Wide phenotype data

Querying semantic phenotypes with transcribed specimen data

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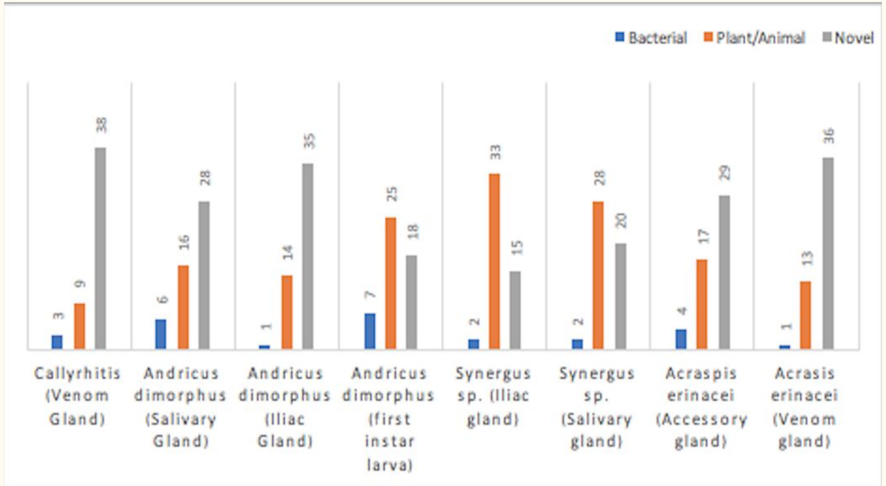
Big data...wide data

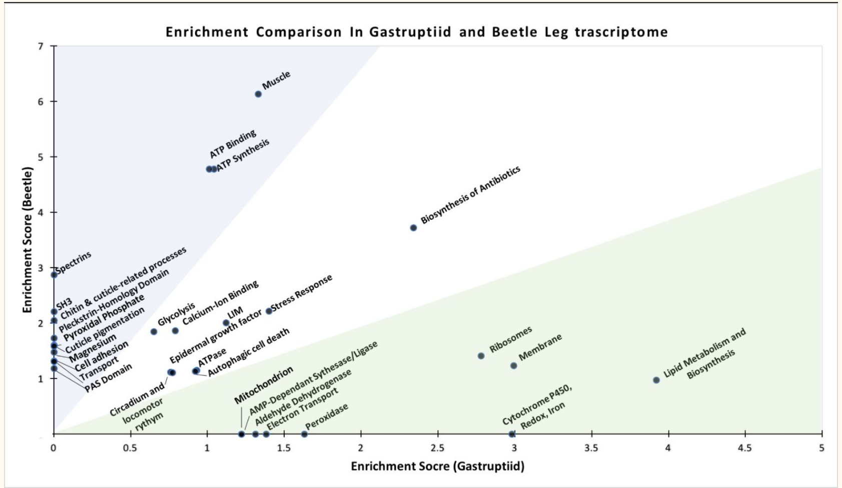
“a term for data sets that are so large or complex that **traditional** data processing application software is **inadequate** to deal with them”

Transcriptomics

Gall induction

Fat in the leg

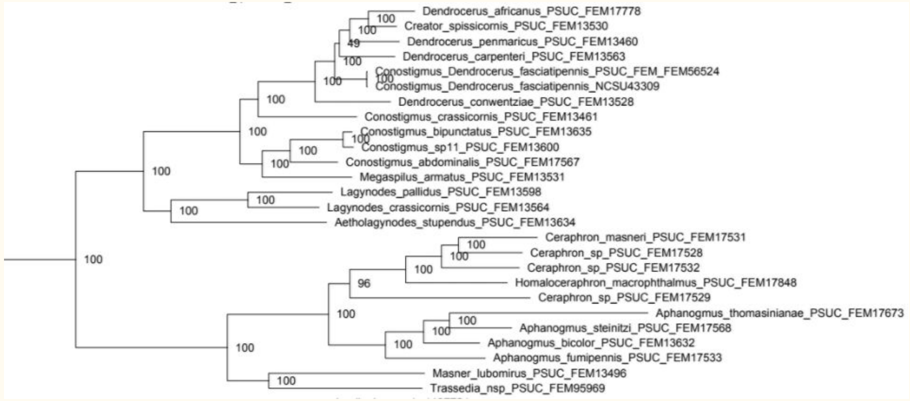




Heather Hines, Sarthok (PSU)

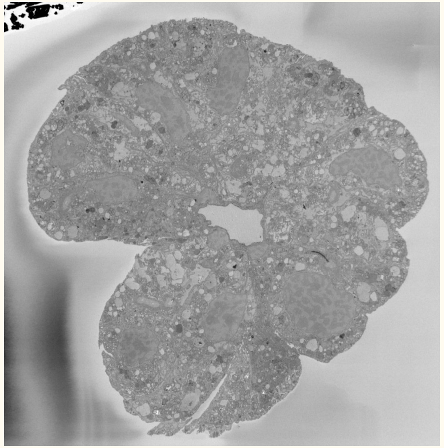
Phylogenomics

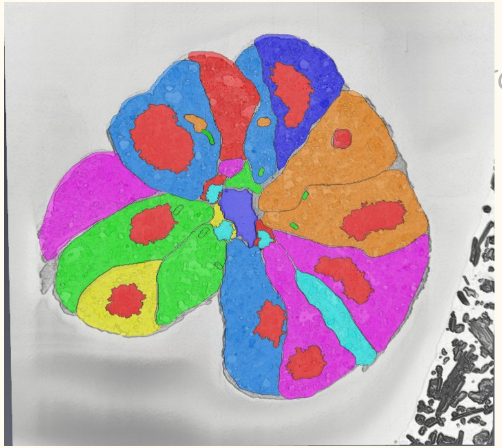
specimen ID	Taxon	LOCI	READ COUNTS
PSUC13601	*Trichosteresis_glabra_BBP343*	**118**	195663
PSUC_FEM13531	*Megaspilus_armatus_BBP344*	**768**	606651
PSUC_FEM17567	*Conostigmus_abdominalis_BBP345*	**1646**	3261473
PSUC_FEM13461	*Conostigmus_crassicornis_BBP346*	**1032**	1113540
PSUC_FEM13635	*Conostigmus_bipunctatus_BBP347*	**1507**	3661418
PSUC_FEM13600	*Conostigmus_sp11_BBP348*	**1335**	2093855
NCSU43309	*Conostigmus_Dendrocerus_fasciatipennis_BBP349*	**1590**	3751733
PSUC_FEM_FEM56524	*Conostigmus_Dendrocerus_fasciatipennis_BBP350*	**1220**	1210643
PSUC_FEM17778	*Dendrocerus_africanus_BBP352*	**990**	1083301
PSUC_FEM13460	*Dendrocerus_penmaricus_BBP353*	**958**	1092439
PSUC_FEM13528	*Dendrocerus_conwentziae_BBP354*	**1416**	3033925
PSUC_FEM13563	*Dendrocerus_carpenteri_BBP355*	**1319**	1367755
PSUC_FEM13566	*Dendrocerus_wollastoni_BBP356*	**61**	140598
PSUC_FEM13530	*Creator_spissicornis_BBP357*	**1219**	2256146
PSUC_FEM13564	*Lagynodes_crassicornis_BBP358*	**1334**	2079628
PSUC_FEM13598	*Lagynodes_pallidus_BBP359*	**1260**	1841397
PSUC_FEM13458	*Aetholagynodes_stupendus_BBP360*	**122**	1755745
PSUC_FEM13634	*Aetholagynodes_stupendus_BBP361*	**444**	4266208
PSUC_FEM13496	*Masner_lubomirus_BBP362*	**826**	1118863
PSUC_FEM13599	*Gnathoceraphron_sp_BBP365_BBP407*	**67**	239480
PSUC_FEM13457	*Elysoceraphron_sp_BBP366*	**151**	933832
PSUC_FEM17533	*Aphanogmus_fumipennis_BBP367*	**1340**	2855879
PSUC_FEM13632	*Aphanogmus_bicolor_BBP368*	**1515**	4115372
PSUC_FEM17603	*Aphanogmus_fasciatipennis_BBP369_BBP408*	**166**	318215
PSUC_FEM17568	*Aphanogmus_steinitzi_BBP370*	**1630**	5800207
PSUC_FEM17531	*Ceraphron_masneri_BBP372*	**1153**	1504156
PSUC_FEM17532	*Ceraphron_sp_BBP373*	**1051**	1197400
PSUC_FEM17528	*Ceraphron_sp_BBP374*	**1167**	1525923
PSUC_FEM13459	*Pteroceraphron_mirabilipennis_BBP377*	**207**	660555
PSUC_FEM17527	*Kenitoceraphron_heptamerus_BBP378*	**58**	216160
PSUC_FEM17708	*Ecitonetes_subapterus_BBP379*	**28**	91307
PSUC_FEM13633	*Cyoceraphron_sp_BBP406*	**202**	113562
PSUC_FEM17673	*Aphanogmus_thomasinianae_BBP409*	**495**	345305
PSUC_FEM17529	*Ceraphron_sp_BBP410*	**755**	742153
PSUC_FEM17848	*Homaloceraphron_macrophthalmus_BBP411*	**936**	3659795
PSUC_FEM95969	*Trassedia_nsp_BBP412*	**671**	3495279

