Integrate across studies & fields by virtue of ontologies

TABLE 1. CHARACTER STATE MATRIX USED FOR PHYLOGENETIC ANALYSIS OF THE PLACEMENT OF <i>B. capapretum</i> WITHIN PIMELODIDAE AND <i>Brachyplatystoma</i> . Character states described in Appendix 1 and text.																		
	12345	67890	1	11111	11112	22222	22223	22222	22223	33333	12345	67890	1	11111	11112	22222	22223	33333
<i>Steindachneridion</i>	11110	00000	00000	21000							12345	67890	1	11111	11112	22222	22223	33333
<i>Phractocephalus-Leiarus group</i>	11110	00000	00000	00000										11110	00000	00000	21000	00000
<i>Pimelodus</i> group	11111	11111	00000	00000							12345	67890	1	11111	00000	00000	00000	00000
<i>Calophysus</i> group	11111	11111	00000	00000										11111	00000	00000	01110	00000
<i>Zungaro</i>	11111	10000	00000	01001										11111	00000	01001	20000	00000
<i>Sorubim</i> group	11111	10000	00000	20001										11111	00000	20001	20000	00011
<i>Platycephalichthys</i>	11111	10000	11000	00000										10000	11000	00000	00000	00000
<i>Brachyplatystoma vaillantii</i>	11111	10000	11111	11000										11110	00000	00000	00000	00001
<i>B. tigrinum</i>	11111	10000	11121	00111										11111	00000	00000	01110	00000
<i>B. platynemum</i>	11111	10000	11120	11111										11111	00000	01001	20000	00010
<i>B. filamentosum</i>	11111	10000	11131	11111										11111	00000	01001	21001	01101
<i>B. cape</i>	11111	10000	11131	11111										10000	11121	00111	11000	00000
<i>B. rousseauxii</i>	11111	10000	11131	11111										10000	11120	11111	11110	00000
Heptapteridae	00000	00000	00000	00001										10000	11111	00000	00000	00000
Pseudopimelodidae	00000	00000	00000	00000										11110	00000	00000	00000	00000
Bagridae	00100	00000	00000	01000										11111	00000	01121	00111	10010
Ictaluridae	00000	00000	00000	00001										11111	00000	01120	11111	00000
<i>Steindachneridion</i>	11110	00000	00000	21000							12345	67890	1	11111	11112	22222	22223	33333
<i>Phractocephalus-Leiarus</i> group	11110	00000	00000	00000										11110	00000	00000	00000	00001
<i>Pimelodus</i> group	11111	11111	00000	00000										11111	00000	00000	00000	00000
<i>Calophysus</i> group	11111	11111	00000	00000										11111	00000	00000	01110	00000
<i>Zungaro</i>	11111	10000	00000	01001										11111	00000	01001	20000	00010
<i>Sorubim</i> group	11111	10000	00000	20001										11111	10000	00000	20000	00011
<i>Platycephalichthys</i>	11111	10000	11000	00000										11111	10000	11000	00000	00000
<i>Brachyplatystoma vaillantii</i>	11111	10000	11111	11000										11110	00000	00000	00000	00000
<i>B. tigrinum</i>	11111	10000	11121	00111										11111	11111	00000	00000	00001
<i>B. platynemum</i>	11111	10000	11120	11111										11111	11111	00000	00000	00000
<i>B. filamentosum</i>	11111	10000	11131	11111										11111	11111	00000	01110	00000
<i>B. capapretum</i>	11111	10000	11131	11111										11111	00000	01001	20000	00010
<i>B. rousseauxii</i>	11111	10000	11131	11111										11111	00000	01001	21001	01101
Heptapteridae	00000	00000	00000	00001										10000	11111	00000	00000	00000
Pseudopimelodidae	00000	00000	00000	00000										11110	00000	00000	00000	00000
Bagridae	00100	00000	00000	01000										11111	00000	01121	00111	10010
Ictaluridae	00000	00000	00000	00001										11111	00000	01120	11111	00000



