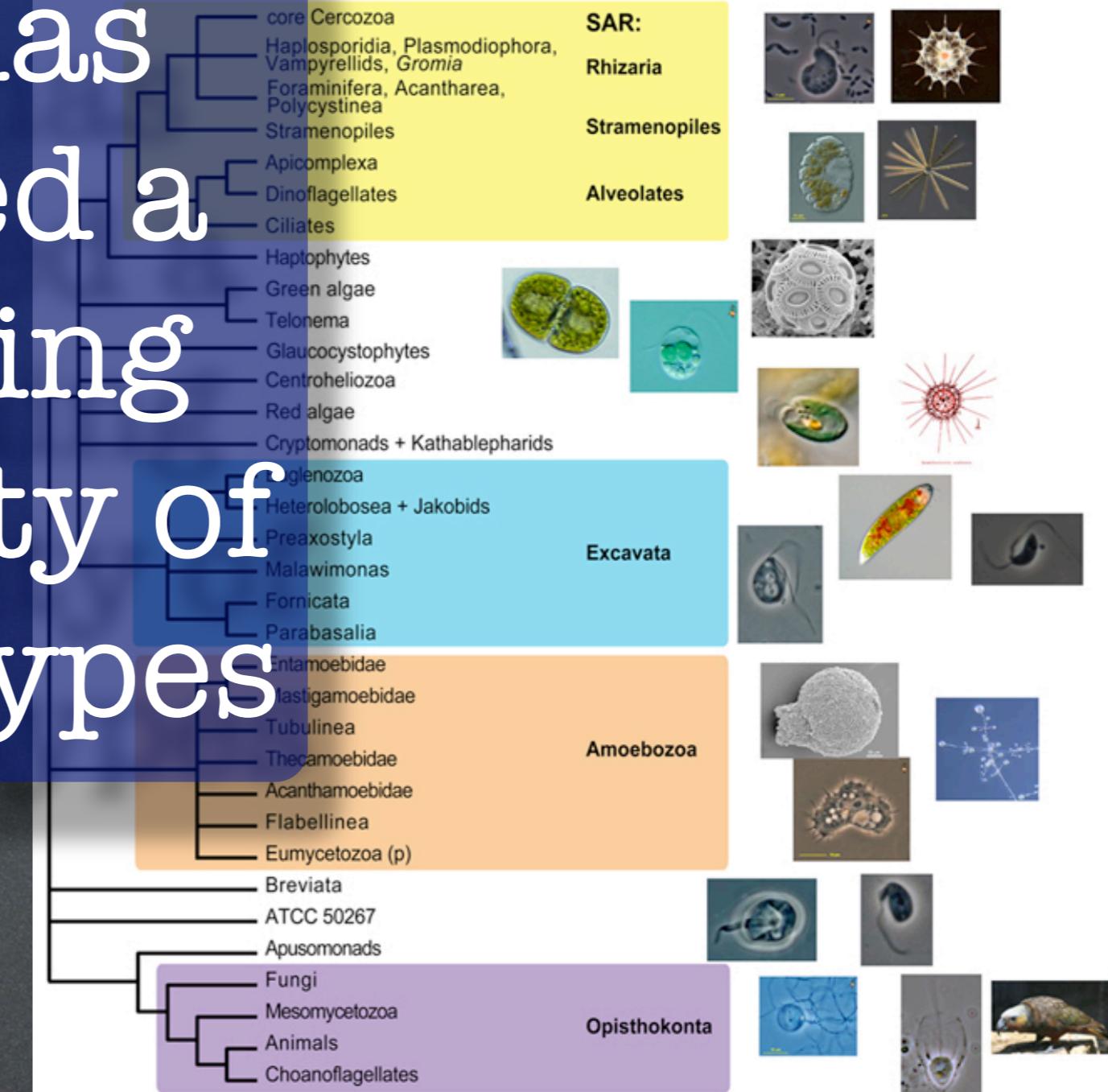
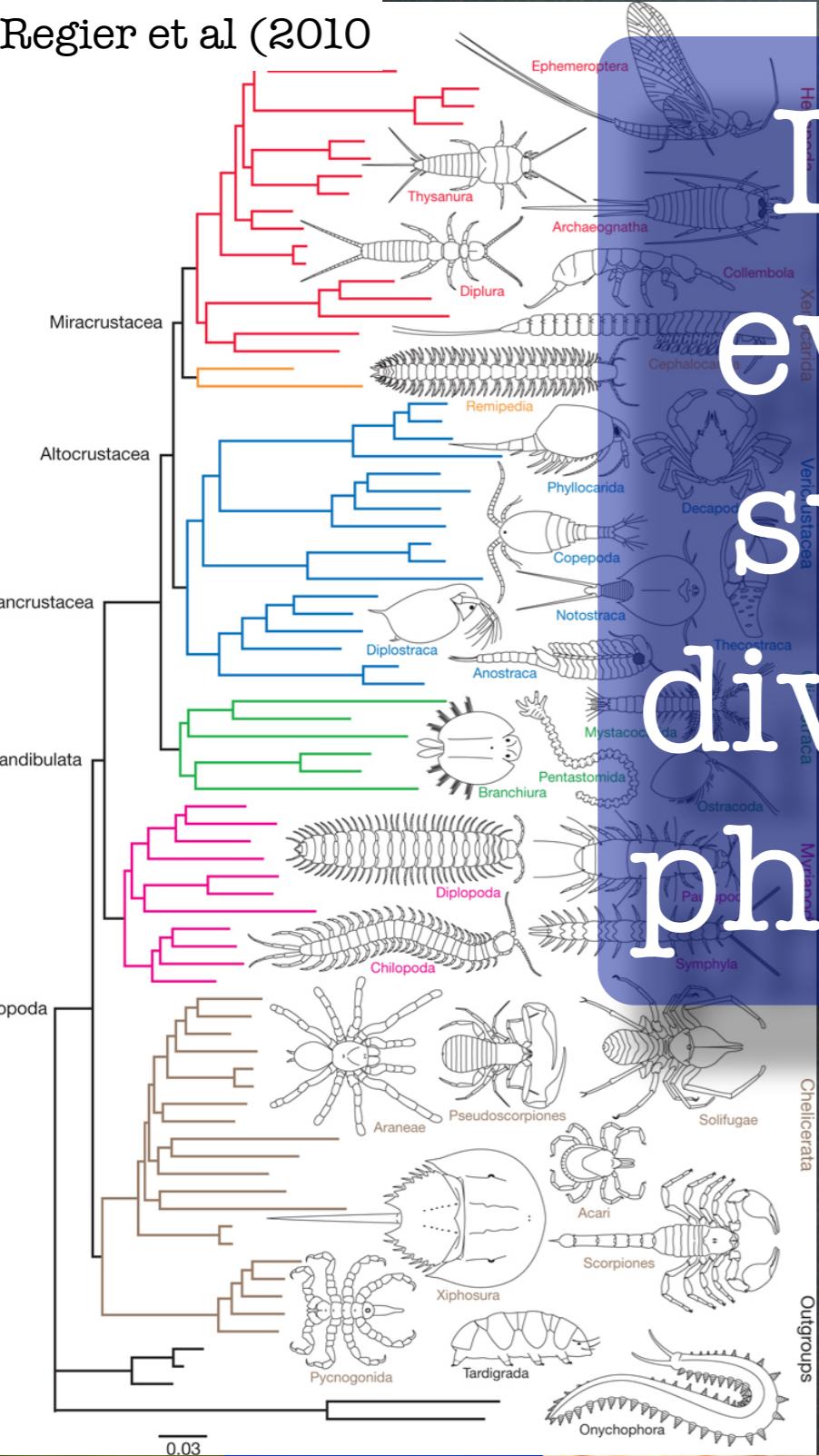


# Reasoning over phenotype diversity, character change, and evolutionary descent

Hilmar Lapp  
National Evolutionary Synthesis Center (NESCent)  
Seminar at University of Florida, March 1, 2011

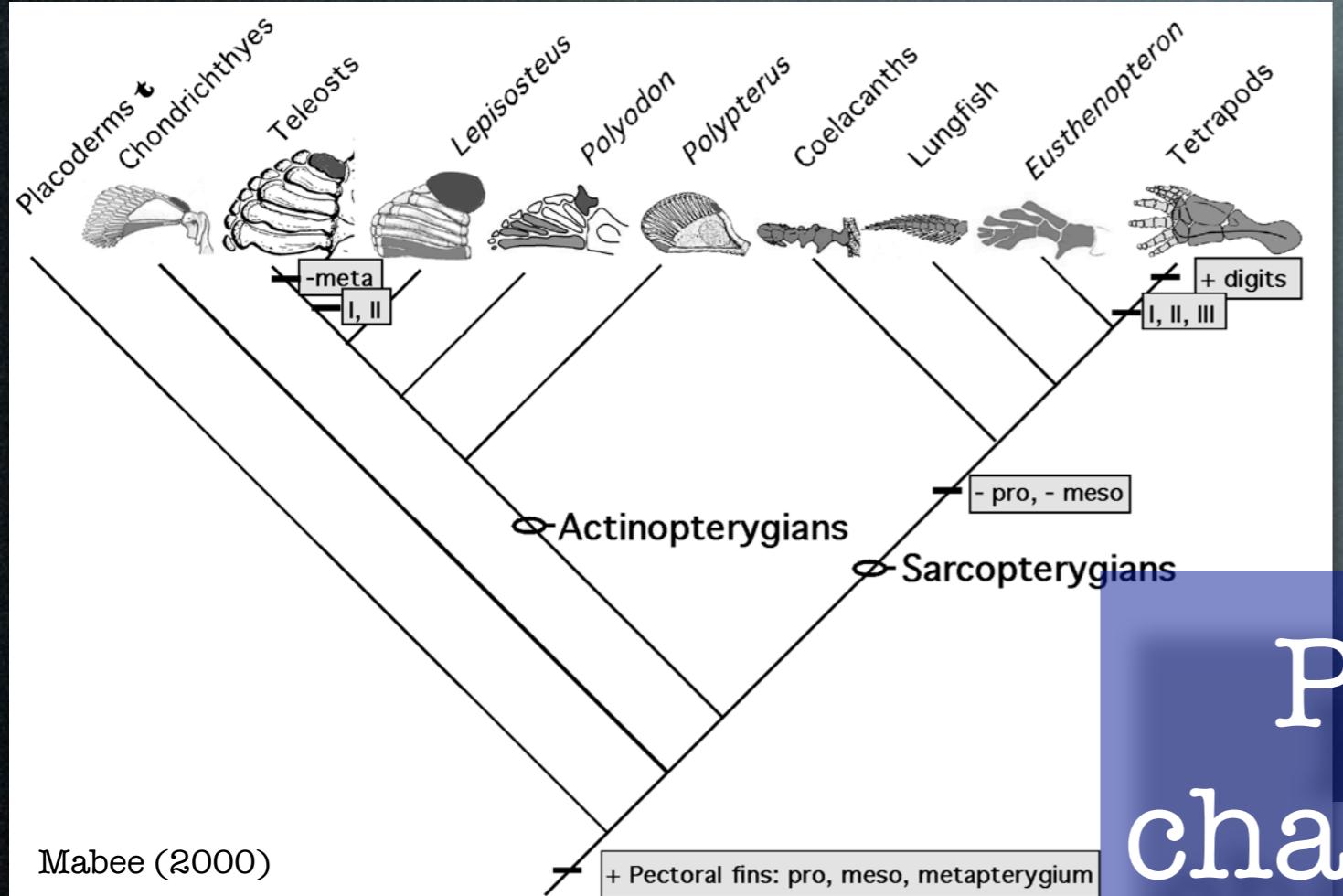
# Life has evolved a stunning diversity of phenotypes



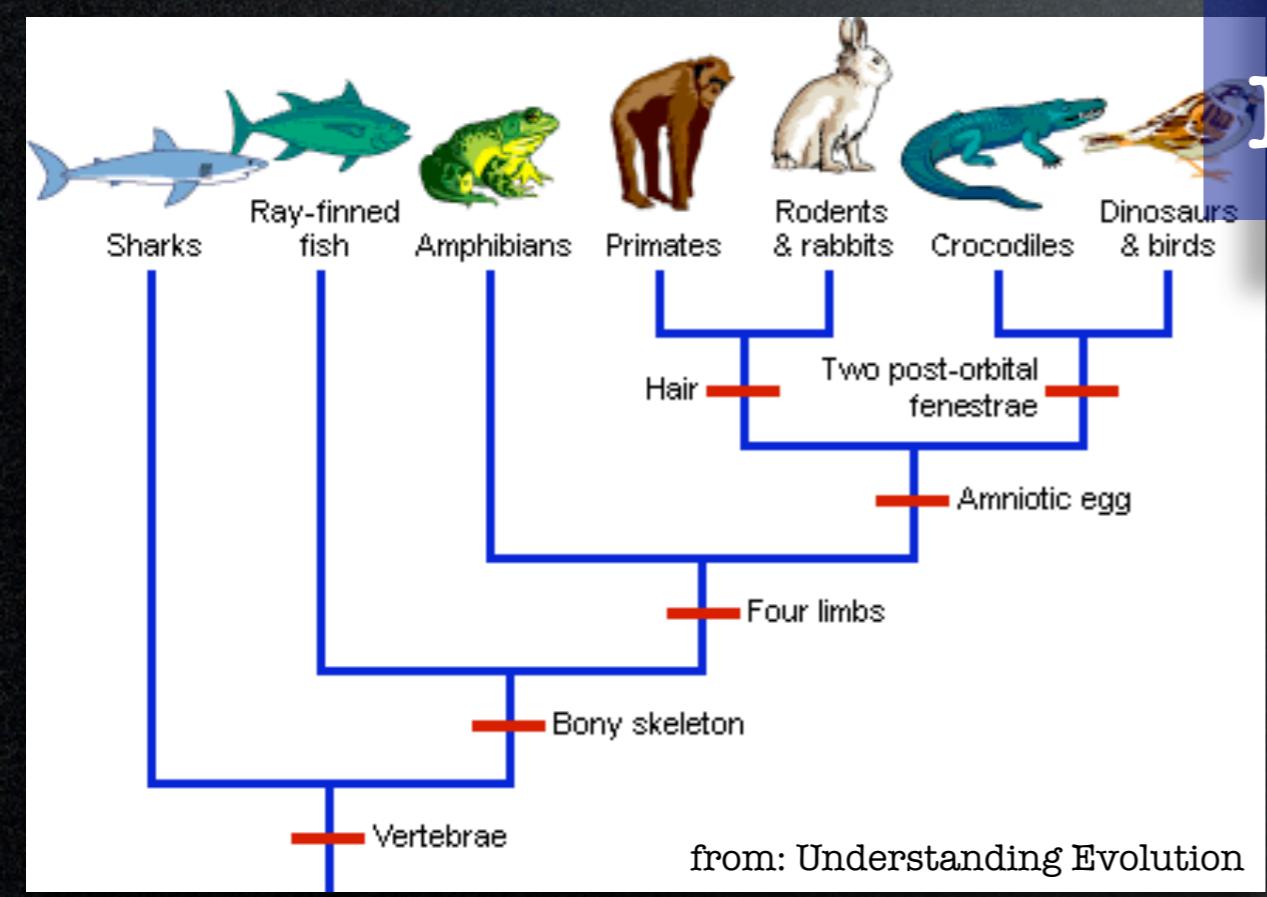
Images: Web Tree of Life (<http://tolweb.org>)





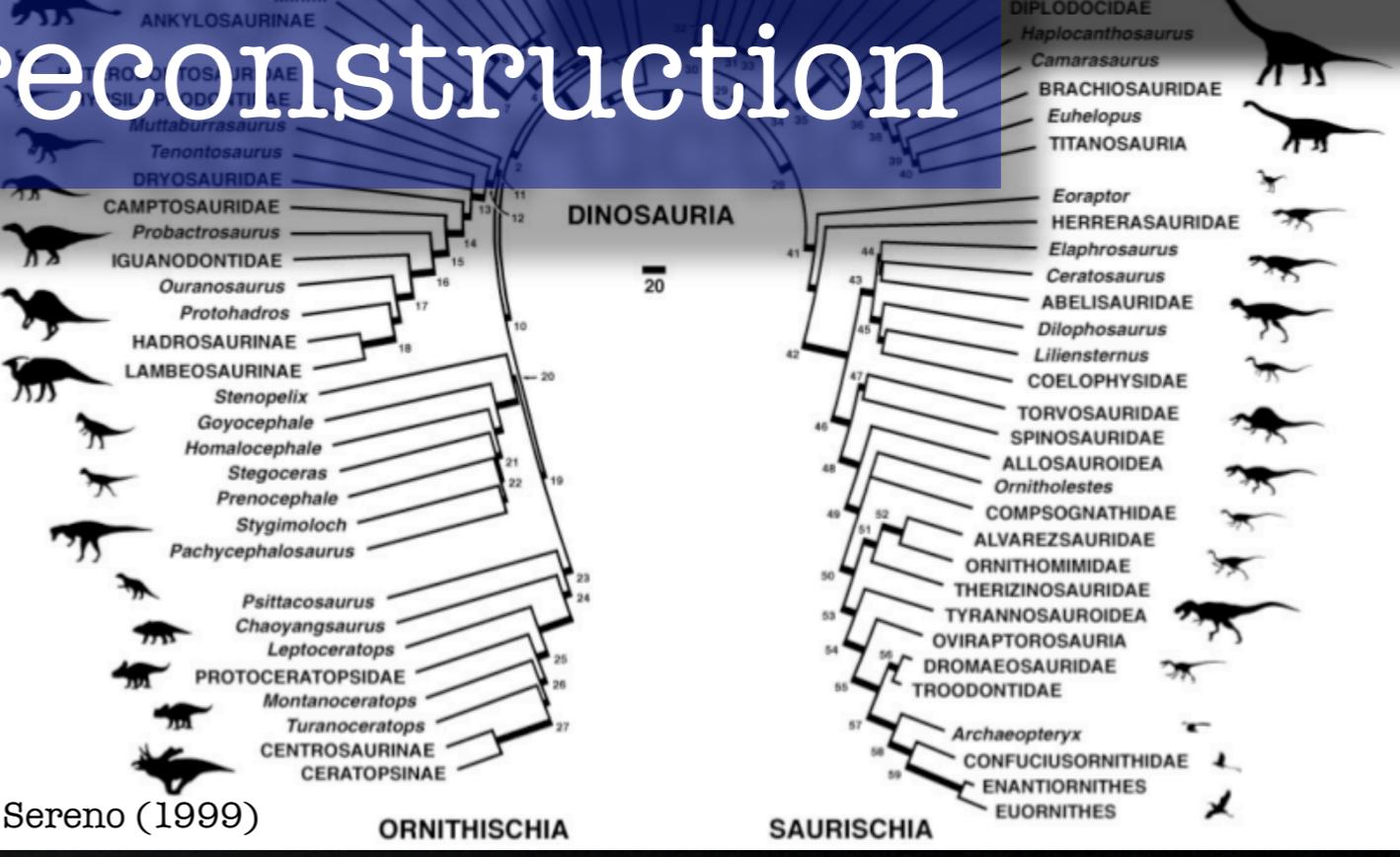


Mabee (2000)

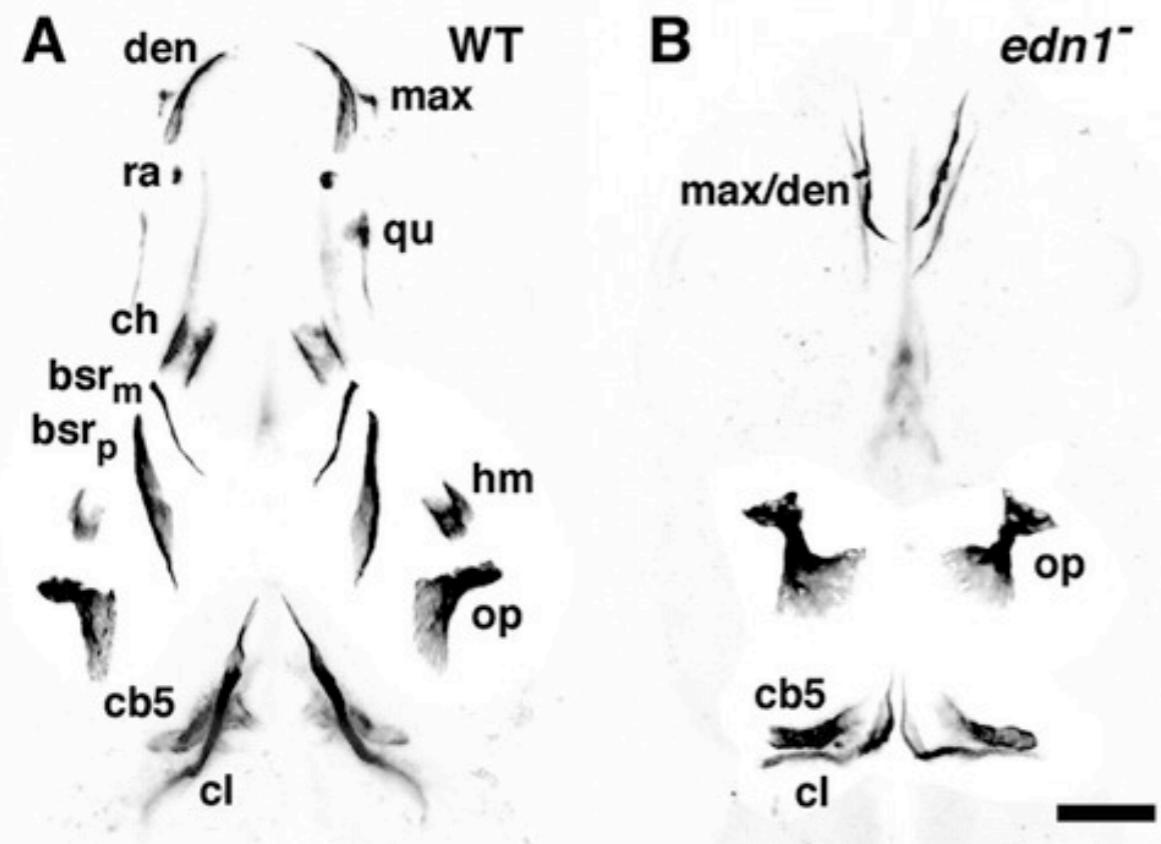


from: Understanding Evolution

# Phenotype changes inform phylogenetic reconstruction



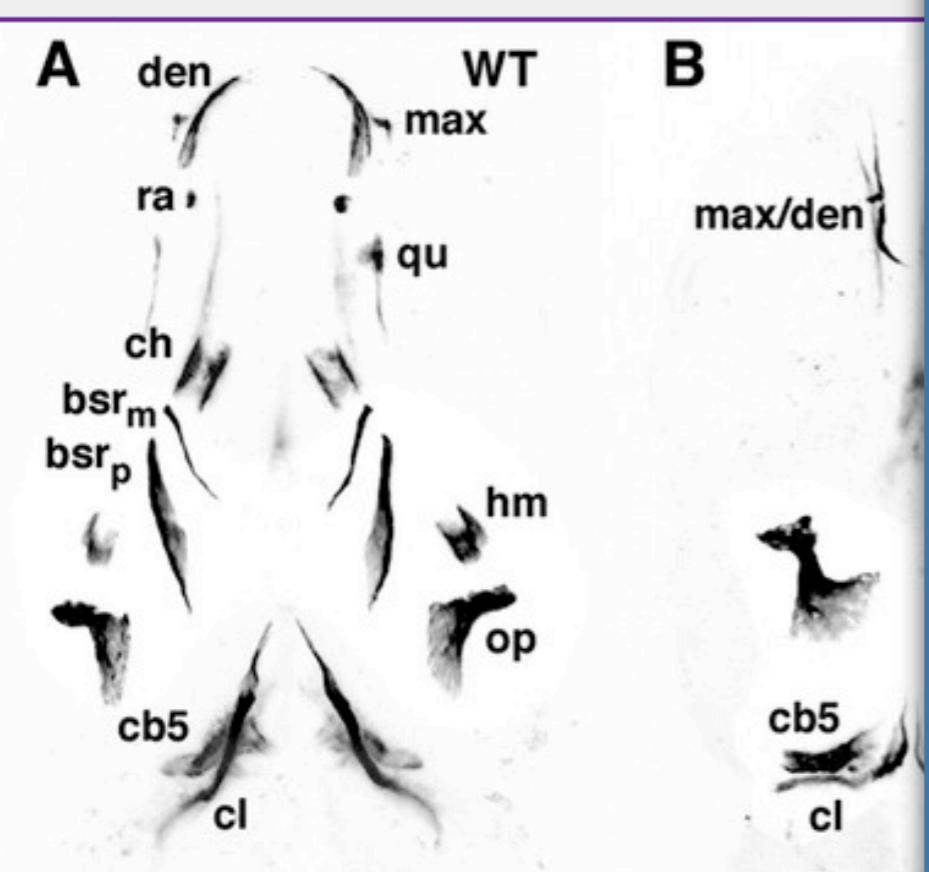
# Phenotype observations important to many fields



**Fig. 2** Ossifications in the young wild-type (WT) zebrafish (A) and homozygous *edn1* mutant (B). Ventral views, anterior to the top, of negative images of bones fluorescently labeled with Calcein in larvae at 7-days postfertilization. Ventral bones of the pharyngeal arches are identified (Cubbage and Mabee, 1996) by their labels on the left side, and dorsal bones are labeled on the right side in both panels, all of them are present as bilateral pairs. (A) The wild type first or mandibular arch includes a dorsal and a ventral dermal bone, the maxilla (max) and dentary (den), and a dorsal and a ventral cartilage-replacement bone, the quadrate (qu) and retroarticular (ra). The second or hyoid arch includes a dorsal and two ventral dermal bones, opercle (op), and two branchiostegal rays ( $bsr_p$  and  $bsr_m$ ), and dorsal and ventral cartilage replacement bones (very incompletely ossified at this stage), the hyomandibula (hm) and ceratohyal (ch). The most posterior arch includes a cartilage-replacement bone, ceratobranchial 5 (cb5). Overlaying ceratobranchial 5 is the cleithrum (cl), a long dermal bone connecting the posterior skull and the pectoral girdle. Two other craniofacial bones present at this stage lie deeper in the tissue and are not labeled, the parasphenoid and the endopterygoid. (B) Many of the anterior ossifications (in the first two arches) are missing in the *edn1* mutant. Ceratobranchial 5 and the cleithrum are present, shortened and somewhat malformed. In the mandibular arch dermal bones (max/den) are present but severely malformed, an example of the 'wicket' phenotype discussed in the text (see also Fig. 3). In the hyoid arch the opercle is present and its joint region (upper part of the bone) is markedly expanded, a mild example of the 'opercle-gain' phenotype described in the text and other Figures. Scale bar: 100  $\mu$ m.

Kimmel et al, 2003

# Phenotype observations important to many fields



this stage), the hyomandibula (hm) and ceratohyaline cartilage (ch), ceratobranchial 5 (cb5). Overlaying ceratobranchial 5 is the opercle (op). Two other craniofacial bones present at this stage are the pectoral girdle. Two other craniofacial bones present at this stage are the endopterygoid. (B) Many of the anterior ossifications are severely malformed, an example of the 'wicket' phenotype discussed in the text (see also Fig. 3). In the hyoid arch the opercle is present and its joint region (upper part of the bone) is markedly expanded, a mild example of the 'opercle-gain' phenotype described in the text and other Figures. Scale bar: 100  $\mu$ m.

