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BioNames: linking taxonomy, texts, and trees

BioNames is a web database of taxonomic names for animals, linked to the primary literature and, wherever possible, to phylogenetic trees. It aims to provide a taxonomic "dashboard" where at a glance we can see a summary of the taxonomic and phylogenetic information we have for a given taxon and hence provide a quick answer to the basic question "what is this taxon?" BioNames combines classifications from the Global Biodiversity Information Facility (GBIF) and GenBank, imagery from the Encyclopedia of Life (EOL), animal names from the Index of Organism Names (ION), and bibliographic data from multiple sources including the Biodiversity Heritage Library (BHL) and CrossRef. The user interface includes display of full text articles, interactive timelines of taxonomic publications, and zoomable phylogenies. It is available at http://bionames.org.

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Introduction

Large-scale digitisation of biodiversity data is underway on at least three broad fronts. The first, and perhaps the only category that is genuinely "born digital" is DNA sequencing (Benson et al. 2012). DNA barcoding (Hebert 2003) and, more recently, "metabarcoding" (Taberlet et al. 2012) is generating a flood of sequence data, much of it tied to a specific place and time. The contents of natural history collections are being digitised (Baird 2000), both the specimens themselves (Blagoderov et al. 2012) and metadata about those specimens. The latter is being aggregated by the Global Biodiversity Information Facility (GBIF; http://data.gbif.org) to provide an overview of the spatial distribution of life on Earth. Much of the biological literature is similarly being converted from physical to digital form, most notably by the Biodiversity Heritage Library (BHL; http://www.biodiversitylibrary.org). Taxonomic publication is becoming increasingly digital through rise of "mega" journals such as *Zootaxa* (http://www.mapress.com/zootaxa/), and semantically enriched journals such as *ZooKeys* (http://www.pensoft.net/journals/zookeys/).

The increasing use of sequence data has made taxonomic relationships readily computable (e.g., by building phylogenetic trees). Yet many DNA sequences are disconnected from classical taxonomy because they lack formal taxonomic names (Page 2011c; Parr et al. 2012). Barcoding has been responsible for a massive influx of these "dark taxa" into the sequence databases (Page 2011c). Many of these unnamed barcode taxa have since been suppressed by GenBank. But even without the barcoding sequences, dark taxa have been steadily increasing in number in recent years. Names may have a special place in the hearts of taxonomists (Patterson et al. 2010), but the pace of biodiversity discovery is outstripping our ability to put names on taxa, as evidenced by the rise of dark taxa in GenBank. There are increasing calls to adopt less formal taxonomic naming schemes (Schindel and Miller 2010), or to focus on describing biodiversity without necessarily naming it (Deans et al. 2012; Maddison et al. 2012). A significant challenge will be determining whether these dark taxa represent newly discovered taxa, or come from known taxa but have not been identified as such (Hibbett and Glotzer 2011; Nagy et al. 2011).

The vision of "Biodiversity Information on Every Desktop" (Edwards 2000) (perhaps updated to "biodiversity on every device") rests on our ability to not only digitise life (and the documents we have generated during centuries of cataloguing and studying biodiversity) but also to integrate the wealth of data emerging from sequencing machines and optical scanners. There are numerous points of contact between these different efforts, such as specimen codes, bibliographic identifiers, and GenBank accession numbers (Page 2008a; 2010). Figure 1 shows a simplified model of the core entities that make up taxonomy and related disciplines (e.g., systematics). The diagram is not meant to be exhaustive, nor does it attempt to rigorously define relationships in terms of one or more available ontologies. Instead, it simply serves as a way to visualise the links between taxon names, the publications (and authors and journals) where those names first appear, the application of those names to taxa, and data associated with those taxa (e.g., DNA sequence-based phylogenies).

Despite the wealth of possible connections between biodiversity data objects, the most commonly shared identifier that spans sequences, specimens, and publications remains the taxonomic name (Sarkar 2007; Patterson et al. 2010). We rely on names to integrate data, despite the potential ambiguity in what a given taxonomic name "means" (Kennedy et al. 2005; Franz and Cardona-Duque 2013). Unfortunately, it is often difficult to obtain information on a taxonomic name, either to track its origins and subsequent use, or to verify that it has been correctly used. Typically when taxonomic literature is cited in databases, it is typically as a text string with no link to the growing corpus of digitised literature. Hence taxonomic databases are little more than online collections of 5×3 index cards, technology taxonomy's founding father Linnaeus himself pioneered (Müller-Wille & Charmantier 2012). Ideally, for any given taxon name we should be able to see the original description, track the fate of that name through successive revisions, and see other related literature. At present this is almost impossible to do, even in well studied taxa.

EOL Challenge

In response to the Encyclopedia of Life (EOL) Computational Data Challenge (http://eol.org/info/323) I constructed BioNames (http://bionames.org) (Page 2012). Its goal is to create a database of taxonomic names linked to the primary literature and, wherever possible, to phylogenetic trees. Using existing globally unique identifiers for taxonomic names, concepts, publications, and sequences rather than cryptic text strings (for example, abbreviated bibliographic citations) simplifies the task of linking — we can rely on exact matching of identifiers rather than approximate matching between names for what may or may not be the same entity. This is particularly relevant once we start to aggregate information from different databases, where the same information (e.g., a publication) may be represented by different strings. Furthermore, if we use existing identifiers we increase the potential to connect to other databases (Page 2008a). This paper outlines how BioNames was built, describes the user interface, and discusses future plans.