Mouse Genome Informatics

Search ▾ Download ▾ More Resources ▾ Submit Data Find Mice (IMSR) Analysis

Explore MGI

Genes Phenotypes & Disease Models Expression Recombinases (cre) Function Pathway Tumors



Xenbase

[2.8.5] Blast Frogs Literature Expression Genes Genome Browsers Anatomy & Development

Search Genes For Search



ZFIN

Research General Information ZIRC

Genes / Markers / Clones Nomenclature Conventions Obtain approval for gene names

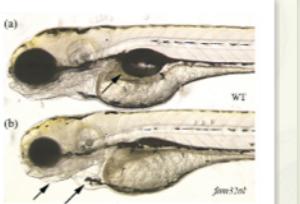
BLAST at ZFIN GBrowse genome browser

Gene Expression Antibodies

Mutants / Morphants / Transgenics Wild-Type Lines Line Designations Submit mutant/transgenic line names

Constructs

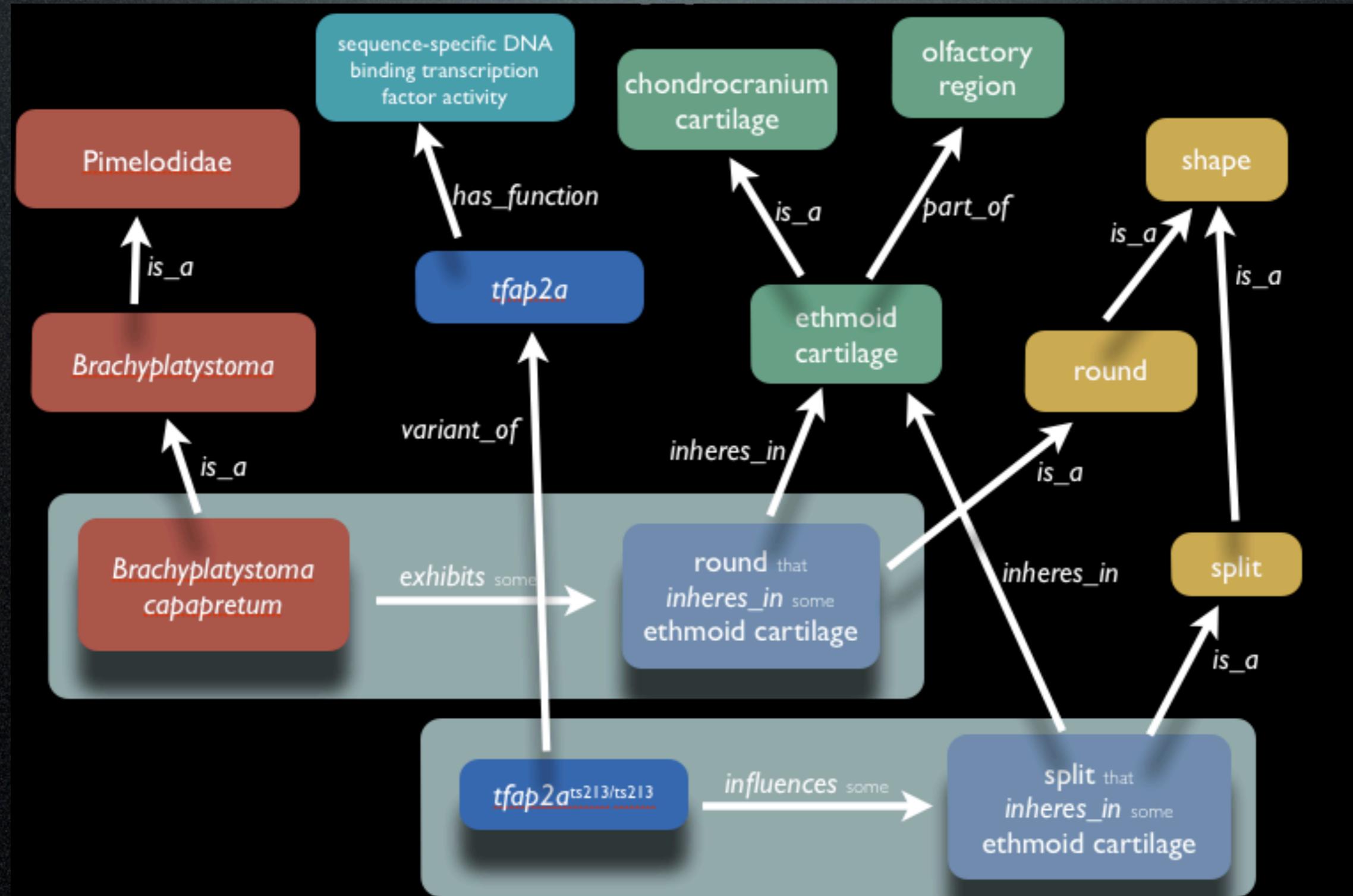
Anatomy / GO Anatomy Atlases and Resources News

