

A Gentle Introduction to Ontologies for Biology

Hilmar Lapp

National Evolutionary Synthesis Center (NESCent)

Ontologies for Ichthyology and Herpetology Workshop
ASIH 2009, Portland, Oregon

Biology is data rich



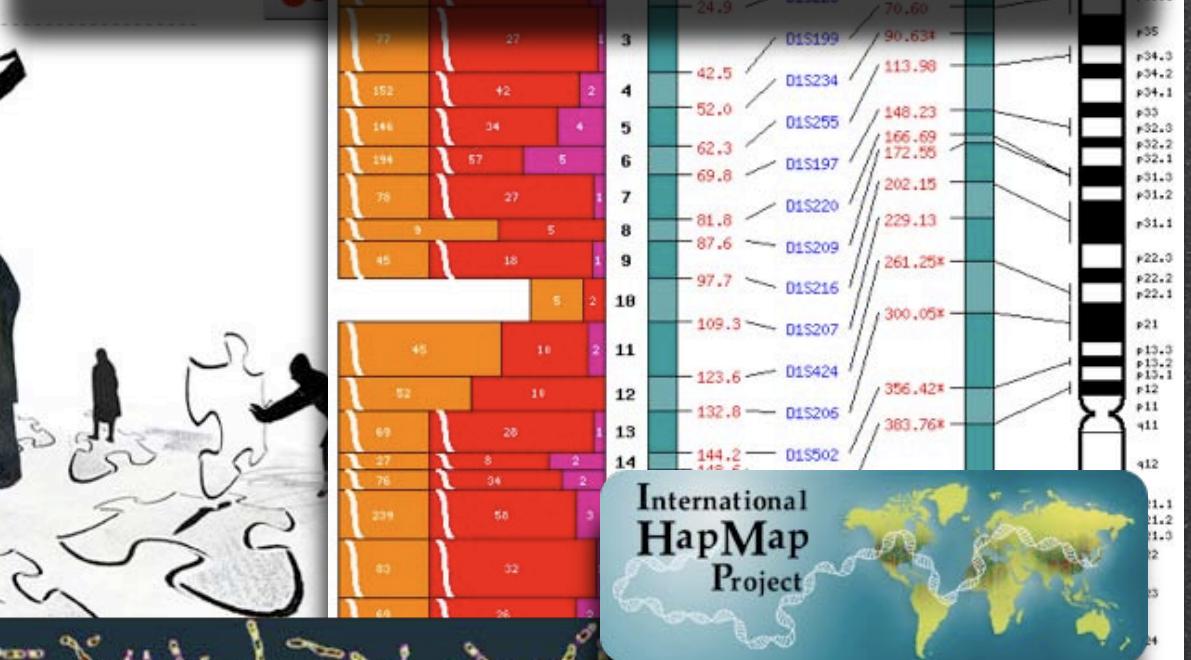
Specials

Big Data

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- [SPECIAL REPORT](#)
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1000 Genomes

A Deep Catalog of Human Genetic Variation



Data integration has to rely on computation

BOLD Systems

<http://www.barcodinglife.org/views/login.php>

BARCODE OF LIFE DATA SYSTEMS
Advancing species identification and discovery through the analysis of short, standardized gene regions

The Barcode of Life Data Systems (BOLD) is an online workbench that aids collection, management, analysis, and use of DNA barcodes. It consists of 3 components (MAS, IDS, and ECS) that each address the needs of various groups in the barcoding community.

MANAGEMENT & ANALYSIS

BOLD-MAS provides a repository for barcode records coupled with analytical tools. It serves as an online workbench for the DNA barcode community.

IDENTIFICATION ENGINE

BOLD-IDS provides a species identification tool that accepts DNA sequences from the barcode region and returns a taxonomic assignment to the species level when possible.

NCBI

Bramocharax caballeroi voucher ECO-CH-P5485A cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Features Sequence

LOCUS EU751721 **DEFINITION** Bramocharax caballeroi voucher ECO-CH-P5485A cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial.

ACCESSION EU751721 **VERSION** EU751721.1 **KEYWORDS** BARCODE.

SOURCE mitochondrial **ORGANISM** *Bramocharax caballeroi*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Characiformes; Characidae; Characidae incertae sedis; Bramocharax. de la Frontera Sur, Av. Centenario Km 5.5, Chetumal, Quintana Roo 77014, Mexico

FEATURES

source Location/Qualifiers
1..652
/organism="Bramocharax caballeroi"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/specimen_voucher="ECO-CH-P5485A"
/db_xref="BOLD:MEFM051-05"
/db_xref="taxon:533334"
/country="Mexico: Veracruz"
/lat lon="18.418 N 95.111 W"
/collection_date="25-Jul-2005"
/collected_by="Martha Valdez"
/identified_by="Martha Valdez"

EXTERNAL

GLOBAL BIODIVERSITY INFORMATION FACILITY

SPECIES COUNTRIES DATABASE

... free and open access to biodiversity data

Ontologies facilitate data integration



Ontologies facilitate data integration

EMAGE

http://www.emouseatlas.org/emagewebapp/pages/emeage_general_query_result.jsf

emage

Quick Search Gene/Protein for *

Home Search Analysis Data Submission EMAP Anatomy Atlas About Help

Query: genes - detected - branchial arch (exact match to structures) - ts1 to ts26

Select All On This Page | Deselect All On This Page Add/Remove Columns Display 10 entries per page

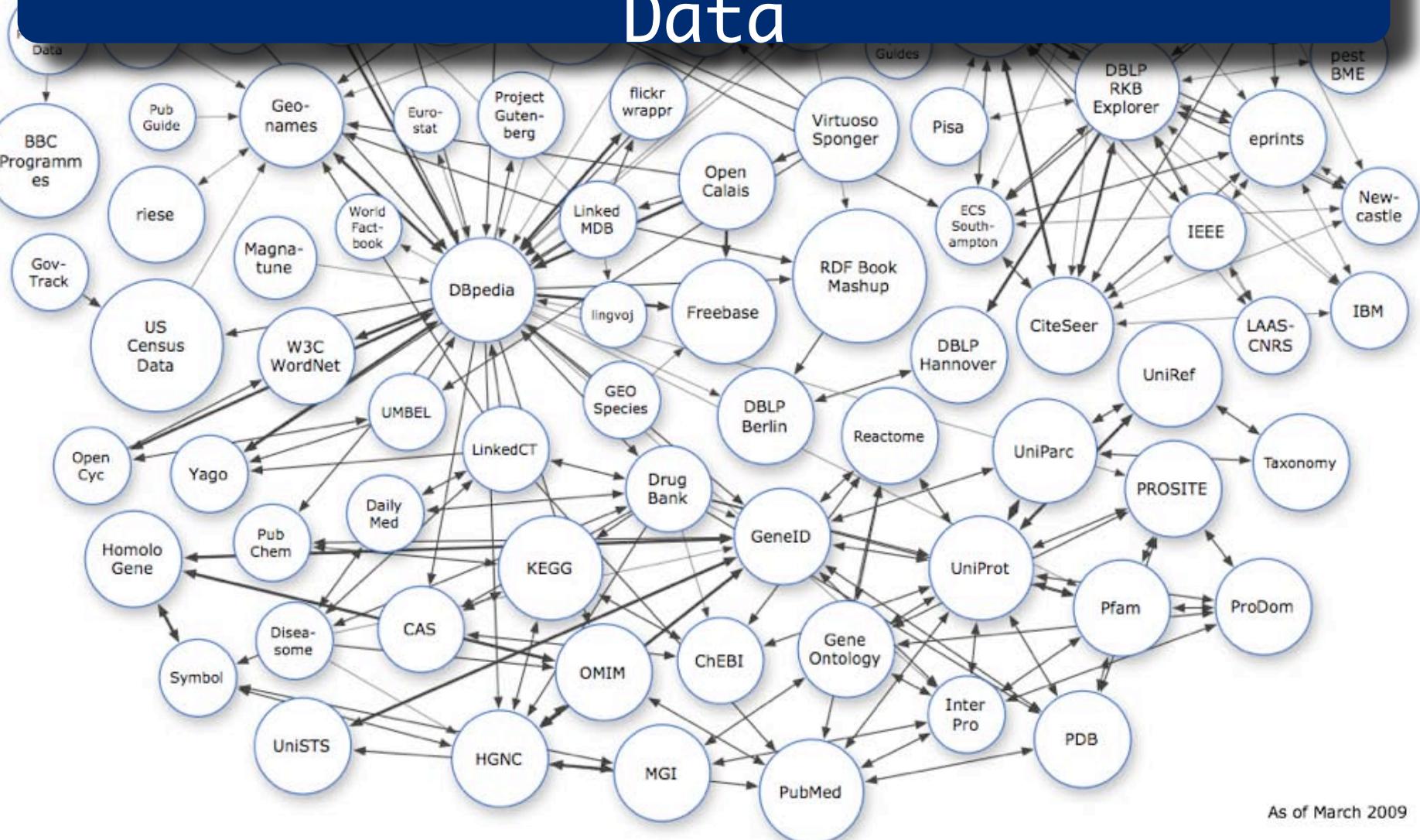
Page 3 of 70 Go to page: Go Flexible Scroll