Materials & Methods

BioNames integrates data on taxonomic names and classifications, literature, and phylogenies from a variety of sources. Given the inevitable differences in how different databases treat the same data (as well as internal inconsistencies within individual databases), considerable effort must be spent cleaning and reconciling data. Much of this process involves mapping "strings" to "things" (Bollacker et al. 2008), or more precisely, mapping strings to identifiers for things.

Taxon names

At present the taxonomic scope of BioNames is restricted to names covered by the International Code of Zoological Nomenclature (animals and those eukaryotes not covered by the International Code of Nomenclature for algae, fungi, and plants). Taxonomic names were obtained from the Index of Organism Names (ION; http://www.organismnames.com). Each name in ION has a Life Science Identifier (LSID) (Martin et al. 2005) which uniquely identifies that name. LSIDs can be dereferenced to return metadata in Resource Description Framework format (RDF) (Page 2008b). ION LSIDs provide basic information on a taxonomic name using the TDWG Taxon Name LSID Ontology (http://rs.tdwg.org/ontology/voc/TaxonName), in many cases including bibliographic details for the publication where the name first appeared (Fig. 2).

The publication in which the name first appeared is listed in the contents of the "PublishedIn" property. In the example in Figure 2 this is the string "Description of a new species of Pinnotheres, and redescription of P. novaezelandiae (Brachyura: Pinnotheridae). New Zealand Journal of Zoology, 10(2) 1983: 151-162. 158 (Zoological Record Volume 120)". I used regular expressions to parse citation strings into their component parts (e.g., article title, journal, volume, pagination), and then attempted to locate the corresponding reference in an external database (see below).

Bibliographic identifiers

When populating BioNames every effort has been made to map each bibliographic string to a corresponding identifier, such as a Digital Object identifier (DOI). While DOIs are the best-known bibliographic identifier, there are several others that are relevant to the taxonomic literature (Page 2009). DOIs are themselves based on Handles (http://hdl.handle.net), an identifier widely used by digital repositories such as DSpace (Smith et al. 2003). A number of journals, such as the *Bulletins* and *Novitates* of the American Museum of Natural History are available in DSpace repositories and consequently have Handles. Other major archives such as JSTOR (http://www.jstor.org/) and the Japanese National Institute of Informatics (CiNii; http://ci.nii.ac.jp/) have their own unique identifiers (typically integer numbers that are part of a URL). Having a variety of identifiers can complicate the task of finding existing identifiers for a particular publication. Whereas for some identifiers, such as DOIs and CiNii NAIDs (National Institute of Informatics Article IDs) there are OpenURL resolvers for this task (Van de Sompel & Beit-Arie 2001), for other identifiers there may be no obvious way to find the identifier other than by using a search engine.

For the example in Figure 2, the citation string "Description of a new species of Pinnotheres, and redescription of P. novaezelandiae (Brachyura: Pinnotheridae). New Zealand Journal of Zoology, 10(2) 1983: 151-162. 158 (Zoological Record Volume 120)" corresponds to the article with the DOI 10.1080/03014223.1983.10423904. Once we have a DOI, we can then use services such as those provided by CrossRef (http://www.crossref.org) to retrieve author and publisher information for an article (see Fig. 11 below for one use of publisher information).

Identifiers also exist for aggregations of publications, such as journals. The historical practice of abbreviating journal titles in citations has led to a plethora of ways to refer to the same journal. For example, the BioStor database (http://biostor.org; Page 2011b) has accumulated more than ten variations on the name of the journal *Bulletin of Zoological Nomenclature* (such as "Bull Zool Nomen", "Bull Zool Nom.", "Bull. Zool. Nomencl.", etc.). This practice, presumably motivated by the desire to conserve space on the printed page, complicates efforts to match citations to identifiers. One approach to tackling this problem is to map abbreviations to journal-level globally unique identifiers, such as International Standard Serial Numbers (ISSNs) (for the *Bulletin of Zoological Nomenclature* the ISSN is 0007-5167). In addition to reducing ambiguity, there are web services such as that provided by WorldCat (http://www.worldcat.org) that take ISSNs and return the history of name changes for a journal, which in turn can help clarify the (often complicated) history of long-lived journals.

Documents

Taxonomic publications are available under a variety of licenses, ranging from explicitly open access licenses (MacCallum 2007) to articles that are "free", to articles that are behind a paywall. Archives such as JSTOR and CiNii have a mixture of free and subscription-based content. Many smaller journals, often published by scientific societies, are providing their content online for free, if not explicitly under an open license. The Biodiversity Heritage Library (the single largest source of taxonomic articles in BioNames, Fig. 11) makes its content available under a Creative Commons license. Where PDFs were available online either "for free" or under open access, these were downloaded and locally cached. Pages were extracted and converted into bitmap images for subsequent display in a web browser.

Closed-access publications that are available online are linked to by their identifier (e.g., DOI). Access to some of these publications may be available for short-term "rent" by services such as DeepDyve (http://www.deepdyve.com): where possible BioNames includes a link those services.