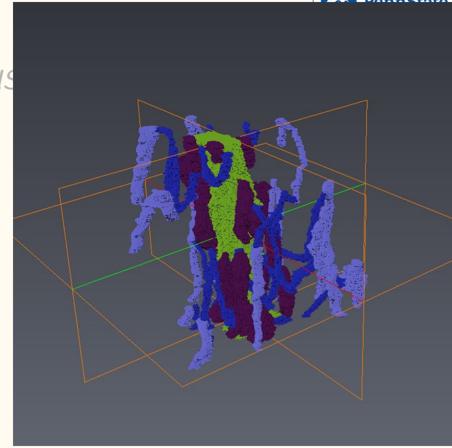


Bonnie Blaimer, Sean Brady, Matthew Buffington (Smithsonean Institute)

3D sr-μCT







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Perspective

Finding Our Way through Phenotypes

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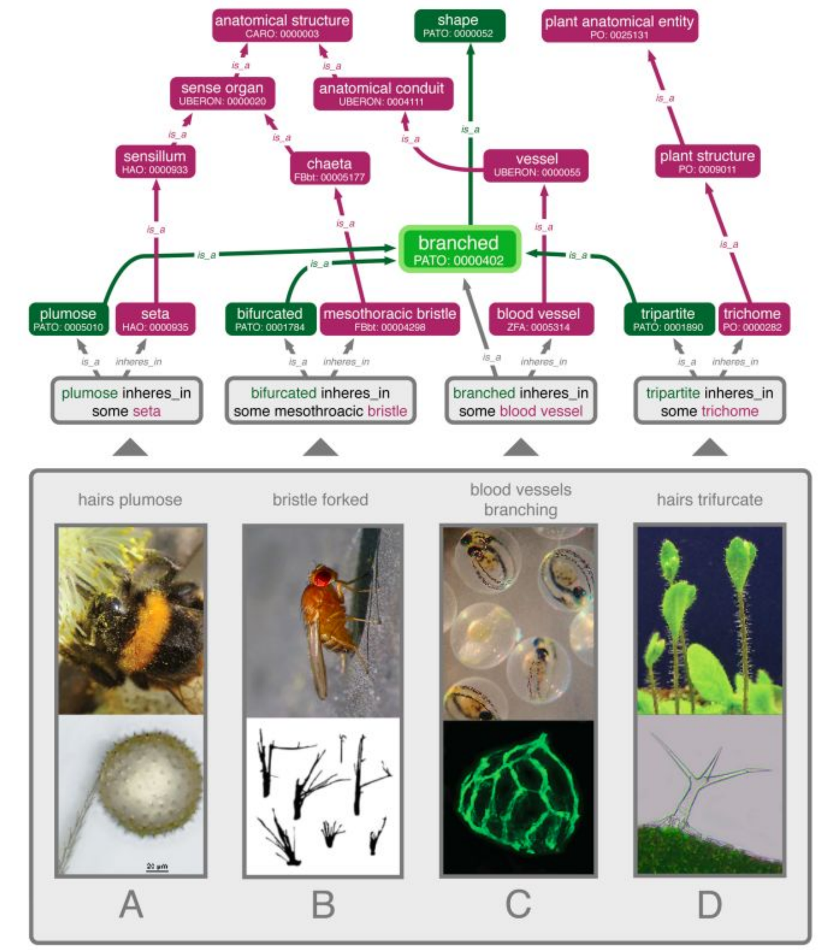
Abstract

Despite a large and multifaceted effort to understand the vast landscape of phenotypic data, their current form inhibits productive data analysis. The lack of a community-wide, consensus-based, human- and machine-interpretable language for describing phenotypes and their genomic and environmental contexts is perhaps the most pressing scientific bottleneck to integration across many key fields in biology, including genomics, systems biology, development, medicine, evolution, ecology, and systematics. Here we survey the current phenomics landscape, including data resources and handling, and the progress that has been made to accurately capture relevant data descriptions for phenotypes. We present an example of the kind of integration across domains that computable phenotypes would enable, and we call upon the broader biology community, publishers, and relevant funding agencies to support efforts to surmount today's data barriers and facilitate analytical reproducibility.



Phenotypes?

Description. Female. Body length 255–358 (n=4, slide specimens) (dry length of one paratype before slide mounting 264). Dark brown (presumably), appendages apparently lighter in colour (cleared specimens so colour not really known). Fore wing margin in apical half narrowly but distinctly margined with brown, otherwise with faint uniform brown suffusion over most of surface except partly behind venation.

Head. Head width 123–135 (n=3). Face with 7 setae on each side (Fig. 9) and with faint reticulate sculpture. Mouthparts (Figs 9, 10) with mandible about as long as maxilla and with 5 teeth, the two ventral ones large, the 3 dorsal ones small and in one specimen a small tooth between the large ventral ones (Figs 9, 10). Occiput with vertexal suture (= supraorbital suture extension onto occiput) long and in line with supraorbital trabecula, only weakly diverging from posterior eye margin.

Antenna. Scape on inner surface and pedicel with longitudinally reticulate sculpture; funicle 5-segmented, with 1 mps on fl_1–fl_4 and 2 mps on fl_5 (Fig. 8, 15), the mps unusually wide (Figs 7, 8); clava with 6 mps. Measurements (length/width, n = 3 or 4) of antennal segments: scape 53–60/12–16, pedicel 29–34/20–22, fl_1 35–37/11–12, fl_2 33–35/10–12, fl_3 32–34/10–11, fl_4 33–35/10–12, fl_5 38–42/13–16, clava 79–86/19–23. Length/width ratios of antennal segments: scape 3.29–4.26, pedicel 1.52–1.66, fl_1 3.10–3.41, fl_2 3.19–3.63, fl_3 3.04–3.44, fl_4 3.04–3.48, fl_5 2.60–2.79, clava ≈3.69–4.55 (clava not always oriented in perfect lateral view).

Mesosoma. Mesoscutum width 82–90 (n=3), with coarse reticulate sculpture, the cells irregularly shaped but more longitudinally stretched on midlobe, more isodiametric anteriorly on lateral lobe (Fig. 7); scutellum with coarse reticulate sculpture, the cells smaller on anterior scutellum, larger and more transversally stretched on frenum (Fig. 7); dorsellum apparently smooth (Figs 11, 12; propodeum with sculpture as on frenum (Figs 11, 12). Mesoscutal midlobe and axilla with relatively long setae.