Select	Gene/Protein	Data Image	Region	Structures	Theiler Stage	Stage Given	ID	Mutant Allele
<input type="checkbox"/>	Akr1a4			tail branchial arch otocyst fronto-nasal process	17	10.5 dpc	EMAGE:4189	wild-type
<input type="checkbox"/>	Alx1			medial-nasal process mesenchyme latero-nasal process mesenchyme 1st arch maxillary part 1st branchial arch	17	10.5 dpc	EMAGE:3606	wild-type
<input type="checkbox"/>	Alx1			1st arch mandibular part	17	10.5 dpc	EMAGE:3608	wild-type
<input type="checkbox"/>	Alx3			medial-nasal process embryo 1st arch mandibular part	17	10.5 dpc	EMAGE:122	wild-type

Link to original image EMAGE:3606

Open "http://www.emouseatlas.org/gxdb/dbl/image/3606/3606.html" in a new window behind the current window

Shared ontologies & identifiers: The Global Web of Data



As of March 2009

But phenotypes are complex, free text

OMIM – SRY-BOX 9; SOX9

<http://www.ncbi.nlm.nih.gov/entrez/dispmim.cgi?id=608160>

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.

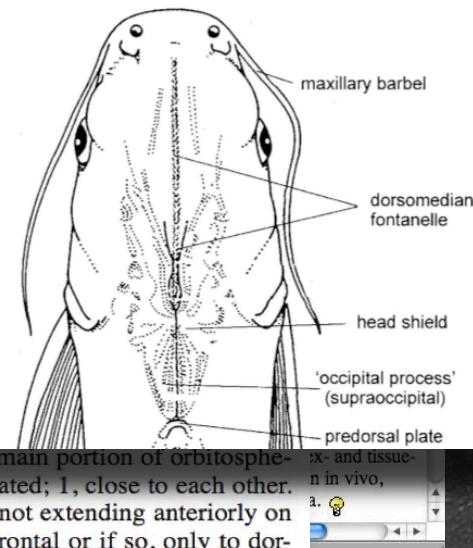
By cell transfection experiments, Sudbeck et al. (1996) showed that SOX9 through the motif AACAAAG, a sequence recognized by other HMG domain proteins, binds to the DNA-binding domain of yeast GAL4, the transactivating factor at the C terminus of SOX9. With 1 exception, all SOX9 nonsense and frameshift mutations lead to truncation of this domain, suggesting that skeletal development in these cases results, at least in part, from loss of the

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AMERICAN MUSEUM NOVITATES

APPENDIX 1. CHARACTER SUMMARY

1. Fifth infraorbital. 0, well developed, without contact between fourth and sixth infraorbitals; 1, greatly reduced, with posteroventral margin of sixth infraorbital in contact with posterodorsal margin of fourth infraorbital.
2. Antorbital-lateral ethmoid contact. 0, no contact; 1, antorbital contacting ventral wing of lateral ethmoid along its entire lateral edge.
3. Antorbital. 0, flat, platelike, without medial process; 1, with a short medial, vertically aligned process at its posterior edge that extends along posterior surface of ventral wing of lateral ethmoid; 2, with enlarged medial, vertically aligned process at its posterior edge that extends along posterior surface of ventral wing of lateral ethmoid.
4. Mesethmoid spine. 0, conical, or with a dif-
- tilaginous surface body of vomer.
14. Portion on vomer. 0, not modified in depression on its anterior tip of maxillary barbel.
15. Ridge on lateral 1, present.
16. Rhinosphenoid. 0
17. Lateral ethmoid-absent; 1, present.
18. Parasphenoid and main portion of orbitosphenoid. 0, well separated; 1, close to each other.
19. Dilatator fossa. 0, not extending anteriorly on dorsal surface of frontal or if so, only to dorsoposterior edge of orbit; 1, highly developed, extending anteriorly on dorsal surface of frontal beyond dorsoposterior edge of orbit.



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*).

Integrating phenotypes can open up new science

Ambystoma talpoideum (Holbrook, 1838)

Mole salamander

Authoritative INFORMATION All

MORPHOLOGY

Physical Description

SOURCE AND ADDITIONAL INFORMATION

AUTHOR Ashlee Behr

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SUPPLIER Animal Diversity Web 

SOURCE URL [View original data object](#)

Mole salamanders are facultatively paedomorphic; they can either become terrestrial adults (metamorphic adults) or retain their aquatic larval form even as they become sexually mature (paedomorphic, branchiate, or neotenic adults). Paedomorphic adults can eventually undergo metamorphosis or they may remain in the aquatic form throughout life. Terrestrial adults live in areas surrounding breeding ponds while paedomorphic adults remain in permanent ponds. Environmental conditions present during larval development can determine which life form an individual salamander will become.