Clustering taxonomic names

Taxonomic names comprise a "canonical" name and the name's authorship, for example *Homo sapiens* Linnaeus comprises the canonical name "Homo sapiens" and the authorship string "Linnaeus". Names in taxonomic databases such as ION display numerous variations in spelling of authors, and instances of the same canonical name published by different authors (e.g., homonyms), so the names were clustered before populating BioNames. For each set of taxon names with the same canonical name the authorship was compared. If one name lacked an author and the other had an author, the names were automatically merged into a cluster. Given more than two names a graph was constructed where the nodes are the authorship strings, and a pair of nodes is connected if their corresponding strings were sufficiently similar. String similarity was computed by converting the strings to a "finger print" comprising lower case letters with all accented characters replaced by non-accented equivalents, and all punctuation removed, then finding the longest common subsequence of the two strings. If the length of the subsequence relative to the input strings was longer than a specified threshold (by default, 0.8, where identical strings have a similarity of 1.0) then the two author strings were connected by an edge in the graph. The components of the graph correspond to clusters of names with similar authorship strings, and were treated as being the same name. Figure 3 shows a graph for the different names that all have "Rhacophorus" as the canonical name.

Mapping names to taxa

BioNames includes two taxonomic classifications, sourced from GBIF (http://uat.gbif.org/dataset/d7dddbf4-2cf0-4f39-9b2a-bb099caae36c) and NCBI (ftp://ftp.ncbi.nih.gov/pub/taxonomy), respectively. These provide the user with a way to navigate through taxonomic names, as well as view data associated with each classification (e.g., phylogenies).

Ideally there would be a one-to-one mapping between a taxonomic name and a taxon, but complications often arise. In addition to the well-known problems of synonymy (more than one name for the same taxon) and homonymy (the same name used for different taxa), name and taxon databases may store slightly different representations of the same name. For example, ION has four records for the name "Nystactes" (each name is followed by its LSID):

Nystactes	urn:lsid:organismnames.com:name:2787598
Nystactes Bohlke	urn:lsid:organismnames.com:name:2735131
Nystactes Gloger 1827	urn:lsid:organismnames.com:name:4888093
Nystactes Kaup 1829	urn:lsid:organismnames.com:name:4888094

GBIF has three taxa with this name (the number is the GBIF species id):

Nystactes Böhlke, 1957	2403398
Nystactes Gloger, 1827	2475109
Nystactes Kaup, 1829	3239722

Note the differences in the name string ("o" versus "ö" in "Böhlke", presence or absence of years and commas). To automate the mapping of names to concepts in cases like this I constructed a bipartite graph where the nodes are taxon names, divided into two sets based upon which database they came from (e.g., one set of names from ION, the other from GBIF). I then connect the nodes of the graph by edges whose weights are the similarity of the two strings computed using the longest common subsequence that the two strings share. For example, Figure 4 shows the graph for "Nystactes". Computing the maximum weighted bipartite matching of this graph creates a map between the two sets of names. Ideally GBIF should have only one entry for *Nystactes* because each animal name (with a few exceptions) must be unique. If a newer name has already been published before, then it should be replaced by a new name. In this case, *Nystactes* (Böhlke 1957) has since been replaced by *Nystactichthys* (Böhlke 1958), and *Nystactes* (Kaup 1829) by *Paramyotis* (Bianchi 1916). Unfortunately these changes have not yet percolated their way from the primary literature into the GBIF taxonomy.

Images

To help the user recognise the taxa being displayed images for as many taxa as possible were obtained using EOL's API, which provides access to both the images, and a mapping between GBIF and NCBI taxon concept identifiers and the corresponding record in EOL.

Phylogenies

Phylogenies were obtained from the PhyLoTA database (http://phylota.net) (Sanderson et al. 2008). This database contains eukaryote phylogenies constructed from automatically assembled clusters of nucleotide sequences (loosely corresponding to "genes"). A MySQL data dump was downloaded (version 184, corresponding to the GenBank release of the same version number) and used to populate a local MySQL database. Metadata for the sequences in each phylogeny was obtained from the European Bioinformatics Institute (EBI; http://www.ebi.ac.uk), and used to populate the MySQL database with basic information such as taxon and locality information, as well as bibliographic details for the sources of the sequences.

Database

Once aggregated, cleaned, and reconciled, the data was converted to JSON (JavaScript Object Notation) and stored in a CouchDB database. CouchDB is a "NoSQL" document database that stores objects in JSON format. Unlike typical SQL databases, CouchDB does not have a database schema and does not support ad hoc queries. Instead CouchDB accepts semi-structured documents, and the user defines fixed queries or "views" (Anderson et al. 2010).

Results

BioNames comprises a CouchDB database and a web interface. Key features of the interface are outlined below.

Search

BioNames features a simple search interface that takes a scientific name and returns matching taxonomic names and concepts, together with any publications and phylogenies that contain the name. Figure 5 shows an example search result.

Document display

BioNames uses the DocumentCloud (https://github.com/documentcloud/document-viewer) viewer to display both PDFs, and page images from digital archives such as BioStor and Gallica (http://gallica.bnf.fr/) (Fig. 6).

Journals

Much of the work in populating BioNames comprises mapping citation to string to bibliographic identifiers and, where possible, linking those citations to full text. For each journal that has a ISSN, BioNames has a corresponding web page that lists all the articles from that journal that are in the database, and provides a graphical summary of how many of those articles have been located online (Fig. 7).