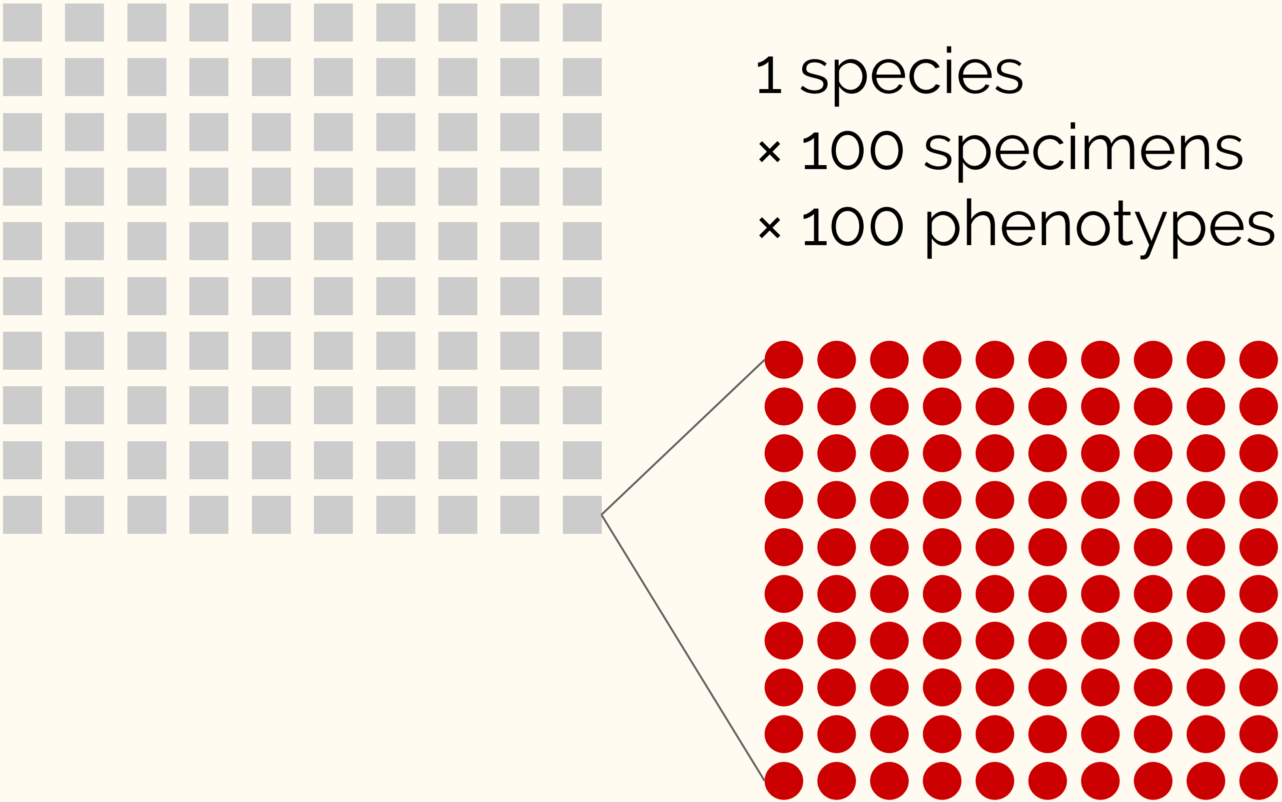
Wings. Fore wing narrow, beyond level of venation with evenly concave posterior margin and surface with one row of about 10 microtrichia extending from stigmal vein almost to wing apex and a second row extending proximally from socketed seta at apex of frenal fold to just past base of parastigma (Fig. 13). Hind wing without microtrichia on surface between the usual anterior and posterior rows. Fore wing length (n=4) 394–428, width 30–33, length/width 13.0–13.5, longest marginal setae ≈106–127. Hind wing length 376–414, width 13–15, longest marginal setae 86–94.

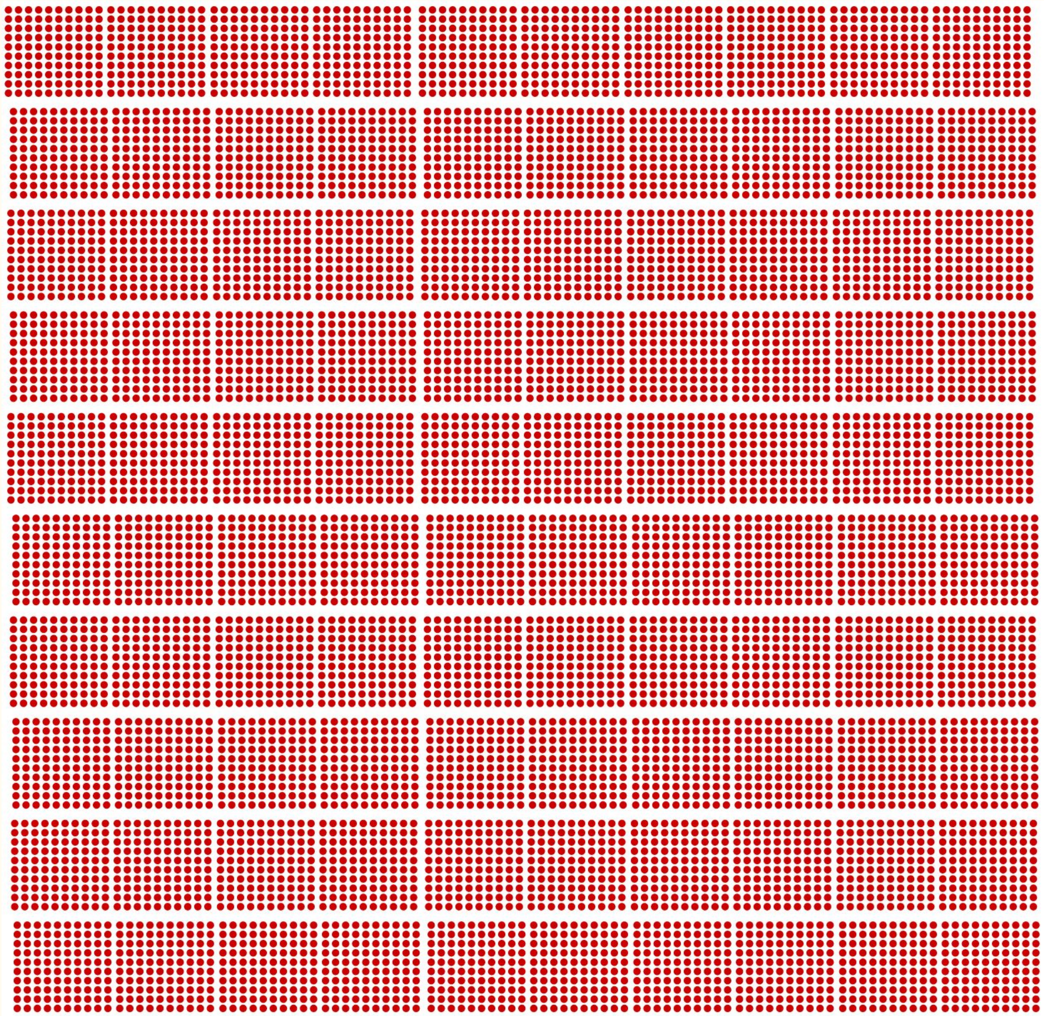
Legs. Metatarsomere 1 0.78–0.92 × as long as metatarsomere 2 (Fig. 14).

Metasoma. Ovipositor length 124–129 (n=4), 1.13–1.20 × as long as metatibia length (104–114) and extending slightly forward of junction between mesosoma and metasoma (Fig. 14, gaster slightly crushed and poorly oriented).