Both mole salamander morphs have short, stout bodies with broad, disproportionately large heads. Body size of terrestrial and aquatic males varies across populations and time. In some years and ponds, aquatic males will be larger, on average, than terrestrial males. In other years, the opposite can be

SWITCH TO COMMON NAMES

CLASSIFICATION : TEXT | GRAPHIC | 

[Animalia](#) +
[Chordata](#) +
[Amphibia](#) +
[Caudata](#) +
[Ambystomatidae](#) +
[Ambystoma](#) +
[Ambystoma talpoideum \(Holbrook, 1838\)](#)

[Archaea](#) +
[Bacteria](#) +
[Chromista](#) +
[Fungi](#) +
[Plantae](#) +
[Protozoa](#) +
[Viruses](#) +

Words often are polysemous

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

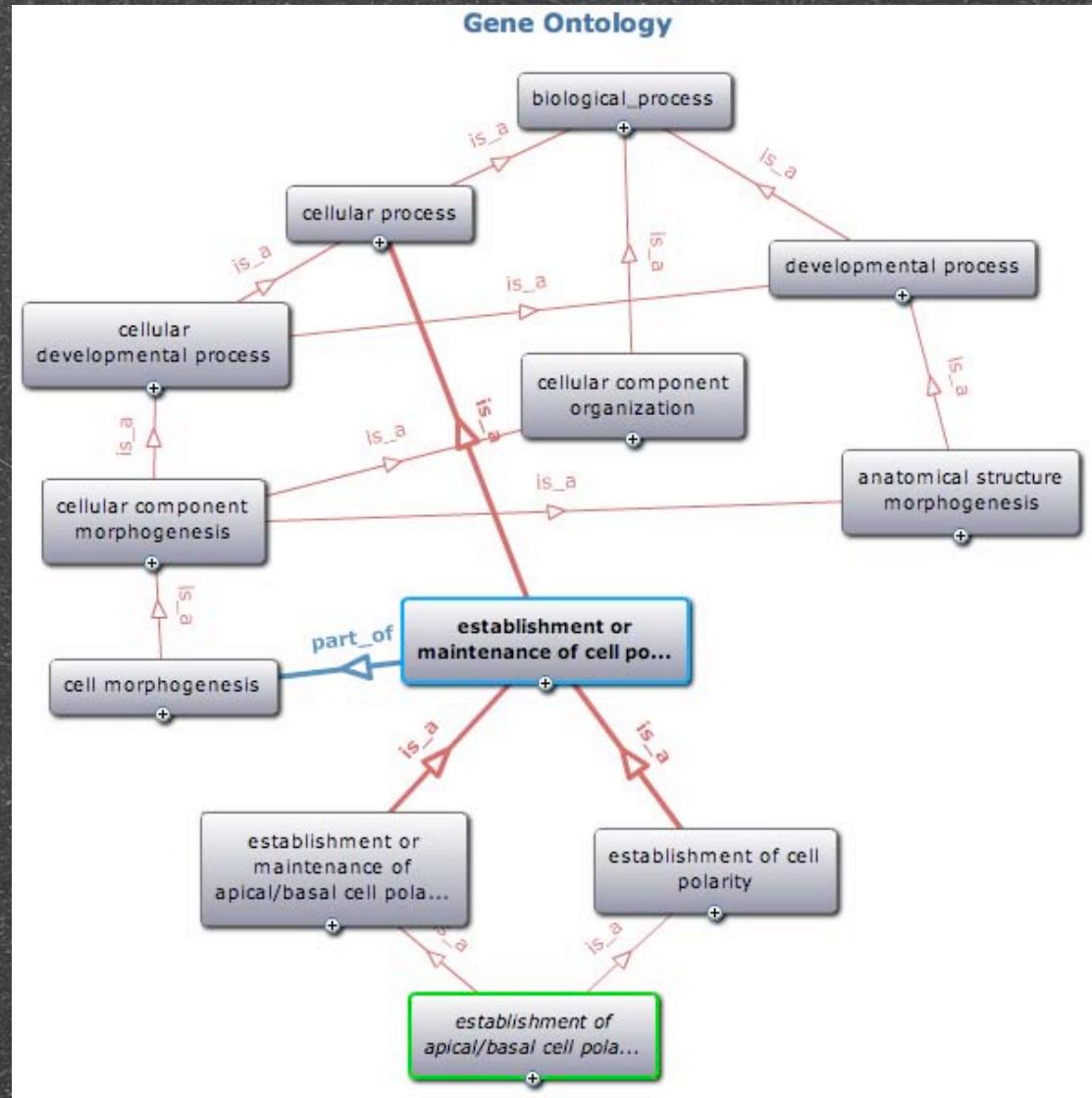
Words often are polysemous

- “Replacement bone that is median and is the anterior-most bone of the ventral hyoid arch”
- basihyal bone
- basihyoid
- glossohyal

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



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

What are ontologies not?

- An ontology is not a database.
 - Databases typically are silos, but ontologies can connect siloed data
- An ontology is not a terminology.
 - Terminologies are built ad-hoc to serve specific application needs.
- An ontology is not data.
 - Ontologies are used to annotate data and make data interoperable.

Ontologies can address the problems with text

List of characters

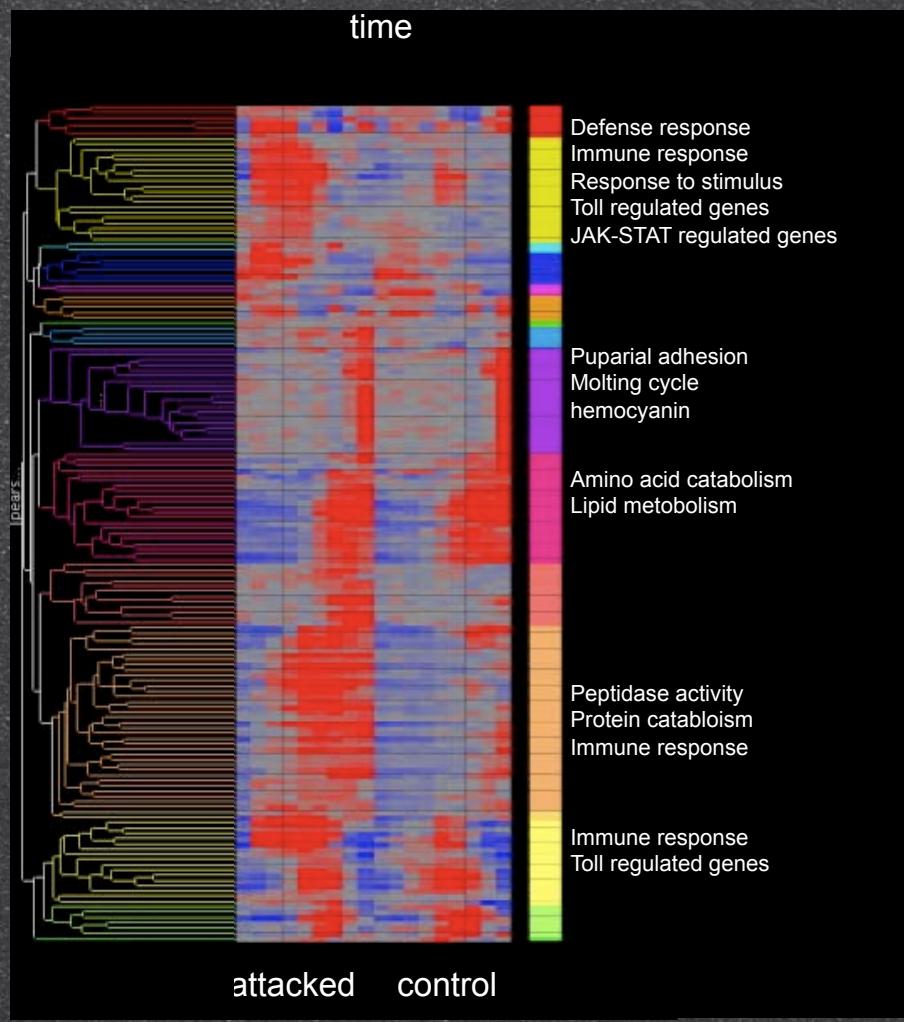
The list of characters, the analysis of certain morphological characters, and the phylogenetic relationships of certain teleosts are based on the features listed below. [0] represents the plesiomorphic character state and [1], [2], [3], and [4] the apomorphic character states. The outgroup used to polarize characters includes †*Watsonulus eugnathoides*, *Amia calva*, *Lepisosteus* spp., and others in different analyses.