Timeline

BioNames can display timelines of the numbers of taxonomic names published in higher taxonomic groups, inspired by Taxatoy (Sarkar et al. 2008) (Fig. 8). For a given node in the taxonomic hierarchy the children of that node are displayed as a treemap where the size of each cell is proportional to the log of the number of taxa in the subtree rooted on that child taxon. The number of names in that taxon published in each year is displayed as an interactive chart. Clicking on an individual year will list the corresponding publications for that year.

Taxa

Each GBIF or NCBI taxon in BioNames has a corresponding web page that lists the associated taxonomic names, publications linked to those names, and other relevant data (e.g., Fig. 9).

Phylogenies

Phylogenies from PhyLOTA are rendered in an interactive viewer using the Scalable Vector Graphics (SVG) format. The user can zoom in and out, and change the drawing style. Terminal taxa with the same label have the same colour (Fig. 10). This makes it easier to recognise clusters of sequences from the same taxon (e.g., conspecific samples), as well as highlight possible errors (e.g., mislabelled or misidentified sequences). At present the colours are arbitrarily chosen, other schemes could be added in future (Lespinats and Fertil 2011).

Dashboard

The BioNames web site features a "dashboard" which displays various summaries of the data it contains. For example, Fig. 11 shows a bubble chart of the number of articles different publishers have made available online. "Publisher" in this context is broadly defined to include digital archives such as BioStor and JSTOR, repositories using DSpace, and commercial publishers such as Elsevier, Informa UK, Magnolia Press, Springer, and Wiley.

Discussion

The EOL Computational Data Challenge imposed a deadline on the first release of BioNames, however development of both the database and web interface is ongoing. Below I discuss some potential applications and future directions.

Links

BioNames makes extensive use of identifiers to clean and link data, but the real value of identifiers becomes apparent when they are shared, that is, when different databases use the same identifiers for the same entities, instead of minting their own. Reusing identifiers can enable unexpected connections between databases. For example, the PubMed biomedical literature database has a record (PMID:948206) for the paper "Monograph on ‘*Lithoglyphopsis*’ *aperta*, the snail host of Mekong River Schistosomiasis" (Davis et al. 1976). The PubMed record contains the abstract for the paper, but not a link to where the user can obtain a digital version of the paper. However, this reference is in a volume that has been scanned by the Biodiversity Heritage Library, and the article has been extracted by BioStor (http://biostor.org/reference/102054). If PubMed was linked to BHL, users of PubMed could go straight to the content of the article. But this is just the start. The Davis et al. paper also mentions museum specimens in the collection of the Academy of Natural Sciences of Drexel University, Philadelphia. Metadata for these specimens has been aggregated by GBIF, and the BioStor page for this article displays those links (http://biostor.org/reference/102054). In an ideal world we should be able seamlessly to traverse the path PubMed → BioStor → GBIF. Likewise, we should be able to traverse the path in the other direction. At present, a user of GBIF simply sees metadata for these specimens and a locality map. They are unaware that these specimens have been cited in a paper (Davis et al. 1976) which demonstrates that the snails host the Mekong River schistosome. This connection would be trivial to make if the reciprocal link was made: GBIF → BioStor. Furthermore, a link BioStor → PubMed would give us access to Medical Subject Headings (MeSH) for the schistosome paper. Hence we could imagine ultimately searching a database of museum specimens (GBIF) using queries from a controlled vocabulary of biomedical terms (MeSH).

Making these connections requires not only that we have digital identifiers, but also that where ever possible we reuse existing identifiers. In practice forging these links can be hard work (Page 2011a), and many links may be missing from existing databases (Miller et al. 2009). However, if we restrict ourselves to project-specific identifiers then we stymie attempts to create a network of connected biodiversity data.

Text mining

Much of the value of a scientific publication lies dormant unless it is accessible to text mining, which requires access to full text. Where possible BioNames stores information on the publisher of each article (Fig. 11), which could then be used to prioritise discussions with publishers on gaining access to full text (Van Noorden 2012). Fortunately, the single largest "publisher" of content in BioNames is BioStor (Page 2011b), which contains scans and OCR text from the Biodiversity Heritage Library. BHL makes its content available under a Creative Commons license, and so can be readily mined. Indeed, the text has already been indexed by tools that can recognise taxonomic names (Akella et al. 2012).

Impact of taxonomic literature

The taxonomic community has long felt disadvantaged by the role of citation-based "impact factor" in assessing the importance of taxonomic research (Garfield 2001; Krell 2000; Werner 2006) especially as much of the taxonomic literature appears in relatively low-impact journals. A common proposal is to include citations to the taxonomic authority for every name mentioned in a scientific paper (Wägele et al. 2011). Regardless of the merits of this idea, in practice these citations are often hard to locate, which is another motivation for BioNames.

There is additional value in surfacing identifiers for the taxonomic literature. In addition to helping construct citation networks, global identifiers can facilitate computing other measures of the value of a taxonomic paper. There is a growing interest in additional measures of post-publication impact of a publication in terms of activity such as social bookmarking, and commentary on web sites ("alt-metrics") (Yan and Gerstein 2011). Gathering these metrics is greatly facilitated by using standard bibliographic identifiers (otherwise, how do we know whether two commentators are discussing the same article or not?). If taxonomic literature is be part of this burgeoning conversation then it needs to be able to be identified unambiguously.