OMIM – SRY-BOX 9; SOX9

NCBI

MIM \*608160  
Cloning  
Mapping  
Gene Function  
Molecular Genetics  
Cytogenetics  
Evolution  
Animal Model  
Allelic Variants  
View List  
References  
Contributors  
Creation Date  
Edit History

Gene map  
Entrez Gene  
N Nomenclature  
R RefSeq  
G GenBank  
P Protein  
U UniGene

LinkOut  
HGMD  
GAD  
MGI

### GENE FUNCTION

[Morais da Silva et al. \(1996\)](#) found that, consistent with its role in sex determination, SOX9 expression closely follows differentiation of Sertoli cells in the mouse testis, in experimental sex reversal when fetal ovaries are grafted to adult kidneys, and in the chick where there is no evidence for an Sry gene. The results suggested to the authors that SOX9 plays an essential role in sex determination, possibly immediately downstream of SRY in mammals, and that it functions as a critical Sertoli cell differentiation factor, perhaps in all vertebrates.

By cell transfection experiments, [Sudbeck et al. \(1996\)](#) showed that SOX9 can transactivate transcription from a reporter plasmid through the motif AACAAAG, a sequence recognized by other HMG domain transcription factors. By fusing all or part of SOX9 to the DNA-binding domain of yeast GAL4, the transactivating function was mapped to a transcription activation domain at the C terminus of SOX9. With 1 exception, all SOX9 nonsense and frameshift mutations in patients with campomelic dysplasia and sex reversal lead to truncation of this domain, suggesting to [Sudbeck et al. \(1996\)](#) that impairment of gonadal and skeletal development in these cases results, at least in part, from loss of the transactivation of genes downstream of SOX9.

During chondrogenesis in the mouse, Sox9 is coexpressed with Col2a1 ([120140](#)), the gene encoding type II collagen, the major cartilage matrix protein. COL2A1 is therefore a candidate regulatory target of SOX9. Regulatory sequences required for chondrocyte-specific expression of the COL2A1 gene have been localized to conserved sequences in the first intron in rats, mice, and humans. [Bell et al. \(1997\)](#) showed that SOX9 protein binds specifically to sequences in the first intron of human COL2A1. Mutation of these sequences abolished SOX9 binding and chondrocyte-specific expression of a COL2A1-driven reporter gene (COL2A1-lacZ) in transgenic mice. Furthermore, ectopic expression of Sox9 transactivated both a COL2A1-driven reporter gene and the endogenous Col2a1 gene in transgenic mice. These results demonstrated that COL2A1 expression is directly regulated by SOX9 protein in vivo and implicated abnormal regulation of COL2A1 during chondrogenesis as a cause of the skeletal abnormalities associated with campomelic dysplasia.

SOX9 is expressed during chondrocyte differentiation and is upregulated in male and downregulated in female genital ridges during sex differentiation. To study the sex- and tissue-specific regulation of SOX9, [Kanai and Koopman \(1999\)](#) defined the transcription start site and characterized the Sox9 promoter region in the mouse. The Sox9 proximal promoter shows moderately high nucleotide similarity between mouse and human. Transient transfection experiments using various deletion constructs at the 6.8-kb upstream region of the mouse Sox9 gene fused to a luciferase reporter showed that the interval between 193 and 73 bp from the transcription start site was essential for maximal promoter activity in cell lines and in primary male and female gonadal somatic cells and liver cells isolated from mouse embryos 13.5 days postcoitum. This minimal promoter region was shown by DNase I hypersensitive site assay to be in an 'open' state of chromatin structure in gonads of both sexes, but not in the liver. Promoter activity was higher in testis than in ovary and liver, but deletion of the region from -193 to -73 bp abolished this difference. [Kanai and Koopman \(1999\)](#) concluded that the proximal promoter region is in part responsible for the sex- and tissue-specific expression of the SOX9 gene, and that more distal positive and negative elements contribute to its regulation in vivo, consistent with the observation that translocations upstream from the SOX9 gene can result in campomelic dysplasia.

# As complex, free text phenotypes are resistant to computing

5. Aortic canal on compound Weberian centrum: ventrally open groove [0]; bony tube [1] (Lundberg et al., 1991b). Within the family a uniquely derived and unreversed synapomorphy of Pimelodidae exclusive of *Steindachneridion* and *Phractocephalus-Leiarius* group, CCI = 1.
6. Position of right cardinal vein foramen (or open trough): vertebra 5 [0]; vertebra 6 [1] (Nass, 1991). Within the family a uniquely derived and unreversed synapomorphy of Pimelodidae exclusive of *Steindachneridion* and *Phractocephalus-Leiarius* group, CCI = 1.
7. Ethmoid plate form: rounded [0]; quadrangular [1] (Lundberg et al., 1991b). Within Pimelodidae a uniquely derived and unreversed synapomorphy of *Pimelodus* group plus *Calophysus* group, CCI = 1.
8. Mesethmoid cornua deflection: none [0]; abruptly deflected ventrally [1] (Lundberg et al., 1991b). Within Pimelodidae a uniquely derived and unreversed synapomorphy of *Pimelodus* group plus *Calophysus* group, CCI = 1.
9. Coronoid process: shallow to moderately inclined [0]; steeply inclined, tall, and a little recurved [1] (Lundberg et al., 1991b). Within Pimelodidae a uniquely derived and unreversed synapomorphy of *Pimelodus* group plus *Calophysus* group, CCI = 1.

47. Shape of posterior dorsomedian fontanelle. An elongate-rectangular posterior fontanelle of most catfishes appears to be the plesiomorphic condition (see also Tilak 1963, 1964, 1965a; Lundberg 1982; Arratia 1987; Grande 1987). An irregularly-shaped or rounded rowing posteriorly [2] (Buitrago, pers. comm.). Within Pimelodidae uniquely derived basally in *Brachyplatystoma* but reversed in *B. tigrinum*, CCI = 0.5; state 2 is independently derived in *Steindachneridion* and *Sorubim* group.
17. Mandibular nerve canal in articular: absent [0]; present [1] (Nass, 1991). Highly homoplastic within Pimelodidae; uniquely derived basally in *Brachyplatystoma* but reversed in *B. tigrinum*, CCI = 0.2.
18. Urohyal vertical keel and posterior process: smooth sided [0]; with lateral ridges [1]. Within Pimelodidae a uniquely derived and unreversed synapomorphy of *Brachyplatystoma* exclusive of *B. vaillantii*, CCI = 1.
19. Orbital notch: present [0]; absent, eye not bounded by lateral ethmoid and sphenotic projections [1]. Within Pimelodidae a uniquely derived and unreversed synapomorphy of *Brachyplatystoma* exclusive of *B. vaillantii*, CCI = 1.
20. Ectopterygoid: present [0]; absent [1]. Within Brachyplatystomatini an unambiguously derived and unreversed synapomorphy of *Brachyplatystoma* exclusive of *B. vaillantii*, but independently derived in some Pimelodidae and other catfishes, CCI = 0.33.

State 0 = frontal broad anteriorly and moderately narrow posteriorly, anterior space reduced (adults) and arms moderately wide; 1 = frontal moderately broad posteriorly, anterior space moderately enlarged; 2 = frontal broad posteriorly, anterior arms narrow, space enlarged.

49. Laminar bone over the anterior vertebrae. The laminar bone is usually continuous medially in ariids (except in *Galeichthys* and *Ancharius*) and is more extensive in larger individuals, an ontogenetic change evidenced in most taxa. However, the excavation of the laminar bone posteromedially and the overlapping of the transverse process bases laterally is variable. I consider that a minimal cover over the aortic groove is plesiomorphic in ariids and interpret a ‘minimal cover’ as exposed transverse process bases and a deep median excavation on the ventral surface. The laminar bone in ariids extends over four to eight vertebra centra. Some ariids possess apomorphic modifications in the laminar shelf, such as depressions (e.g., *Guiritinga barbus*, *Cinetodus froggatti*) or median single keel (e.g., high and acute in *Batrachocephalus*, *Nemapteryx armiger*) or double keel (e.g., *Bagre marinus*).

# Finding similar information in free-text is difficult

“lacrymal bone...flat”

Mayden 1989

“lacrimal...small, flat”

Grande and Poyato-  
Ariza 1999

“lacrimal...triangular”

Royer 1999

“first infraorbital (lachrimal)  
shape...flattened”

Kailola 2004

“fourth infraorbital...anterior and  
posterior margins...in parallel”

Zanata and Vari 2005

# Meaning of words depends on context

- Burrowing insectivorous mammals in the family Talpidae
- A spy buried secretly within an organization or country
- The SI unit used in chemistry for the amount of a substance
- A small, sometimes raised area of skin, usually with darker pigment
- A Mexican sauce made from chili peppers and other spices, including chocolate
- A massive structure, usually of stone, used as a pier, jetty, or breakwater between places separated by water

# Meaning of words depends on context

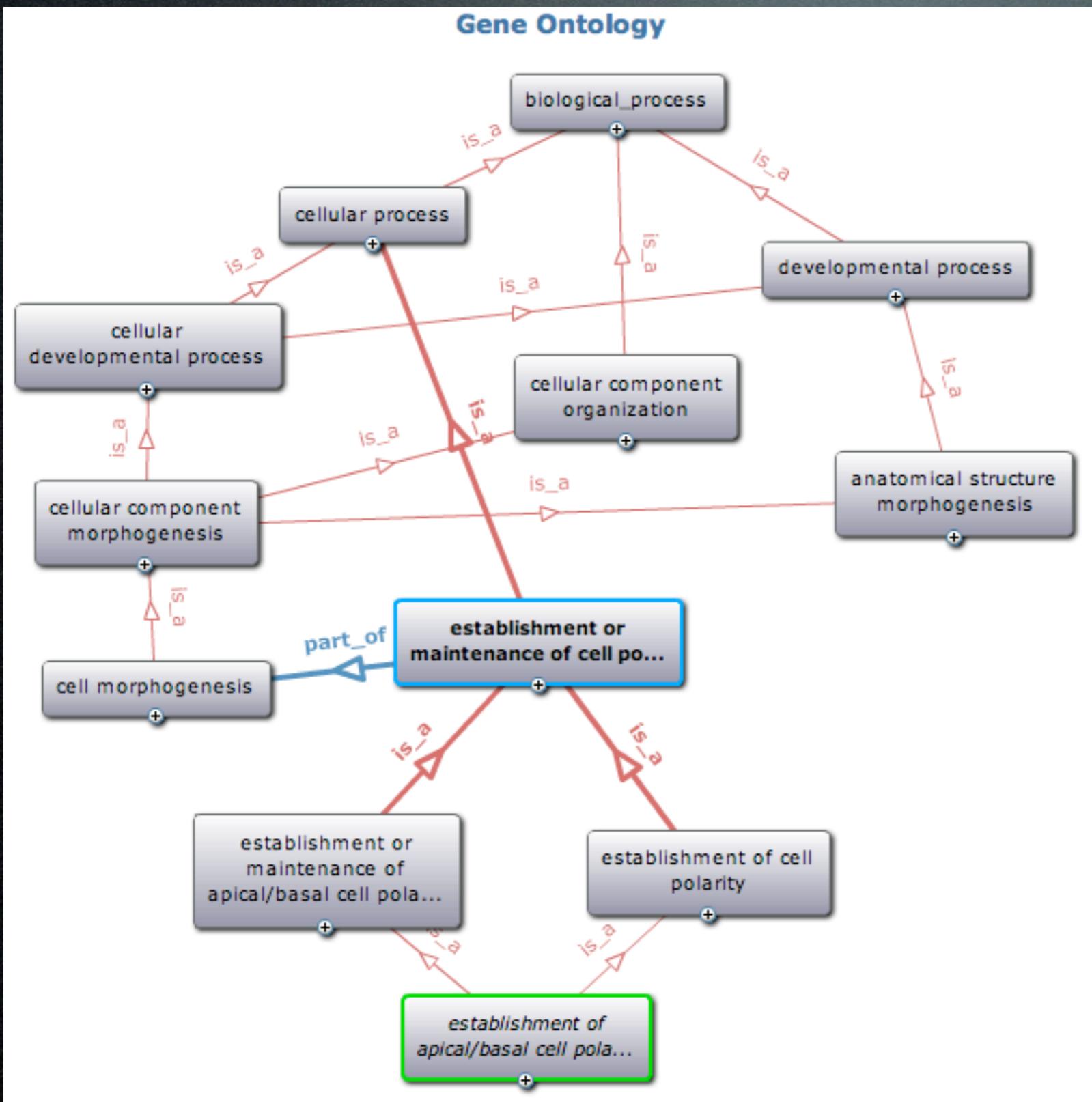
## Mole:

- Burrowing insectivorous mammals in the family Talpidae
- A spy buried secretly within an organization or country
- The SI unit used in chemistry for the amount of a substance
- A small, sometimes raised area of skin, usually with darker pigment
- A Mexican sauce made from chili peppers and other spices, including chocolate
- A massive structure, usually of stone, used as a pier, jetty, or breakwater between places separated by water

# What is an ontology?

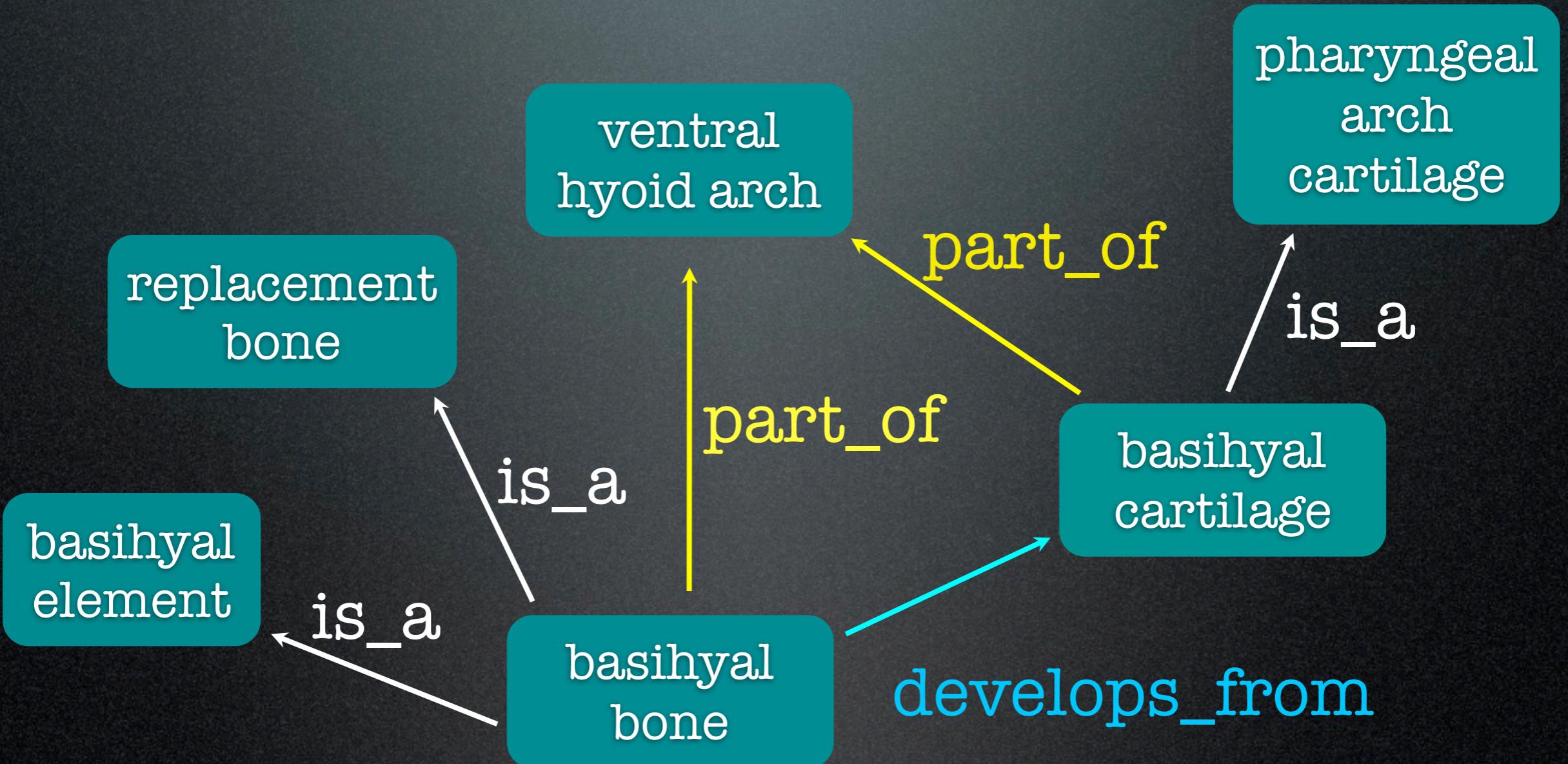
- An ontology is a type of vocabulary with well-defined terms and the logical relationships that hold between them.
- An ontology represents the knowledge about its subject domain.

# Ontologies support reasoning



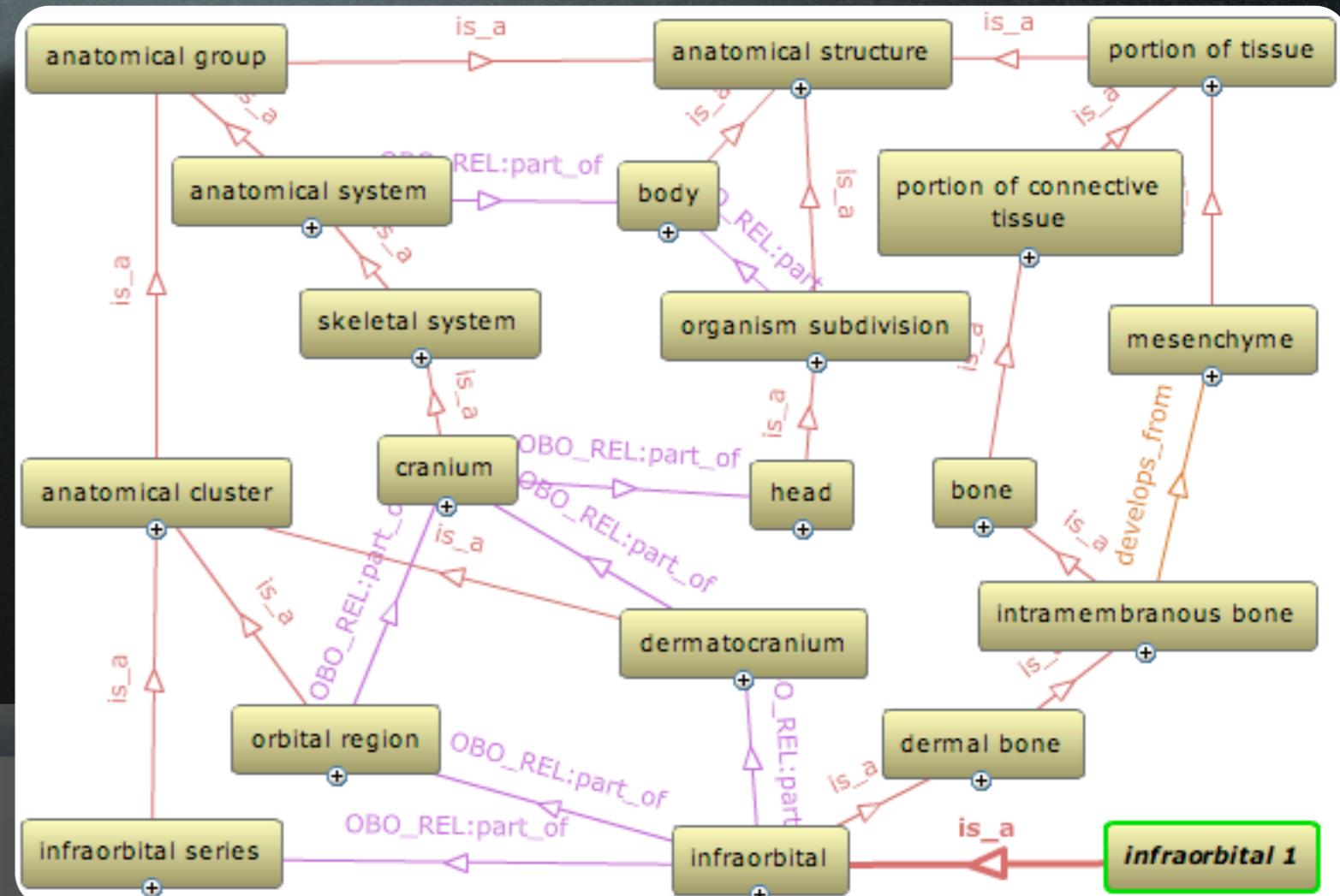
- Relationships (“assertions”) induce a hierarchical structure.
- Ontologies can be processed by machines to make inferences.

# The same principles apply to anatomy

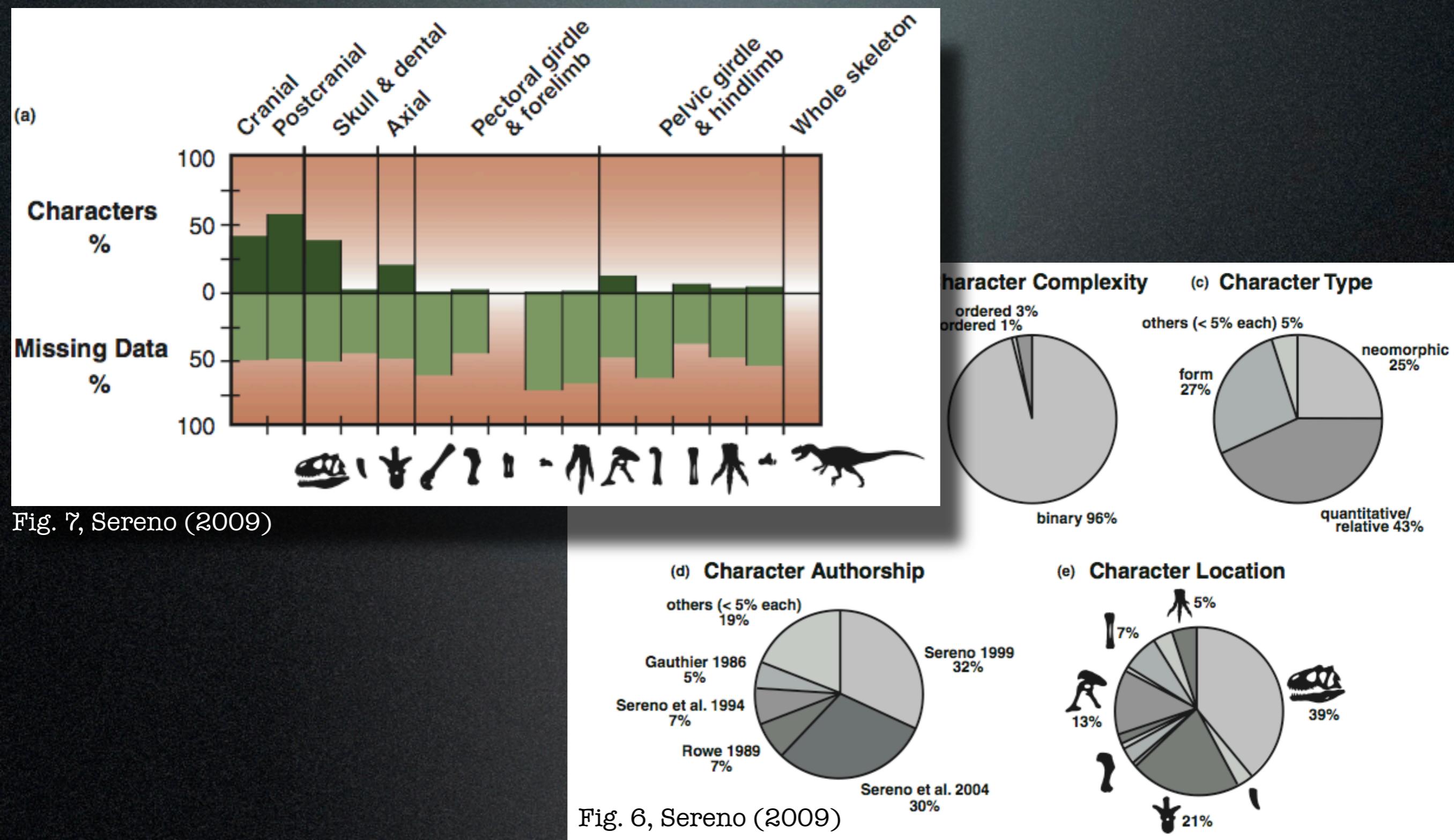


# The same principles apply to anatomy

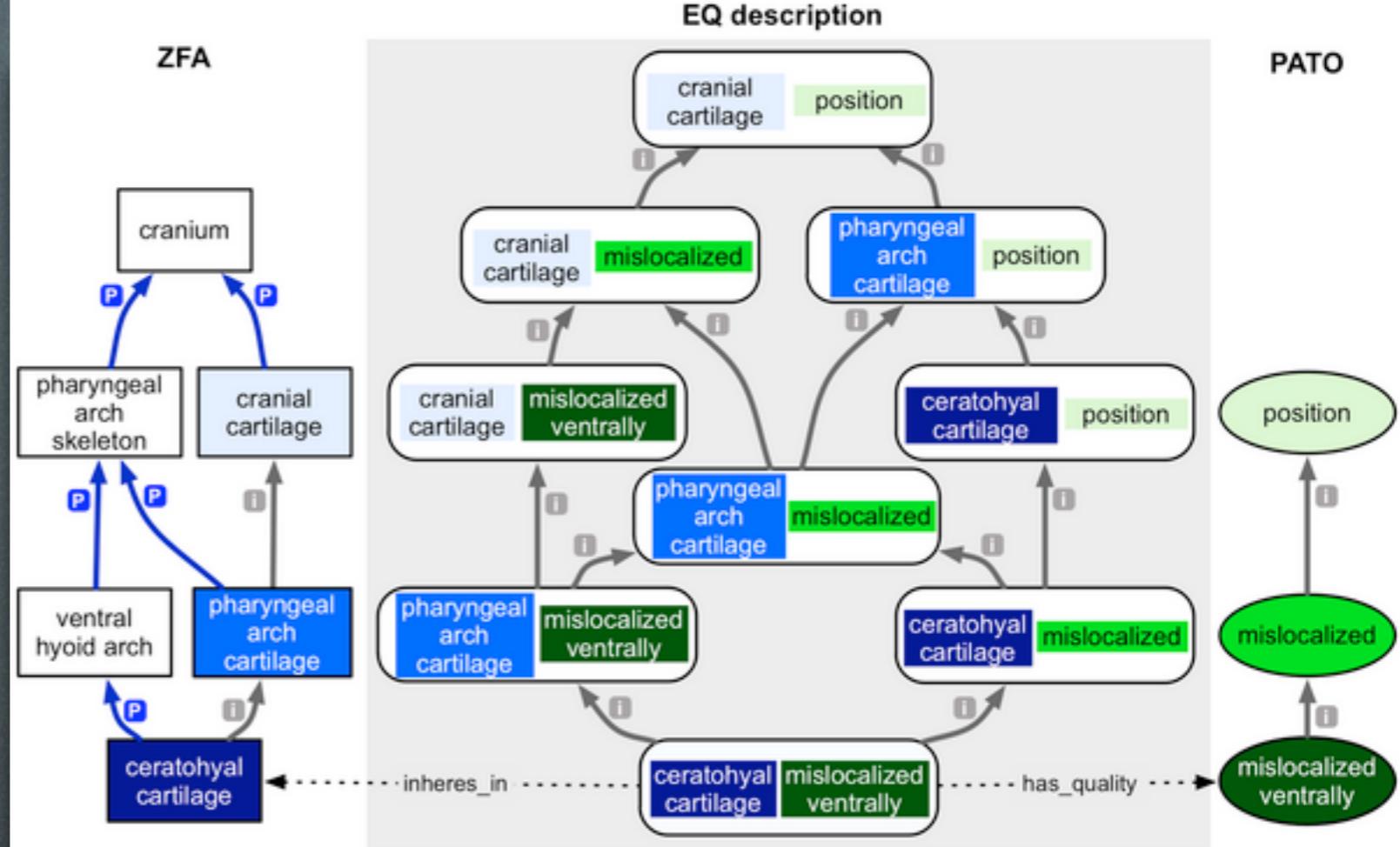
Details for infraorbital 1 [Teleost Anatomy Ontology]	
ID	TAO:0000223
Name	infraorbital 1
Children	0
Definition	Infraorbital that is the first (anteriormost) bone of the infraorbital series.
xref_definition	ZFIN:curator
RELATED SYNONYM	lachrymal bone
RELATED SYNONYM	lacrimal bone
RELATED SYNONYM	lacrymal bone