With the exceptions indicated, characters 1 to 167 are from ARRATIA (1991, 1996b, 1997) or are new characters. Because of the use of different outgroups, characters 26, 27, 28, 36, 76, 77, 78, 92, 122, 124, 125, 126, 128, 129, 130, 137, 140, and 157 changed their polarization with respect to ARRATIA (1996b, 1997), and in other cases, the presentation of some characters was slightly modified (indicated below). Characters 168 to 175 are from GRANDE & BEMIS (1998); characters 176 to 191 are taken from PINNA (1996); and characters 192 to 196 are from BRITO (1997).

1. Ethmopalatine ossification in the floor of nasal capsule articulating with autopalatine: [0] absent; [1] present. (PATTERSON & ROSEN 1977.)
2. Two paired endoskeletal ethmoidal ossifications: [0] absent; [1] present.
3. Parietal bones fused in a median element: [0] absent; [1] present.

Arratia, 1999. Zoological Journal of the Linnean Society 151:691-757.

Ontologies can address the problems with text



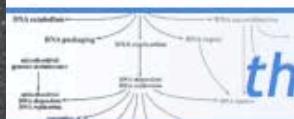
Annotating data with ontologies: Gene annotation as an example

Annotation objectives

- Where and when is a particular gene product involved (cell part, cell type, body part, development stage)?
- Which functions does the gene product exert?
- With which biological processes is the gene product associated?
- In abnormal or wild-type phenotype?

Gene Ontology (GO)

- Covers cellular component, molecular function, biological process
- Multi-species, multi-disciplinary, open-source
- Annotated gene products allow information-theoretic computation
 - E.g., quantitative assessment of commonalities among and across sets of genes



the Gene Ontology

AmiGO

[Search](#) [Browse](#) [GOOSE](#) [Other Tools](#) [Help](#)Search GO 

terms



genes or proteins



exact match

establishment of apical/basal cell polarity

[Term information](#) ▾ [Term lineage](#) ▾ [External references](#) ▾ [17 gene product associations](#) ➔

Term Information

Accession	GO:0035089
Ontology	biological process
Synonyms	None
Definition	The specification and formation of the polarity of a cell along its apical/basal axis. [source: GOC:bf]
Comment	None
Subset	None
Community	There have been 0 comments for this term. If you would like to view or participate in the community annotation, please continue to the GONUTS page.

[Back to top](#)

Term Lineage

[Switch to viewing term parents, siblings and children](#) [Filter tree view](#) [?](#)[Filter Gene Product Counts](#)[View Details](#)

Term Lineage

Switch to viewing term parents, siblings and children

▼ Filter tree view ?

Filter Gene Product Counts

Data source

Species

- All
- AspGD
- CGD
- dictyBase

- All
- Agrobacterium tum...
- Anaplasma phagocy...
- Arabidopsis thaliana

View Options

Tree view

 Full Compact[Set filters](#)[Remove all filters](#) all : all [245476 gene products]

- GO:0008150 : biological_process [172247 gene products]
 - GO:0016043 : cellular component organization [12771 gene products]
 - GO:0032989 : cellular component morphogenesis [2548 gene products]
 - GO:0000902 : cell morphogenesis [2181 gene products]
 - GO:0007163 : establishment or maintenance of cell polarity [448 gene products]
 - GO:0030010 : establishment of cell polarity [183 gene products]
 - GO:0035089 : establishment of apical/basal cell polarity [17 gene products]
 - GO:0045198 : establishment of epithelial cell apical/basal polarity [13 gene products]
 - GO:0035088 : establishment or maintenance of apical/basal cell polarity [65 gene products]
 - GO:0035089 : establishment of apical/basal cell polarity [17 gene products]
 - GO:0045198 : establishment of epithelial cell apical/basal polarity [13 gene products]
 - GO:0045197 : establishment or maintenance of epithelial cell apical/basal polarity [47 gene products]
 - GO:0045198 : establishment of epithelial cell apical/basal polarity [13 gene products]
 - GO:0045199 : maintenance of epithelial cell apical/basal polarity [6 gene products]
 - GO:0035090 : maintenance of apical/basal cell polarity [10 gene products]
 - GO:0045199 : maintenance of epithelial cell apical/basal polarity [6 gene products]
 - GO:0030011 : maintenance of cell polarity [28 gene products]
 - GO:0035090 : maintenance of apical/basal cell polarity [10 gene products]
 - GO:0045199 : maintenance of epithelial cell apical/basal polarity [6 gene products]

[Actions...](#)

Last action: Opened

GO:0035090

[Graphical View](#)[Reset tree](#)[View in tree browser](#)[Download...](#)[OBO](#)[RDF-XML](#)[GraphViz dot](#)[View gene products associated with this term](#)

Gene Product Associations to establishment of apical/basal cell polarity ; GO:0035089 and children

Download all association information in: [gene association format](#) [RDF-XML](#)

[Filter associations displayed](#)

establishment of apical/basal cell polarity ; GO:0035089 [\[show def\]](#) [\[view in tree\]](#)

	Symbol, full name	Information	Qualifier	Evidence	Reference	Assigned by
<input type="checkbox"/>	baz bazooka	38 associations gene from <i>Drosophila melanogaster</i> BLAST		IMP	FB:FBrf0167999	FlyBase
<input type="checkbox"/>	Foxj1 forkhead box J1	18 associations gene from <i>Mus musculus</i> BLAST		IMP With MGI:MGI:2181746	MGI:MGI:3037476	MGI
<input type="checkbox"/>	Prkci protein kinase C, iota	9 associations gene from <i>Mus musculus</i> BLAST		IMP With MGI:MGI:3526850 Inferred from Mutant Phenotype; click to view documentation With MGI:MGI:360694	MGI:MGI:3607414	MGI
<input type="checkbox"/>	Prkci protein kinase C, iota	16 associations gene from <i>Rattus norvegicus</i> BLAST		ISO With RGD:1331958	RGD:1624291	RGD

establishment of epithelial cell apical/basal polarity ; GO:0045198 [\[show def\]](#) [\[view in tree\]](#)

	Symbol, full name	Information	Qualifier	Evidence	Reference	Assigned by
<input type="checkbox"/>	crb crumbs	33 associations gene from <i>Drosophila melanogaster</i>		TAS	FB:FBrf0054006	FlyBase
<input type="checkbox"/>	Crb3 crumbs homolog 3 (Drosophila)	4 associations gene from <i>Mus musculus</i> BLAST		ISA With EMBL:AY103469	MGI:MGI:2668769	MGI
<input type="checkbox"/>	ds	24 associations gene from <i>Drosophila melanogaster</i> BLAST		IMP	FB:FBrf0155499	FlyBase