Dark taxa

One of the original motivations for constructing BioNames is the rise of "dark taxa" in genomics databases (Page 2011c). It is clear that some dark taxa do, in fact, have names. For example, consider the frog "*Gephyromantis* aff. *blanci* MV-2005" (NCBI taxonomy id 321743), which has a single DNA sequence AY848308 associated with it. This sequence was published as part of a

DNA barcoding study (Vences et al. 2005). If we enter the accession number AY848308 into Google we find two documents, one the supplementary table for (Vences et al. 2005), the other a subsequent paper (Vences and Riva 2007) that describes the frog with this sequence as a new species, *Gephyromantis runewsweeki*. This example is relatively straightforward, but it still required significant time to track down the species description. A key question facing attempts to find names for dark taxa is whether the methods available can be scaled to handle the magnitude of the problem.

Alternatively, one could argue that newer technologies such as DNA barcoding make classical taxonomy less relevant, and perhaps the effort in digitising older literature and exposing the taxonomic names it contains is misplaced. A counter argument would be that the taxonomic literature potentially contains a wealth of information on ecology, morphology and behaviour, often for taxa in areas that have been subsequently altered by human activity. Given the rarity of many taxa (Lim et al. 2011), and the uneven taxonomic and geographic distribution of taxonomic expertise (May 1998; Gaston and May 1992), for many species the only significant data on their biology may reside in the legacy literature (possibly under a different name (Solow et al. 1995)). As this legacy becomes more accessible through projects such as BHL (and services that build upon that project; Page 2011a) there will be considerable opportunities to mine that literature for basic biological data (Thessen et al. 2012).

Publishing platform

Recently some taxonomic journals have begun to mark up taxonomic names and descriptions (Penev et al. 2010), which is a precursor to linking names and data together. But these developments leave open the problem of what these links will point to. If we have a database of all taxonomic names and the associated literature (such as BioNames aims to be for zoological names), then such a database would provide an obvious destination for those links. Indeed, ultimately, we could envisage publishing new taxonomic publications within such a database, so that each new publication becomes simply another document within the database (Gerstein and Junker 2002). In the same way, we could use automated methods to extend the process of tagging names, specimens and literature cited to the legacy literature (Page 2010), so that the entire body of taxonomic knowledge becomes a single interwoven web of names, citations, publications, and data.

Availability

BioNames is accessible at http://bionames.org. The source code used to build the web site is available on GitHub http://github.com/rdmpage/bionames. Scripts used to fetch, clean, and reconcile the data are archived in http://github.com/rdmpage/bionames-data

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References

Akella, L., Norton, C. N., & Miller, H. (2012). NetiNeti: discovery of scientific names from text using machine learning methods. BMC Bioinformatics, 13(1), 211. doi:10.1186/1471-2105-13-211

Anderson, J. Chris, Jan Lehnardt and Noah Slater (2010). CouchDB: The Definitive Guide. O'Reilly, ISBN: 978-0-596-15589-6

Baird, R. (2010). Leveraging the fullest potential of scientific collections through digitisation.Biodiversity Informatics, 7(2). https://journals.ku.edu/index.php/jbi/article/view/3987

Benson, Dennis A., Ilene Karsch-Mizrachi, Karen Clark, David J. Lipman, James Ostell, and Eric W. Sayers (2012). GenBank. Nucl. Acids Res. (2012) 40 (D1): D48-D53. doi:10.1093/nar/gkr1202

Bianchi 1916. Annuaire du Musee Zoologique de l'Academie d. Sciences de St. Petersbourg 21:xxiii-xxxii (not seen)

Blagoderov, V., Kitching, I., Livermore, L., Simonsen, T., & Smith, V. (2012). No specimen left behind: industrial scale digitization of natural history collections. ZooKeys, 209(0), 133–146. doi:10.3897/zookeys.209.3178

Bollacker, K., Evans, C., Paritosh, P., Sturge, T., & Taylor, J. (2008). Freebase. Proceedings of the 2008 ACM SIGMOD international conference on Management of data - SIGMOD '08 (p. 1247). Association for Computing Machinery. doi:10.1145/1376616.1376746

Böhlke, J. E. (1957). On the Occurrence of Garden Eels in the Western Atlantic, with a Synopsis of the Heterocongrinae. Proceedings of the Academy of Natural Sciences of Philadelphia, 109: 59-79. http://www.jstor.org/stable/4064494

Böhlke, J. E. (1958). Substitute Names for *Nystactes* Bohlke and *Lucaya* Bohlke, Preoccupied. Copeia, 1958(1), 59. doi:10.2307/1439557

Conle, Oskar V, and Frank H Hennemann (2002) Revision of neotropic Phasmatodea: The tribe Anisomorphini sensu Bradley & Galil 1977: (Insecta, Phasmatodea, Pseudophasmatidae). Spixiana Supplement 28: 1–141. http://biostor.org/reference/118220

Davis GM, Kitikoon V, Temcharoen P (1976) Monograph on "*Lithoglyphopsis*" *aperta*, the snail host of Mekong River schistosomiasis. Malacologia 15(2): 241-87. http://biostor.org/reference/102054