# Integrating across studies?



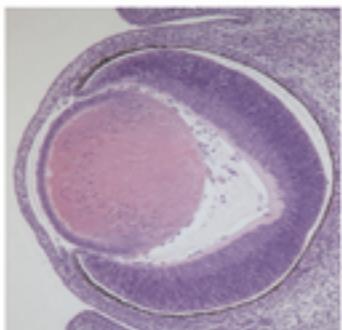
# Computing example: Search by Similarity



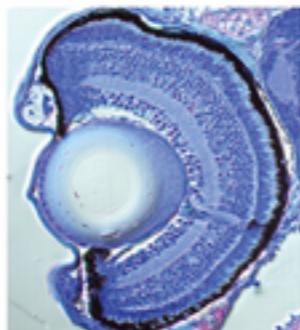
Human



Mouse



Zebrafish



Drosophila

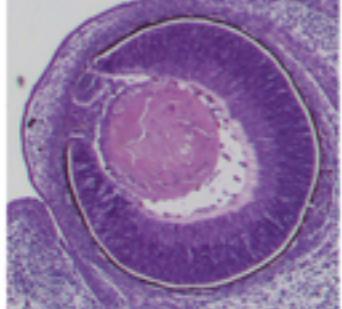


Fig. 3, Washington et al (2009)

WT

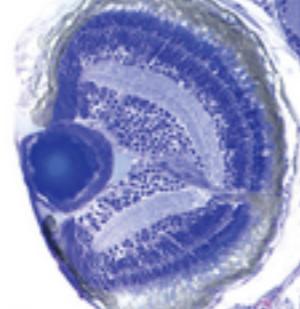


*PAX6*<sup>+/-</sup>



*Pax6*<sup>-/-</sup>

mut



*pax6b*<sup>-/-</sup>



*ey*<sup>-/-</sup>

EQs

cornea opaque  
iris absent  
retina degenerate  
lens opaque  
aqueous humor of eyeball increased pressure

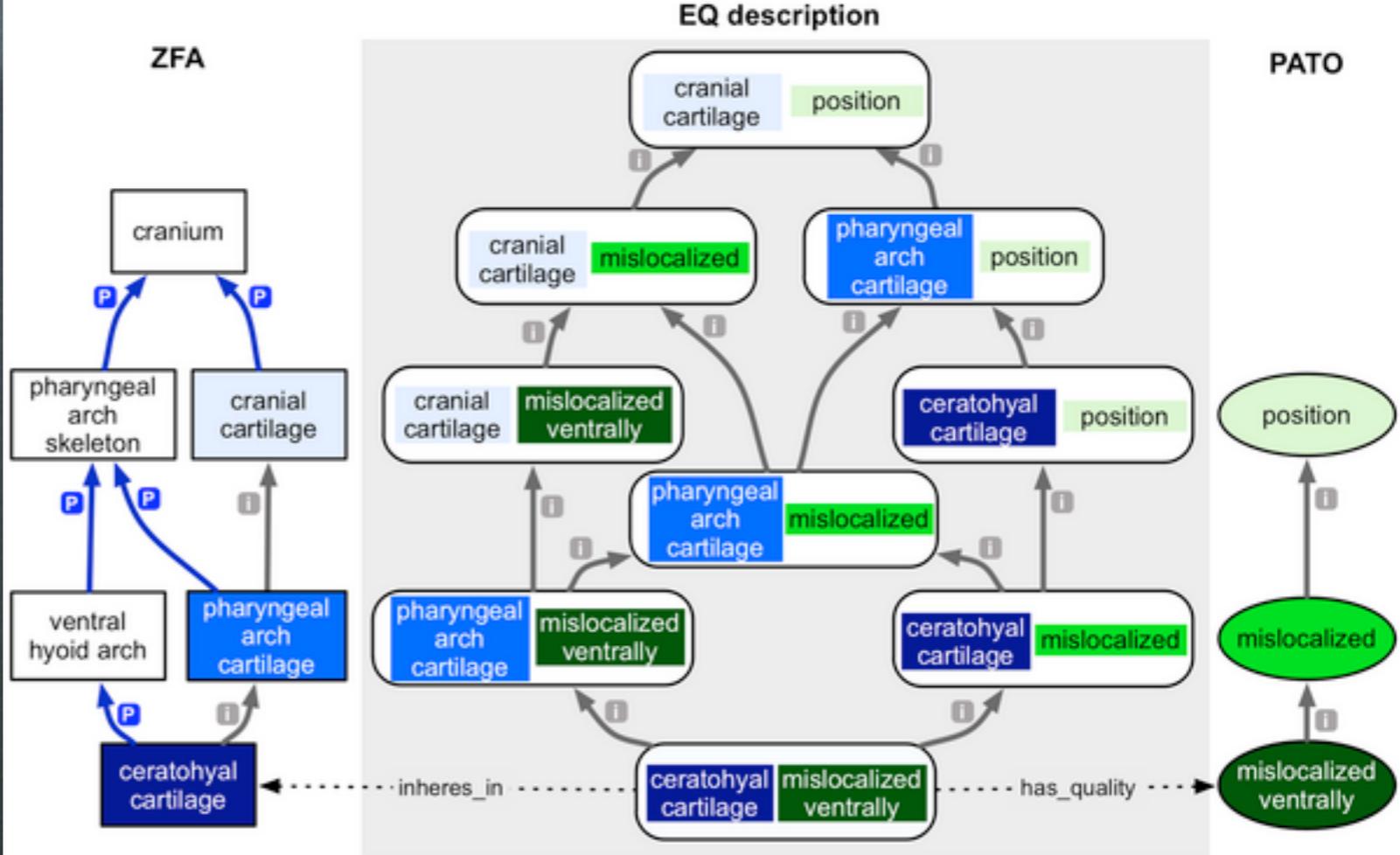
eye decreased size  
lens fused\_to cornea  
iris morphology  
anterior chamber absent

eye decreased size  
lens decreased size  
retina malformed

eye absent

Fig. 1, Washington et al (2009)

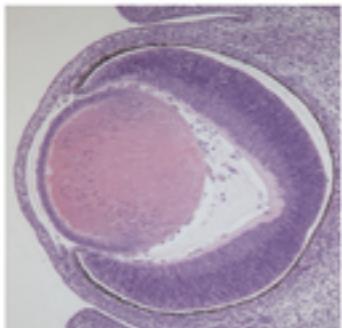
# Computing example: Search by Similarity



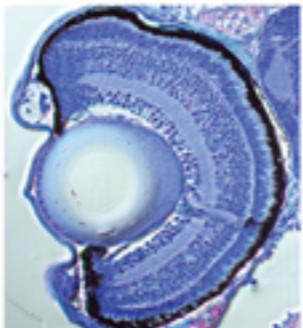
Human



Mouse



Zebrafish

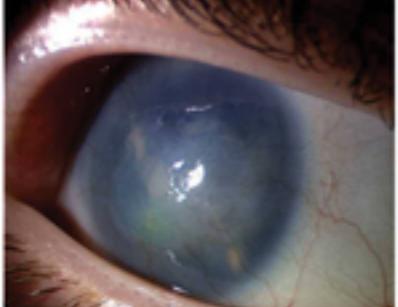


Drosophila



Fig. 3, Washington et al (2009)

WT



*PAX6<sup>+/-</sup>*

EQs

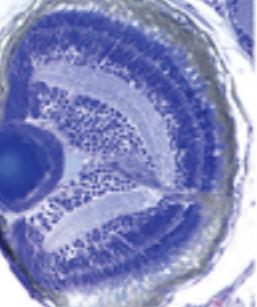
- cornea opaque
- iris absent
- retina degenerate
- lens opaque
- aqueous humor of eyeball increased pressure



*Pax6<sup>+/-</sup>*

EQs

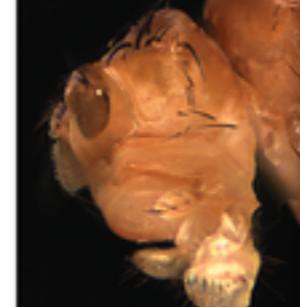
- eye decreased size
- lens fused\_to cornea
- iris morphology
- anterior chamber absent



*pax6b<sup>+/-</sup>*

EQs

- eye decreased size
- lens decreased size
- retina malformed



*ey<sup>+/-</sup>*

EQs

- eye absent



<http://tolweb.org/Trogloglanis/69910>

Fig. 1, Washington et al (2009)

# Computing over comparative morphology?



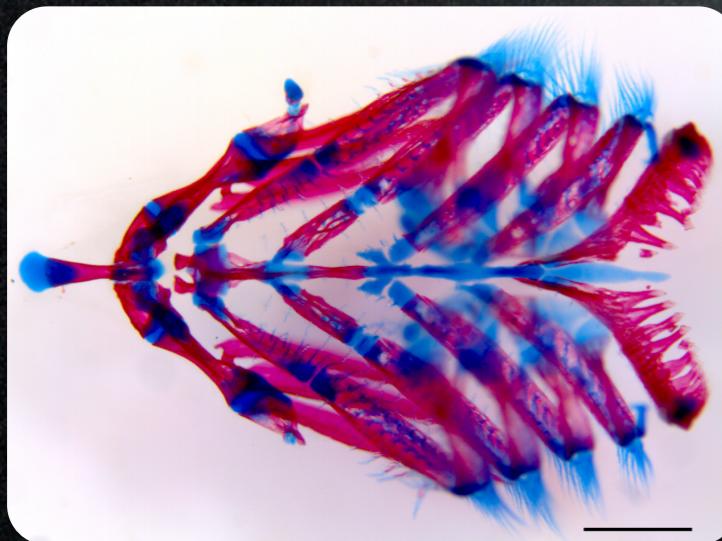
*Cyprinus carpio*



*Pangio anguillaris*



*Nemacheilus fasciatus*



*Catostomus commersoni*



*Gyrinocheilus aymonieri*



*Phenacogrammus interruptus*

# Knowledge mining & hypothesis generation



Model Organism

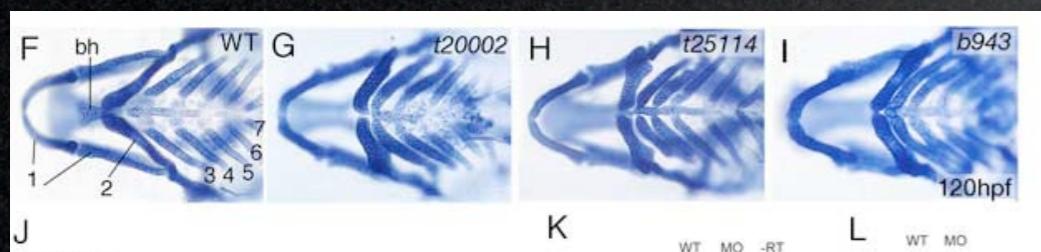
Mutagenesis



Mutant or missing protein at specific developmental stage



Phenotype change(s) to wildtype



Laue et al (2008)

Non-model organisms

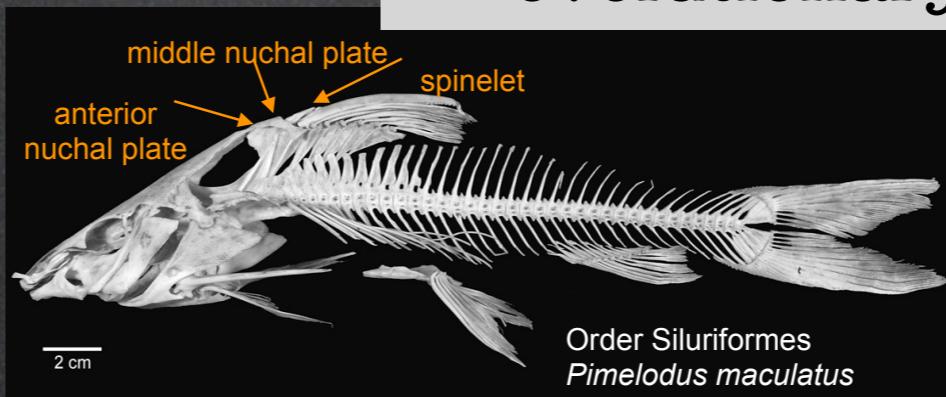
Mutation, selection, drift, gene flow



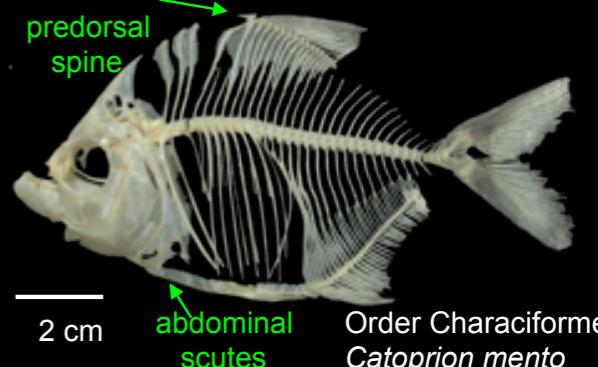
Altered expression or function of protein



Phenotype changes between evolutionary lineages



Order Siluriformes  
*Pimelodus maculatus*



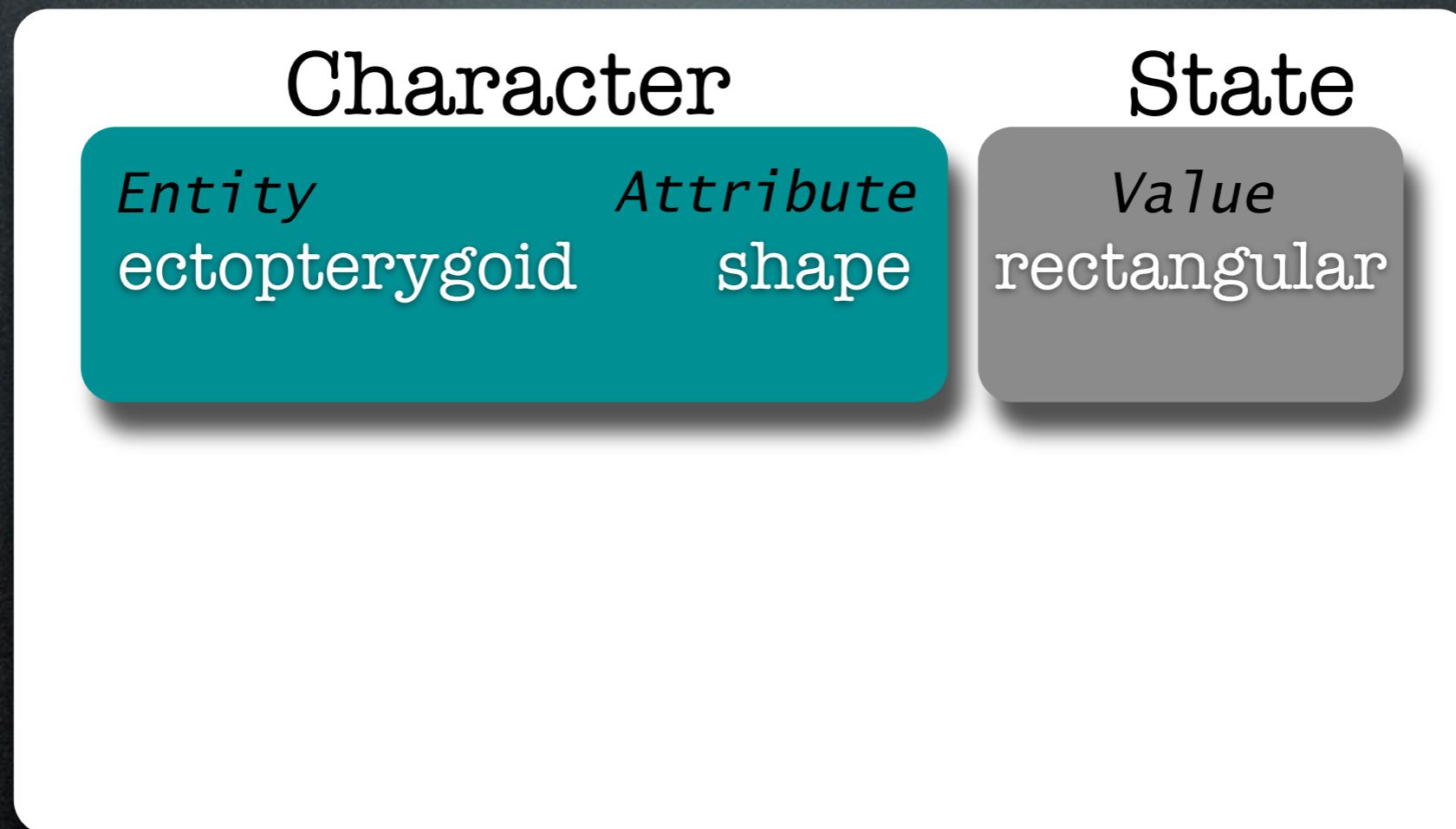
Order Characiformes  
*Catoprion mento*

# Phenoscape

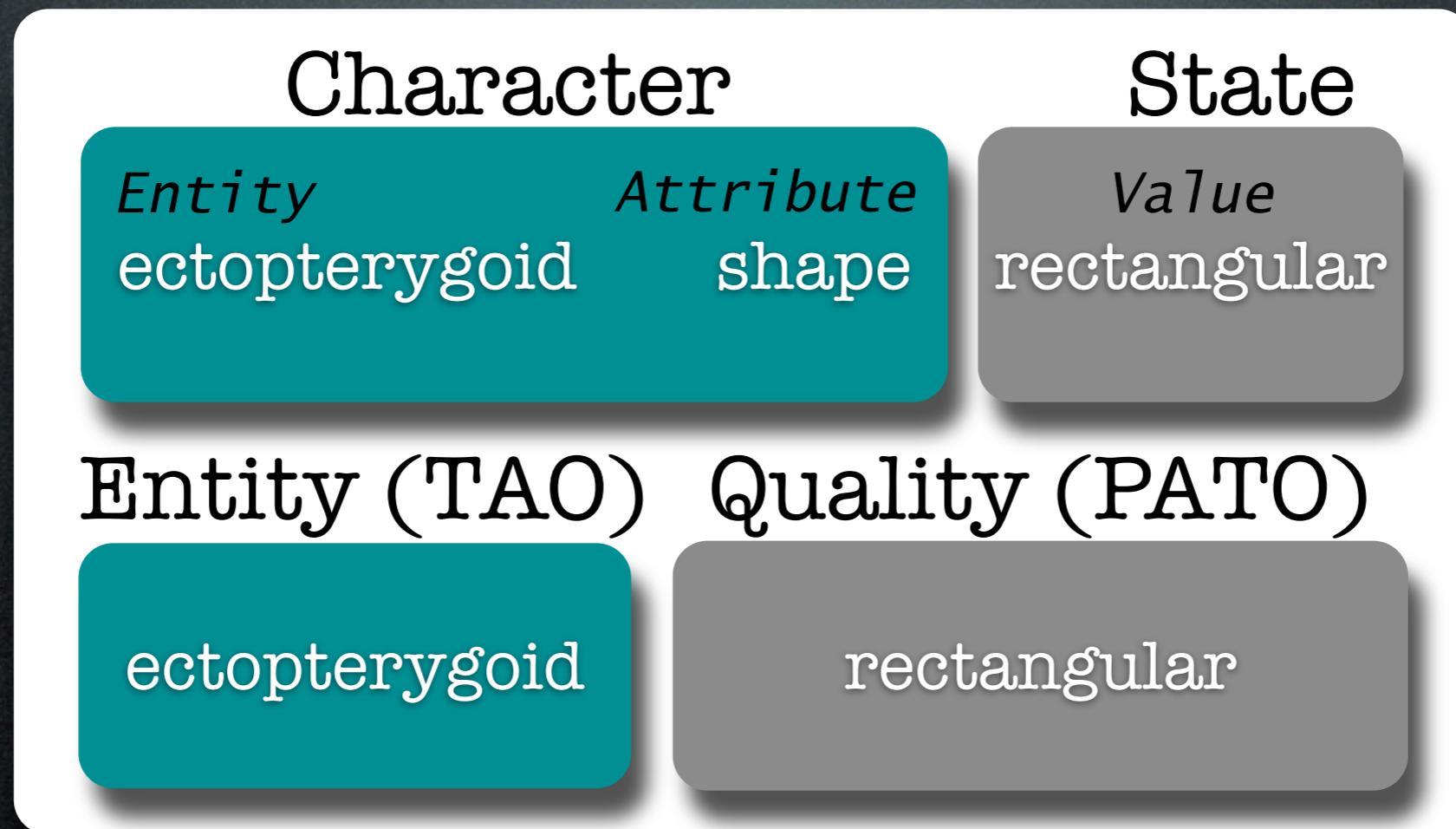


- Collaboration between P. Mabee (PI, U. South Dakota), M. Westerfield (ZFIN), and Todd Vision (UNC, NESCent)
- Aim: Foster devo-evo synthesis by
  - Prototyping a database of curated, machine-interpretable evolutionary phenotypes.
  - Integrating these with mutant phenotypes from model organisms.
  - Enabling data-mining and discovery for candidate genes of evolutionary phenotype transitions.
- Informatics for the project is developed and hosted at NESCent

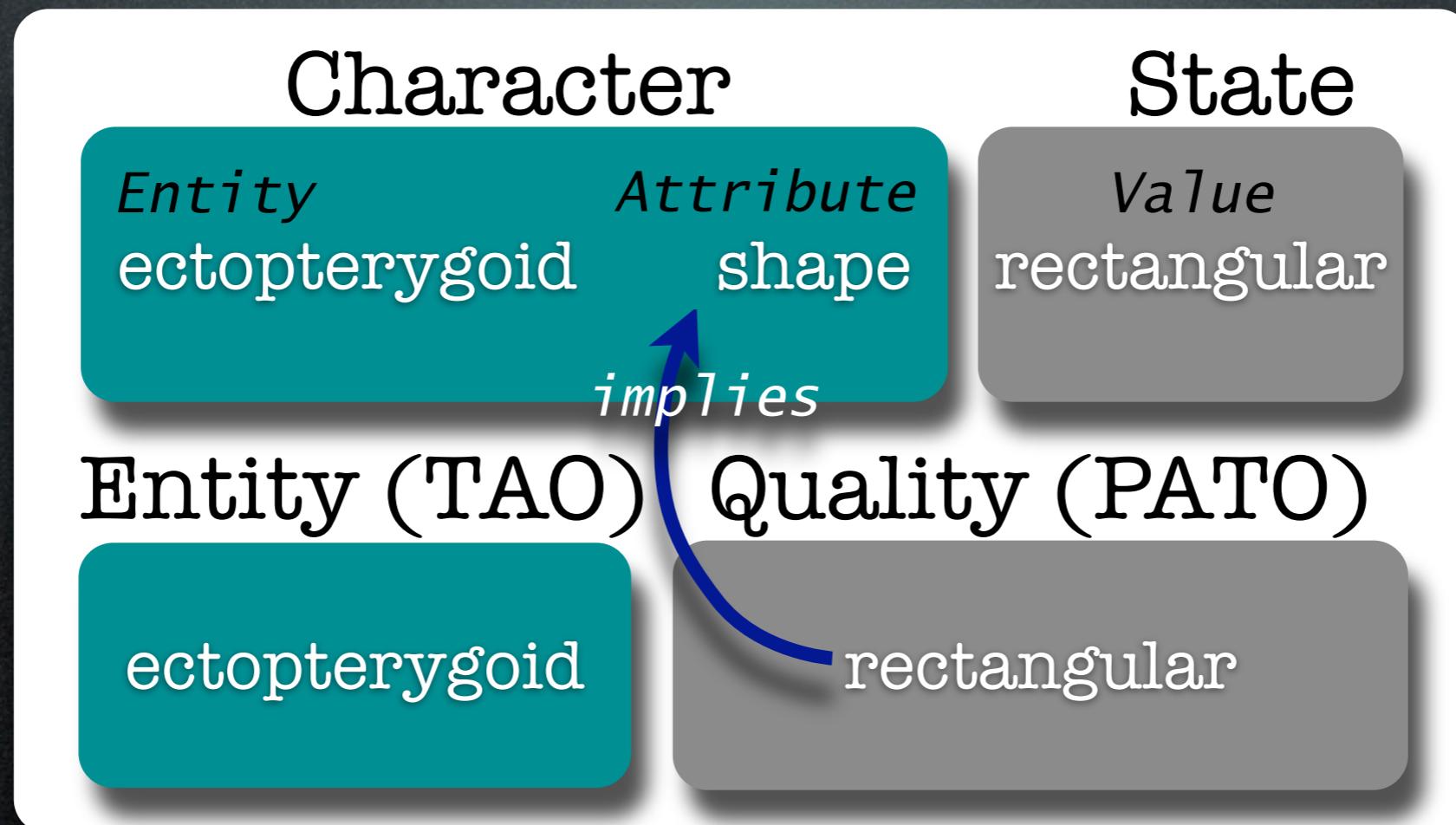
# Entity-Quality Model for Evolutionary Phenotypes