Your Input Welcome



Prkci^{tm1Kido} Targeted Allele Detail

Allele	Symbol: Prkci ^{tm1Kido} Name: targeted mutation 1, Yoshiaki Kido ID: MGI:3526850																																									
Synonyms	PRClambda ^{flx}																																									
Allele details	Allele Type: Targeted (Floxed/Frt) ES Cell Line: Not Specified Mutation: Insertion LoxP sites flanked exon 5 by homologous recombination. (J:95378) International Mouse Strain Resource: (Search for IMSR strains with Prkci mutations) References and Additional Notes: (See Below)																																									
Gene information	Symbol: Prkci Human Ortholog: PRKCI Name: protein kinase C, iota Chromosome: 3:30894669-30951663 bp, + strand Genetic Position: 13.8 cM																																									
Phenotype summary	<p>Phenotype Summary by Mammalian Phenotype terms Key:</p> <table border="1"> <tr> <td>hm</td> <td>homozygous</td> <td>ht</td> <td>heterozygous</td> </tr> <tr> <td>cn</td> <td>conditional genotype</td> <td>cx</td> <td>complex: > 1 genome feature</td> </tr> <tr> <td>tg</td> <td>involves transgenes</td> <td>ot</td> <td>other: hemizygous, indeterminate,...</td> </tr> <tr> <td>N</td> <td>normal phenotype</td> <td>∅</td> <td>expected model not found</td> </tr> </table> <p>(show or hide all annotated terms)</p> <p>Genotypes are listed in the next section.</p> <table border="1"> <thead> <tr> <th>Affected Systems</th> <th>Genotypes:</th> <th>cn1</th> <th>cn2</th> </tr> </thead> <tbody> <tr> <td>digestive/alimentary system</td> <td>▶</td> <td>✓</td> <td></td> </tr> <tr> <td>endocrine/exocrine glands</td> <td>▶</td> <td>✓</td> <td></td> </tr> <tr> <td>homeostasis/metabolism</td> <td>▶</td> <td>✓</td> <td></td> </tr> <tr> <td>nervous system</td> <td>▶</td> <td></td> <td>✓</td> </tr> <tr> <td>vision/eye</td> <td>▶</td> <td></td> <td>✓</td> </tr> </tbody> </table>		hm	homozygous	ht	heterozygous	cn	conditional genotype	cx	complex: > 1 genome feature	tg	involves transgenes	ot	other: hemizygous, indeterminate,...	N	normal phenotype	∅	expected model not found	Affected Systems	Genotypes:	cn1	cn2	digestive/alimentary system	▶	✓		endocrine/exocrine glands	▶	✓		homeostasis/metabolism	▶	✓		nervous system	▶		✓	vision/eye	▶		✓
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Phenotypic data by genotype	<p>Phenotypic Data by Genotype</p> <p>(show or hide all phenotypic details)</p> <table border="1"> <thead> <tr> <th>Genotype</th> <th>Allelic Composition</th> <th>Genetic Background</th> </tr> </thead> <tbody> <tr> <td>▶ cn1</td> <td>Prkci^{tm1Kido}/Prkci^{tm1Kido} Tg(Ins2-cre)25Mgn/0</td> <td>involves: 129/Sv * C57BL/6 * DBA/2</td> </tr> <tr> <td>▶ cn2</td> <td>Prkci^{tm1Kido}/Prkci^{tm1Kido} Tg(Crx-cre)1Tfur/0</td> <td>Not Specified</td> </tr> </tbody> </table>		Genotype	Allelic Composition	Genetic Background	▶ cn1	Prkci ^{tm1Kido} /Prkci ^{tm1Kido} Tg(Ins2-cre)25Mgn/0	involves: 129/Sv * C57BL/6 * DBA/2	▶ cn2	Prkci ^{tm1Kido} /Prkci ^{tm1Kido} Tg(Crx-cre)1Tfur/0	Not Specified																															
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Ontology community resources & infrastructure: NCBO Bioportal and OBO Foundry

NCBO Bioportal: Welcome to the NCBO Bioportal

<http://bioportal.bioontology.org/>

BioPortal Browse Search Projects Annotate All Mappings All Resources Sign In Reg

Experimental Factor Ontology NCI Thesaurus Gene Ontology

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Find an ontology [Explore](#)
[Browse Ontologies >](#)

Search resources
[Advanced Resource Search](#)

Ontology	Version	Notes	Mappings
Human disease	1.50	0	17732
Mouse adult gross anatomy	1.194	0	3905
NCI Thesaurus	08.12d	9	3798
Foundational Model of Anatomy	3.0	0	1997
Zebrafish anatomy and development	1.21	0	791

Statistics	
Ontologies	145
Concepts	723,806
Resources Indexed	11

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<http://bioontology.org/>

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- [Working With The Center](#)
- [The Promise of Semantic Web Technology](#), by Matthew Dublin for Genome Web, features an interview with Mark Musen about the future of the Semantic Web's use in biology.

Current News

- October 17, 2009 - Call for Paper/Exhibition Submissions - [BME09-CISP09](#)
- August 10, 2009 - Call for Papers - [SWESE2009](#)
- August 7, 2009 - Call for papers - [Workshop on Semantic Web Applications in Scientific Discourse](#)
- July 31, 2009 - Call for papers - [The First International Workshop on Role of Semantic Web in Provenance Management \(SWPM 2009\)](#)
- July 24, 2009 - [ICBO: program now available](#).
- July 20, 2009 - Call for papers - [8th Terminology and Artificial Intelligence Conference \(TIA 2009\)](#)

The National Center for Biomedical Ontology is a consortium of leading biologists, clinicians, informaticians,

ONTOLOGY NAME	FORMAT	VERSION	AUTHOR	UPLOADED ON	GROUP	STATUS
Amphibian gross anatomy (AAO)	OBO Format	1.8	AmphiAnat list	07/30/2008	OBOFoundry	Explore
C. elegans gross anatomy (WBbt)	OBO Format	1.21	Http://bioportal Administrators	07/22/2008	OBOFoundry	Explore
Dictyostelium discoideum anatomy (DDANAT)	OBO Format	1.9	Rex			
Drosophila gross anatomy (FBbt)	OBO Format	1.30	Http://bioportal Administrators			
Fungal gross anatomy (FAO)	OBO Format	1.3	Fungi			
Human developmental anatomy, abstract version (EHDAA)	OBO Format	1.3	EMA			
Human developmental anatomy, timed version (EHDA)	OBO Format	1.3	EMA			
Medaka fish anatomy and development (MFO)	OBO Format	1.1	Medaka			
Mosquito gross anatomy (TGMA)	OBO Format	1.10	C. L.			
Mouse adult gross anatomy (MA)	OBO Format	1.194	Ana			
Mouse gross anatomy and development (EMAP)	OBO Format	1.2	EMA	07/30/2008	OBOFoundry	Explore
Plant structure (PO)	OBO Format	1.63	Po_anatomy Administrators	04/03/2009	OBOFoundry	Explore
Spider Ontology (SPD)	OBO Format	1.11	Martin Ramirez	07/24/2009	OBOFoundry	Explore
Teleost anatomy and development (TAO)	OBO Format	1.117	Wasila Dahdul	07/22/2009	OBOFoundry	Explore
Tick gross anatomy (TADS)	OBO Format	1.2	Http://www Administrators	07/30/2008	OBOFoundry	Explore
Xenopus anatomy and development (XAO)	OBO Format	1.17	Erik Segerdell	07/22/2009	OBOFoundry	Explore
Zebrafish anatomy and development (ZFA)	OBO Format	1.21	ZFIN administrators	06/23/2009	OBOFoundry	Explore