Deans, A. R., Yoder, M. J., & Balhoff, J. P. (2012). Time to change how we describe biodiversity. Trends in Ecology & Evolution, 27(2), 78–84. doi:10.1016/j.tree.2011.11.007

Edwards, J. L. (2000). Interoperability of Biodiversity Databases: Biodiversity Information on Every Desktop. Science, 289(5488), 2312–2314. doi:10.1126/science.289.5488.2312)

Faulkes, C. G., Bennett, N. C., Cotterill, F. P. D., Stanley, W., Mgode, G. F., & Verheyen, E. (2011). Phylogeography and cryptic diversity of the solitary-dwelling silvery mole-rat, genus *Heliophobius* (family: Bathyergidae). (A. Kitchener, Ed.)Journal of Zoology, 285(4), 324–338. doi:10.1111/j.1469-7998.2011.00863.x

Franz, N. M., & Cardona-Duque, J. (2013). Description of two new species and phylogenetic reassessment of *Perelleschus* O'Brien & Wibmer, 1986 (Coleoptera: Curculionidae), with a complete taxonomic concept history of *Perelleschus* sec. Franz & Cardona-Duque, 2013 . Systematics and Biodiversity, 11(2), 209–236. doi:10.1080/14772000.2013.806371

Garfield, E. (2001).Nature, 413(6852), 107–107. doi:10.1038/35093267

Gaston, K. J., & May, R. M. (1992). Taxonomy of taxonomists. Nature, 356(6367), 281–282. doi:10.1038/356281a0

Gerstein, M. and Jochen Junker (2002). Blurring the boundaries between scientific 'papers' and biological databases. Nature http://www.nature.com/nature/debates/e-access/Articles/gernstein.html

Hebert, P. D. N., Cywinska, A., Ball, S. L., & deWaard, J. R. (2003). Biological identifications through DNA barcodes. Proceedings of the Royal Society B: Biological Sciences, 270(1512), 313–321. doi:10.1098/rspb.2002.2218

Hibbett, D., & Glotzer, D. (2011). Where are all the undocumented fungal species? A study of *Mortierella* demonstrates the need for sequence-based classification. New Phytologist, 191(3), 592–596. doi:10.1111/j.1469-8137.2011.03819.x

Kaup, J. J., & Stejneger, L. (1829). Skizzirte Entwickelungs-Geschichte und natürliches System der europäischen Thierwelt : Erster Theil welcher die Vogelsäugethiere und Vögel nebst Andeutung der Entstehung der letzteren aus Amphibien enthält /. Smithsonian Institution Biodiversity Heritage Library. doi:10.5962/bhl.title.63915

Kennedy, J. B., Kukla, R., & Paterson, T. (2005). Scientific Names Are Ambiguous as Identifiers for Biological Taxa: Their Context and Definition Are Required for Accurate Data Integration (pp. 80–95). Springer-Verlag. doi:10.1007/11530084_8

Krell, F.-T. (2000).Nature, 405(6786), 507–508. doi:10.1038/35014664

Lespinats, Sylvain, & Bernard Fertil. (2011). ColorPhylo: A Color Code to Accurately Display Taxonomic Classifications. Evolutionary Bioinformatics, 257. doi:10.4137/EBO.S7565

Lim, G. S., Balke, M., & Meier, R. (2011). Determining Species Boundaries in a World Full of Rarity: Singletons, Species Delimitation Methods. Systematic Biology, 61(1), 165–169. doi:10.1093/sysbio/syr030

MacCallum, C. J. (2007). When Is Open Access Not Open Access? PLoS Biology, 5(10), e285. doi:10.1371/journal.pbio.0050285

Maddison, D. R., Guralnick, R., Hill, A., Reysenbach, A.-L., & McDade, L. A. (2012). Ramping up biodiversity discovery via online quantum contributions. Trends in Ecology & Evolution, 27(2), 72–77. doi:10.1016/j.tree.2011.10.010

Martin, S., Hohman, M. M., & Liefeld, T. (2005). The impact of Life Science Identifier on informatics data. Drug Discovery Today, 10(22), 1566–1572. doi:10.1016/S1359-6446(05)03651-2

MAY, R. M. (1988). How Many Species Are There on Earth? Science, 241(4872), 1441–1449. doi:10.1126/science.241.4872.1441

Miller, H., Norton, C. N., & Sarkar, I. N. (2009). GenBank and PubMed: How connected are they? BMC Research Notes, 2(1), 101. doi:10.1186/1756-0500-2-101

Müller-Wille, S., & Charmantier, I. (2012). Natural history and information overload: The case of Linnaeus. Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences, 43(1), 4–15. doi:10.1016/j.shpsc.2011.10.021

Nagy, L. G., Petkovits, T., Kovács, G. M., Voigt, K., Vágvölgyi, C., & Papp, T. (2011). Where is the unseen fungal diversity hidden? A study of *Mortierella* reveals a large contribution of reference collections to the identification of fungal environmental sequences. New Phytologist, 191(3), 789–794. doi:10.1111/j.1469-8137.2011.03707.x

Page, R. D. M. (1983). Description of a new species of *Pinnotheres* , and redescription *of P. novaezelandiae* (Brachyura: Pinnotheridae) . New Zealand Journal of Zoology, 10(2), 151–162. doi:10.1080/03014223.1983.10423904