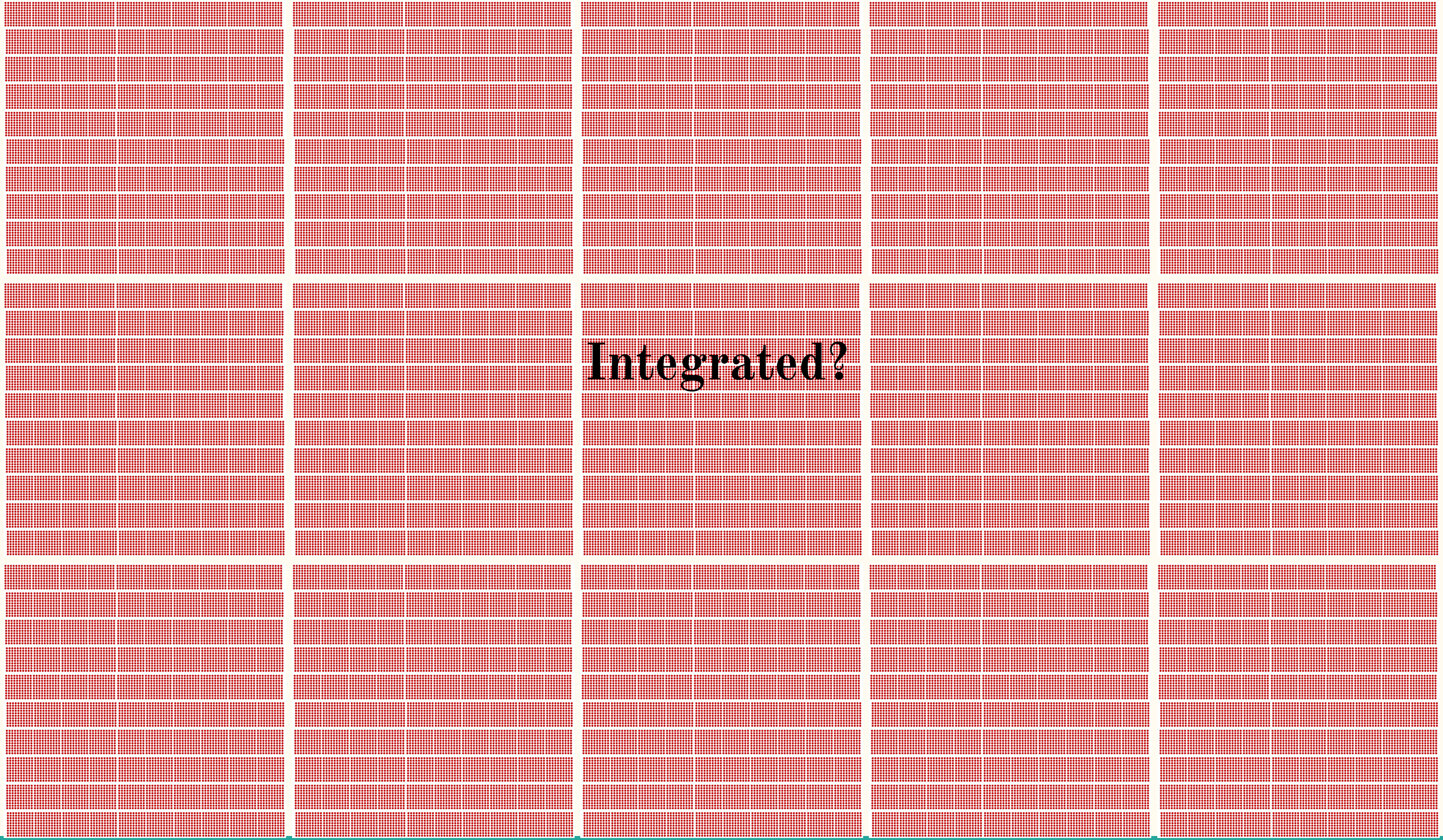
Huber and Triapitsyn (2013)

1 species
× 100 specimens
× 100 phenotypes per specimen





10,000 phenotypes per species


Integrated?

Approaches to phenotype data integration

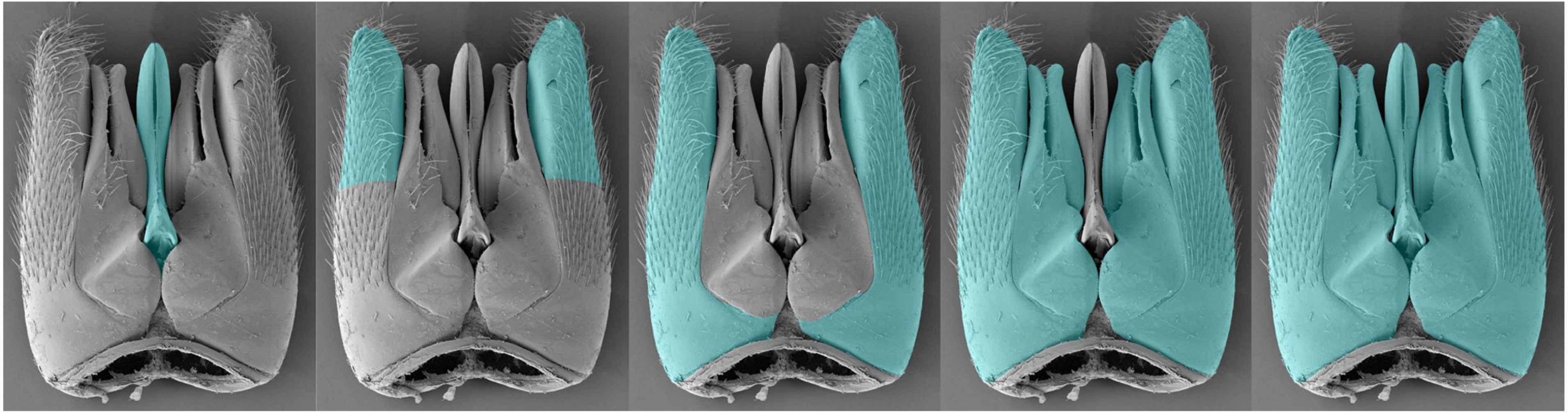
Legacy data processing (mining phenotypes from published works)

- Charaparser (Cui 2012)
- Phenex (Balhoff 2010)

De-novo semantic phenotypes

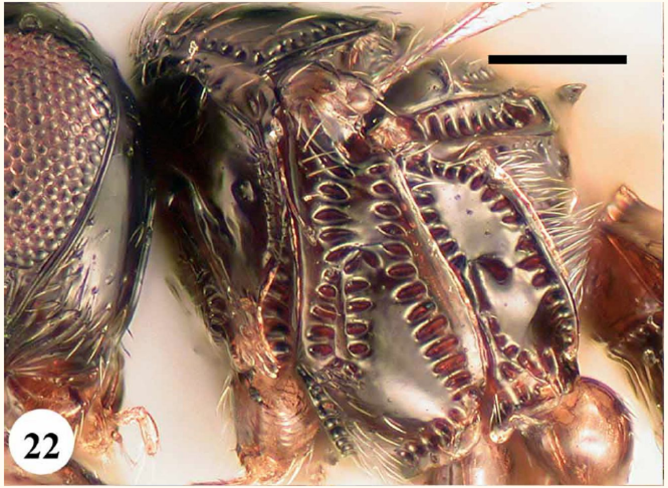
- SP's Balhoff et al. 2013

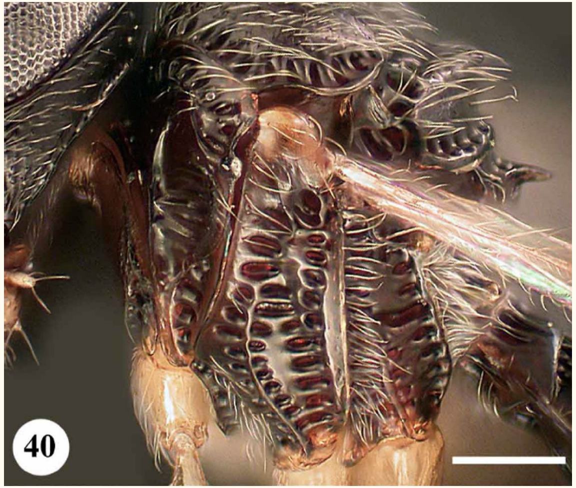
Data mining application based on label match
Homonymy



DOI: 10.1371/journal.pone.0015991

Anatomy descriptions = Figure legends



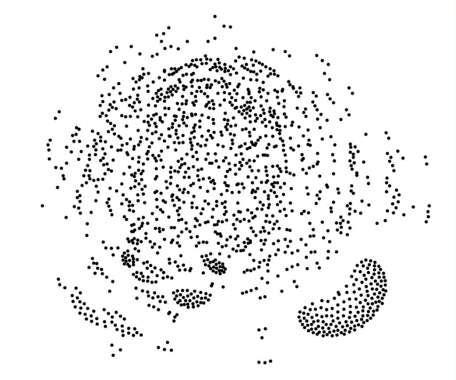


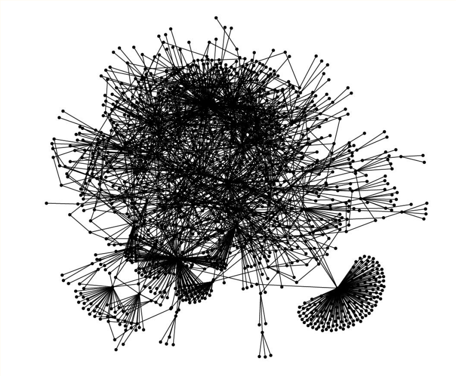
"Mesopleural carina incomplete"