OB0 Foundry coverage

RELATION TO TIME	CONTINUANT			OCCURRENT	
GRANULARITY	INDEPENDENT			DEPENDENT	
ORGAN AND ORGANISM	Organism (NCBI Taxonomy)	Anatomical Entity (FMA, CARO)	Organ Function (FMP, CPRO)	Phenotypic Quality (PaTO)	Biological Process (GO)
CELL AND CELLULAR COMPONENT	Cell (CL)	Cellular Component (FMA, GO)	Cellular Function (GO)		
MOLECULE		Molecule (ChEBI, SO, RnaO, PrO)	Molecular Function (GO)	Molecular Process (GO)	

OBO Foundry as a community resource

- Provides ontology building know-how:
 - Tested ontology building and community best-practices
 - Incremental, modular, bottoms-up approach to evidence-based terminology
 - Principles for developing definitions and relationships
- Provides peer-review and community feedback

Consistent definitions for terms

- Genus-differentia: A is a type of <parent of A> that <differentia>
- Example: premaxilla is-a dermal bone
 - def: "Dermal bone that forms the anteriormost element of the upper jaw. It articulates with the maxilla posterodorsally and its antimere medially. The premaxilla is paired."

Interoperability: Reuse of relations

OBO Relations Ontology (RO)

Foundational

*is_a
part_of*

Spatial

*located_in
contained_in
adjacent_to*

Temporal

*transformation_of
derives_from
preceded_by*

Participation

*has_participant
has_agent*

“Relations in Biomedical Ontologies”, Genome Biology, April 2005

Ontological needs for computable phenotypes

“Meckel’s cartilage greatly reduced”



Meckel’s cartilage
Entity (E)

Meckel’s cartilage
Entity
Character

decreased size
Quality (Q)

size:
Attribute
Character State

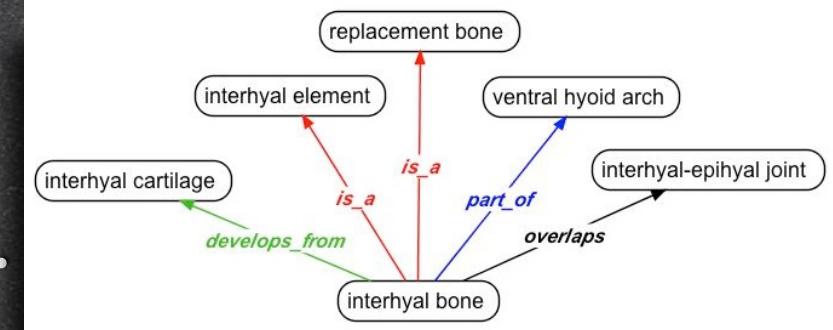
decreased

Value

- In addition, need ontologies for
 - who exhibits the phenotype (taxonomy)
 - evidence

Teleost Anatomy Ontology (TAO)

- Initiated in 2007 as a clone of the zebrafish anatomy ontology.
- 2371 terms, 395 new.
- Multi-species: teleosts.
- Terms are defined based on structure, homology is not implied.
- Focus is on the skeletal system as the ontology is driven by annotation.