Page, R. D. M. (2008a). Biodiversity informatics: the challenge of linking data and the role of shared identifiers. Briefings in Bioinformatics, 9(5), 345–354. doi:10.1093/bib/bbn022

Page, R. D. (2008b). LSID Tester, a tool for testing Life Science Identifier resolution services. Source Code for Biology and Medicine, 3(1), 2. doi:10.1186/1751-0473-3-2

Page, R. D. (2009). bioGUID: resolving, discovering, and minting identifiers for biodiversity informatics. BMC Bioinformatics, 10(Suppl 14), S5. doi:10.1186/1471-2105-10-S14-S5

Page, R. D. M. (2010). Enhanced display of scientific articles using extended metadata. Web Semantics: Science, Services and Agents on the World Wide Web, 8(2-3), 190–195. doi:10.1016/j.websem.2010.03.004

Page, R. D. M. (2011a). Linking NCBI to Wikipedia: a wiki-based approach. PLoS Currents, 3, RRN1228. doi:10.1371/currents.RRN1228

Page, R. D. (2011b). Extracting scientific articles from a large digital archive: BioStor and the Biodiversity Heritage Library. BMC Bioinformatics, 12(1), 187. doi:10.1186/1471-2105-12-187

Page, R. D. M. (2011c). Dark taxa: GenBank in a post-taxonomic world. http://iphylo.blogspot.co.uk/2011/04/dark-taxa-genbank-in-post-taxonomic.html

Page, R. D. M. 2012. EOL Computable Data Challenge. doi 10.6084/m9.figshare.92091

Parr, C. S., Guralnick, R., Cellinese, N., & Page, R. D. M. (2012). Evolutionary informatics: unifying knowledge about the diversity of life. Trends in Ecology & Evolution, 27(2), 94–103. doi:10.1016/j.tree.2011.11.001

Patterson, D. J., Cooper, J., Kirk, P. M., Pyle, R. L., & Remsen, D. P. (2010). Names are key to the big new biology. Trends in Ecology & Evolution, 25(12), 686–691. doi:10.1016/j.tree.2010.09.004

Penev, L., Agosti, D., Georgiev, T., Catapano, T., Miller, J., Blagoderov, V., Roberts, D., et al. (2010). Semantic tagging of and semantic enhancements to systematics papers: ZooKeys working examples. ZooKeys, 50(0). doi:10.3897/zookeys.50.538

Sanderson, M., Boss, D., Chen, D., Cranston, K., & Wehe, A. (2008). The PhyLoTA Browser: Processing GenBank for Molecular Phylogenetics Research. Systematic Biology, 57(3), 335–346. doi:10.1080/10635150802158688

Sarkar, I. N. (2007). Biodiversity informatics: organizing and linking information across the spectrum of life. Briefings in Bioinformatics, 8(5), 347–357. doi:10.1093/bib/bbm037

Sarkar, I., Schenk, R., & Norton, C. N. (2008). Exploring historical trends using taxonomic name metadata. BMC Evolutionary Biology, 8(1), 144. doi:10.1186/1471-2148-8-144

Schindel DE, Miller SE (2010) Provisional nomenclature: the on-ramp to taxonomic names. In: Polaszek A (Ed) Systema Naturae 250 - The Linnaean Ark. CRC Press, 109-115 pp.

Smith, M., Barton, M., Branschofsky, M., McClellan, G., Walker, J. H., Bass, M., Stuve, D., et al. (2003). DSpace. D-Lib Magazine, 9(1). doi:10.1045/january2003-smith

Solow, A. R., Mound, L. A., & Gaston, K. J. (1995). Estimating the Rate of Synonymy. Systematic Biology, 44(1), 93–96. doi:10.1093/sysbio/44.1.93

TABERLET, P., COISSAC, E., POMPANON, F., BROCHMANN, C., & WILLERSLEV, E. (2012). Towards next-generation biodiversity assessment using DNA metabarcoding. Molecular Ecology, 21(8), 2045–2050. doi:10.1111/j.1365-294X.2012.05470.x

Thessen, A. E., Cui, H., & Mozzherin, D. (2012). Applications of Natural Language Processing in Biodiversity Science. Advances in Bioinformatics, 2012, 1–17. doi:10.1155/2012/391574

Van de Sompel, H., & Beit-Arie, O. (2001). Open Linking in the Scholarly Information Environment Using the OpenURL Framework. D-Lib Magazine, 7(3). doi:10.1045/march2001-vandesompel

Van Noorden, R. (2012). Trouble at the text mine. Nature, 483(7388), 134–135. doi:10.1038/483134a

Vences M, Riva IDL (2007) A new species of *Gephyromantis* from Ranomafana National Park, south-eastern Madagascar (Amphibia, Anura, Mantellidae). Spixiana 30(1): 135-143.