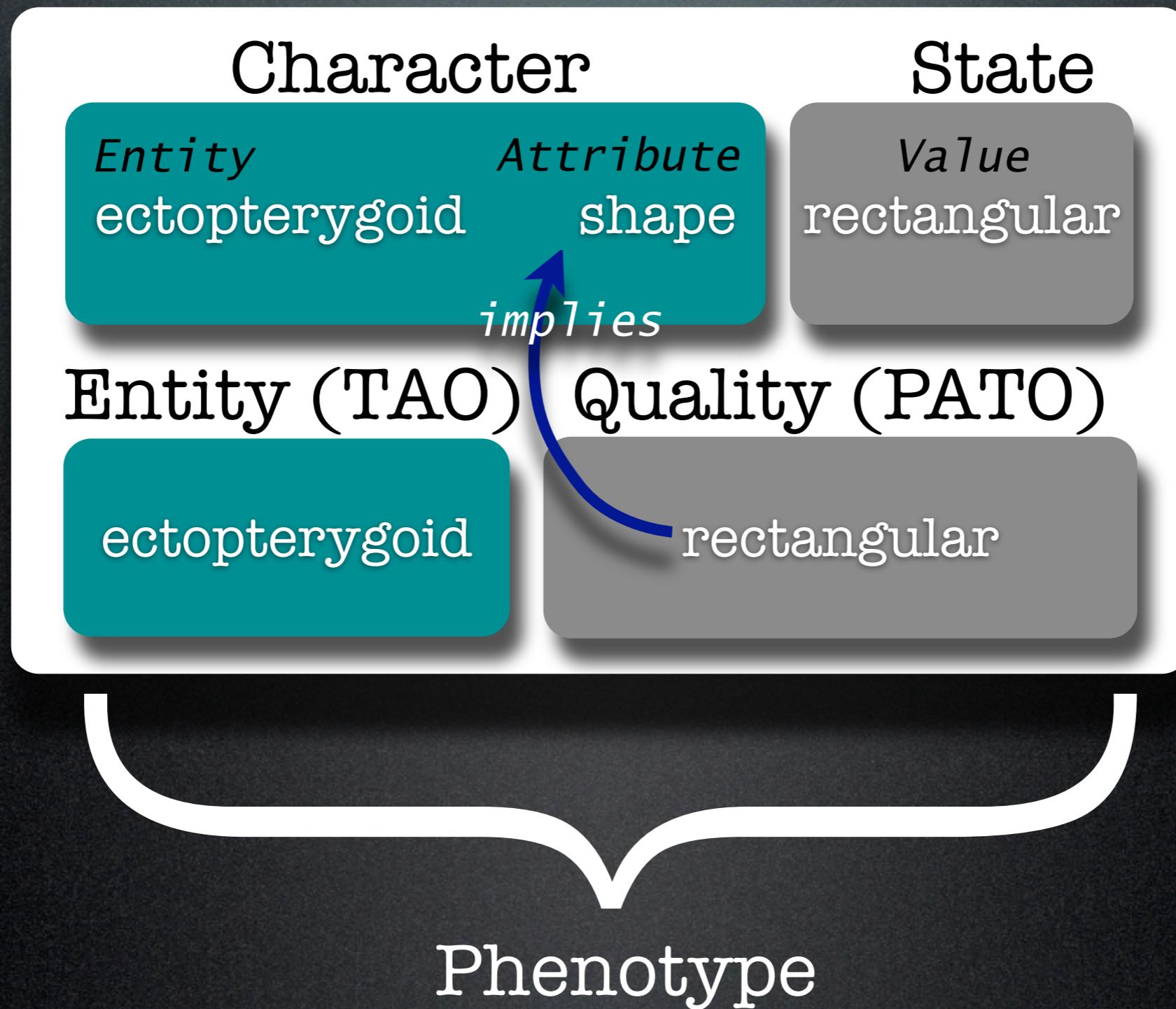
# Entity-Quality Model for Evolutionary Phenotypes



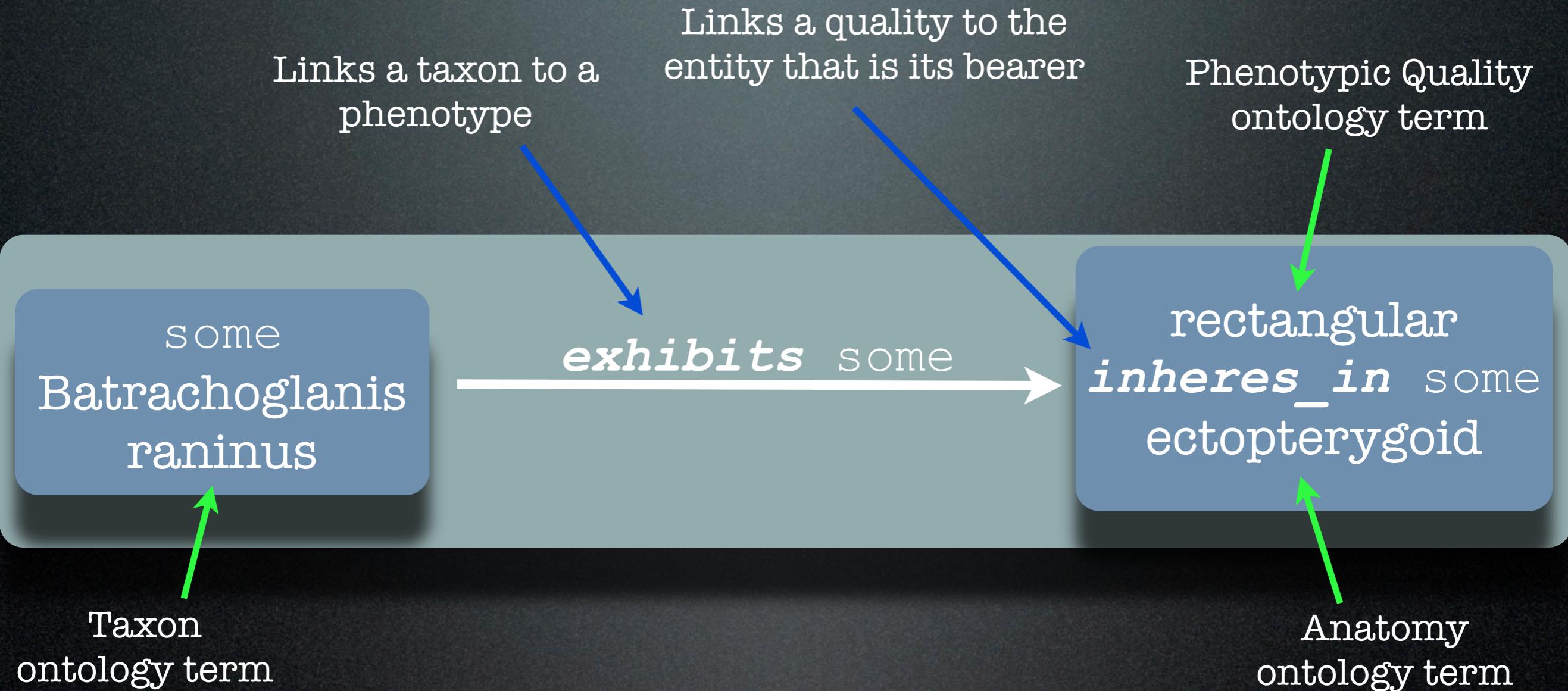
# Entity-Quality Model for Evolutionary Phenotypes



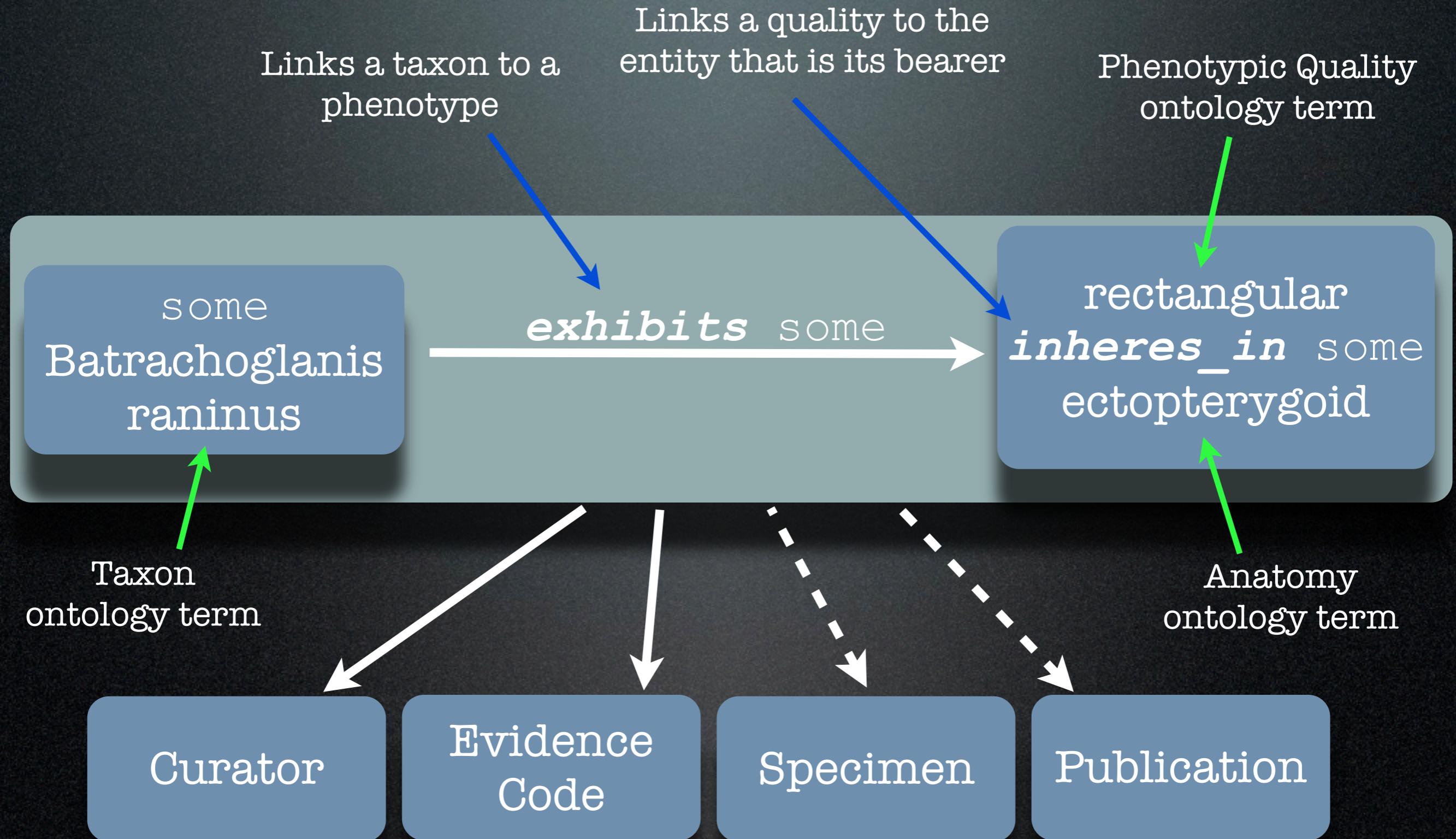
# Entity-Quality Model for Evolutionary Phenotypes



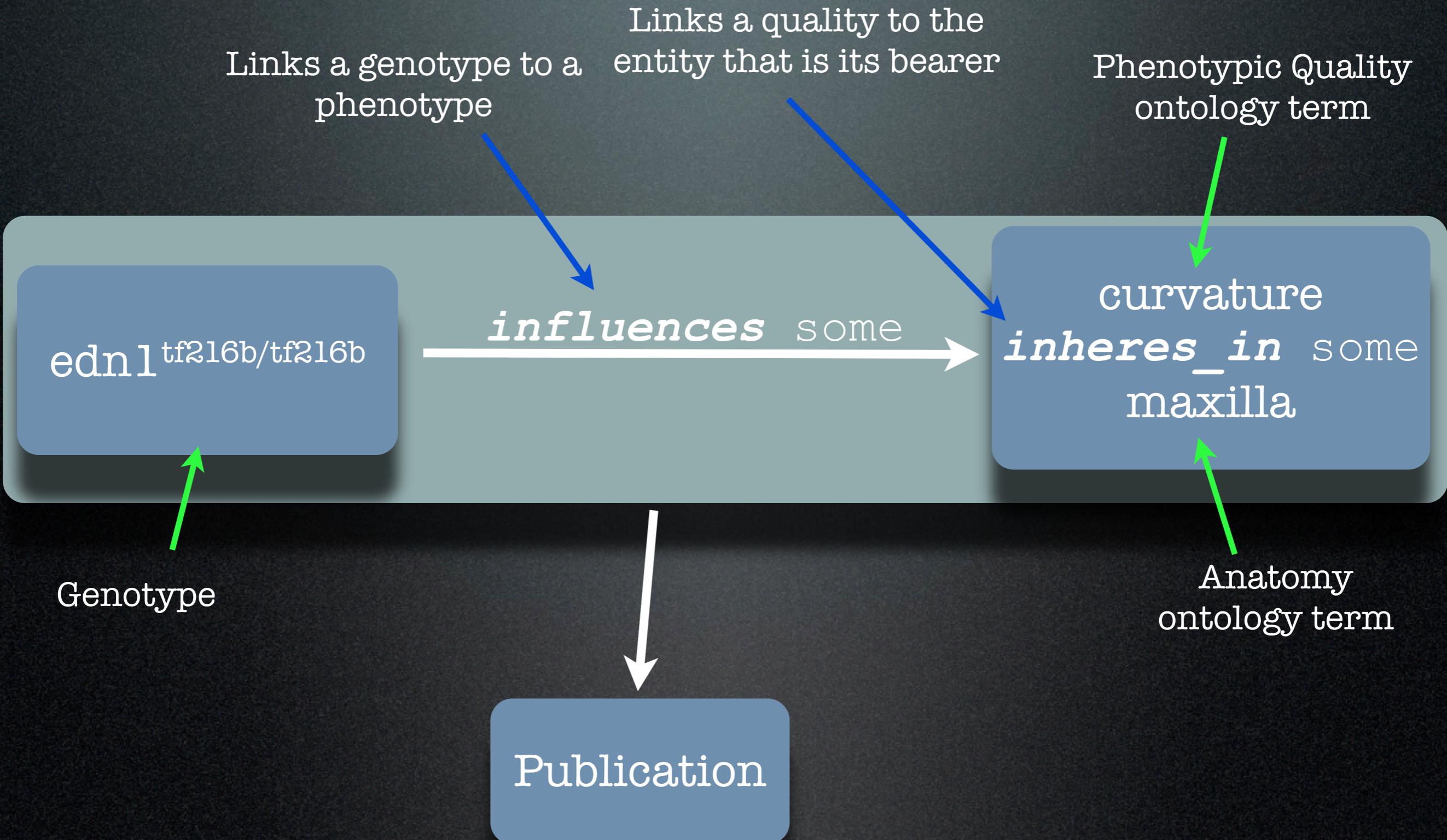
# Taxon phenotype assertion



# Taxon phenotype assertion



# Gene phenotype assertion



# Full workflow: free-text → EQ → integrated KB

## legacy free-text character data

56. *Naked body*. A scaleless body is a derived condition in the ostariophysans. Most cypriniforms, characiforms and most primitive teleosts and gonorhynchiforms possess scales on all or part of the body, while the majority of catfishes (including ariids) and gymnotoids lack scales – although scales are often represented by ossified lateral line tubes (Roberts 1973; Fink and Fink 1981). Some catfishes (doradids, Kailola (2004)

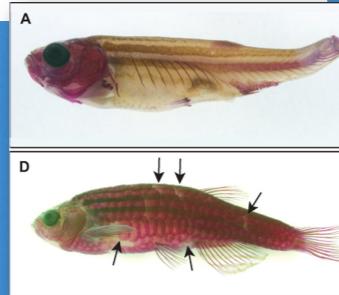


© Jean Ricardo Simões Vitule

## mutant phenotype

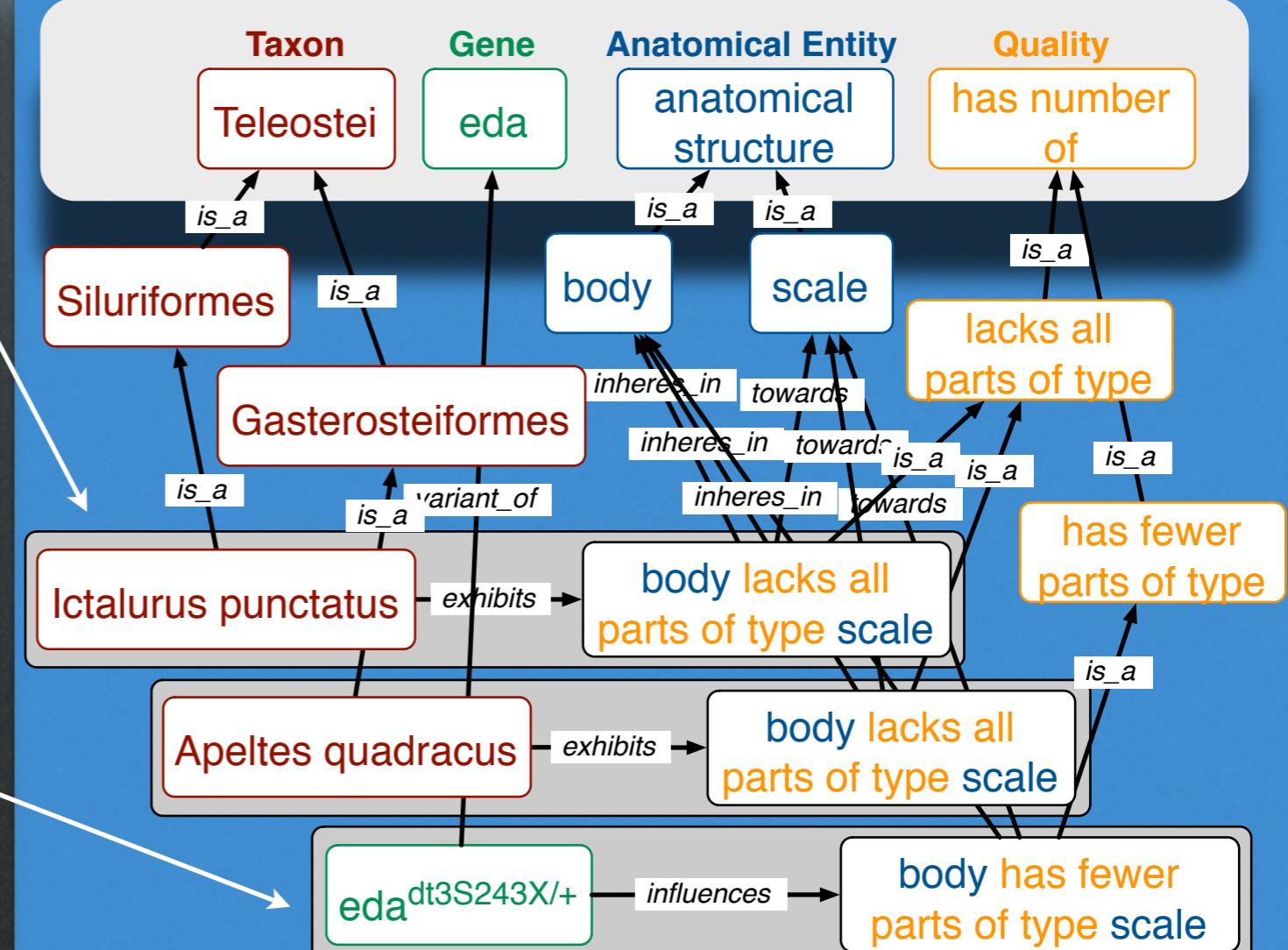
Here, we describe the phenotypic and molecular characterization of a set of mutants showing loss of adult structures of the dermal skeleton, such as the rays of the fins and the scales, as well as the pharyngeal teeth. The mutations represent adult-viable, loss of function alleles in the *ectodysplasin* (*eda*) and *ectodysplasin receptor* (*edar*) genes.

Harris et al. (2008)



**EQ = body  
lacks all  
parts of type  
scale**

**EQ = body  
has fewer  
parts of type  
scale**



# Full workflow: free-text → EQ → integrated KB

## legacy free-text character data

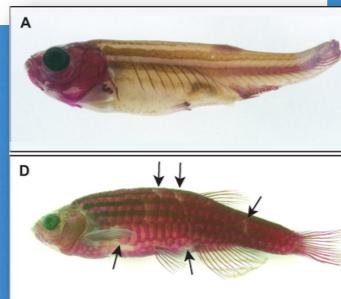
56. *Naked body*. A scaleless body is a derived condition in the ostariophysans. Most cypriniforms, characiforms and most primitive teleosts and gonorynchiforms possess scales on all or part of the body, while the majority of catfishes (including arids) and gymnotoids lack scales – although scales are often represented by ossified lateral lines (Fink and Fink 1981). Some Kailola (2004)

- 501,862 taxon phenotype annotations
- Curated from 4,732 characters in 2,474 species from 52 papers
- From ZFIN: 21,829 phenotype annotations about 3,893 genes

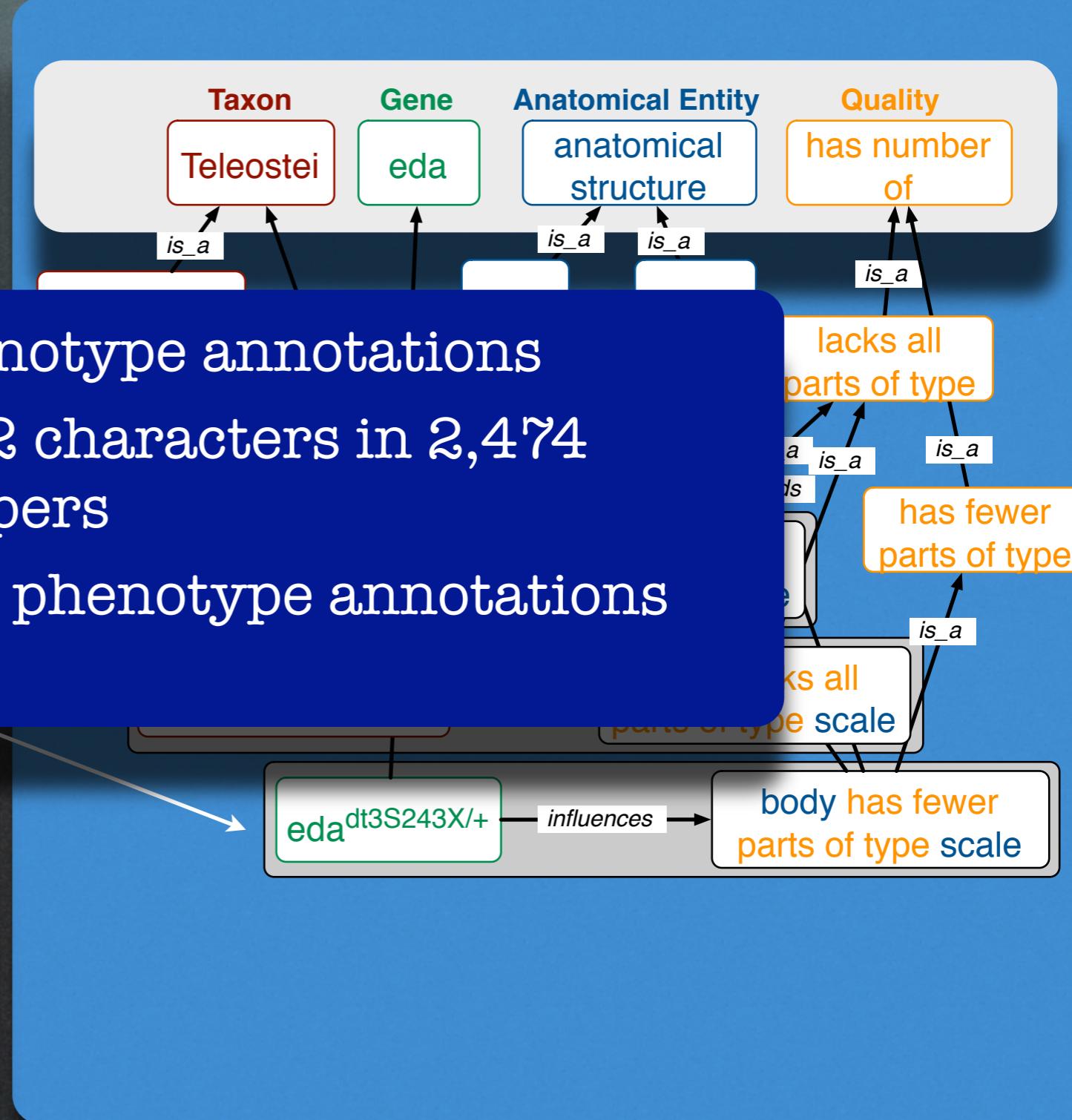
## mutant phen

Here, we describe the phenotypic and molecular characterization of mutants showing loss of the dermal skeleton, such as the rays of the fins and the scales, as well as the pharyngeal teeth. The mutations represent adult-viable, loss of function alleles in the *ectodysplasin* (*eda*) and *ectodysplasin receptor* (*edar*) genes.

Harris et al. (2008)



**EQ = body  
lacks all  
parts of type  
scale**



# Phenoscape Knowledgebase

Phenoscape Knowledgebase (BETA)

<http://kb.phenoscape.org/>

The Phenoscape Knowledgebase is currently in BETA testing - we would greatly value your feedback as we continue its development.

**BETA**

[Home](#) [Provide Feedback](#) [About](#) [Acknowledgments](#)

**Search the Phenoscape Knowledgebase**

basih|  matches, basihyal e names or

- basihyal bone**
- basihyal cartilage
- basihyal element
- basihyal tooth
- basihyal toothplate synonym for basihyal tooth plate
- basihyal tooth plate
- basihyoid synonym for basihyal bone

Anatomical entities Phenotype annotations to genes  
Phenotypic qualities Taxa  
Genes Genes  
Comparative publications Comparative publications

**Phenoscape News**

Third beta release of Phenoscape Knowledgebase 2.0 by Jim - Feb 07, 2011  
Phenoscape Knowledgebase 2.0 beta release 3 is now available at <http://kb.phenoscape.org/>. This version includes an enhanced ...

Introducing the Vertebrate Anatomy Ontology by wdahdul - Jan 12, 2011  
The Vertebrate Anatomy Ontology (VAO) was recently developed as a high-level, bridging ontology for existing and future single ...

Matching Phenotypes by pmidford - Dec 17, 2010  
An important goal for the Phenoscape project is to be

For further information about the Phenoscape project and project partners, please see our [project wiki](#).

The Knowledgebase currently contains 501,862 phenotype statements about 2,474 taxa, sourced from 52 publications, as well as 21,829 phenotype statements about 3,893 genes, retrieved from ZFIN. The data were last loaded into the Knowledgebase on 2011-02-10.



The Phenoscape Knowledgebase is currently in BETA testing - we would greatly value your feedback as we continue its development.

Site search:

Enter entity terms (e.g. basihyal bone), phenotypic qualities (e.g. shape, size), taxonomic names (e.g. Ictaluridae), gene names or symbols (e.g. cadherin 6, cdh6), or publications.

[Home](#) [Provide Feedback](#) [About](#) [Acknowledgments](#)

## Query for:

Phenotype annotations to taxa

### Taxon is:

*Ictalurus*

and

### Phenotype is:

Any

and

### Publication is:

Any

**Include inferred annotations**

[\[help\]](#)

[« Previous](#)

Results 1 - 20 of 2450

[Next »](#)

### Phenotype [\[help\]](#)

Taxon	Entity	Quality	Related Entity	Source
<i>Ictalurus australis</i>	posterior region of supraoccipital crest	bifid		
<i>Ictalurus australis</i>	process of occipital region	shape		
<i>Ictalurus australis</i>	facial foramen	position		
<i>Ictalurus australis</i>	pectoral fin spine	shape		
<i>Ictalurus australis</i>	anatomical margin of process of dorsal side of cranium	round		
<i>Ictalurus australis</i>	Weberian apparatus	depth		
<i>Ictalurus australis</i>	lateral ethmoid wing	increased length		
<i>Ictalurus australis</i>	frontal bone	structure	adductor mandibulae complex	
<i>Ictalurus australis</i>	epihyal-ceratohyal joint	cartilaginous		



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Site search:

Go

Enter entity terms (e.g. basihyal bone), phenotypic qualities (e.g. shape, size), taxonomic names (e.g. Ictaluridae), gene names or symbols (e.g. cadherin 6, cdh6), or publications.