Taxonomically variable relationships

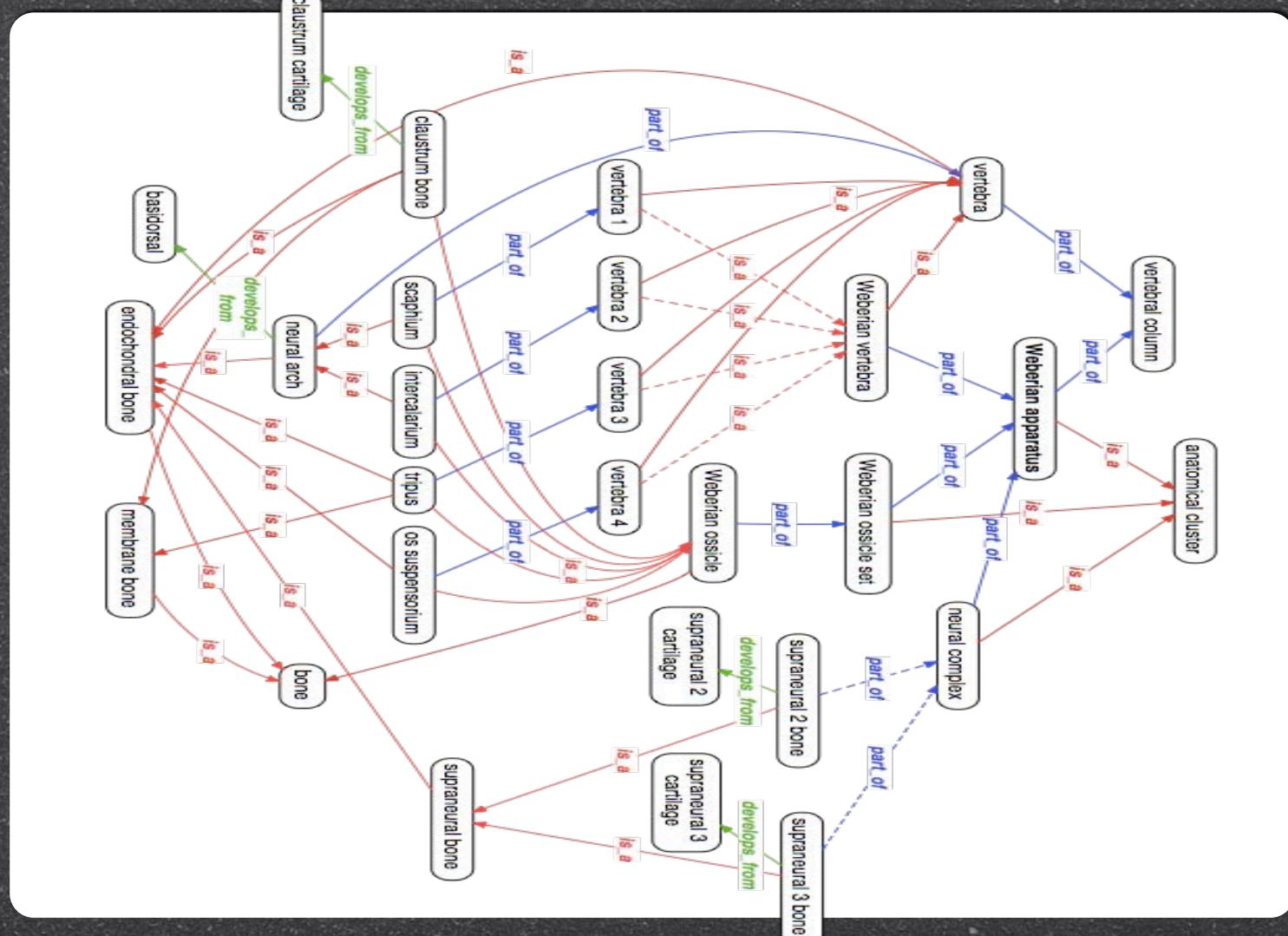


Image Record: [460945] Chromobotia macracanthus

<p>Contributor: Cypriniform Tree of Life [edit]</p> <p>Submitter: Paula Mabee [edit]</p> <p>Date Submitted: 2008-09-08</p> <p>Last Modified: 2008-09-08</p> <p>Publish Date: 2008-09-07</p> <p>CCToL</p> <p>Description: basihyal From spreadsheet line 417</p> <p>CToLDateSubmitted: 14-Jun-11</p> <p>CToLSubmittedBy: Ericka Grey</p> <p>Magnification: NULL</p> <p>Dimension (px): 1280x1024</p> <p>Resolution (PPI): 100</p> <p>Submitted as: jpg</p> <p>Original File Name: Boba_macracanthus_1165_25x_EG_Basihyal_501.jpg</p> <p>View id: 459122</p> <p>Specimen part: basihyal</p> <p>Angle: Dorsal</p> <p>Technique: Digital Camera</p> <p>Preparation: Cleared and counterstained for bone (Alizarin red) and cartilage (Alician blue)</p> <p>Download: tiff (1.21 MB) jpeg (131.37 KB)</p> <p>Copyright: Ericka Grey and Paula Mabee</p> <p>Licensor: </p>	 <p>FSI Viewer</p>
<p>Specimen</p> <p>Specimen id: 460920</p> <p>Basis of record: [S] - Specimen</p> <p>Sex: unknown</p> <p>Form: unknown</p> <p>Stage: Juvenile/Adult</p> <p>Catalog number: 199848</p> <p>Collector:</p> <p>Date collected:</p>	<p>Locality</p> <p>Locality Id:</p> <p>Continent/ocean:</p> <p>Country:</p> <p>Locality:</p> <p>Latitude:</p>
<p>Determination</p> <p>Class: Actinopterygii [edit]</p> <p>Order: Cypriniformes [edit]</p> <p>Family: Cobitidae [edit]</p> <p>Genus: Chromobotia [edit]</p> <p>Species: Chromobotia macracanthus [edit]</p>	<p>(Add Annotation...)</p>
<p>External links/identifiers</p> <p>External identification: CTOL-S:0001165</p> <p>External identification: CTOL-I:0000501</p> <p>Ontology:</p> <p>Teleost Anatomy Ontology TAO:0000316</p>	<p>Other Annotations (Add Annotation...)</p>

Basihyal
bone

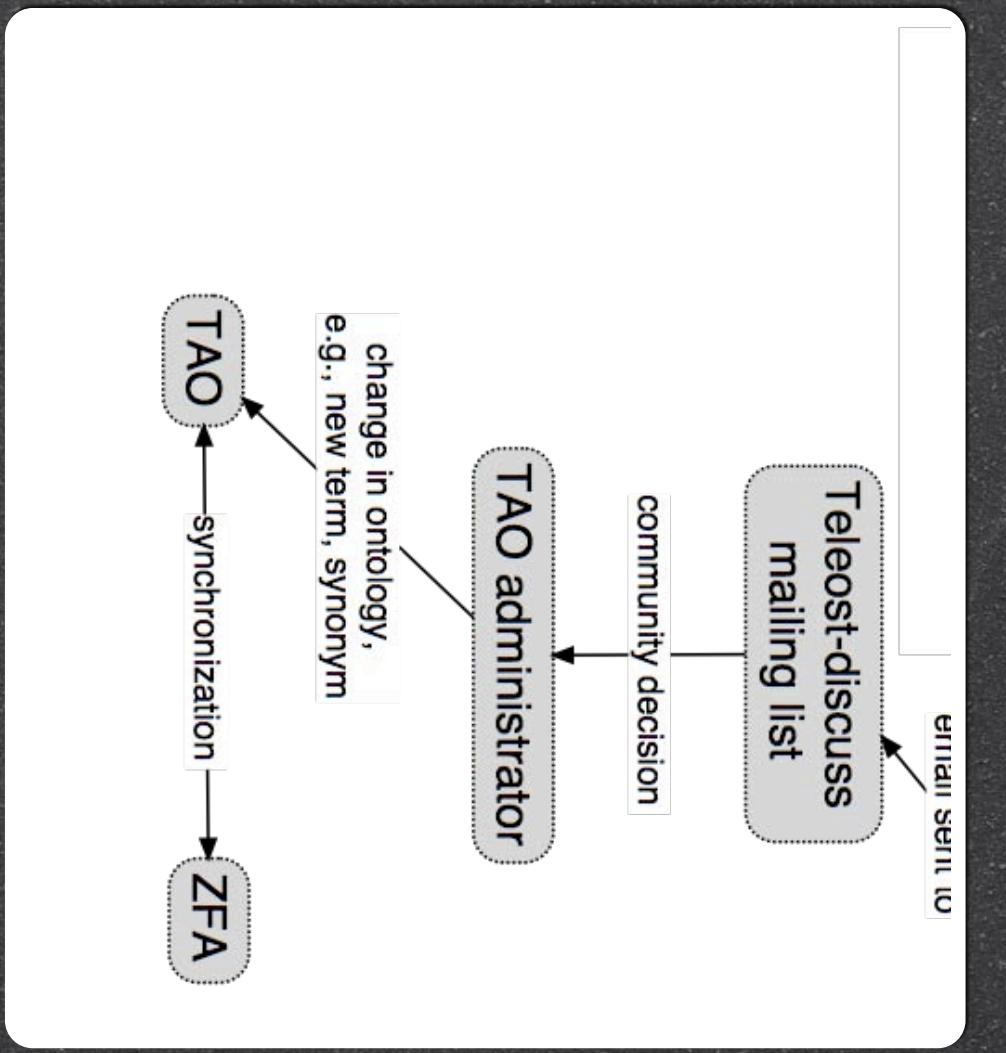
- TAO is already being used to link data

Teleost Taxonomy Ontology (TTO)

- Based on and regularly updated from Bill Eschmeyer's Catalog of Fishes
- Includes custom additions, such as fossil taxa and higher order taxa.
- 36,060 terms (taxa), 38,000 synonyms

Community ownership of ontology development

- OBO ontologies have a request tracker
- Participation is open
- Subject (biology) experts are key to ensure usefulness
- Ontology building is a collaborative effort



SourceForge.net: Open Biomedical Ontologies: Teleost Anatomy (TAO) term requests
http://sourceforge.net/tracker/?group_id=76834&atid=994764 Google

Open Biomedical Ontologies

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Tracker: Teleost Anatomy (TAO) term requests

Search: Advanced Options RSS

Page: 1 2 3 ... 34 Next » 1 - 10 of 339 Results - Display 10

ID	Summary	Status	Opened	Assignee	Submitter	Resolution	Priority
2812852	Pharyngobranchial series	Open	2009-06-26	nobody	nobody	None	5
2808769	syn: operculare	Open	2009-06-19	nobody	pmabee	None	5
2808159	Parurohyal	Open	2009-06-18	nobody	pmabee	None	5
2808155	unbranched anal fin ray	Open	2009-06-18	nobody	pmabee	None	5
2808135	dorsal fin pterygiophore 1	Open	2009-06-18	wdahdul	wdahdul	None	5
2808115	palate	Open	2009-06-18	nobody	pmabee	None	5
2808111	gill arch preferred term	Open	2009-06-18	wdahdul	wdahdul	None	5
2807822	surangular	Open	2009-06-17	nobody	tgrande	None	5
2807821	craniotemporal muscle	Open	2009-06-17	nobody	tgrande	None	5
2807819	diplospondyly	Open	2009-06-17	nobody	tgrande	None	5

Artifact ID: Filter Reset Permalink

Page: 1 2 3 ... 34 Next » 1 - 10 of 339 Results - Display 10

On Mar 25, 2008, at 5:11 PM, Vari, Richard wrote:

Hi,

Brian has pointed out some important points in noting the variation in the infraorbitals. The relative size of IO1 is often a function of head shape and it is rare that it is the largest element among characiforms. At least in some gymnotiforms it is reduced to a tubular canal not notably larger than the other elements in the series. In general it lies between the anteroventral margin of eye and the upper jaw.