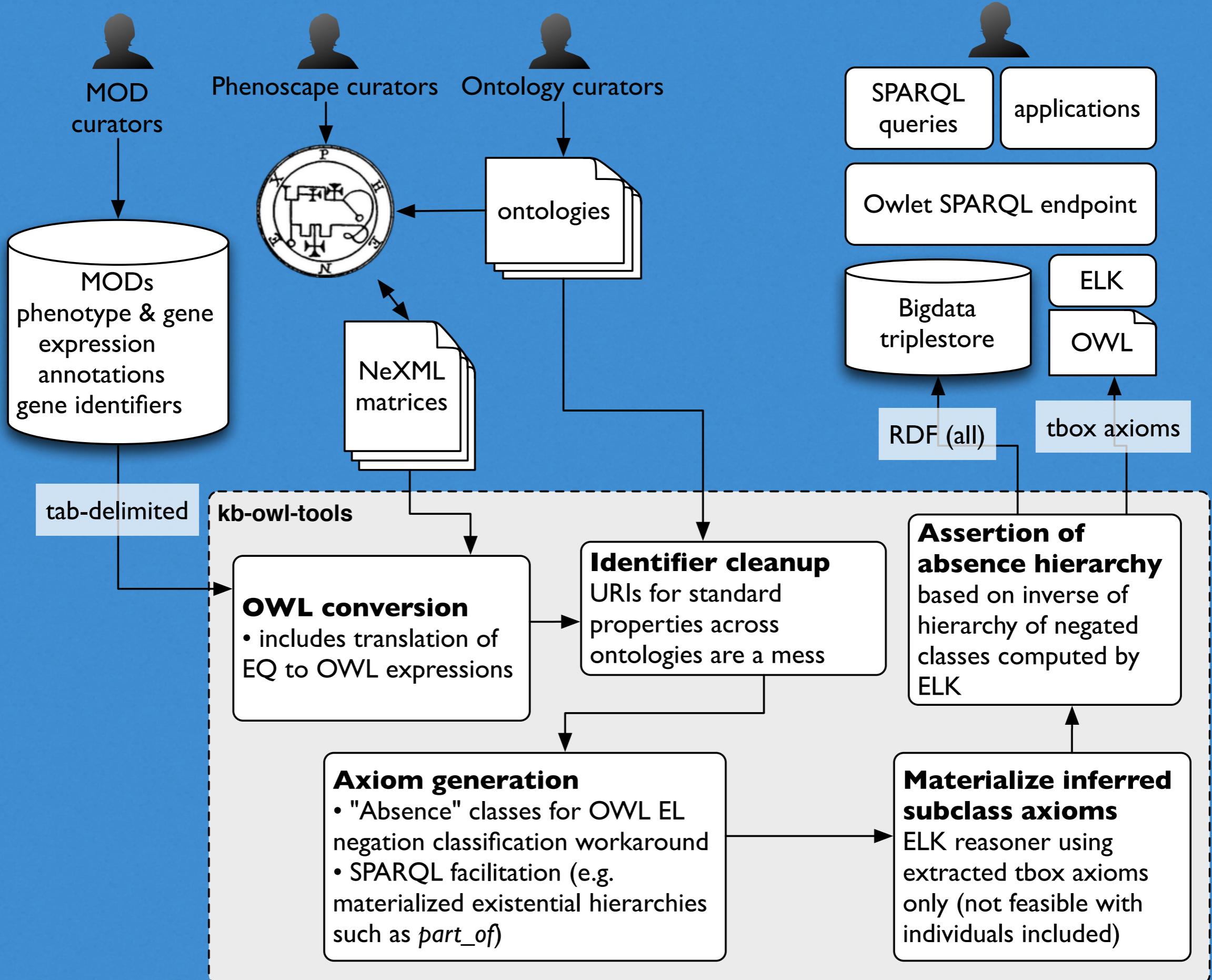


Comparative studies
= Phenoscape Knowledgebase

Model organism datasets

Computable via shared ontologies, rich semantics, OWL reasoning





Ontology axiom authoring at scale is cumbersome

- If a developmental precursor is absent, the structure is absent.

“For every anatomical structure, assert that the class of things not having the structure as a part is a subclass of the class of things not having the structure’s developmental precursor structure as a part.”