Mikó et al. 2010

Formalized Anatomy: the foundation for big phenotypes data

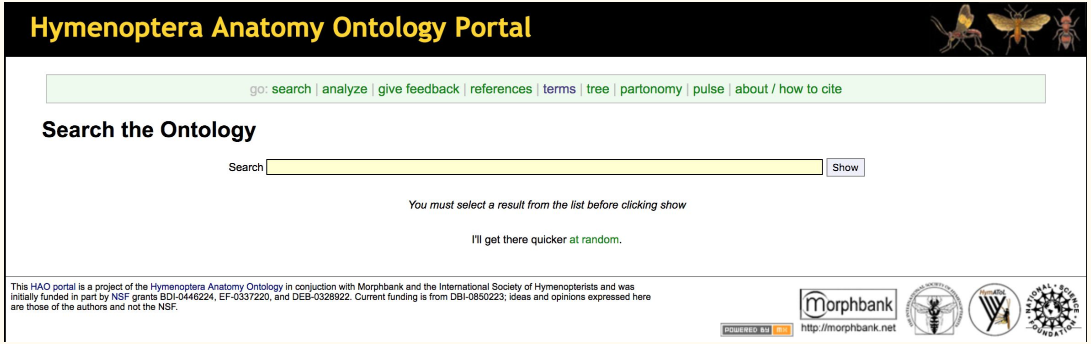
Ontologies and other knowledge organization systems

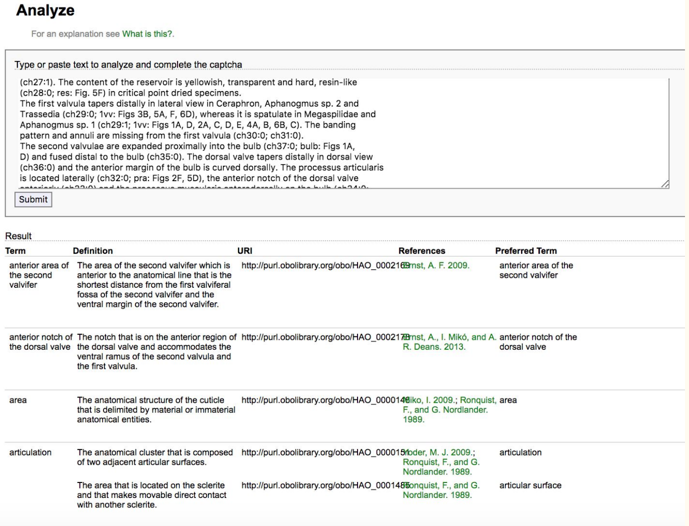




Hymenoptera Anatomy Ontology

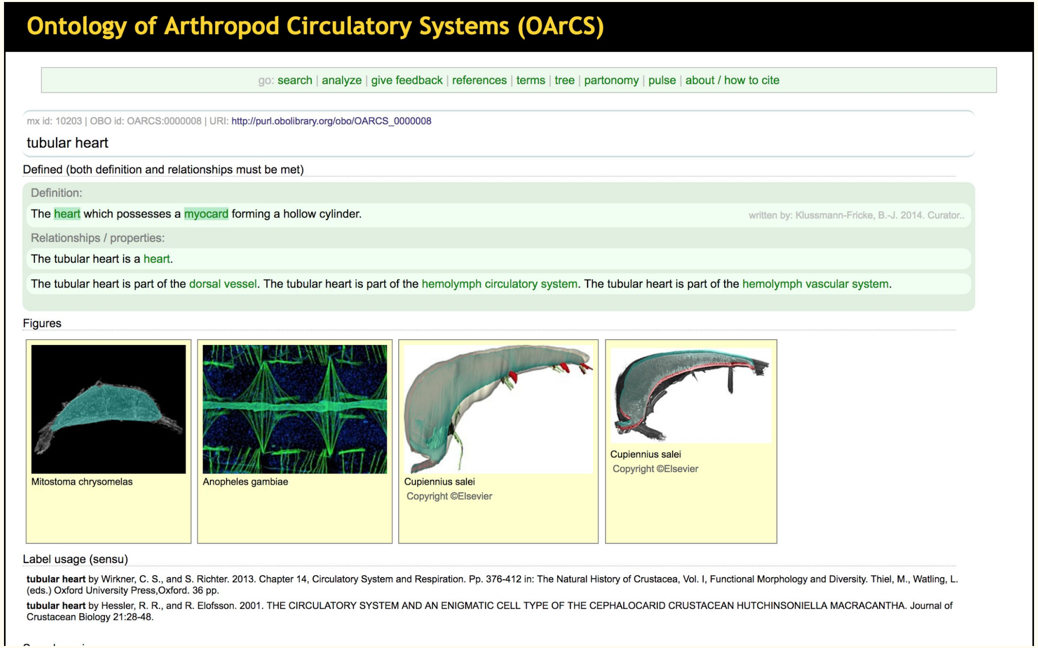
HAO Portal, URI tables





Term	Definition	URI	References	Preferred Term
anterior area of the second valvifer	The area of the second valvifer which is anterior to the anatomical line that is the shortest distance from the first valviferal fossa of the second valvifer and the ventral margin of the second valvifer.	http://purl.obolibrary.org/obo/HAO_0002169	Ernst, A. F. 2009.	anterior area of the second valvifer
anterior notch of the dorsal valve	The notch that is on the anterior region of the dorsal valve and accommodates the ventral ramus of the second valvula and the first valvula.	http://purl.obolibrary.org/obo/HAO_0002178	Ernst, A., I. Mikó, and A. R. Deans. 2013.	anterior notch of the dorsal valve
area	The anatomical structure of the cuticle that is delimited by material or immaterial anatomical entities.	http://purl.obolibrary.org/obo/HAO_0000146	Miko, I. 2009.; Ronquist, F., and G. Nordlander. 1989.	area
articulation	The anatomical cluster that is composed of two adjacent articular surfaces.	http://purl.obolibrary.org/obo/HAO_0000151	Yoder, M. J. 2009.; Ronquist, F., and G. Nordlander. 1989.	articulation
	The area that is located on the sclerite and that makes movable direct contact with another sclerite.	http://purl.obolibrary.org/obo/HAO_0001485	Ronquist, F., and G. Nordlander. 1989.	articular surface

OArCS



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The First Organ-Based Ontology for Arthropods (Ontology of Arthropod Circulatory Systems - OArCS) and its Integration into a Novel Formalization Scheme for Morphological Descriptions