[Home](#) [Provide Feedback](#) [About](#) [Acknowledgments](#)

### Query for:

Phenotype annotations to taxa

#### Taxon is:

*Ictalurus*

[Add](#)

and

#### Phenotype is:

mesethmoid bone • shape

[\[broaden/refine\]](#)

including parts

[Add](#)

and

#### Publication is:

Any

[Add](#)

[Include inferred annotations](#)

[\[help\]](#)

[Apply Filter](#)[« Previous](#)

Results 1 - 11 of 11

[Next »](#)

#### Phenotype [\[help\]](#)

Taxon	Entity	Quality	Related Entity	Source
<i>Ictalurus australis</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus balsanus</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus dugesii</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus furcatus</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus lupus</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus meridionalis</i>	mesethmoid bone	shape		
<i>Ictalurus mexicanus</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus pricei</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus punctatus</i>	mesethmoid cornu	bifurcated		
<i>Ictalurus punctatus</i>	mesethmoid bone	shape		
<i>Ictalurus punctatus</i>	medial region of anterior margin of mesethmoid bone	notched		



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Site search:



Enter entity terms (e.g. basihyal bone), phenotypic qualities (e.g. shape, size), taxonomic names (e.g. Ictaluridae), gene names or symbols (e.g. cadherin 6, cdh6), or publications.

[Home](#) [Provide Feedback](#) [About](#) [Acknowledgments](#)

## Query for:

Phenotype annotations

## Taxon is:

Ictalurus

and

## Phenotype is:

mesethmoid bone

[broaden/refine]

 including parts

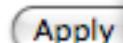
and

## Publication is:

Any

 Include inferred

[help]

[« Previous](#)

## mesethmoid bone

**Source:** Teleost Anatomy Ontology**Synonyms:** ethmoid**Definition:** Endochondral bone that extends forward from the frontal bones and articulates posterolaterally with the lateral ethmoids and the vomer and parasphenoid ventrally. The mesethmoid is an unpaired median bone.**ID:** TAO:0000323**overlaps:** mesethmoid-frontal joint, mesethmoid-lateral ethmoid joint, mesethmoid-nasal joint, mesethmoid-premaxillary joint, mesethmoid-vomer joint, neurocranium**develops from:** ethmoid cartilage, neurocranial trabecula**is part of:** chondrocranium, olfactory region**is a type of:** endochondral bone**may have part:** lateral mesethmoid wing, mesethmoid cornu, mesethmoid ventral diverging lamella[View details for mesethmoid bone](#)

Results 1 - 11 of 11

[Next »](#)

Phenotype <small>[help]</small>			
Entity	Quality	Related Entity	Source
mesethmoid cornu	bifurcated		
<a href="#">mesethmoid bone</a>	shape		
mesethmoid cornu	bifurcated		
mesethmoid cornu	bifurcated		
mesethmoid cornu	bifurcated		
mesethmoid bone	shape		
region of anterior margin of mesethmoid bone	notched		



The Phenoscape Knowledgebase is currently in BETA testing - we would greatly value your feedback as we continue its development.

Site search:

Go

## Source Data

### *Ictalurus australis*

anatomical margin of process of dorsal side of cranium

round

**Query for:**

## Phenotype annotation

## Taxon is:

Ictalurus 

and

**Phenotype is:**

**Any**

and

**Publication is:**

Any

## Include infer

[help]

ADE

## *Ictalurus australis*

frontal bone

## structure

## adductor mandibulae complex

## *Ictalurus australis*

epihyal-ceratohyal joint

**cartilaginous**



# publication: Lundberg 1992

source: Phenoscape-annotated publications

[Overview](#)[Data Matrix](#)[Specimens](#)

Original character-by-taxon data matrix from publication **Lundberg 1992**. You can also query for all phenotype annotations curated from this matrix.

	1. Posterior flap of adipose fin	2. Gill membranes	3. Orbital rim	4. Caudal fin
<i>Amelurus brunneus</i>	free from back and caudal fin	divergent	free	scarcely emarginate to rounded
<i>Amelurus catus</i>	free from back and caudal fin	divergent	free	forked with rounded lobes
<i>Amelurus melas</i>	free from back and caudal fin	divergent	free	scarcely emarginate to rounded
<i>Amelurus natalis</i>	free from back and caudal fin	divergent	free	scarcely emarginate to rounded
<i>Amelurus nebulosus</i>	free from back and caudal fin	divergent	free	scarcely emarginate to rounded
<i>Amelurus platycephalus</i>	free from back and caudal fin	divergent	free	scarcely emarginate to rounded
<i>Amelurus serracanthus</i>	free from back and caudal fin	divergent	free	scarcely emarginate to rounded
<i>Ictalurus australis</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus balsanus</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus dugesii</i> as <i>Ictalurus dugesi</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus furcatus</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus lupus</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus mexicanus</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus pricei</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Ictalurus punctatus</i>	free from back and caudal fin	divergent	free	forked with pointed lobes
<i>Noturus flavus</i>	adnate to back and broadly joined to caudal fin	divergent	united to cornea, eye subcutaneous	scarcely emarginate to rounded
<i>Noturus insignis</i>	adnate to back and broadly joined to caudal fin	divergent	united to cornea, eye subcutaneous	scarcely emarginate to rounded
<i>Noturus stigmosus</i>	adnate to back and partly joined to caudal fin	divergent	united to cornea, eye subcutaneous	scarcely emarginate to rounded
<i>Priatella phreatophila</i>	adnate to back and broadly joined to caudal fin	divergent	?	scarcely emarginate to rounded



# publication: Lundberg 1992

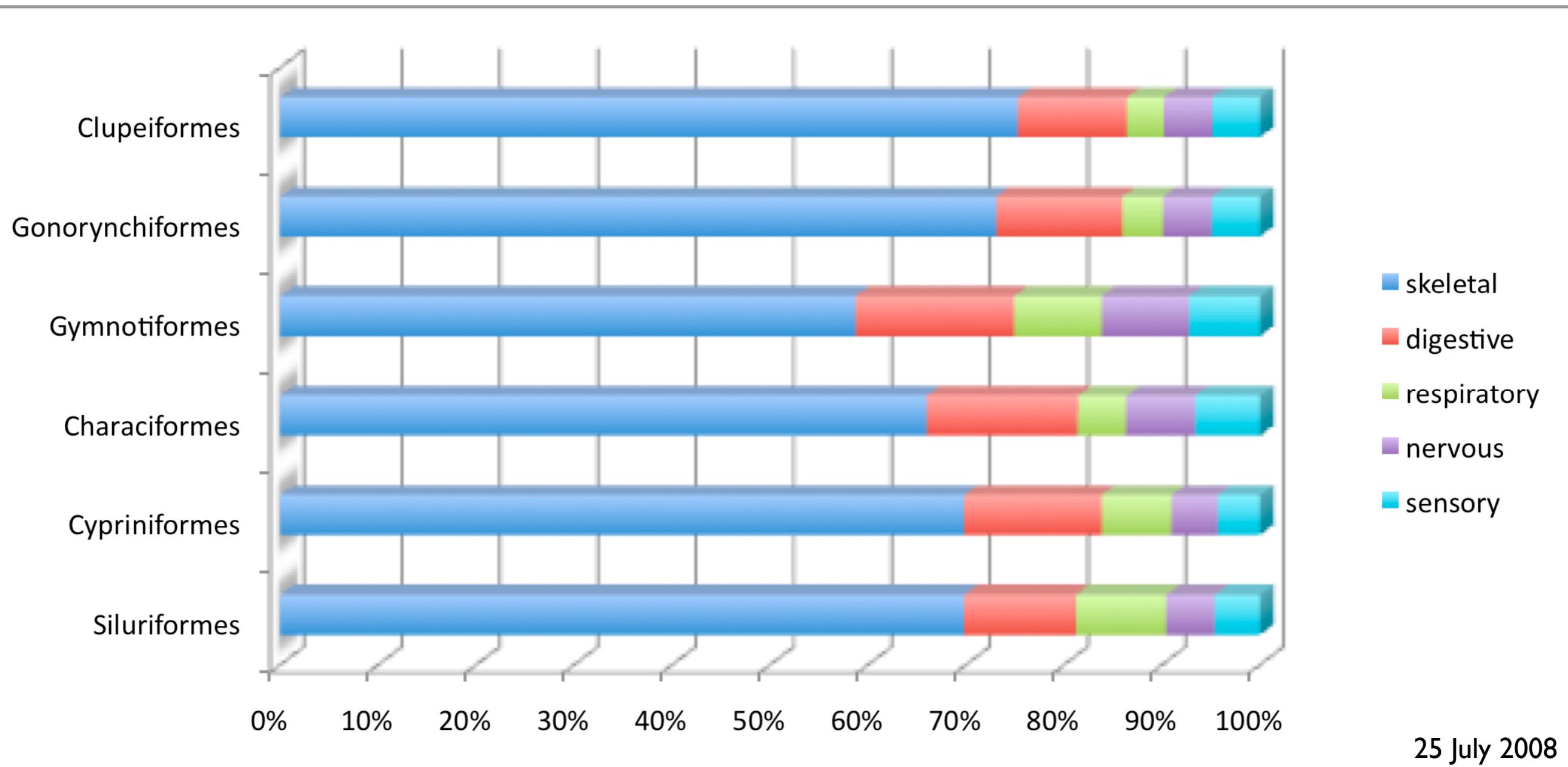
source: Phenoscape-annotated publications

[Overview](#)[Data Matrix](#)[Specimens](#)

## Taxa and specimens used in this study

Taxon name used in publication	Valid taxon	Specimens	Comment
<i>Noturus nocturnus</i>	<i>Noturus nocturnus</i>	<a href="#">UMMZ 165883</a> , <a href="#">UMMZ 167214</a>	
<i>Satan eurystomus</i>	<i>Satan eurystomus</i>		WMM not in collection code list
<i>Noturus flavus</i>	<i>Noturus flavus</i>	<a href="#">UMMZ 126366</a> , <a href="#">UMMZ 126365</a> , <a href="#">UMMZ 182039</a> , <a href="#">UMMZ 111724</a> , <a href="#">UMMZ 165852</a> , <a href="#">UMMZ 165842</a> , <a href="#">UMMZ 165833</a> , <a href="#">UMMZ 189178</a>	
<i>Ictalurus lupus</i>	<i>Ictalurus lupus</i>	<a href="#">UMMZ 169619</a> , <a href="#">UMMZ 17????4</a> , <a href="#">UMMZ 186503</a> , <a href="#">UMMZ 179822</a>	One of the specimen ID numbers for UMMZ was partially unreadable. I replaced the unreadable numbers with question marks.
<i>Pylodictis olivaris</i>	<i>Pylodictis olivaris</i>	<a href="#">UMMZ 186652</a> , <a href="#">UMMZ 173452</a> , <a href="#">UMMZ 169029</a> , <a href="#">UMMZ 103107</a> , <a href="#">UMMZ 152549</a> , <a href="#">UMMZ 160732</a> , <a href="#">UMMZ 170129</a> , <a href="#">UMMZ 97069</a> , <a href="#">UMMZ 186266</a>	
		<a href="#">UW 3276</a> , <a href="#">UW 3275</a> , <a href="#">AMNH 9499</a> , <a href="#">USNM 3983</a> , <a href="#">USNM 3982</a> , <a href="#">USNM 3981</a> , <a href="#">USNM 3985</a> , <a href="#">USNM 8122</a> , <a href="#">AMNH 6387</a> , <a href="#">AMNH 6388</a> , <a href="#">USNM 167588</a> , <a href="#">USNM 167590</a> , <a href="#">USNM 167590</a> , <a href="#">USNM 2170</a>	PF not in list of

# Major taxonomic groups have similar distribution of entities among phenotypes



# Some notable differences for skeletal characters

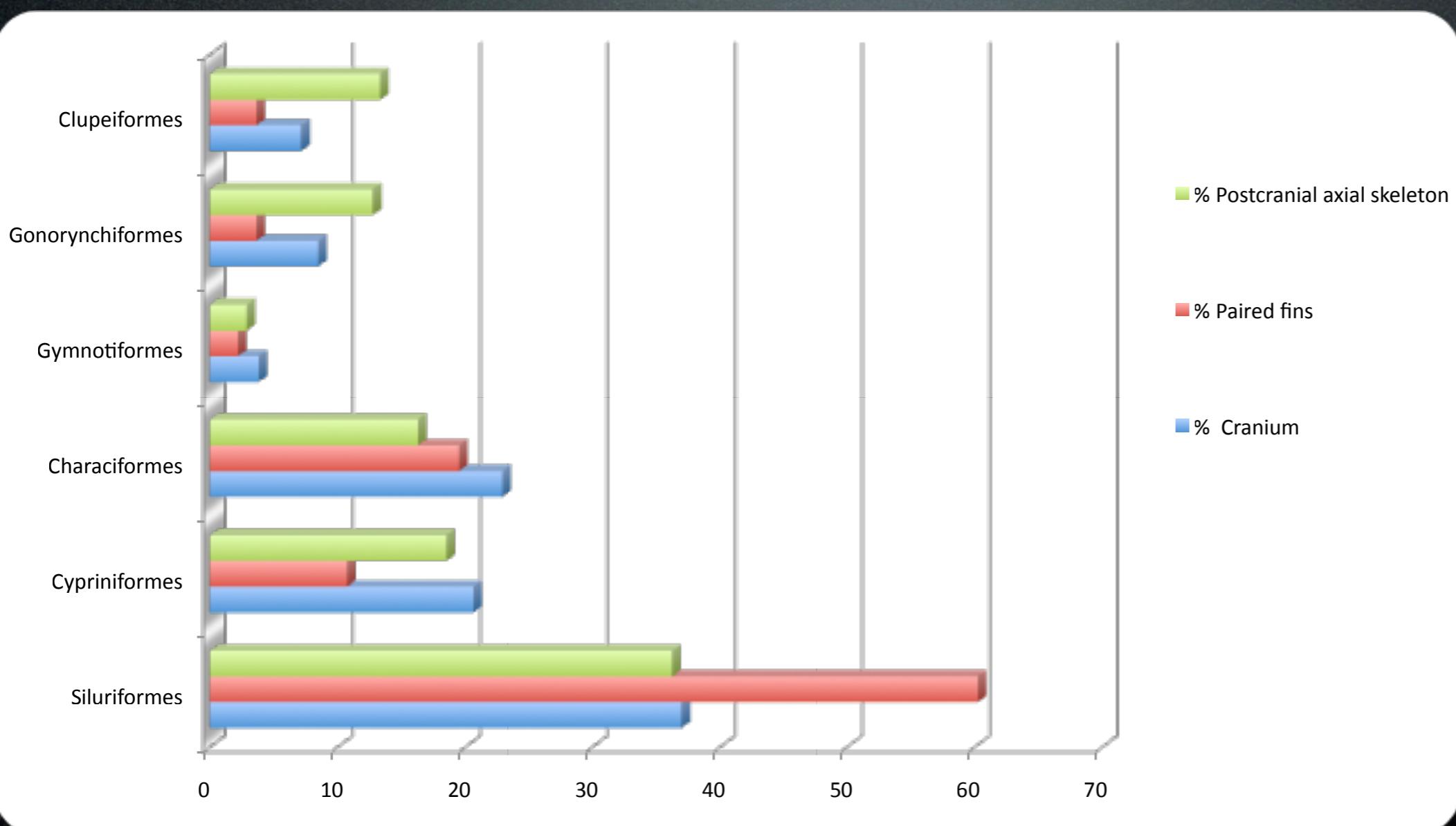
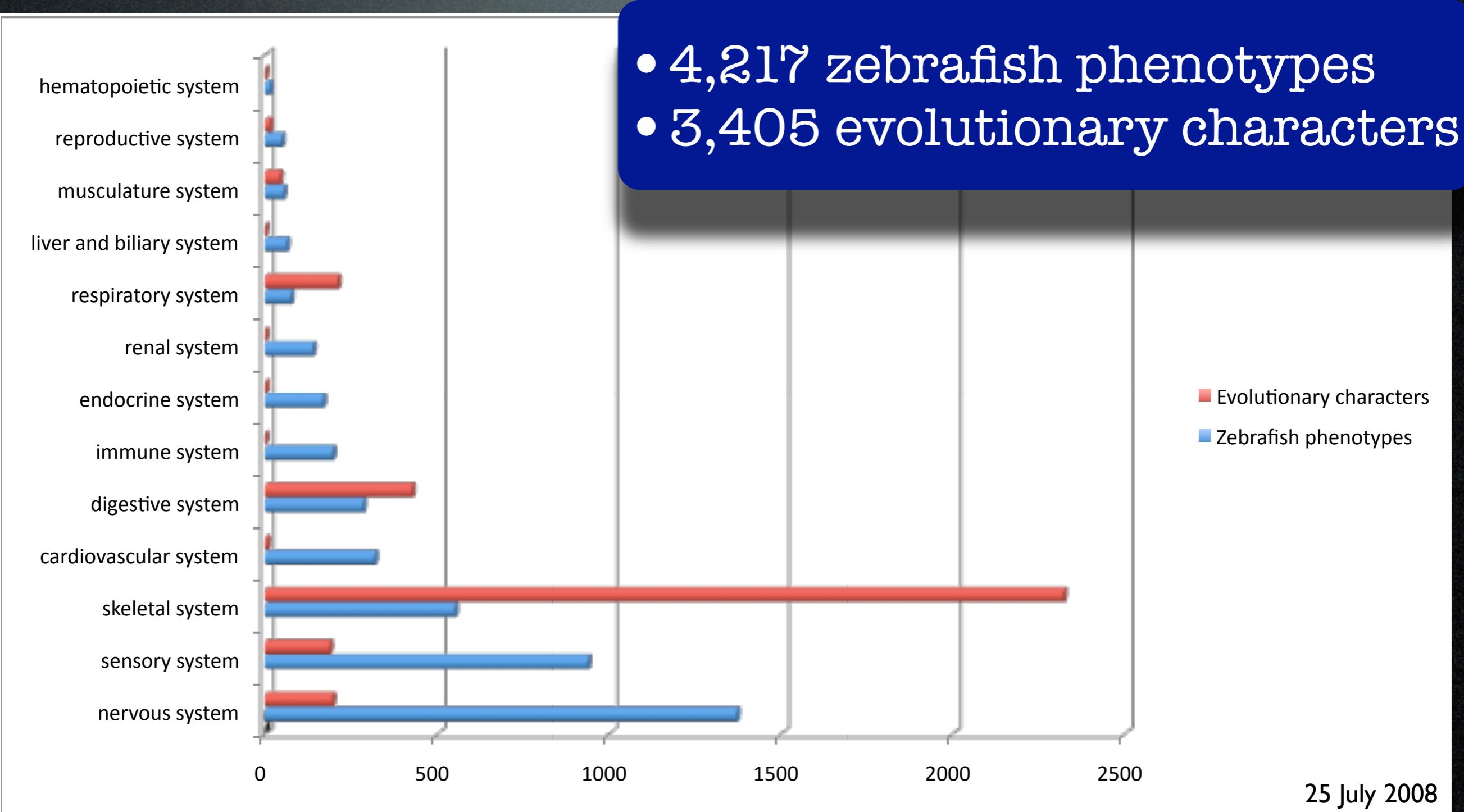


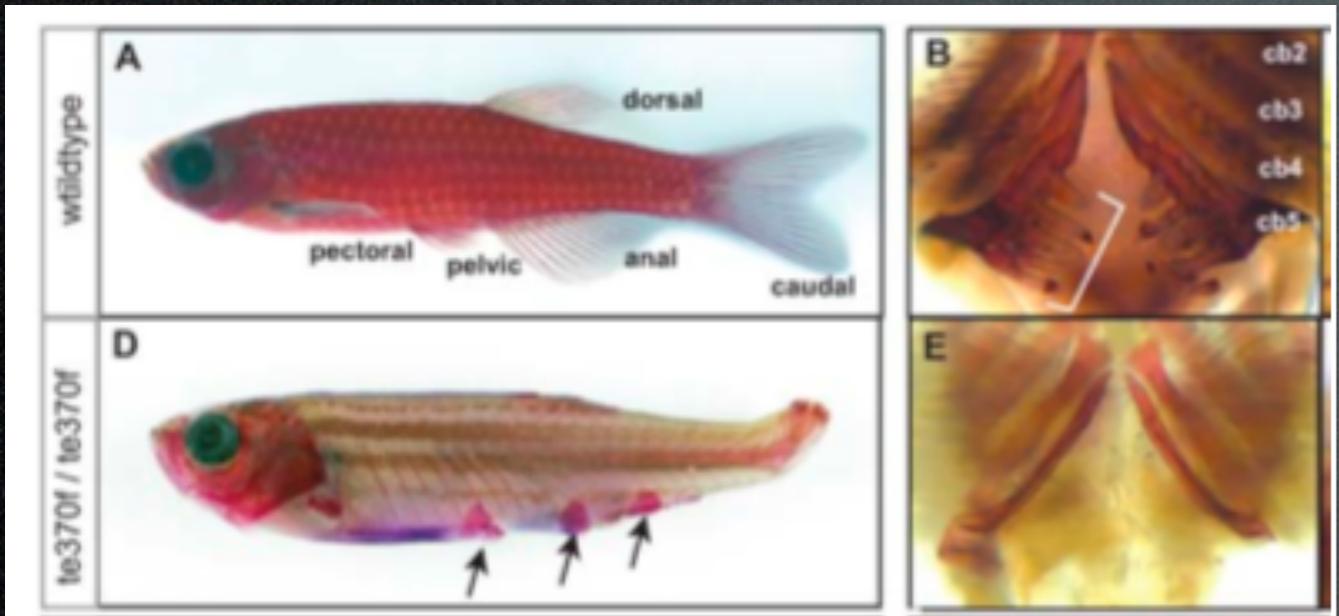
Image from Sabaj-Perez

# Substantial overlap between model organism and evolutionary phenotypes



# Hypothesis generation: Genetic basis for scale loss in Siluriformes

Mutation of *eda* gene  
in *Danio*:



Harris et al., 2007

*Ictalurus punctatus*:

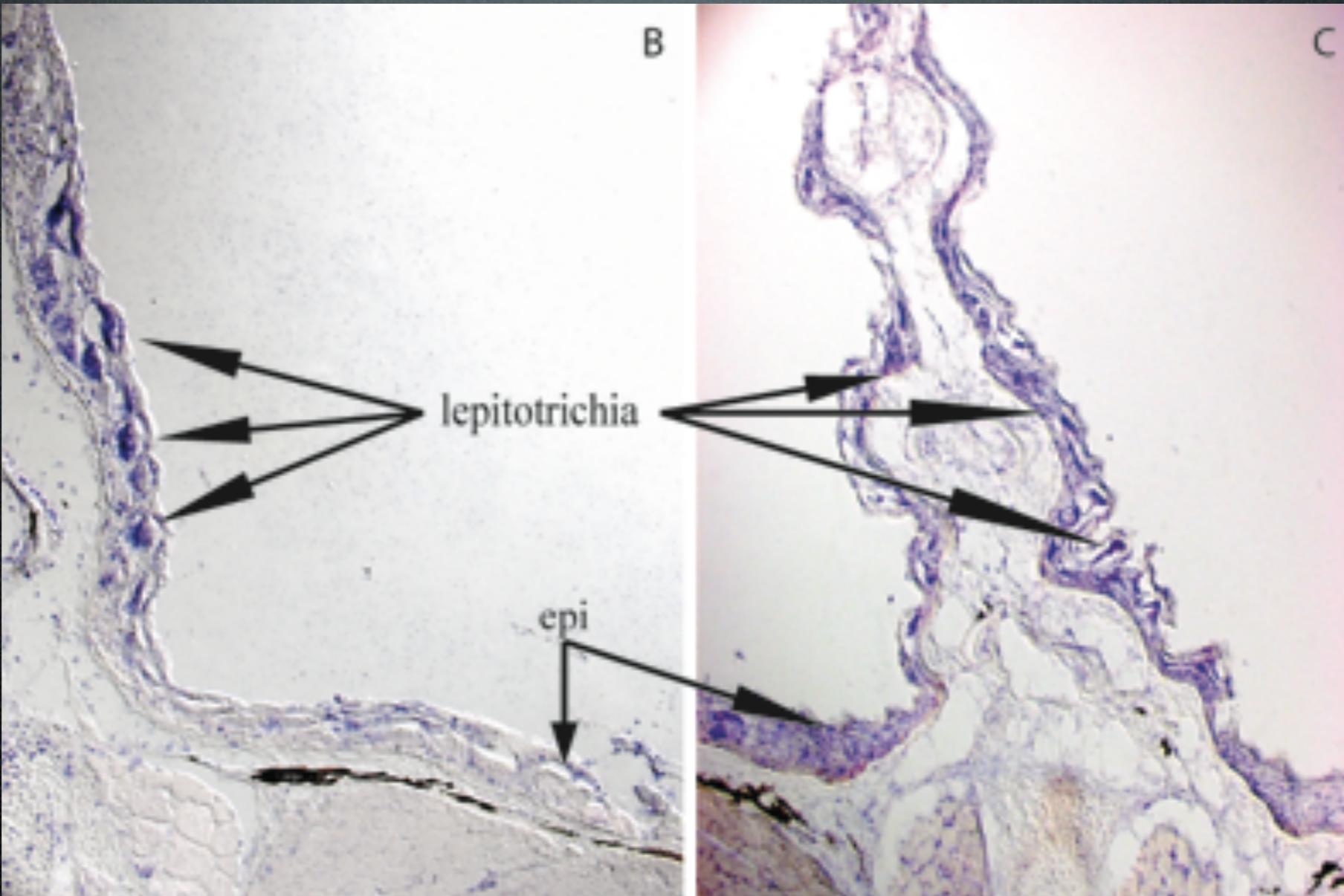


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# Wet lab test

(Work by Richard Edmunds)