(See Balhoff et al, Phenotype Day, <http://phenoday2014.bio-lark.org/pdf/11.pdf>)

Scowl: marrying programming to ontology language

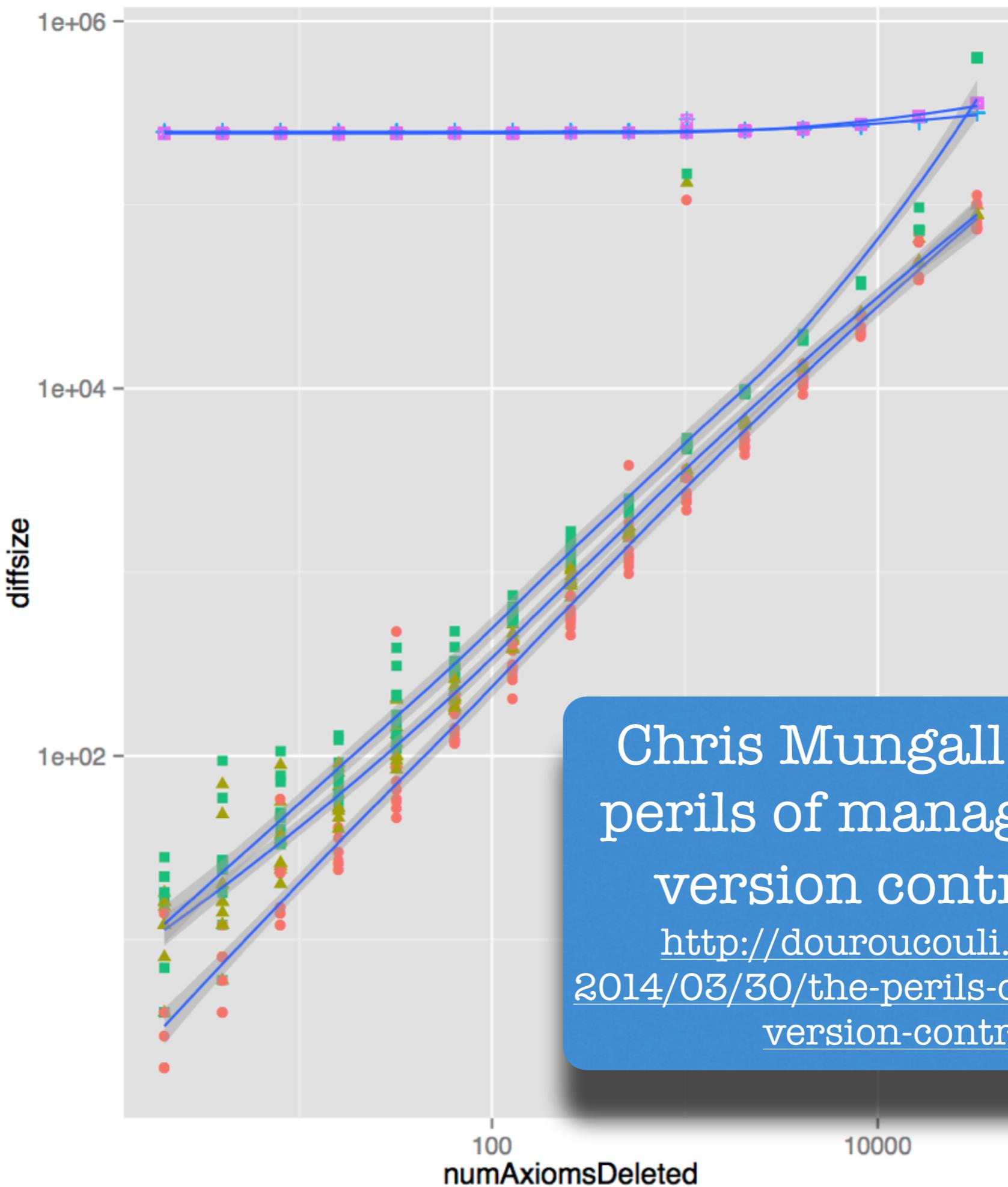
“For every anatomical structure, assert that the class of things not having the structure as part is a subclass of the class of things not having the structure’s developmental precursor as part.”

```
for {  
    term <- reasoner.getSubclasses(anatomical_structure)  
} yield  
(not (hasPart some term)) SubClassof (not (hasPart some (developsFrom  
some term)))
```