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Abstract.—Morphology, the oldest discipline in the biosciences, is currently experiencing a renaissance in the field of comparative phenomics. However, morphological/phenotypic research still suffers on various levels from a lack of standards. This shortcoming, first highlighted as the "linguistic problem of morphology", concerns the usage of terminology and also the need for formalization of morphological descriptions themselves, something of paramount importance not only to the field of morphology but also when it comes to the use of phenotypic data in systematics and evolutionary biology. We therefore argue, that for morphological descriptions, the basis of all systematic and evolutionary interpretations, ontologies need to be utilized which are based exclusively on structural qualities/properties and which in no case include statements about homology and/or function. Statements about homology and function constitute interpretations on a different or higher level. Based on these "anatomy ontologies", further ontological dimensions (e.g., referring to functional properties or homology) may be exerted for a broad use in evolutionary phenomics. To this end we present the first organ-based ontology for the most species-rich animal group, the Arthropoda. Our Ontology of Arthropod Circulatory Systems (OArCS) contains a comprehensive collection of 383 terms (i.e., labels) tied to 296 concepts (i.e., definitions) collected from the literature on phenotypic aspects of circulatory organ features in arthropods. All of the concepts used in OArCS are based exclusively on structural features, and in the context of the ontology are independent of homology and functional assumptions. We cannot rule out that in some cases, terms are used which in traditional usage and previous accounts might have implied homology and/or function (e.g. heart, sternal artery). Concepts are composed of descriptive elements that are used to classify observed instances into the organizational framework of the ontology. That is, descriptions in ontologies are only descriptions of individuals if they are necessary/and or sufficient representations of attributes (independently) observed and recorded for an individual. In addition, we here present for the first time an entirely new approach to formalizing phenotypic research, a semantic model for the description of a complex organ system in a highly disparate taxon, the arthropods. We demonstrate this with a formalized morphological description of the hemolymph vascular system in one specimen of the European garden spider *Araneus diadematus*. Our description targets five categories of descriptive statement: "position", "spatial relationships", "shape", "constituents", and "connections", as the corresponding formalizations constitute exemplary patterns useful not only when talking about the circulatory system, but also in descriptions in general. The downstream applications of computer-parsable morphological descriptions are widespread, with their core utility being the fact that they make it possible to compare collective description sets in computational time, that is, very quickly. Among other things, this facilitates the identification of phenotypic plasticity and variation when single individuals are compared, the identification of those traits which correlate between and within taxa, and the identification of links between morphological traits and genetic (using GO, Gene Ontology) or environmental (using ENVO, Environmental Ontology) factors. [Arthropoda; concept; function; hemolymph vascular system; homology; terminology.]

Morphology Needs Ontologies

Well-established, linked, and consolidated resources for describing phenotypic features are standard for genetic data (e.g., "NCBI, http://www.ncbi.nlm.nih.gov", "http://flybase.org", etc.), but despite previous calls for more investment in the area of phenotypic research (e.g. Trelease 2006; Houle et al. 2010), analogous resources for morphology are in their infancy (Deans et al. 2015). Federated and integrated morphological knowledge bases cannot be derived from classical phenotypic characterizations using classical terminology, as the use of different vocabularies means that such characterizations are often not comparable. This central and well-known problem has been termed the "linguistic problem of morphology" (Vogt et al. 2010)—and it extends from the lack of a commonly accepted, standardized, and taxon-independent morphological terminology to the lack of a commonly accepted standardized and formalized method for describing morphological traits. An increasingly popular solution to the lack of standardized vocabularies is the use of software-based ontologies. Ontologies make the semantic scope of a given term comparable, inferable, and queryable. This means that through the properties linking different concepts with each other, a term is understandable in its context.

As nothing in biology makes sense except in the light of evolution (Dobzhansky 1973), phenotypic research is necessarily concerned, among other things, with one of the most central evolutionary concepts,

Wirkner et al. 2017. *Systematic Biology*

Semantic statement model Entity attribute: value

Antennal shelf count: absent	not (has part some antennal shelf)	not (has part some antennal shelf)	
Antennal shelf count: present	has part some antennal shelf	has part some antennal shelf	
Anterior tentorial pit count: present	has part some anterior tentorial pit		
Anterior tentorial pit shape: elongate	has part some (anterior tentorial pit and (bearer of some elongated))		
Anterior tentorial pit shape: point-like	has part some (anterior tentorial pit and (bearer of some punctiform))		
Anterodistal notch of the fore wing count: absent	not (has part some anterodistal notch of the fore wing)		
Anterodistal notch of the fore wing count: present	has part some anterodistal notch of the fore wing		
Anterolateral mesopectal projection 2-d shape: isosceles triangular	has part some (anterolateral mesopectal projection and (has part some (lateral side and (bearer of some isosceles triangular))))	has part some (mesopectus and (has part some (corner and (is bearer of some isosceles triangular))))	

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A Semantic Model for Species Description Applied to the Ensign Wasps (Hymenoptera: Evaniidae) of New Caledonia

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Associate Editor: Thomas Buckley

Abstract.—Taxonomic descriptions are unparalleled sources of knowledge of life's phenotypic diversity. As natural language prose, these data sets are largely refractory to computation and integration with other sources of phenotypic data. By formalizing taxonomic descriptions using ontology-based semantic representation, we aim to increase the reusability and computability of taxonomists' primary data. Here, we present a revision of the ensign wasp (Hymenoptera: Evaniidae) fauna of New Caledonia using this new model for species description. Descriptive matrices, specimen data, and taxonomic nomenclature are gathered in a unified Web-based application, mx, then exported as both traditional taxonomic treatments and semantic statements using the OWL Web Ontology Language. Character:character-state combinations are then annotated following the entity–quality phenotype model, originally developed to represent mutant model organism phenotype data; concepts of anatomy are drawn from the Hymenoptera Anatomy Ontology and linked to phenotype descriptors from the Phenotypic Quality Ontology. The resulting set of semantic statements is provided in Resource Description Framework format. Applying the model to real data, that is, specimens, taxonomic names, diagnoses, descriptions, and redescriptions, provides us with a foundation to discuss limitations and potential benefits such as automated data integration and reasoner-driven queries. Four species of ensign wasp are now known to occur in New Caledonia: *Szepligetella levipetiolata*, *Szepligetella deercreeki* Deans and Mikó sp. nov., *Szepligetella irwini* Deans and Mikó sp. nov., and the nearly cosmopolitan *Evania appendigaster*. A fifth species, *Szepligetella sericea*, including *Szepligetella impressa*, syn. nov., has not yet been collected in New Caledonia but can be found on islands throughout the Pacific and so is included in the diagnostic key. [Biodiversity informatics; Evaniidae; New Caledonia; new species; ontology; semantic phenotypes; semantic species description; taxonomy.]

Taxonomic descriptions constitute an invaluable source of knowledge about phenotypic diversity across the living world. However, these phenomic annotations are not readily accessed and reused by other biological scientists (Deans et al. 2012). Instead, they are "locked away" in the taxonomic literature, written for, and consumed almost exclusively by, taxonomists. While electronic availability of taxonomic treatments is rapidly growing, reflected in changes to publication requirements (International Commission on Zoological Nomenclature 2012), and accelerated by digitization efforts such as the Biodiversity Heritage Library (http://www.biodiversitylibrary.org/ last accessed May 13, 2013), the constituent phenotypic descriptions are composed in natural language (NL), typically making use of specialized anatomical terminology. These phenotypic descriptions are difficult to data-mine (though see Cui (2012); Thessen et al. (2012)); one reason for this is rampant homonymy and synonymy across anatomical concepts (Yoder et al. 2010). We recently proposed that the application of ontological annotation to taxonomic descriptions, as semantic phenotypes (SPs), would allow a broader array of researchers to apply powerful data integration, search, and automated reasoning techniques to these data, increasing the value of taxonomic work and promoting its reuse (Deans et al. 2012).

An ontology is a formal representation of concepts within a domain and the logical relationships between those concepts, supporting knowledge representation with explicit semantics. By referencing standard, shared concepts, diverse data sets can be aggregated and computed over coherently (Washington et al. 2009; Walls et al. 2012). Biological ontologies have become a standard tool for organizing and accessing genomic and phenotypic data from taxonomically isolated model species (Mungall et al. 2010). Applying these tools to the representation and dissemination of comparative descriptive data offers a means to make connections of phenotypic and genomic information across these different, but closely related, sciences (Mabee et al. 2007; Deans et al. 2012).