*Ictalurus punctatus*



*eda* expression is lacking in the epidermis

# Hypothesis generation: Genetic basis for absence of the basihyal bone in Siluriformes

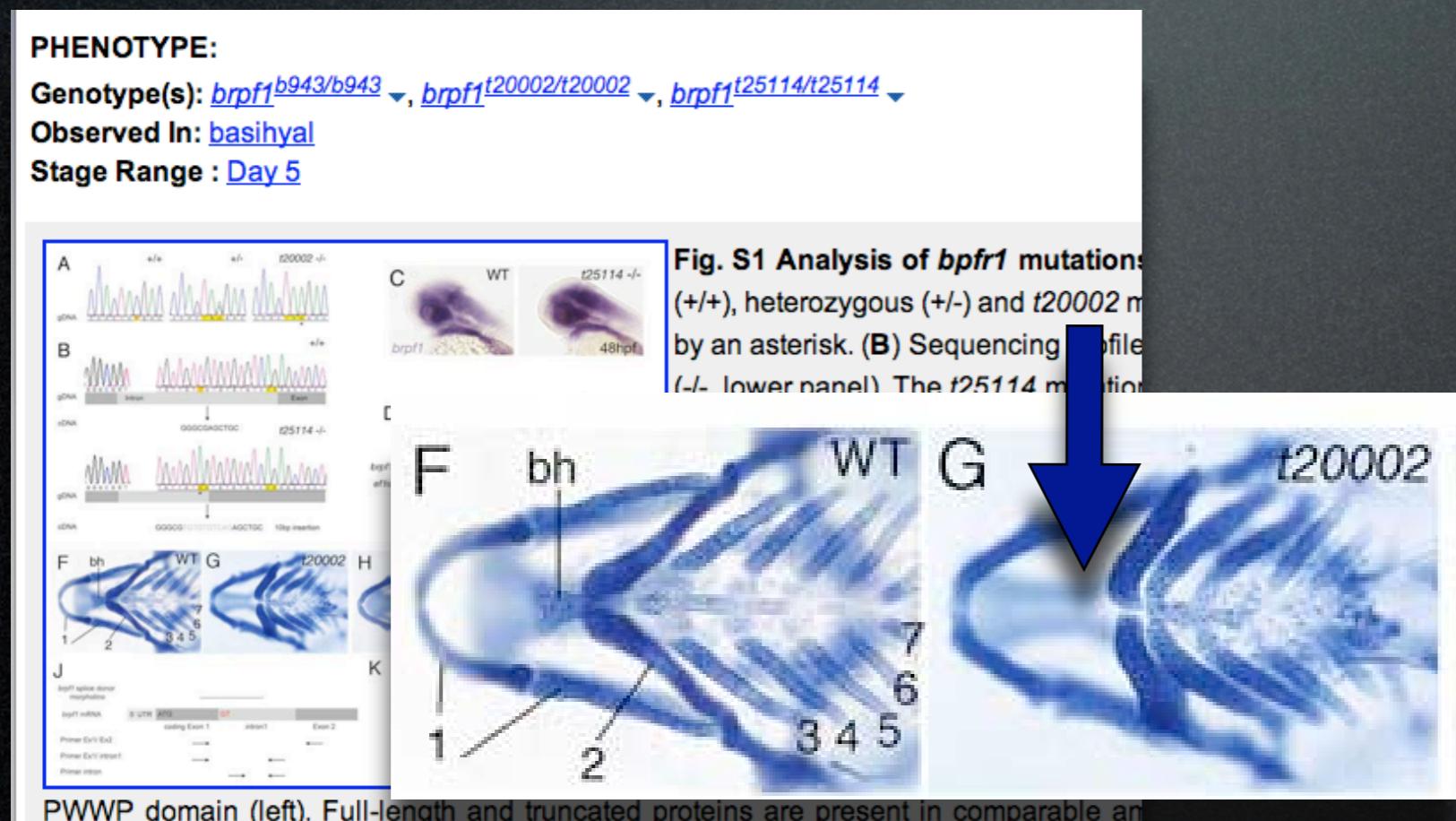
Mutation of *brpf1* gene  
in *Danio*:

## PHENOTYPE:

Genotype(s): [brpf1<sup>b943/b943</sup>](#), [brpf1<sup>t20002/t20002</sup>](#), [brpf1<sup>t25114/t25114</sup>](#)

Observed In: basihyal

Stage Range : Day 5



Laue et al (2008)

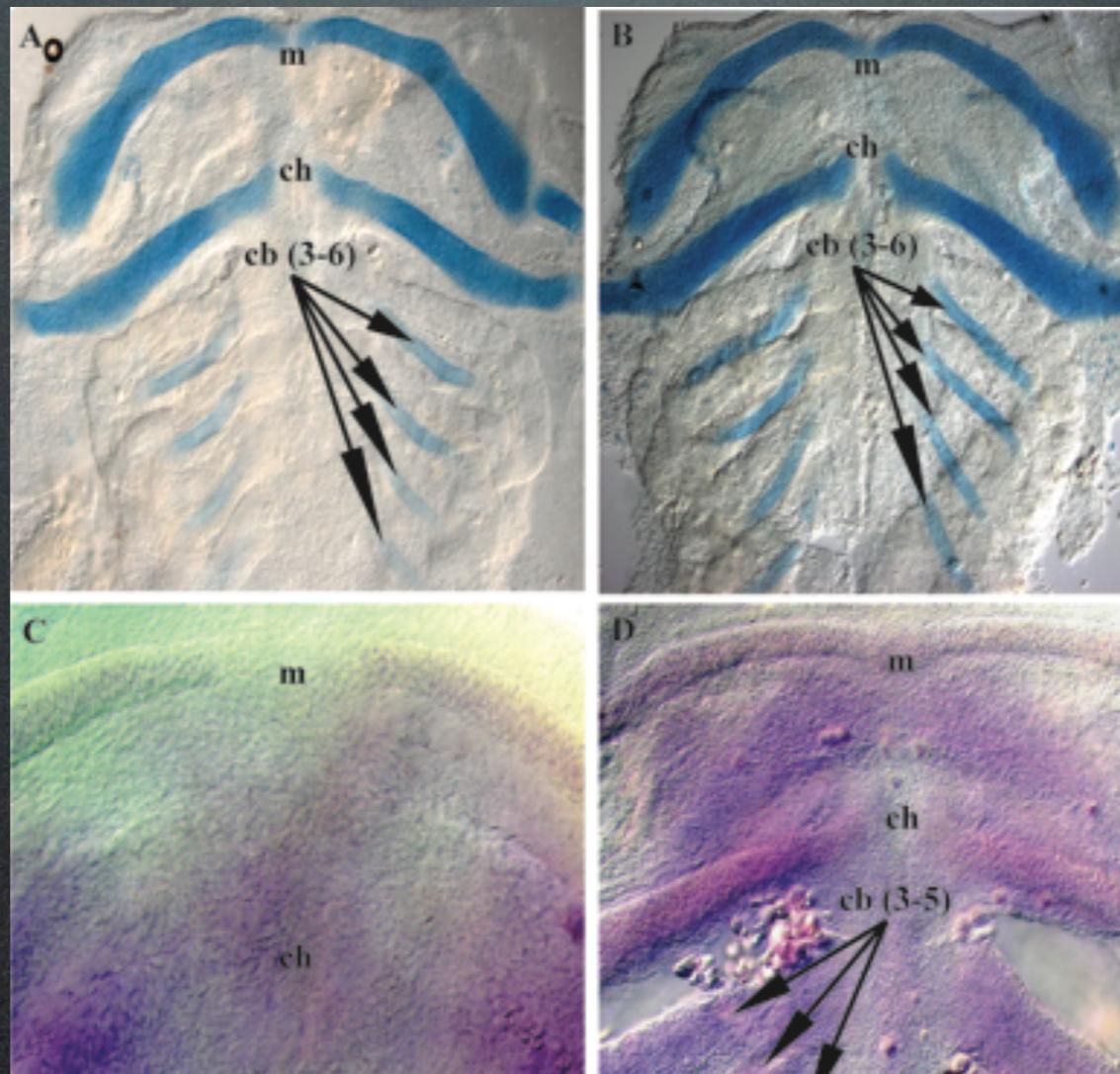
*Ictalurus punctatus*:



# Wet lab test

(Work by Richard Edmunds)

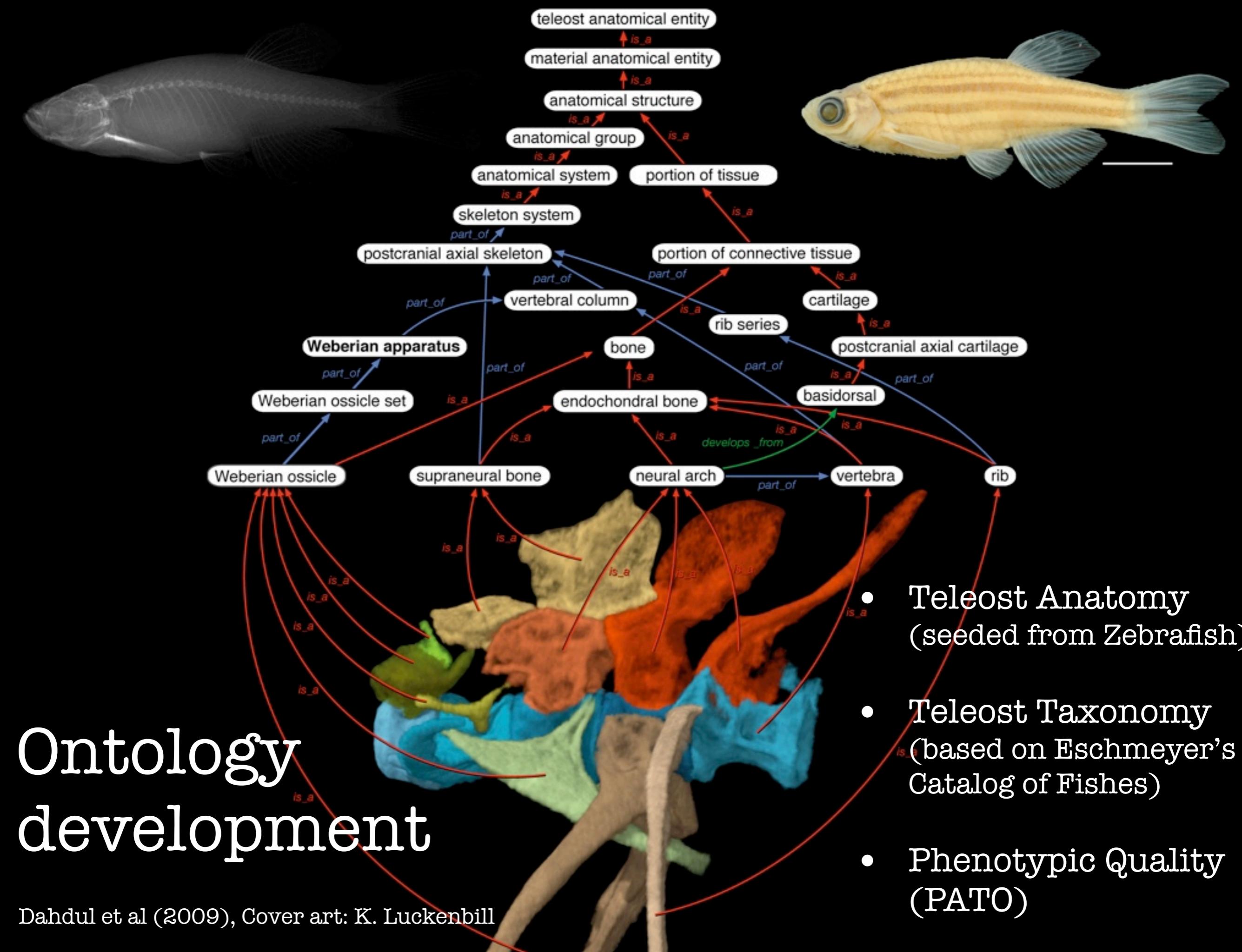
*Ictalurus punctatus*



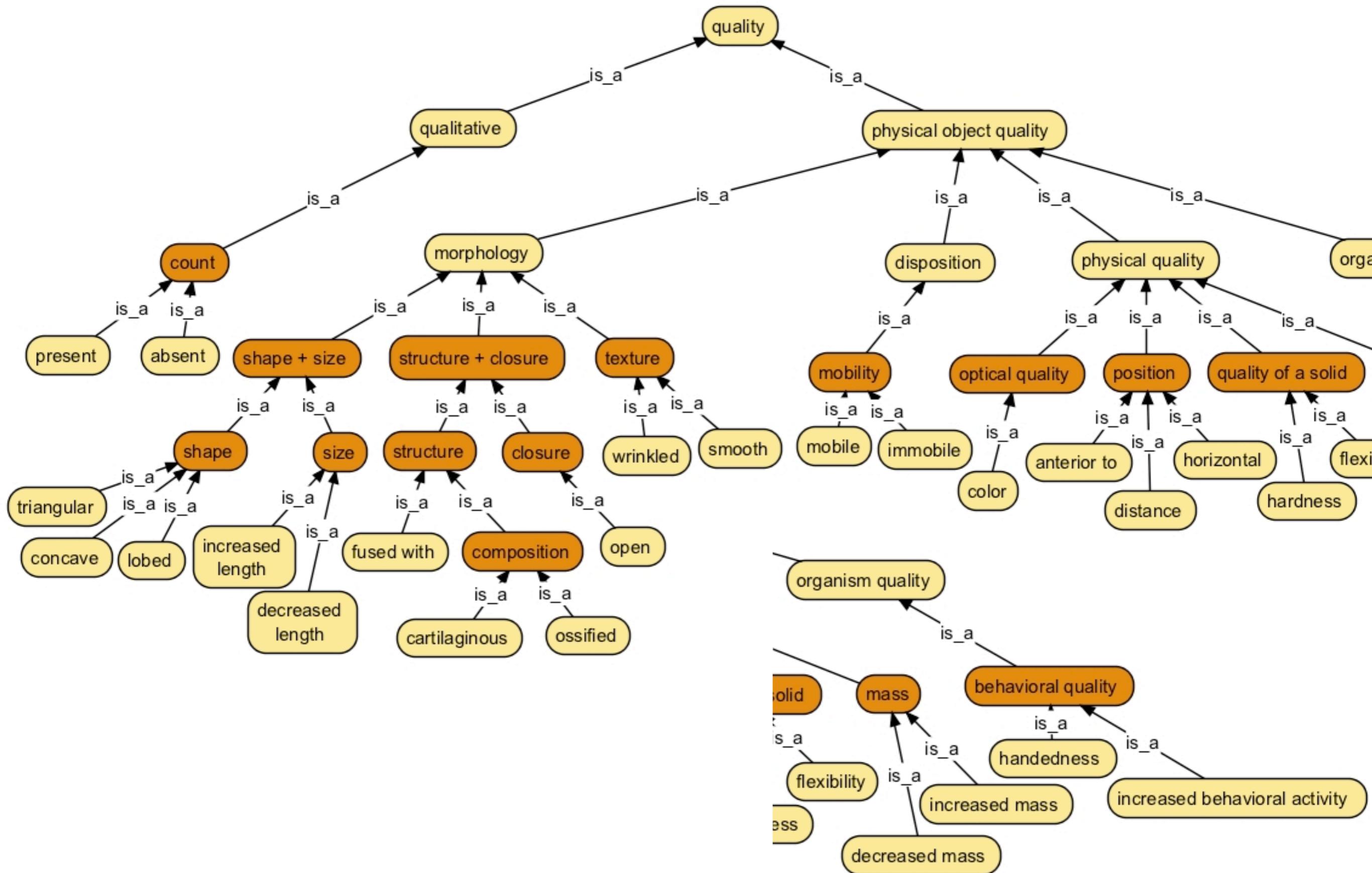
*brpf1* lacks expression in the basihyal

# The parts to make this work

- Ontologies that capture the knowledge domains
- Efficient data curation workflow
- Expressive and scalable inference engine



# Making PATO usable for evolutionary data



# Getting ontologies right is a challenge

- What is the right axis of classification?
  - Structure versus function
  - Relational vs monadic qualities
  - PATO: shape and size vs natural language  
"Interopercle shape: expanded posteroventrally"
- Different ways to observe or generate a phenotypic quality
  - Color as color hue (radiation quality) or pigmentation (structural quality)
  - Relative sizes don't have a universal reference

# Curation

Dahdul et al., 2010 PLoS ONE



1. Students:  
gather publications  
(scan hard copies,  
produce OCR PDFs)



The Phylogeny of Ictalurid Catfishes:  
A Synthesis of Recent Work

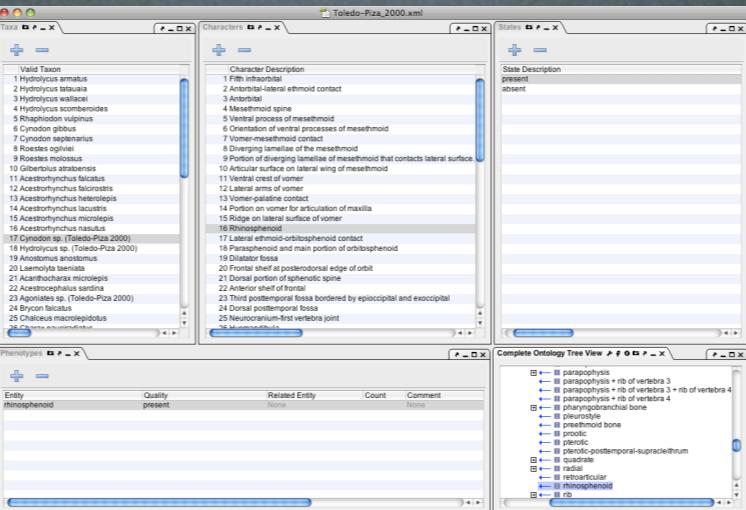
John G. Lundberg

ting evolutionary patterns and problems for hat ictalurids originated and diversified only s autochthony restricts the number of paleo-influenced their history. Their relatively good metric framework, provides minimum ages of evolutionary novelties, and, thereby, estimates of fishes present an ample diversity of ecologic variation of adult body sizes (from about 50 and habitat preferences (from large rivers to on channels). The independent evolution of species within the family also offers a special situation. Furthermore, the highly uneven phylogenetic distribution of characters among genera raises interesting evolutionary questions and/or extinction. An understanding of these is central to the investigation of these and evolutionary history.

about 50 living species of North American catfishes, and fossils record at least 14 extinct species and one extinct, plesiomorphic genus. Ictalurid diversity at the generic and species levels includes: *Astephus*—two extinct species; *Ictalurus*—about eight extant and four extinct species; *Ameiurus*—seven extant and seven extinct species; *Noturus*—25 extant species; *Pylodictis*, *Priacanthus*, *Satan*, and *Troglomimus*—each with one extant species.

Total ictalurid diversity is approximately 100 extant and 20 fossil species.

2. Students:  
Manual entry of free  
text character  
descriptions, matrix,  
taxon list, specimens  
and museum numbers  
using **Phenex**



3. Character  
annotation by experts:  
Entry of phenotypes  
and homology  
assertions using  
**Phenex**

PHENOSCAPE

Search the Phenoscape Knowledgebase

The Phenoscape Knowledgebase uses ontologies to integrate phenotypic data from genetic studies of zebrafish with evolutionary variable phenotypes from the systematic literature of ostariophysan fishes. Users can explore the data by searching for anatomical terms, taxa, or gene names.

The Knowledgebase currently contains 333,987 phenotype statements about 2310 taxa, sourced from 51 publications, as well as 11,267 phenotype statements about 2953 genes, retrieved from ZFIN.

Type at least 4 characters to choose a search term from the popup menu. If there are many matches, the autocomplete menu may take a few seconds to respond.

Most frequently used terms (anatomy, taxon, gene):

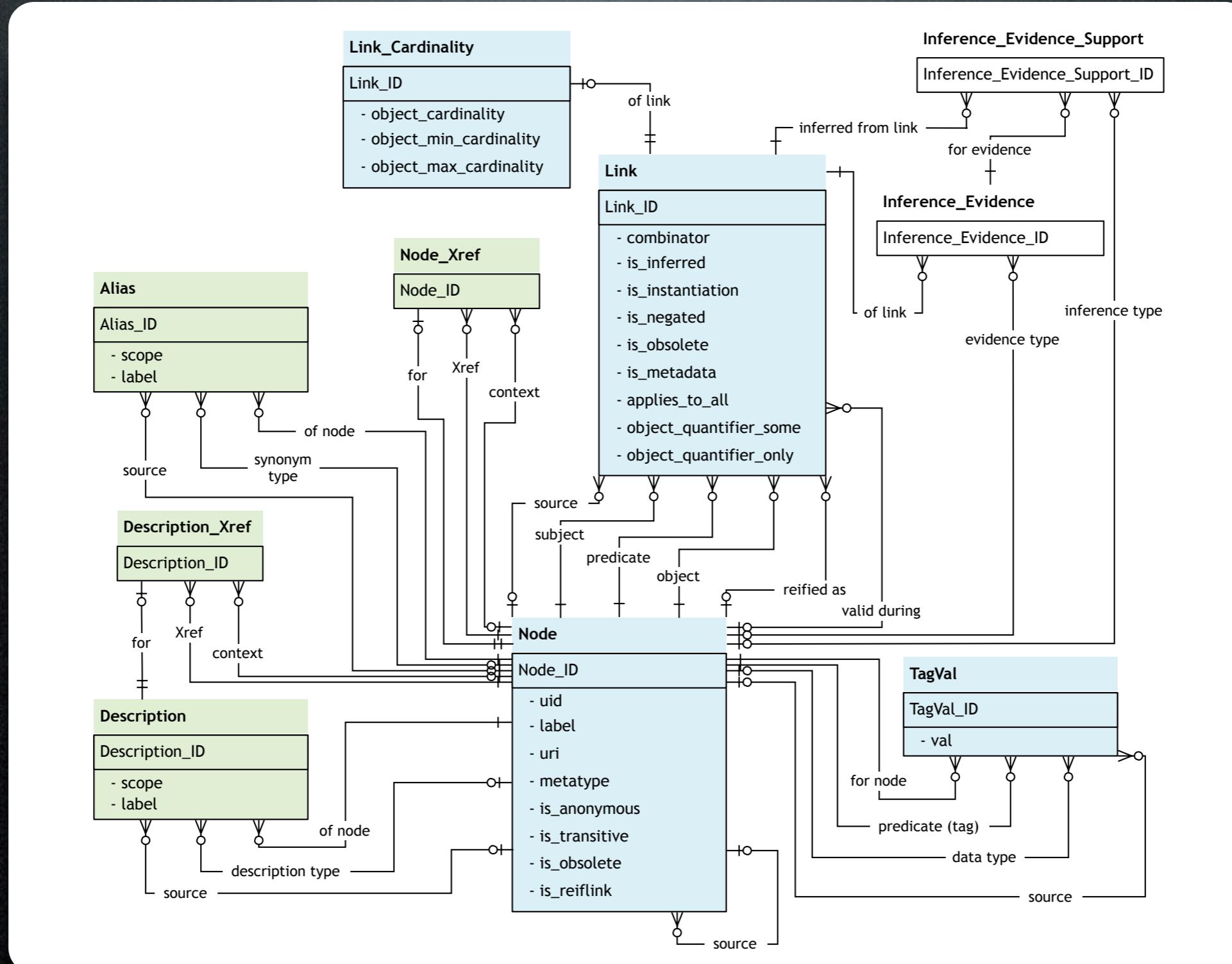
- ache shrt1 Amblyopsis mangoi Amelius nebulosus Amphilius asteueanus anterior limb of parapophysis 4 Antoploscelis apodus Apodus apodus Autoploscelis bernardi
- autopalatine Chrysichthys au epibranchial 2 element Ictalurus punctatus infr
- mib mycbp2 Mystus posterior process of basipt

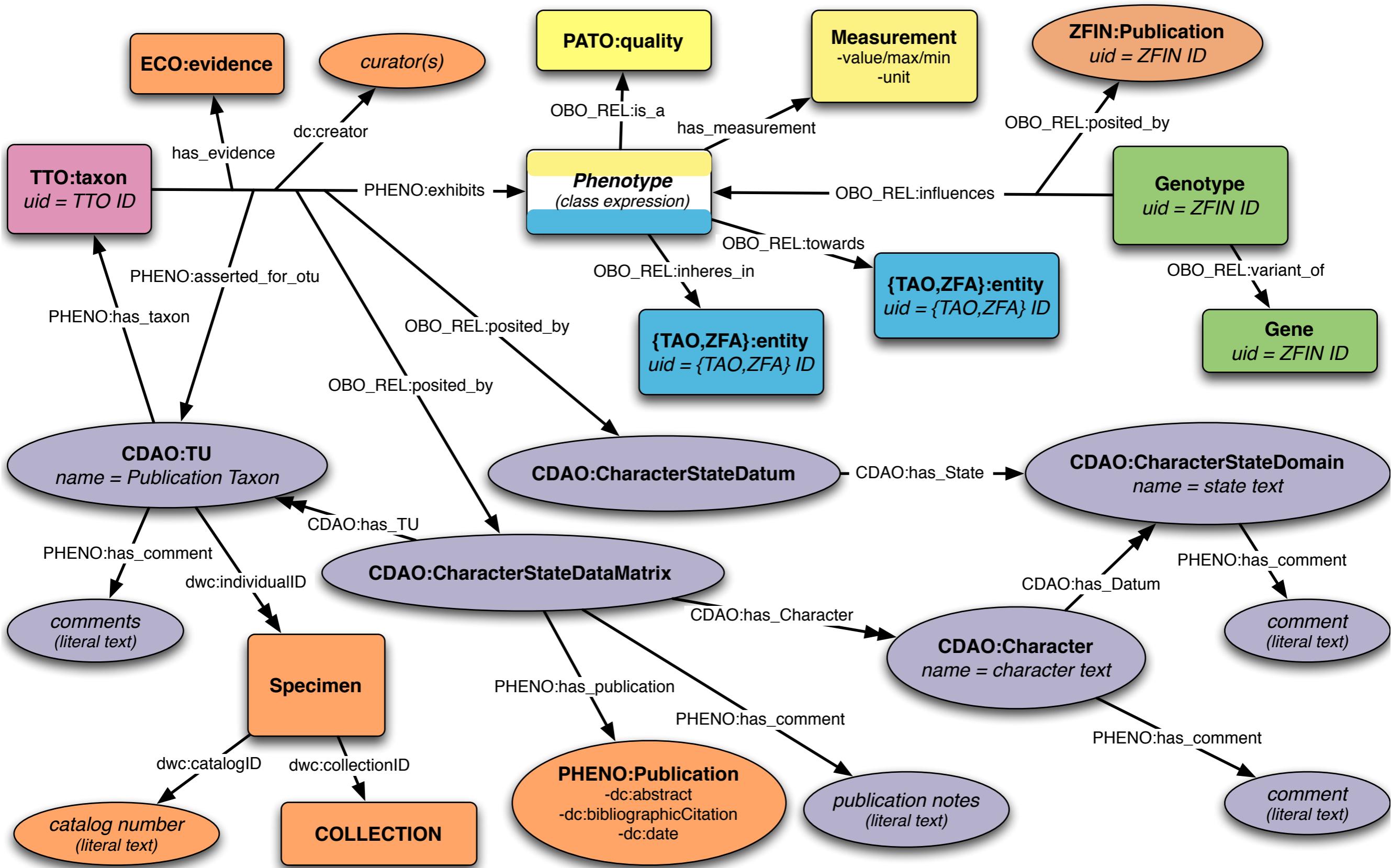
Curators:  
Wasila Dahdul  
Miles Coburn  
Jeff Engeman  
Terry Grande  
Eric Hilton  
John Lundberg  
Paula Mabee  
Richard Mayden  
Mark Sabaj Pérez

4. Consistency  
checks, upload of  
data to public view of  
Phenoscape KB

# KB is based on OBD (Ontology-Based Database)

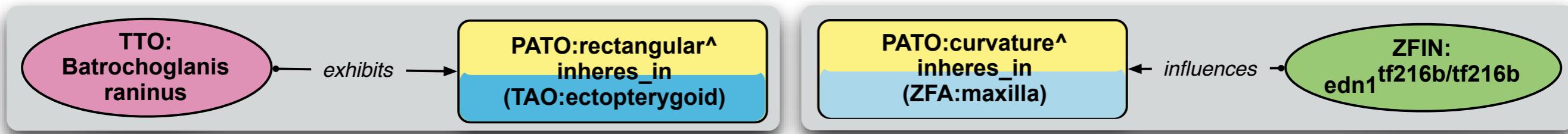
(C. Mungall, LBL)