IO3 and 4 are standarly separate with fusion of IO4 being with IO5 when present.

Comments about canals should be qualified with "when present" since canals are absent in some taxa, usually of smaller body sizes.

Date: Tue, 25 Mar 2008 10:36:37 -0400
From: Brian Sidlauskas <bls16@duke.edu>
Subject: Re: [Obo-teleost-discuss] [obo-Zebrafish Anatomy (ZFA) term requests-1924376] infraorbital definition
To: Wasila Dahdul <dahdul@anat.umd.edu>

A few comments on these definitions:

> Infraorbital 1 [synonym=lachrymal]
> Dermal bone that covers the region
> eye and the upper jaw. Infraorbital 1 (the lachrymal) is the first
> and
> largest bone in the infraorbital series. Bears the anterior most part
> of the infraorbital canal.

IO1 is definitely not always the largest. In many characiforms IO3 is the biggest by far.

> infraorbital 2
> Plate like dermal bone, variable in size, though usually one of the
> smallest in the series. Bears 2-3 neuromast pores enclosed within the
> infraorbital canal (Nelson, 1969).
>
> infraorbital 3
> Plate like dermal bone, variable in size, but usually largest in the
> series. Usually fused with IO4 (eg. Opsariichthys, Nelson (1969)).
> Usually bears 3 neuromast pores enclosed within the infraorbital
> canal
> (Nelson, 1969).

0 and 1 are possible pore numbers for these bones.

IO5 canal forms are highly variable, with canal absent in some taxa.

I did not follow the argument for the need for the dermosphenotic rather than IO6. IO6 seems to be readily identified elements even when there are losses as a consequence of fusion between elements or loss

Date: Tue, 25 Mar 2008 11:13:48 -0500
From: "Arratia, Gloria" <garratia@ku.edu>
Subject: Re: [Obo-teleost-discuss] [obo-Zebrafish Anatomy (ZFA) term requests-1924376] infraorbital definition
To: <bls16@duke.edu>, "Wasila Dahdul" <dahdul@anat.umd.edu>

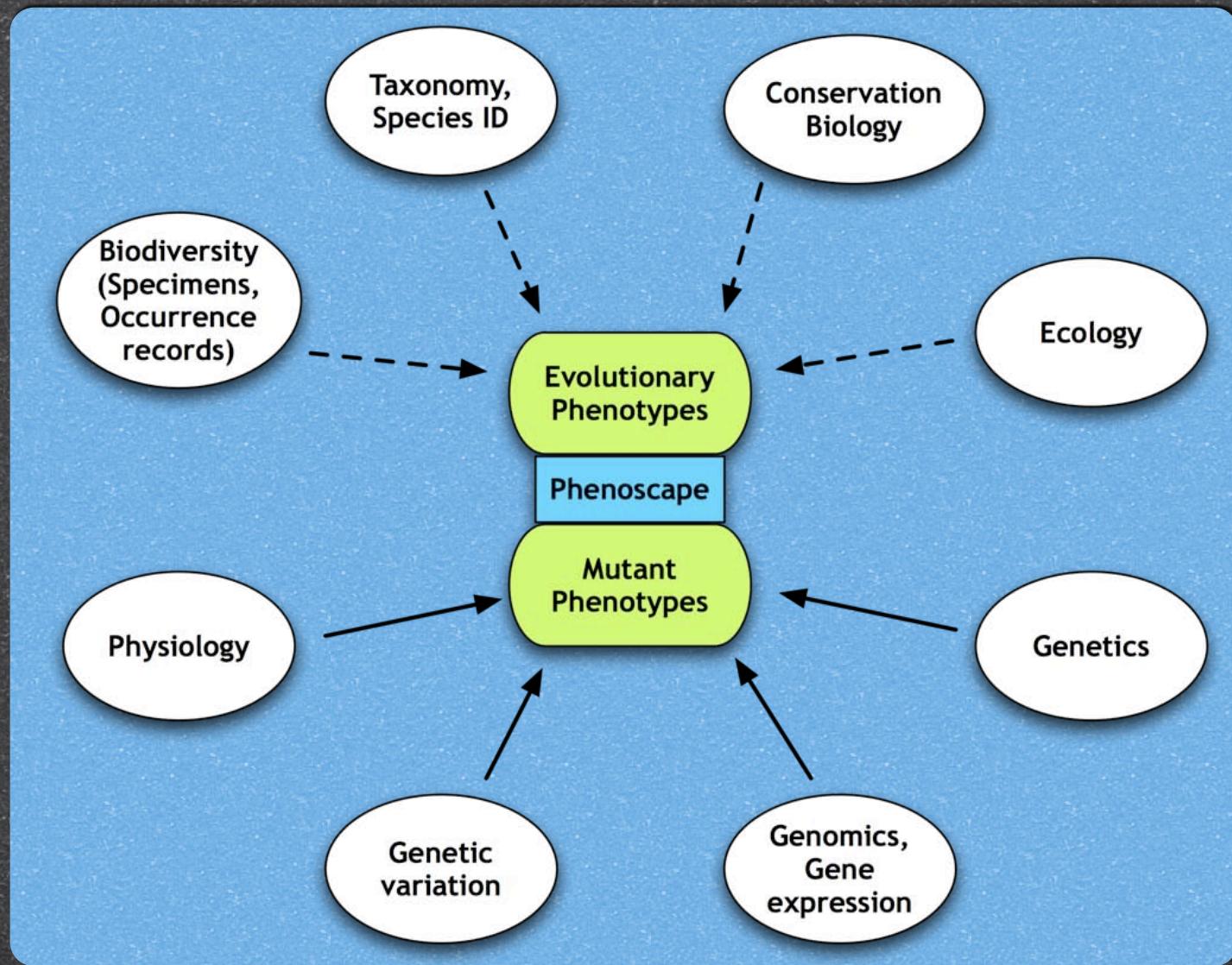
Dear Colleagues,

A few questions: At what level are you trying to define the infraorbital series of bones? At the teleostean basal level or at the ostariophysi level? The possible definitions presented in the last messages show a combination of alternatives that result from the fact that different teleostean levels are being used.

Probably, it may help if I define for you the conditions at the basal teleostean level:

The series of infraorbital bones at the basal teleostean level may have > the 7th or the 6th bone (the most dorsoposterior element). At this level, the common condition for the bone named dermosphenotic is the division of the canal in two branched: one that it may be associated to the supraorbital canal (or end blind in the bone) and other that is the infraorbital canal that joins the otic canal. From this pattern, there are many evolutionary transformation so that infraorbital 7 and 6 are lost, so that the dermosphenotic becomes the 5th bone of the series. Also the connections of the infraorbital canal with the supraorbital and or otic canals may be lost or modified in different teleostean subgroups.

Systematic morphology can be part of data-rich biology



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S. Lewis, C. Mungall