The Phenoscape project has pioneered the application of ontological annotation to evolutionary phenotypes, by annotating morphological character matrix data sets from the published fish systematics literature (Dahdul et al. 2010a), and demonstrating semantic correspondences to mutant phenotype annotations from the Zebrafish Information Network, ZFIN (Mabee et al. 2012). We believe that taxonomists can build on this approach by incorporating ontological annotation into descriptions at the time of publication, thereby increasing the efficiency and scalability of SP annotation. As taxonomists adopt this approach, tools may be developed that facilitate referencing and integrating with existing semantic data as part of the process of creating new descriptions. Here, we discuss our first steps toward meeting this goal by describing a

Insect Systematics & Evolution 44 (2013) 261–347

Male terminalia of Ceraphronoidea: morphological diversity in an otherwise monotonous taxon

István Mikó, Lubomir Masner, Eva Johannes, Matthew J. Yoder and Andrew R. Deans

ZooKeys 569: 53–69 (2016) doi: 10.3897/zookeys.569.6629

RESEARCH ARTICLE

***Dendrocerus mexicali* (Hymenoptera, Ceraphronoidea, Megaspilidae): Novel antennal morphology, first description of female, and expansion of known range into the U.S.**

Kyle N. Burks, István Mikó, Andrew R. Deans

PeerJ

Malagasy *Conostigmus* (Hymenoptera: Ceraphronoidea) and the secret of scutes

István Mikó, Carolyn Trietsch, Emily L. Sandall, Matthew Jon Yoder, Heather Hines and Andrew Robert Deans

JHR 46: 137–150 (2015) doi: 10.3897/JHR.46.5534

RESEARCH ARTICLE

Redescription of *Conostigmus albovarius* Dodd, 1915 (Hymenoptera, Megaspilidae), a metallic ceraphronoid, with the first description of males

Carolyn Trietsch, Andrew R. Deans, István Mikó

PLOS ONE

Folding Wings like a Cockroach: A Review of Transverse Wing Folding Ensign Wasps (Hymenoptera: Evaniidae: *Afrevania* and *Trissevania*)

István Mikó, Robert S. Copeland, James P. Balhoff, Matthew J. Yoder, Andrew R. Deans

ZooKeys 223: 1–38 (2012) doi: 10.3897/zookeys.223.3572

RESEARCH ARTICLE

A revision of *Evaniscus* (Hymenoptera, Evaniidae) using ontology-based semantic phenotype annotation

Patricia L. Mullins, Ricardo Kawada, James P. Balhoff, Andrew R. Deans

Syst. Biol. 66(5):754–768, 2017

The First Organ-Based Ontology for Arthropods (Ontology of Arthropod Circulatory Systems - OArCS) and its Integration into a Novel Formalization Scheme for Morphological Descriptions

Christian S. Wirkner, Torben Göpel, Jens Runge, Jonas Keiler, Bastian-Jesper Klussmann-Fricke, Katarina Huckstorf, Stephan Scholz, István Mikó, Matthew J. Yoder, and Stefan Richter

PLOS ONE

RESEARCH ARTICLE

Taxonomic Synopsis of the Ponto-Mediterranean Ants of *Temnothorax nylanderi* Species-Group

Sándor Csősz, Jürgen Heinze, István Mikó

JHR 53: 77–162 (2016) doi: 10.3897/jhr.53.9890

RESEARCH ARTICLE

New *Dryocosmus* Giraud species associated with *Cyclobalanopsis* and non-*Quercus* host plants from the Eastern Palaearctic (Hymenoptera, Cynipidae, Cynipini)

Chang-Ti Tang, István Mikó, James A. Nicholls, Szabina Schwéger, Man-Miao Yang, Graham N. Stone, Frazer Sinclair, Miklós Bozsó, George Melika, Zsolt Pénzes

JHR 49: 1–23 (2016) doi: 10.3897/JHR.49.7714

RESEARCH ARTICLE

Revision of *Dvivarnus* (Scelionidae, Teleasinae)

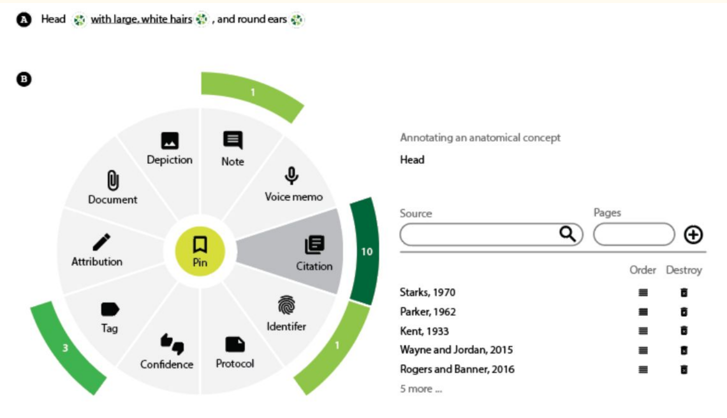
Elijah J. Talamas, István Mikó, Robert S. Copeland

Semantic statement model refined

tubular heart (count: 1) (xref: OARCS:0000008):
- shape: fusiform (PATO:000240) AND sigmoid (PATO:0001878) AND tubular (PATO:0002299)
- position: anterior-posterior axis (BSPO_0000013) AND dorso-medial region (BSPO_0000069) AND posterior region (BSPO_0000072)
- spatial relation: located_in (RO_0001025) opisthosoma (SPD_0000003) AND anterior margin (BSPO_0000671): posterior margin (BSPO_0000672) pedicel (SPD_0000006) AND posterior margin (BSPO_0000672): 2nd dorsoventral muscle (OARCS:000000)) AND parallel_to (BSPO.obo#parallel_to) dorso-medial region   (BSPO_0000069): opisthosoma (SPD:0000003) AND dorsal_to (BSPO_0000089) posterior midgut (SPD:0000131)
- constituents: first ostium (xref: OARCS:0000143) AND second ostium (xref: OARCS:0000142) AND third ostium (xref: OARCS:0000093) AND epicard (xref: OARCS:0000187) AND myocard (xref: OARCS:0000018)
- connections: gives_rise_to (Xref: OArCS:gives_rise): anterior aorta system (xref: OARCS:0000102) AND posterior aorta system (xref: OARCS:0000080) AND first cardiac artery system (xref: OARCS:0000025) AND second cardiac artery system (xref: OARCS:0000097) AND third cardiac artery system (xref: OARCS:0000098) AND attached_to (RO_0002371): dorsal ligament (xref: OARCS:0000203) (count: 10) AND lateral ligament (xref: OARCS:0000196) (count: 9 pairs) AND ventral ligament (xref: OARCS:0000200) (count: 3 pairs)

has part exactly 1 (tubular heart and ((attached to exactly 3 (ventral ligament and (contralateral_to exactly 1 ventral ligament))) and (attached to exactly 9 (lateral ligament and (contralateral_to exactly 1 lateral ligament)))) and (part of some dorso-medial region) and (part of some posterior region) and (part of some opisthosoma) and (has part some myocard) and (has partsome epicard) and (has part some (anterior margin and (adjacent to some (posterior margin and (part of some pedicel))))) and (has part some (posterior margin and (adjacent to some second dorsoventral muscle))) and (dorsal_to some posterior midgut) and (bearer of some sigmoid) and (bearer of some tubular) and (bearer of some fusiform) and (_gives_rise some posterior aorta system) and (_gives_rise some anterior aorta system) and (parallel_to some anterior-posterior axis) and (parallel_to some (dorso-medial region and (part of some opisthosoma))) and (has component exactly 2 (third ostium and (contralateral_to exactly 1 third ostium))) and (has component exactly 2 (second ostium and (contralateral_to exactly 1 second ostium))) and (has component exactly 2 (first ostium and (contralateral_to exactly 1 first ostium))) and (attached toexactly 10 dorsal ligament) and (_gives_rise exactly 1 (first cardiac artery system and (contralateral_to exactly 1 first cardiac artery system))) and (_gives_rise exactly 1 (second cardiac artery system and (contralateral_to exactly 1 second cardiac artery system))) and (_gives_rise exactly 1 (third cardiac artery system and (contralateral_to exactly 1 third cardiac artery system)))

Interfaces



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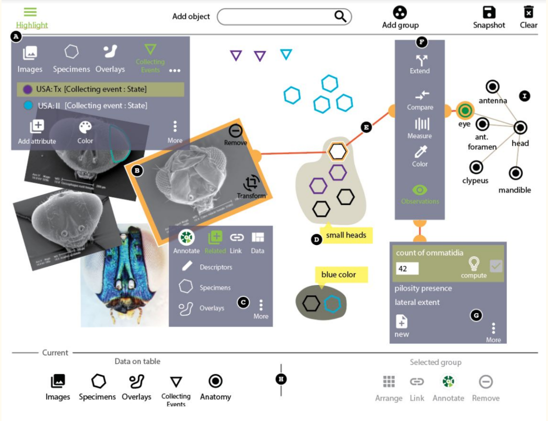
Starks, 1970
Parker, 1962
Kent, 1933
Wayne and Jordan, 2015
Rogers and Banner, 2016
5 more ...