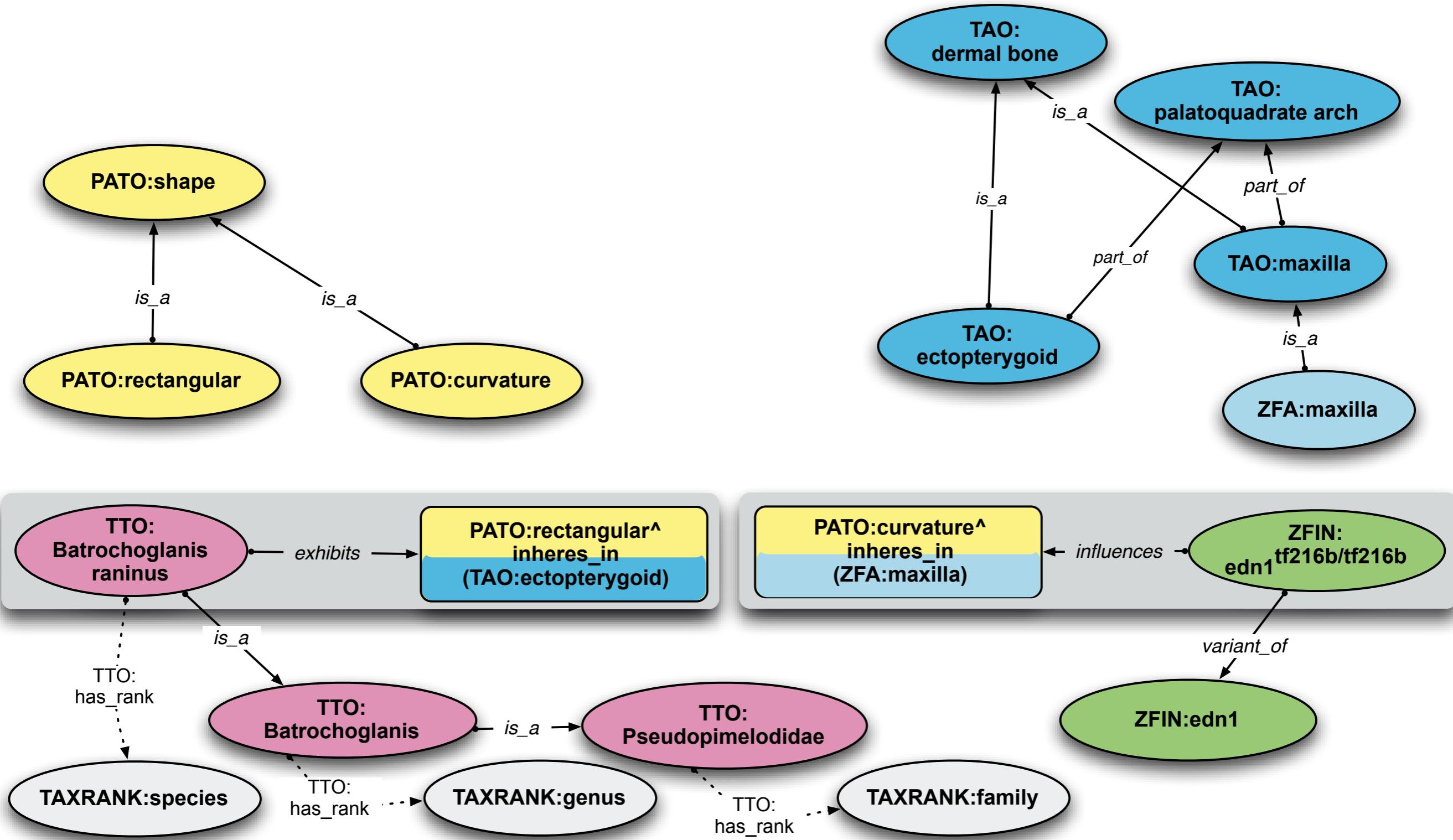


# How does reasoning work?

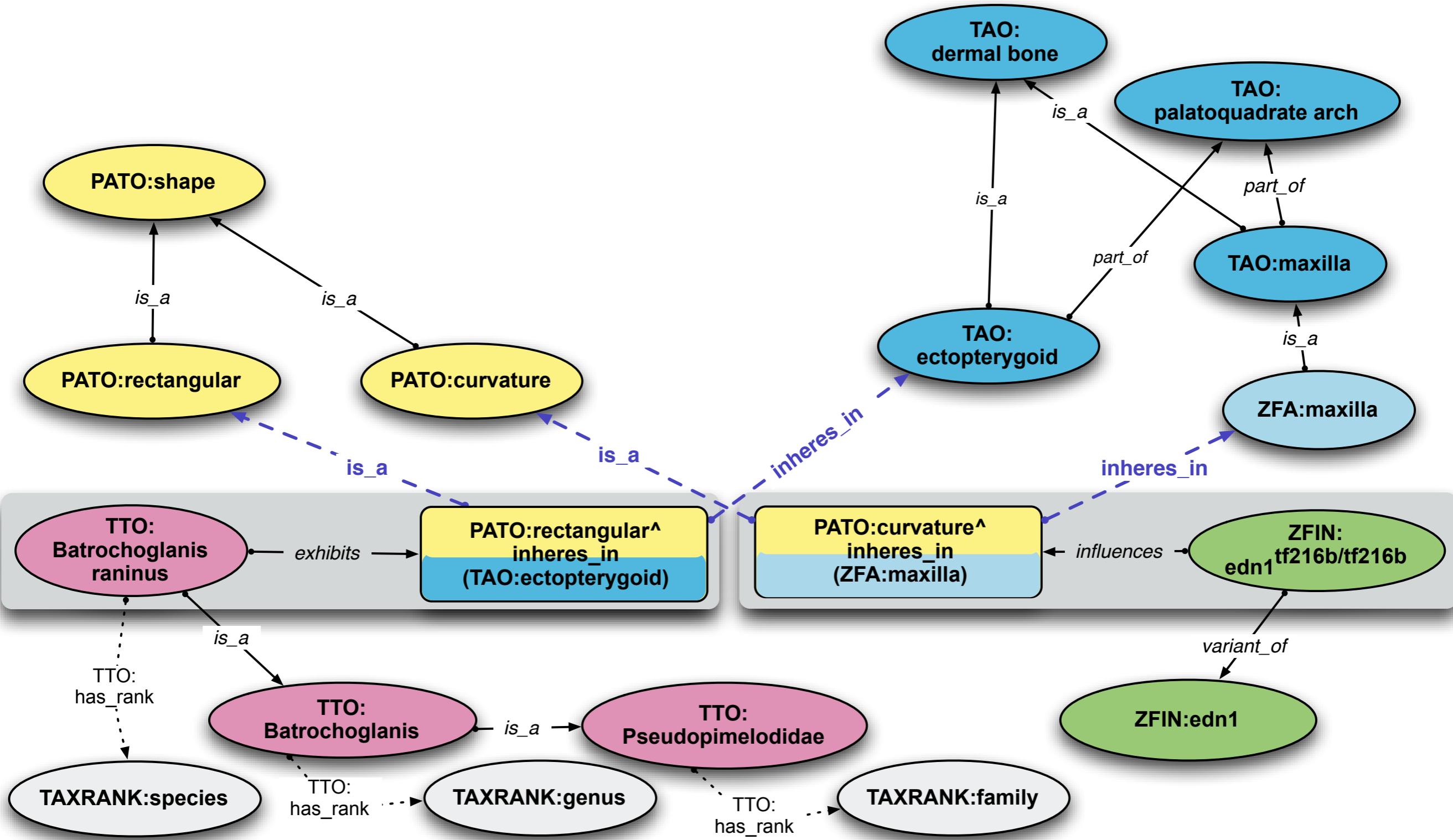
# How does reasoning work?



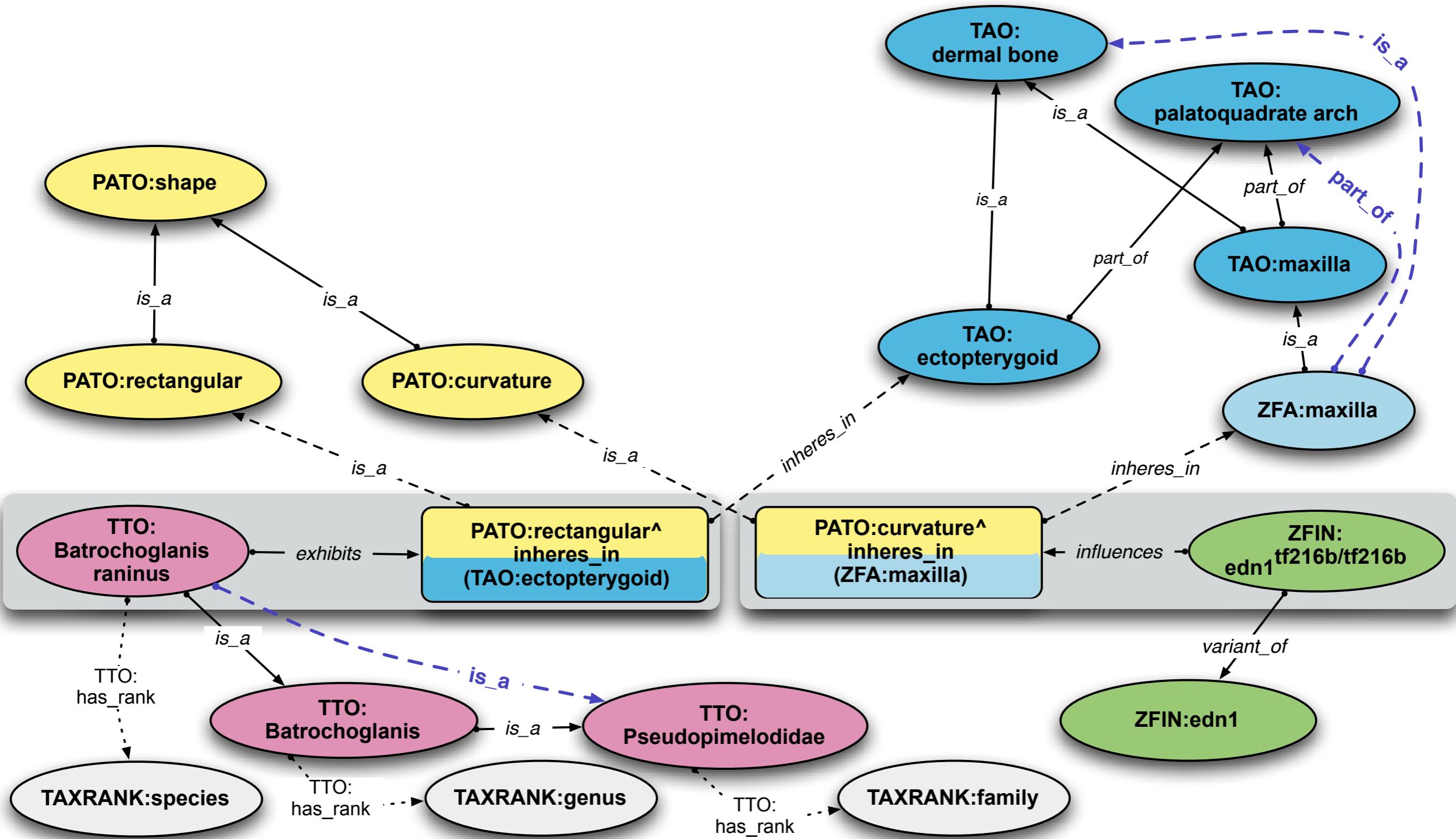
# How does reasoning work?



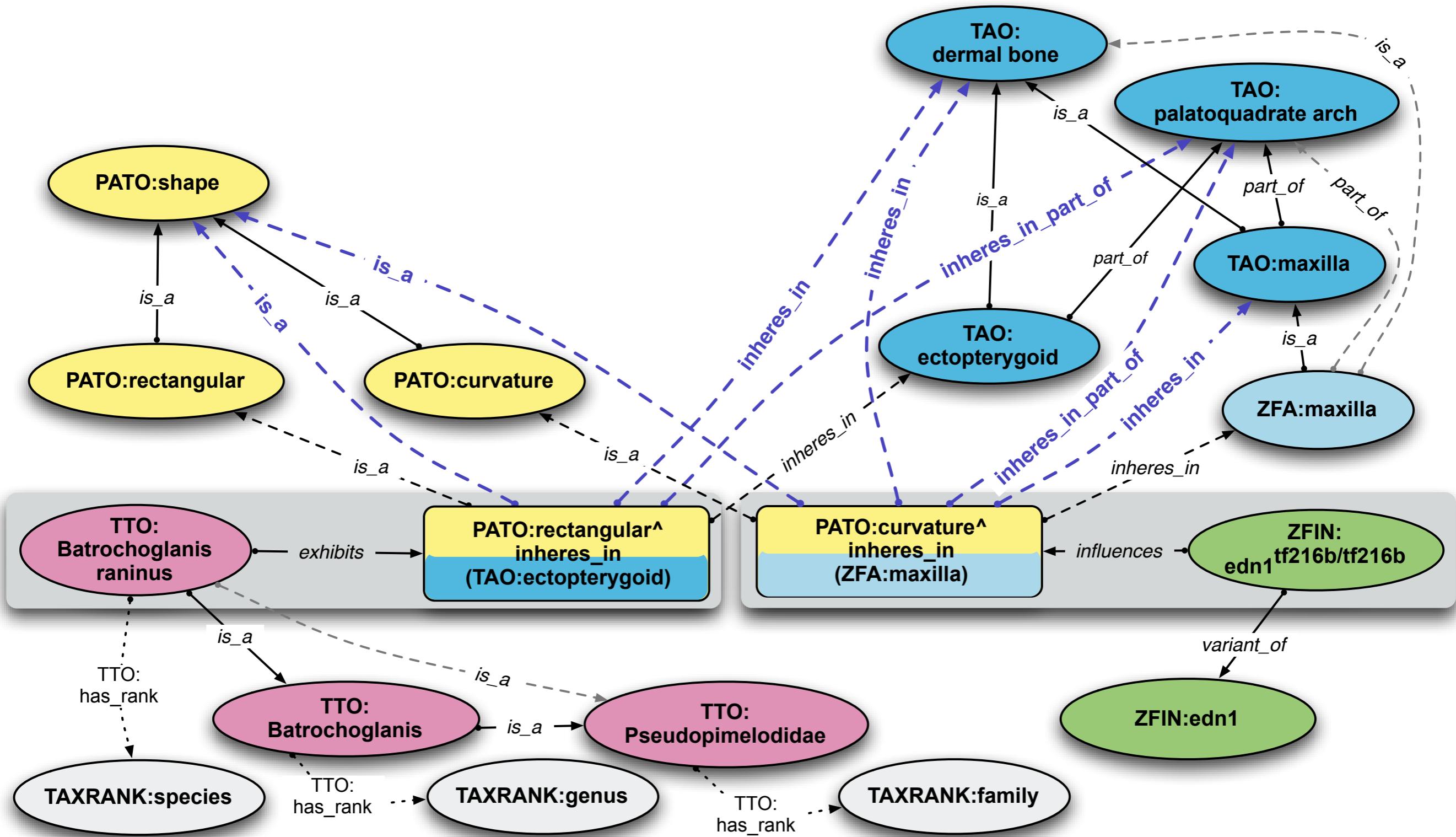
# How does reasoning work?



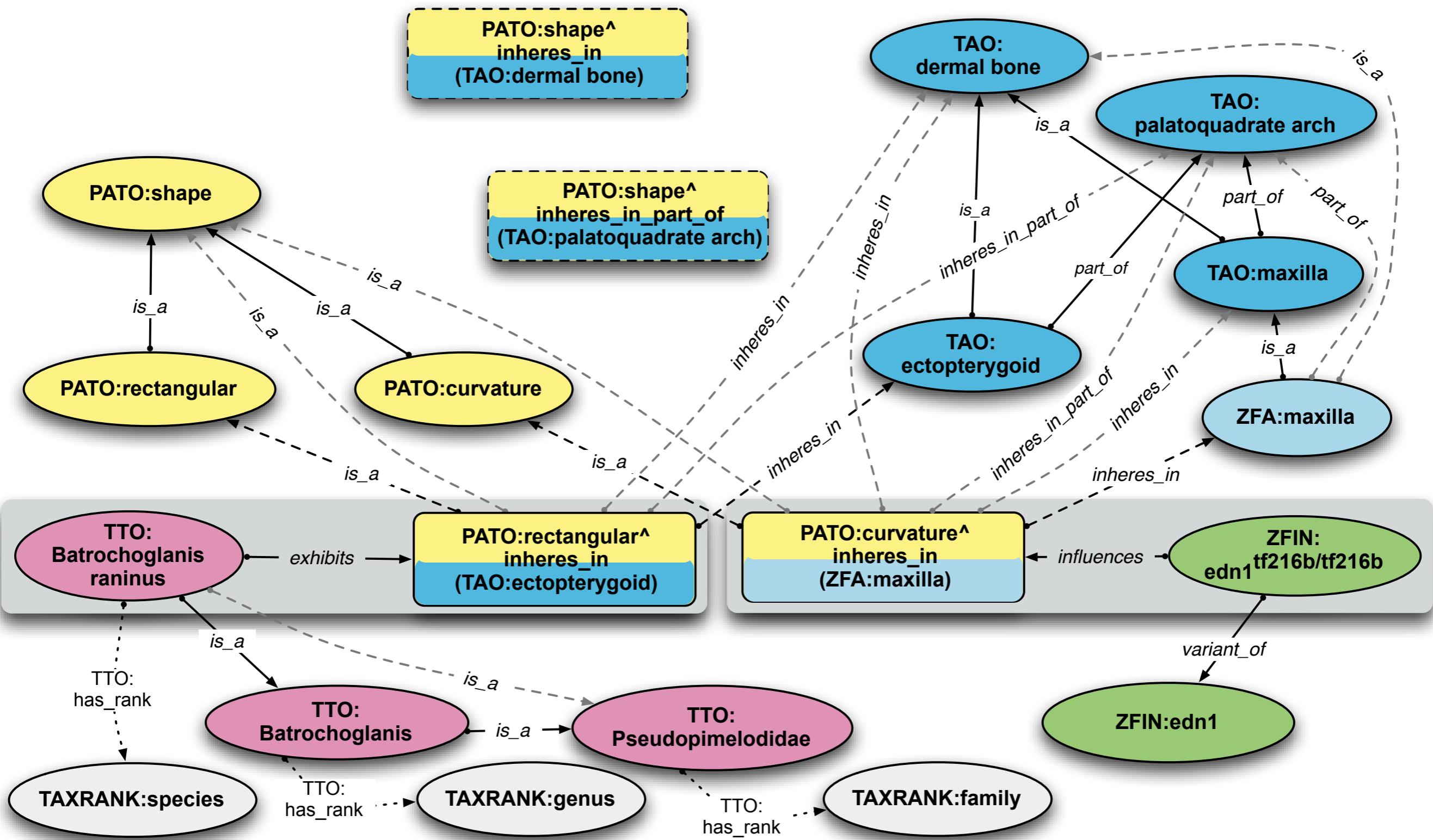
# How does reasoning work?



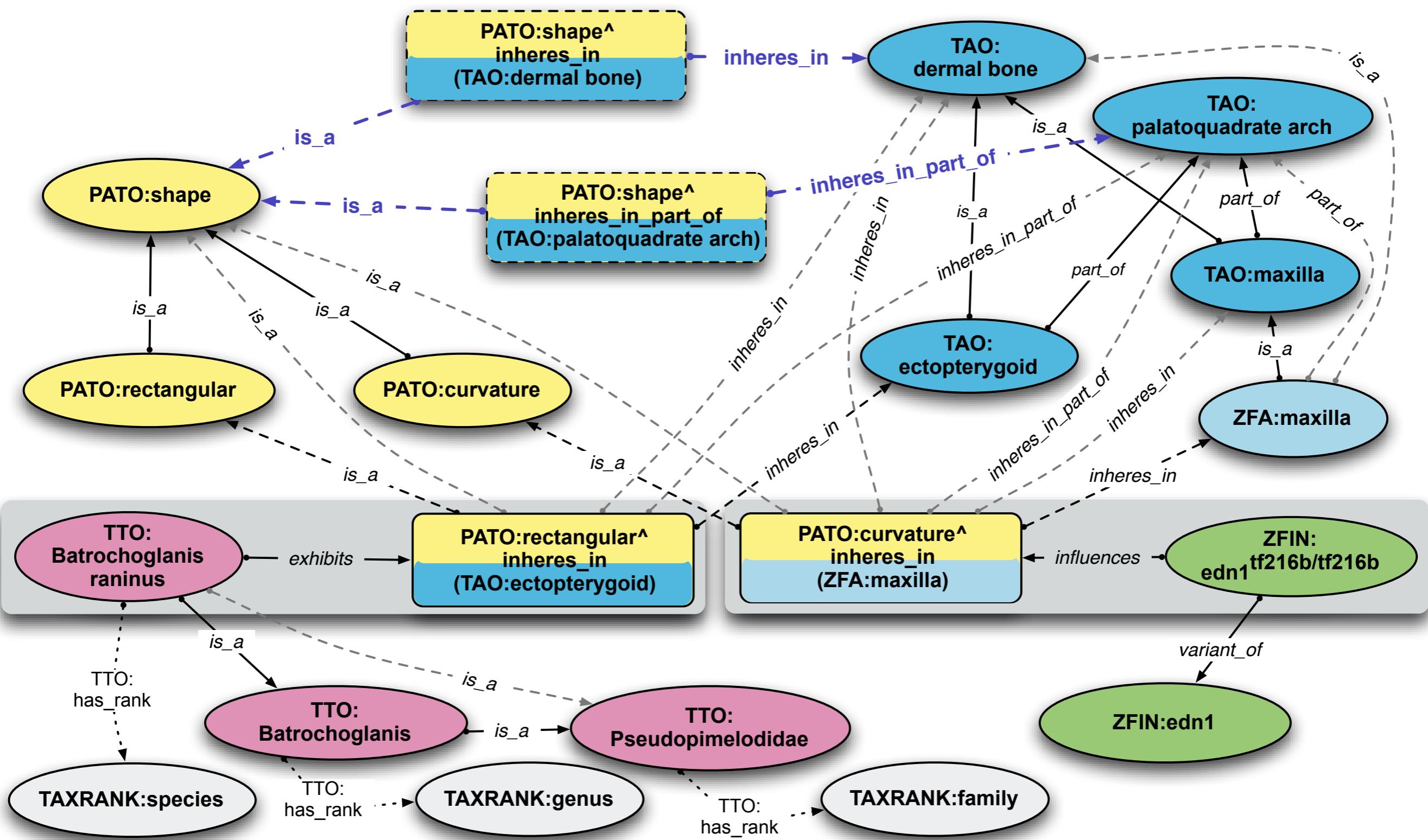
# How does reasoning work?



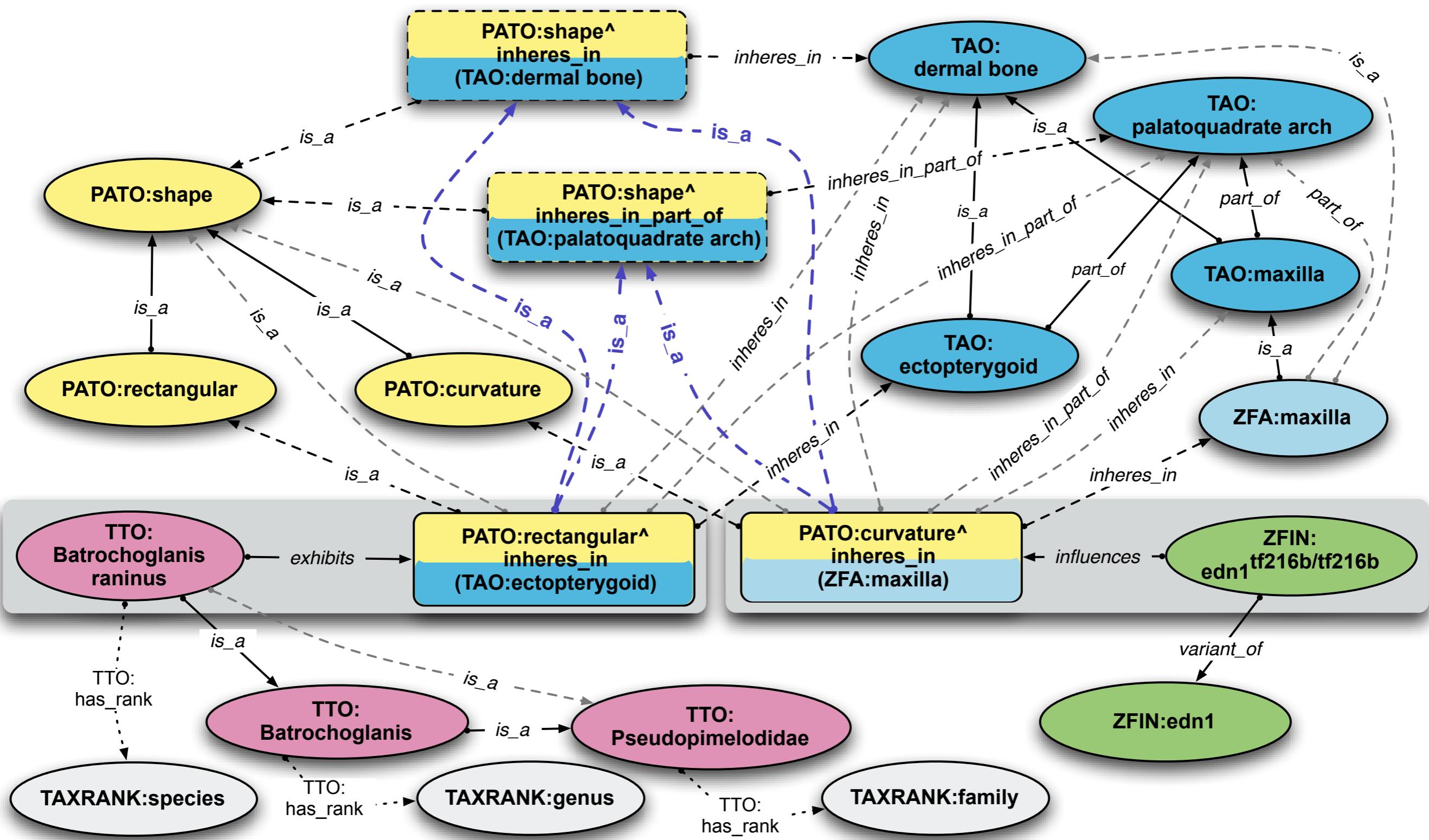
# How does reasoning work?