Scowl

- Allows declarative approach to composing OWL expressions and axioms using the OWL API.
- Implemented as a library in Scala
- Exploits ‘implicit class’ construct in Scala
 - Compiler turns declarative expressions into JVM instructions
- Class, Annotation, Property axioms

```
val hasFather = ObjectProperty("http://example.org/hasFather")
val hasBrother = ObjectProperty("http://example.org/hasBrother")
val hasUncle = ObjectProperty("http://example.org/hasUncle")
val axiom = hasUncle SubPropertyChain (hasFather o hasBrother)
```



Chris Mungall (2014) “The
perils of managing OWL in a
version control system”
[http://douroucouli.wordpress.com/
2014/03/30/the-perils-of-managing-owl-in-a-
version-control-system/](http://douroucouli.wordpress.com/2014/03/30/the-perils-of-managing-owl-in-a-version-control-system/)

```
object AnatomyOntology extends App {  
  
    val factory = OWLManager.getOWLDataFactory  
    val ns = "http://example.org/anatomy.owl#"  
    val head = Class(ns + "001")  
    val body = Class(ns + "002")  
    val hand = Class(ns + "003")  
    val arm = Class(ns + "004")  
    val anatomical_structure = Class(ns + "005")  
    val part_of = ObjectProperty(ns + "006")  
    val label = factory.getRDFSLabel  
  
    val ontology = Ontology("http://example.org/anatomy.owl", Set(  
        head Annotation (label, "head"),  
        head SubClassOf anatomical_structure,  
        head SubClassOf (part_of some body),  
        head SubClassOf (not(part_of some arm)),  
  
        body Annotation (label, "body"),  
        body SubClassOf anatomical_structure,  
  
        arm Annotation (label, "arm"),  
        arm SubClassOf anatomical_structure,  
        arm SubClassOf (part_of some body),  
  
        hand Annotation (label, "hand"),  
        hand SubClassOf anatomical_structure,  
        hand SubClassOf (part_of some arm)))  
  
    ontology.getOWLOntologyManager.saveOntology(  
        ontology,  
        IRI.create(new File(args(0))))  
}
```

Similarly motivated effort: Tawny-OWL

- By Phil Lord
- Allows construction of OWL ontologies in Clojure.
- “the ontology engineering equivalent of R”
- <https://github.com/phillord/tawny-owl>