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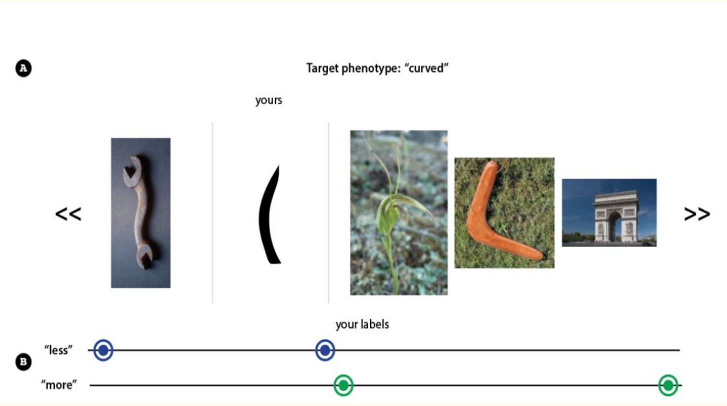

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Target phenotype: "curved"
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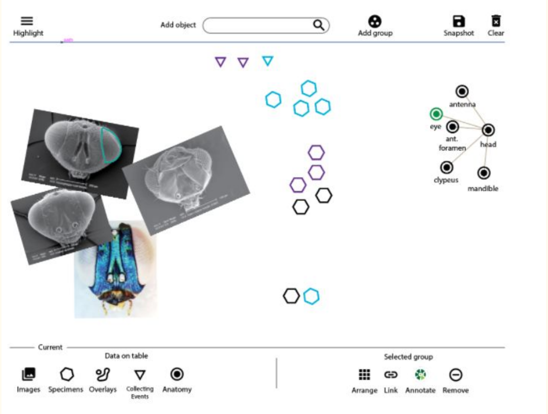
"more"



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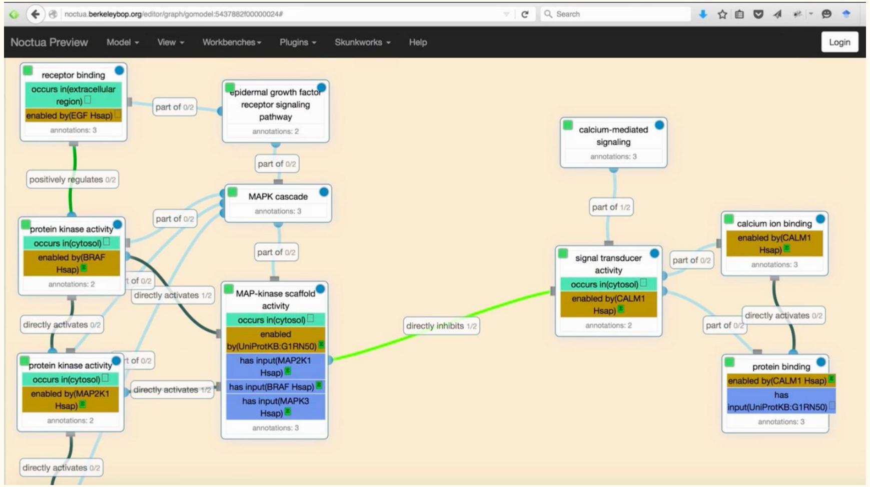
Konclude?



Computable evolutionary phenotype knowledge: a hands-on workshop

The Phenoscape project is hosting a hands-on workshop on Dec 11-14, 2017, at Duke University in Durham, North Carolina.

Evolutionary phenotype data that is amenable to computational data science, including computation-driven discovery, remains relatively new to science. Therefore use-cases and applications that effectively exploit these new capabilities are only beginning to emerge. If you are interested in discovering, linking to, recombining, or computing with machine-interpretable evolutionary phenotypes, this is the workshop for you!

The event will bring together a diverse group of people to collaboratively design and work hands-on on targets of their interest that take advantage and promote reuse of Phenoscape's online evolutionary data resources and services. The event is designed as a hands-on unconference-style workshop. Participants will break into subgroups to collaboratively tackle self-selected work targets.

The full Call for Participation, including motivation and scope, is posted here: https://hackmd.io/s/Sk6Xa7Eq-#

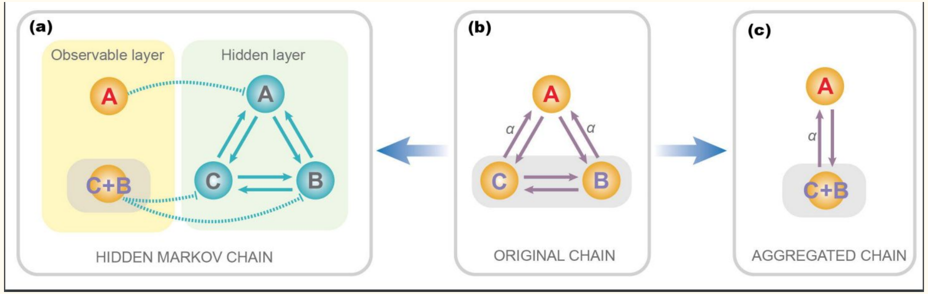
To apply to participate in the event, please fill out the application form by Oct 9, 2017. Travel sponsorship is available but limited, as is space.

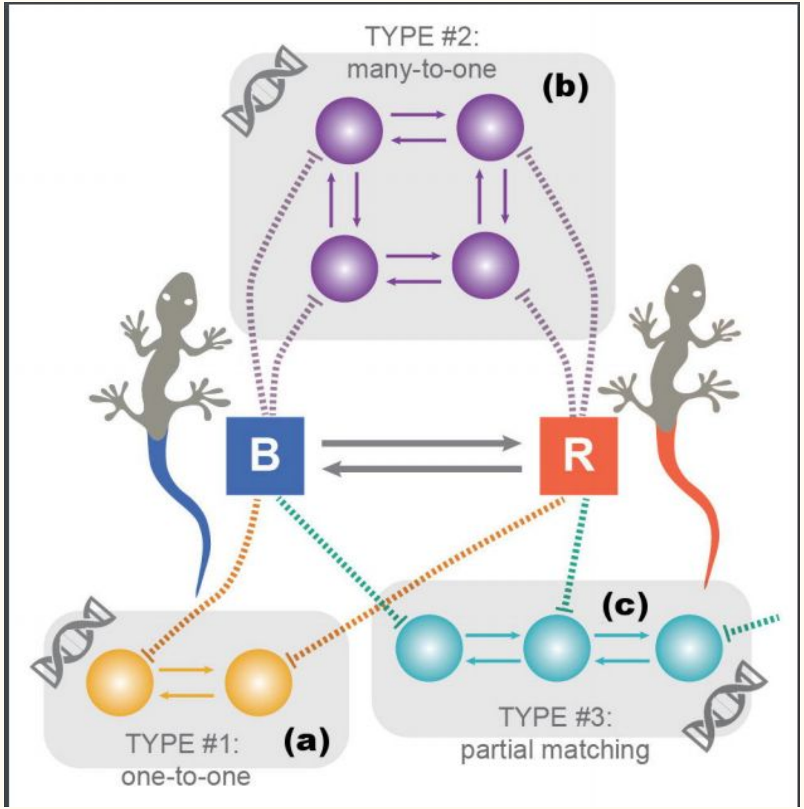
source

A new framework for modeling discrete phenotypic traits

Integration of anatomy ontologies and Evo-Devo using structured Markov chains

$$(A \otimes I_B + I_A \otimes B) \otimes I_C + I_{AB} \otimes C. \quad (7)$$





Tarasov 2017 http://dx.doi.org/10.1101/188672.

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- Thomas van de Kamp (Karlsruhe Institute of Technology)
- Aaron Smith (Northern Arizona University)

http://dx.doi.org/10.6084/m9.figshare.1606223