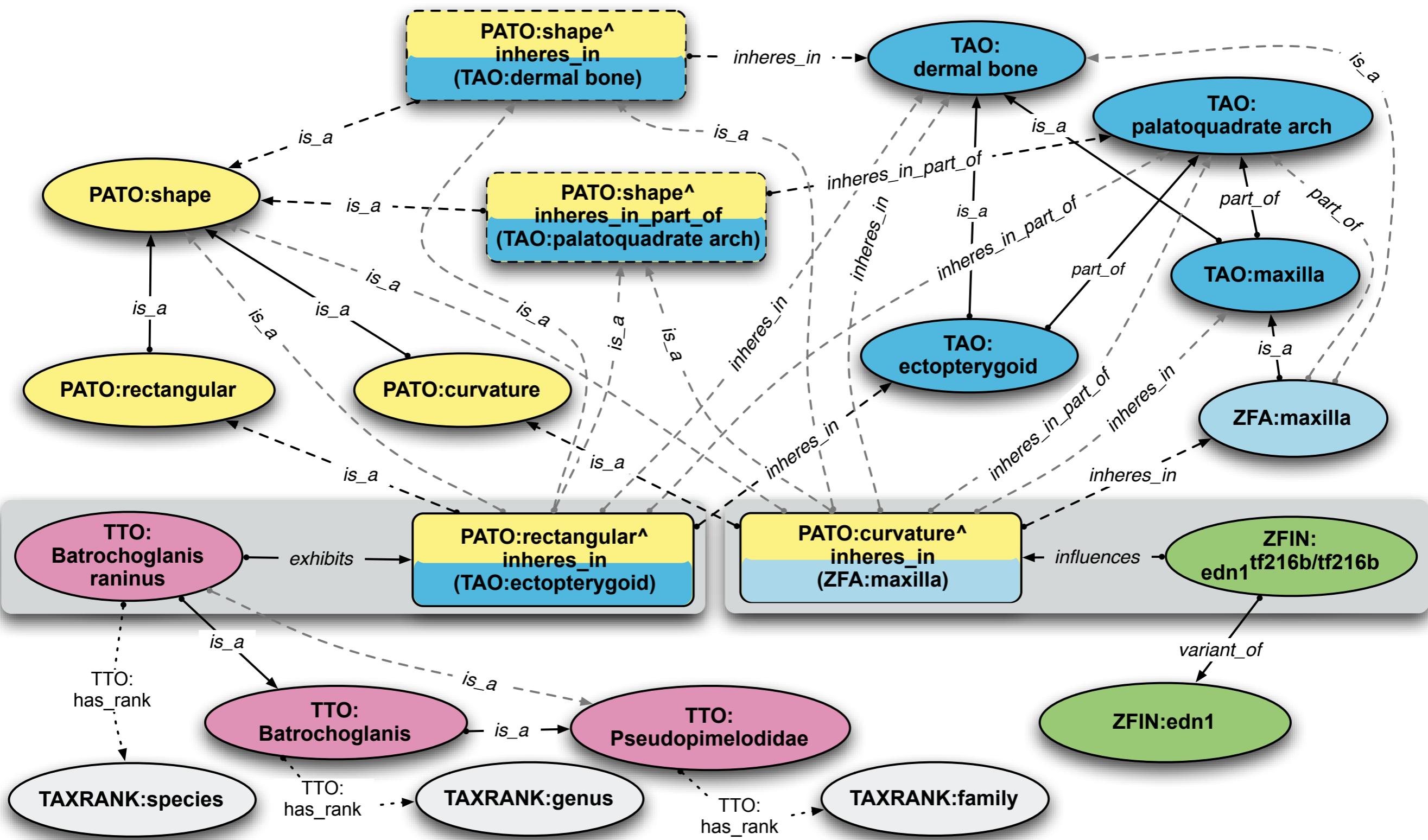
# How does reasoning work?



# How does reasoning work?



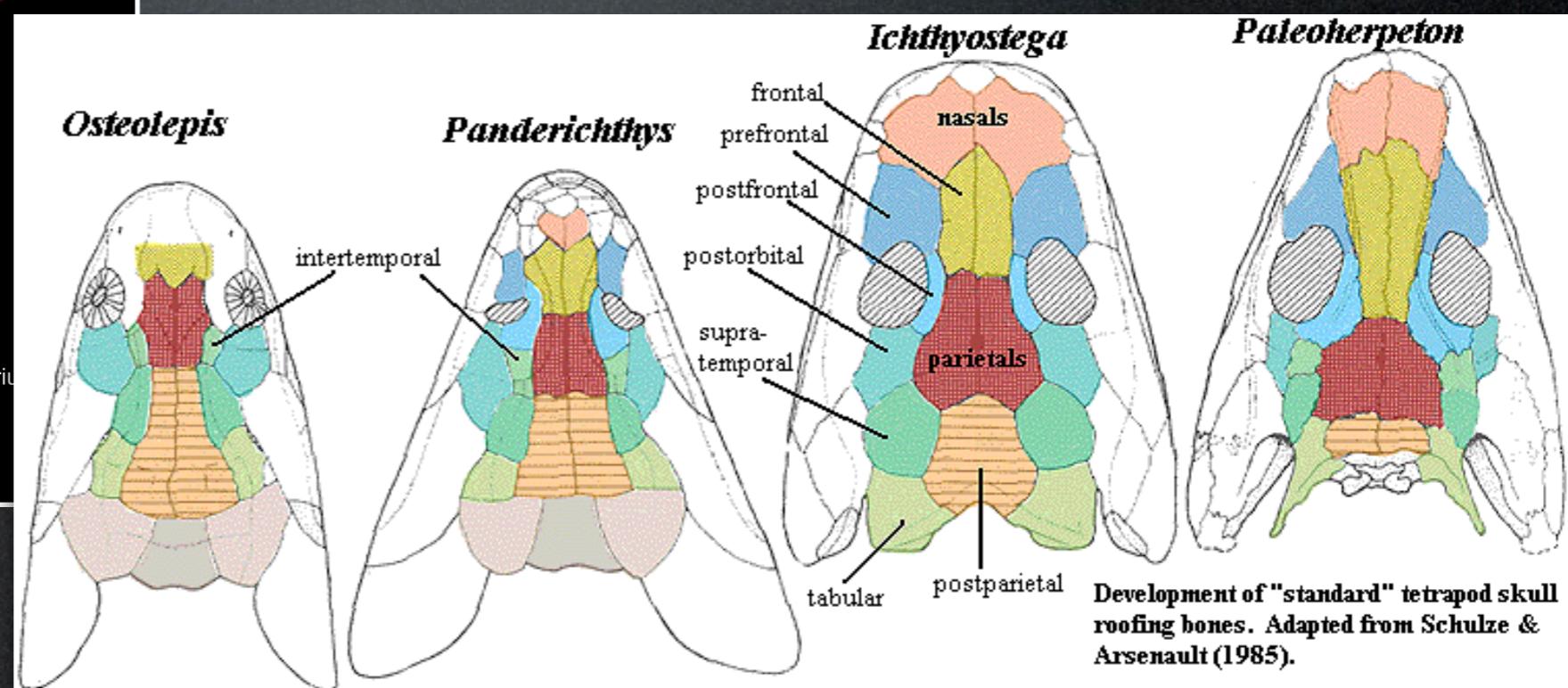
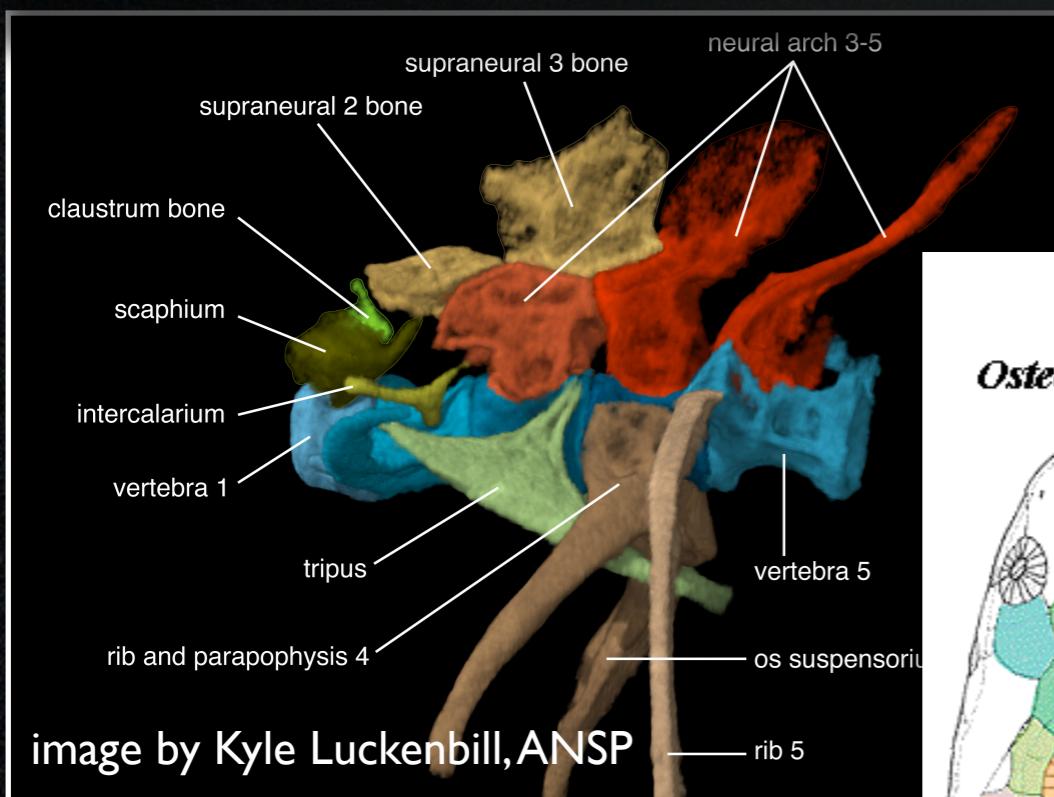
# How does reasoning work?



# Future Directions:

- Reasoning over homology

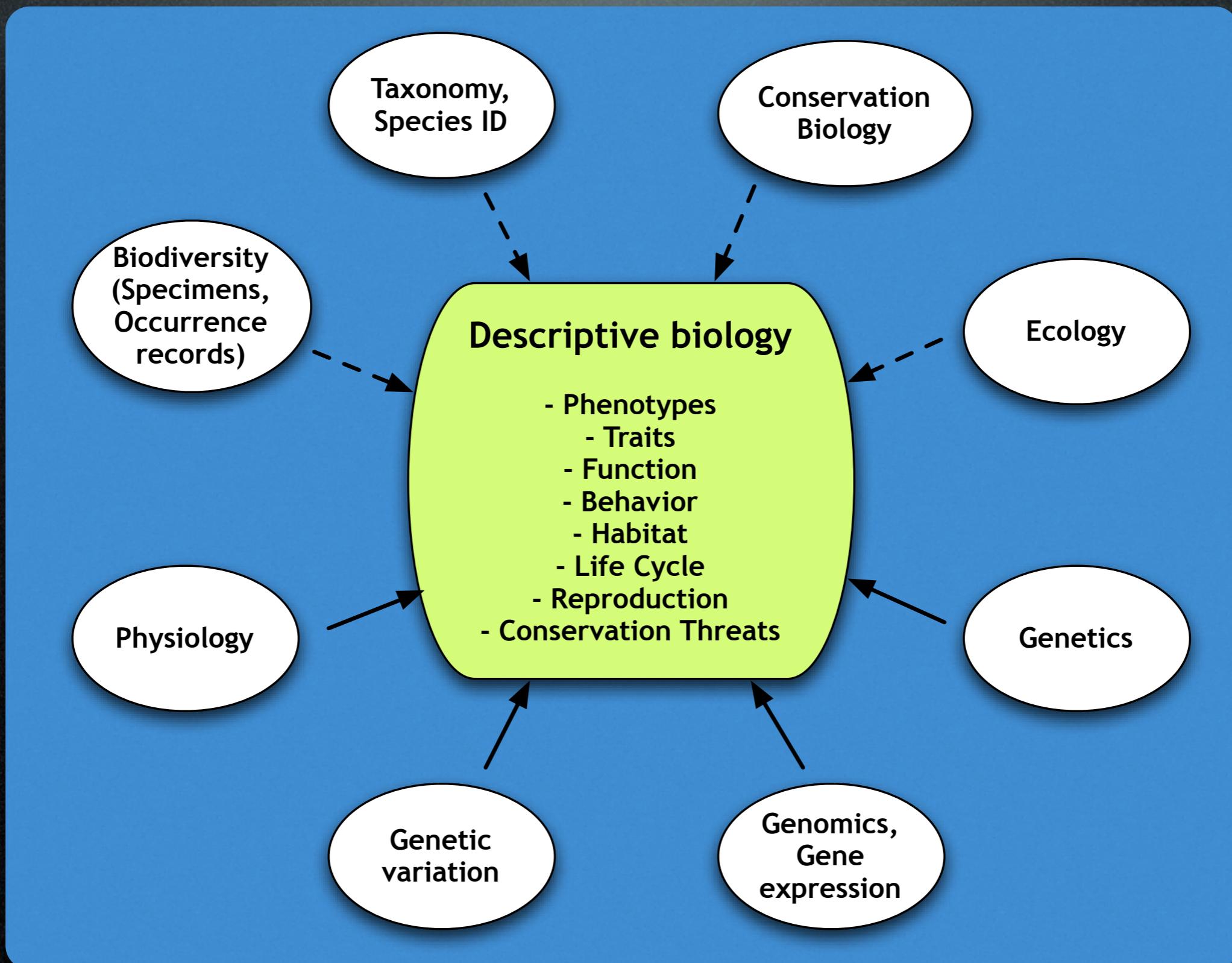
Entity 1	Taxon 1	Relationship	Entity 2	Taxon 2	Evidence	Reference(s)
scaphium	Otophysi	homologous_to	neural arch 1	Teleostei	IDS, IMS, IPS	(Fink and Fink, 1981; Rosen and Greenwood, 1970)
intercalarium	Otophysi	homologous_to	neural arch 2 (ventral portion)	Teleostei	IDS, IMS, IPS	(Rosen and Greenwood, 1970)
intercalarium	Otophysi	homologous_to	neural arch 2	Teleostei	NAS	(Fink and Fink, 1981)
intercalarium	Otophysi	homologous_to	neural arch 2	Teleostei	IMS	(Hora, 1922)
intercalarium	Otophysi	homologous_to	rib of vertebra 2	Teleostei	TAS	(Hora 1922)
tripus	Otophysi	homologous_to	parapophysis + rib of vertebra 3	Teleostei	IDS, IMS, IPS	(Fink and Fink, 1981; Rosen and Greenwood, 1970)



# What next?

- Modeling and reasoning over homology
- Efficient searching and scoring of semantic similarity
- Reducing the bottlenecks in data curation

# Opening descriptive biological data to computing can enable new science



# Acknowledgements

- Phenoscape Personnel & PIs:  
P. Mabee,  
M. Westerfield,  
T. Vision,  
J. Balhoff,  
C. Kothari,  
W. Dahdul,  
P. Midford
- Phenoscape curators & workshop participants
- Berkeley Bioinformatics & Ontologies Project (BBOP):  
C.Mungall, S.Lewis
- National Evolutionary Synthesis Center (NESCent)
- NSF (DBI 0641025)



# Phenotypic similarity matches taxa to candidate genes

Similarity (IC)	Taxon (subsuming taxon with variable phenotypes in subsumed taxa)	Taxon phenotype (one of two or more subsumed variable taxon phenotypes)	Candidate Gene(s) (zebrafish)	Gene phenotype	Subsuming phenotype
15.16	<i>Danio</i>	<i>Danio rerio</i> : epural separated from urostyle	trpm7	epural, composition	epural, structure
14.45	Otophysi	Siluriformes: scales, absent	eda	scales, absent	scales, count
13.25	Siluriformes	Siluriformes: basihyal cartilage, absent	brpf1, disc l and 10 more	basihyal cartilage, absent	basihyal cartilage, count
10.0	<i>Tachysurus</i>	process of Meckel's cartilage, adjacent to coronoid process	edn1, foxd3 and 22 more	Meckel's cartilage, mislocalized posteriorly	Meckel's cartilage, position

# Mapping EQs back to characters is a challenge

- Properties of “good” phylogenetic characters:
  - Exclusivity of states
  - Distinguishability of states
  - Independence of characters
- Finding exclusive states requires incompatible phenotypes. How to determine incompatibility?
  - Two phenotypes are incompatible iff they cannot both inhere in the same specimen.
  - Two qualities are incompatible iff an entity cannot bear both.

# Which EQs and qualities are incompatible?

- Incompatible Qs
  - present vs. absent
  - triangular vs. round
  - absent vs. any other quality
- Incompatible EQs
  - (Q inheres\_in bone E) vs (cartilage E absent)
- Compatible Qs
  - present vs. any other quality (except absent)
  - serrated vs. round
  - some colors

# Detecting phenotype change and variation

**Hemiodus argenteus**

```
{shape:bent inheres_in supraorbital bone,  
count:absent inheres_in upper pharyngeal  
5 tooth}
```

**Hemiodus**

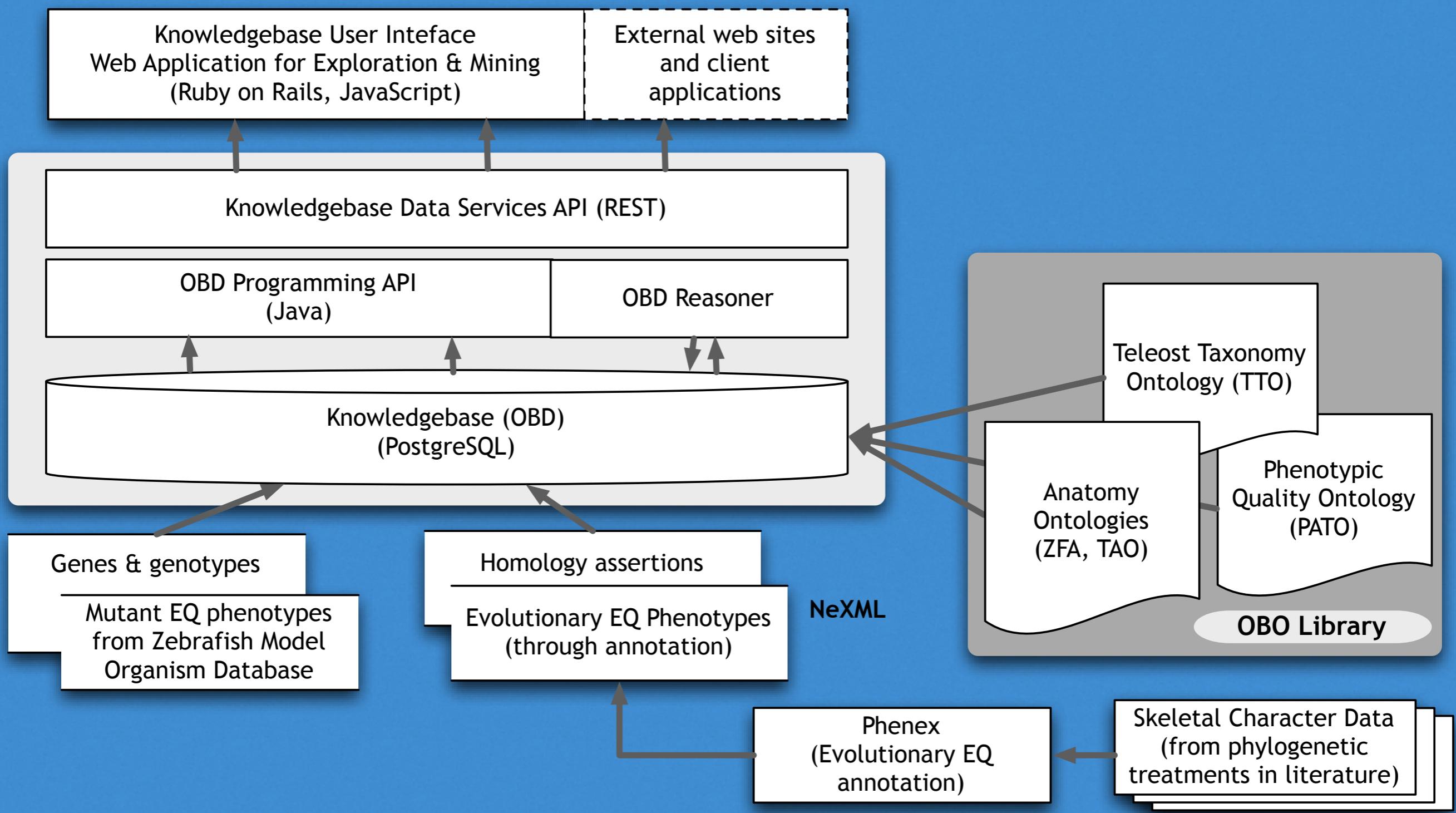
```
{shape:bent inheres_in supraorbital bone,  
shape:straight inheres_in supraorbital bone,  
count:absent inheres_in upper pharyngeal 5 tooth,  
count:present inheres_in upper pharyngeal 5 tooth}
```

**Hemiodus unimaculatus**

```
{shape:straight inheres_in supraorbital  
bone,  
count:present inheres_in upper  
pharyngeal 5 tooth}
```

```
{Change in: shape inheres_in supraorbital bone,  
Change in: count inheres_in upper pharyngeal 5 tooth}
```

# System architecture



# Formalizing homology relationships

- Formal pattern is ternary:

*E1 in\_taxon T1 homologous\_to E2 in\_taxon T2 as E3 in\_taxon T3*

- Classifying homology relationships

- 1-1 homology (phylogenetic homology)

- serial homology

- A *iso\_homologous\_to* B as C

⇒ *all A derived\_by\_descent\_from some*

*(C and has\_derived\_by\_descendent some B)*

*and*

*all B derived\_by\_descent\_from some*

*(C and has\_derived\_by\_descendent some A)*

- *shares\_ancestor\_with* as a relation chain:

*derived\_by\_descent\_from o has\_derived\_by\_descendent*

# Option 1: Asserting homology at higher-level taxa

homology-relations (http://purl.obolibrary.org/obo/homology-relations) - [/Users/lapp/Devel/phenoscape/trunk/vocab/homology/utest\_homol-exp-mod.owl]

homology-relations (http://purl.obolibrary.org/obo/homology-relations)

Active Ontology Entities Classes Object Properties Data Properties Individuals OWLViz DL Query

Asserted class hierarchy Inferred class hierarchy

**Asserted class hierarchy: 'forelimb Mammalia'**

- Thing
  - file:/Users/lapp/Devel/phenoscape/trunk/vocab/homology-relations.owl#root
  - taxonomic\_rank
  - 'anatomical entity'
    - 'material anatomical entity'
    - 'anatomical structure'
      - 'multi-cellular organism'
      - 'organism subdivision'
        - wing
          - 'wing Aves'
          - 'wing Gallus gallus'
    - appendage
      - limb/fin
        - limb
          - forelimb
            - 'forelimb Mammalia'
            - 'forelimb Mus musculus'
            - 'forelimb Homo sapiens'
      - hindlimb
        - 'hindlimb Mus musculus'
        - 'hindlimb Gallus gallus'
        - 'hindlimb Homo sapiens'
      - 'pelvic spur'
        - 'pelvic spur Python'
      - 'anterior region of body'
      - 'posterior region of body'
    - 'vestigial structure'

**Usage: 'forelimb Mammalia'**

Show:  this  disjoint  named sub/superclasses

Found 5 uses of 'forelimb Mammalia'

- 'forelimb Mammalia'
  - 'forelimb Mammalia' equivalentTo forelimb and PHENOSCAPE\_in\_taxon some Mammalia  
'forelimb Mammalia' label "forelimb Mammalia"@en  
Class('forelimb Mammalia')
  - 'forelimb Mammalia' subClassOf derived\_by\_descent\_from some (has\_derived\_by\_descendant some 'forelimb Mammalia' and has\_derived\_by\_descendant some 'wing Aves')
- 'wing Aves'
  - 'wing Aves' subClassOf derived\_by\_descent\_from some (has\_derived\_by\_descendant some 'forelimb Mammalia' and has\_derived\_by\_descendant some 'wing Aves')

**Description: 'forelimb Mammalia'**

Equivalent classes +

- 'forelimb' and PHENOSCAPE\_in\_taxon some 'Mammalia'

Superclasses +

- derived\_by\_descent\_from some (has\_derived\_by\_descendant some 'wing Aves' and has\_derived\_by\_descendant some 'forelimb Mammalia')

Members +

Inferred anonymous superclasses

- 'part of' some 'multi-cellular organism'
- 'part of' some 'anterior region of body'
- 'anterior\_to' some hindlimb

Disjoint classes +

# Option 2: Asserting homology at species level

homology-relations (<http://purl.obolibrary.org/obo/homology-relations>) - [/Users/lapp/Devel/phenoscape/trunk/vocab/homology/utest\_homol-exp-mod.owl]

homology-relations (<http://purl.obolibrary.org/obo/homology-relations>)

Active Ontology Entities Classes Object Properties Data Properties Individuals OWLViz DL Query

Asserted class hierarchy Inferred class hierarchy

Asserted class hierarchy: 'pelvic spur Python'

- Thing
  - file:/Users/lapp/Devel/phenoscape/trunk/vocab/homology-relations
- root
- taxonomic\_rank
- 'anatomical entity'
  - 'material anatomical entity'
  - 'anatomical structure'
    - 'multi-cellular organism'
    - 'organism subdivision'
      - wing
        - wing Aves
        - wing Gallus gallus
  - appendage
  - limb/fin
  - limb
    - forelimb
      - 'forelimb Mammalia'
      - 'forelimb Mus musculus'
      - 'forelimb Homo sapiens'
    - hindlimb
      - 'hindlimb Mus musculus'
      - 'hindlimb Gallus gallus'
      - 'hindlimb Homo sapiens'
  - 'pelvic spur'
    - 'pelvic spur Python'
  - 'anterior region of body'
  - 'posterior region of body'
  - 'vestigial structure'

Usage: 'pelvic spur Python'

Show:  this  disjoint  named sub/superclasses

Found 4 uses of 'pelvic spur Python'

- 'hindlimb Mus musculus'
  - 'hindlimb Mus musculus' subClassOf derived\_by\_descent\_from some (has\_derived\_by\_descendant some 'hindlimb Mus musculus' and has\_derived\_by\_descendant some 'pelvic spur Python')
- 'pelvic spur Python'
  - 'pelvic spur Python' subClassOf derived\_by\_descent\_from some (has\_derived\_by\_descendant some 'hindlimb Mus musculus' and has\_derived\_by\_descendant some 'pelvic spur Python')
  - 'pelvic spur Python' equivalentTo 'pelvic spur'
    - and PHENOSCAPE\_in\_taxon some Python
  - 'pelvic spur Python' label "pelvic spur Python"@en

Description: 'pelvic spur Python'

Equivalent classes +

'pelvic spur'  
and PHENOSCAPE\_in\_taxon some Python

Asserted in: <http://purl.obolibrary.org/obo/homology-relations>

Superclasses +

derived\_by\_descent\_from some (has\_derived\_by\_descendant some 'hindlimb Mus musculus' and has\_derived\_by\_descendant some 'pelvic spur Python')

'pelvic spur'

Inferred anonymous superclasses

'part of' some 'multi-cellular organism'

Members +

Disjoint classes +

# Validation through standard OWL-DL reasoning

Query (class expression)

```
shares_ancestor_with some ('forelimb' and PHENOSCAPE_in_taxon some 'Amniota')
```

Execute Add to ontology

Query results

Sub classes (2)

- 'forelimb Mammalia'
- 'wing Aves'

Descendant classes (5)

- 'forelimb Homo sapiens'
- 'forelimb Mammalia'
- 'forelimb Mus musculus'
- 'wing Aves'
- 'wing Gallus gallus'

Query (class expression)

```
shares_ancestor_with some ('hindlimb' and PHENOSCAPE_in_taxon some 'Amniota')
```

Execute Add to ontology

Query results

Sub classes (4)

- 'hindlimb Gallus gallus'
- 'hindlimb Homo sapiens'
- 'hindlimb Mus musculus'
- 'pelvic spur Python'

Descendant classes (4)

- 'hindlimb Gallus gallus'
- 'hindlimb Homo sapiens'
- 'hindlimb Mus musculus'
- 'pelvic spur Python'