Scowl

- Home:
<http://github.com/phenoscape/scowl>
- MIT-licensed

Ontology-driven querying in SPARQL is not pretty

SPARQL: genes expressed in head muscles

```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX ao: <http://purl.obolibrary.org/obo/my-anatomy-ontology/>
PREFIX owl: <http://www.w3.org/2002/07/owl#>
SELECT DISTINCT ?gene
WHERE
{
?gene ao:expressed_in ?structure .
?structure rdf:type ?structure_class .
# Triple pattern selecting structure:
?structure_class rdfs:subClassOf "ao:muscle" .
?structure_class rdfs:subClassOf ?restriction
?restriction owl:onProperty ao:part_of .
?restriction owl:someValuesFrom "ao:head" .
}
```

- Awkward, lengthy, complicated
- Error-prone
- Slow

Owlet: bridging from SPARQL to DL queries

- Want to allow arbitrary selection of structures of interest, using rich semantics:
(part_of some (limb/fin or girdle skeleton))
or (connected_to some girdle skeleton)
- RDF triplestores provide very limited reasoning expressivity, and scale poorly with large ontologies.
- However, ELK can answer class expression queries within seconds.

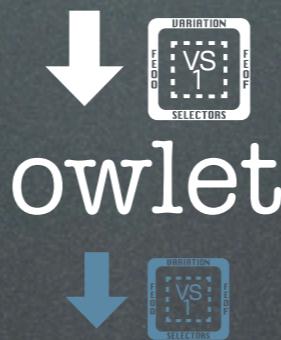
owlet: A little OWL in SPARQL

- **owlet** interprets OWL class expressions embedded within SPARQL queries
- Uses any OWL API-based reasoner to preprocess query.
 - We use ELK that holds terminology in memory.
 - Replaces OWL expression with FILTER statement listing matching terms

```

PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX ao: <http://purl.obolibrary.org/obo/my-anatomy-ontology/>
PREFIX ow: <http://purl.org/phenoscape/owlet/syntax#>
SELECT DISTINCT ?gene
WHERE
{
?gene ao:expressed_in ?structure .
?structure rdf:type ?structure_class .
# Triple pattern containing an OWL expression:
?structure_class rdfs:subClassOf "ao:muscle and (ao:part_of some ao:head)"^^ow:omn .
}

```



```

PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX ao: <http://purl.obolibrary.org/obo/my-anatomy-ontology/>
PREFIX ow: <http://purl.org/phenoscape/owlet/syntax#>
SELECT DISTINCT ?gene
WHERE
{
?gene ao:expressed_in ?structure .
?structure rdf:type ?structure_class .
# Filter constraining ?structure_class to the terms returned by the OWL query:
FILTER(?structure_class IN (ao:adductor_mandibulae, ao:constrictor_dorsalis, ...))
}

```

owlet: A little OWL in SPARQL

- Implemented in Scala, can be used in Java
- Home: <http://github.com/phenoscape/owlet>
- MIT-licensed
- Unique to owlet, compared to some related efforts (e.g., SPARQL-DL, Terp in Pellet):
 - Any SPARQL endpoint / OWL API-based reasoner combination
 - No non-standard syntax

owlery: REST web services for owllet

- Allows federation via SERVICE keyword in SPARQL
- <http://github.com/phenoscape/owlery>

```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX ao: <http://purl.obolibrary.org/obo/my-anatomy-ontology/>
PREFIX ow: <http://purl.org/phenoscape/owlet/syntax#>
SELECT DISTINCT ?gene
WHERE
{
?gene ao:expressed_in ?structure .
?structure rdf:type ?structure_class .
# Triple pattern containing an OWL expression, handled by federated query:
SERVICE <http://owlery.example.org/sparql> {
?structure_class rdfs:subClassOf
    "ao:muscle and (ao:part_of some ao:head)"^^ow:omn .
}
}
```

Summary

- Programming and computing with OWL is more complicated than need be
- Need a thriving ecosystem of small tools that fill common gaps
- Scowl, Owlet, and Owlery are small steps in that direction
- Vision: programming with ontologies as easy and ubiquitous as with alignments

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