Vences, M., Thomas, M., van der Meijden, A., Chiari, Y., & Vieites, D. R. (2005).Frontiers in Zoology, 2(1), 5. doi:10.1186/1742-9994-2-5

Wägele, H., Klussmann-Kolb, A., Kuhlmann, M., Haszprunar, G., Lindberg, D., Koch, A., & Wägele, J. W. (2011). The taxonomist - an endangered race. A practical proposal for its survival. Frontiers in Zoology, 8(1), 25. doi:10.1186/1742-9994-8-25

Werner, Y. L. (2006). The case of impact factor versus taxonomy: a proposal. Journal of Natural History, 40(21-22), 1285–1286. doi:10.1080/00222930600903660

Yan, K.-K., & Gerstein, M. (2011). The Spread of Scientific Information: Insights from the Web Usage Statistics in PLoS Article-Level Metrics. (A. Vespignani, Ed.)PLoS ONE, 6(5), e19917. doi:10.1371/journal.pone.0019917

Figure 1

Taxonomy data model

Simplified diagram of the relationships between the core entities that make up taxonomy, such as authors, publications, taxon names, and taxa. Relationships between entities are represented by lines, those in black are the focus of BioNames.

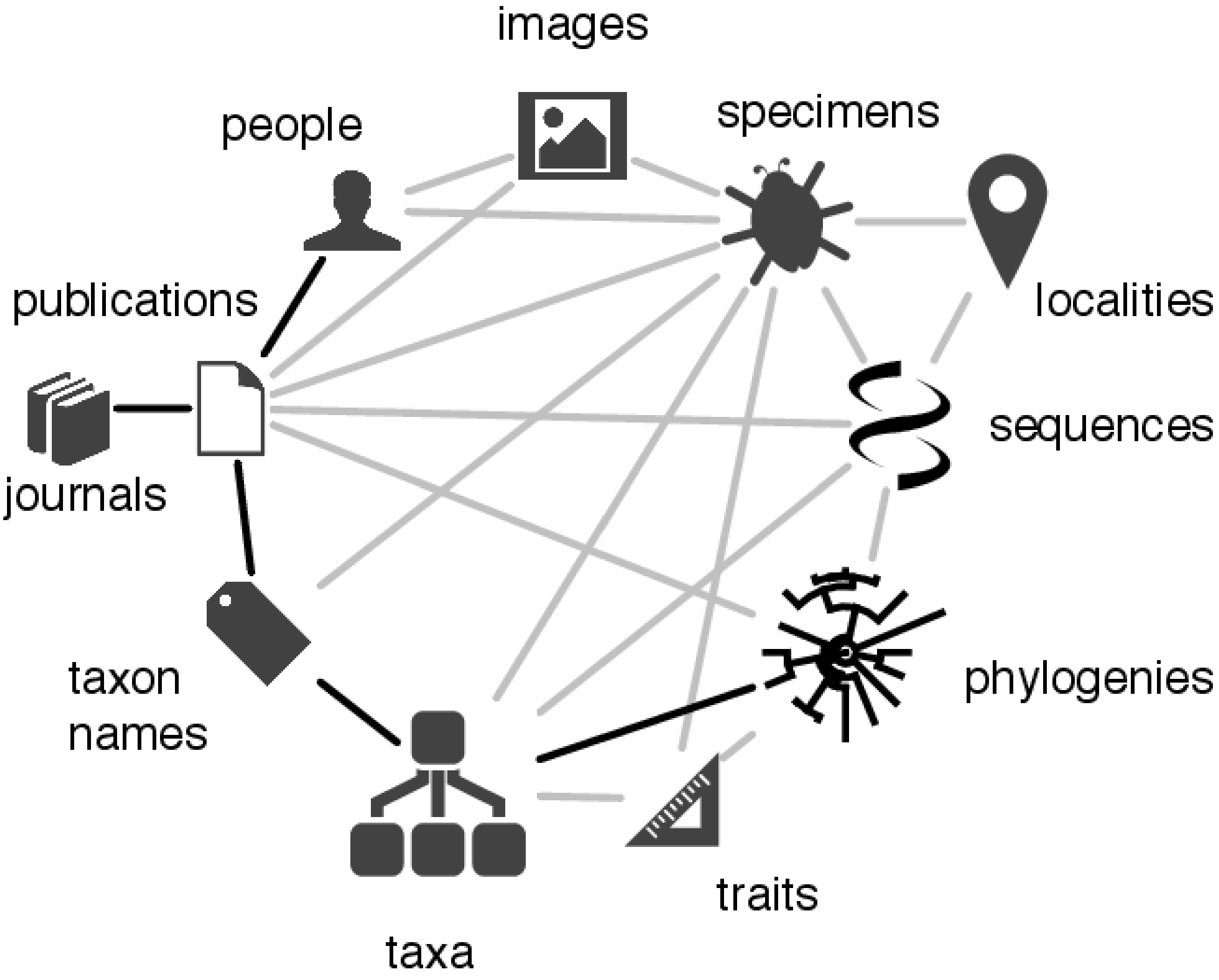

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Figure 2

RDF for taxon name

The RDF retrieved by dereferencing the LSID urn:lsid:organismnames.com:name:371873, which identifies the taxonomic name *Pinnotheres atrinicola*.

```
<?xml version="1.0"?>
<rdf:RDF xmlns:dc="http://purl.org/dc/elements/1.1/" xmlns:dcterms="http://purl.org/dc/terms/" xmlns:rdf="http://
www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:rdfs="http://www.w3.org/2000/01/rdf-schema#"
xmlns:tdwg_co="http://rs.tdwg.org/ontology/voc/Common#" xmlns:tdwg_pc="http://rs.tdwg.org/ontology/voc/
PublicationCitation#" xmlns:tdwg_tn="http://rs.tdwg.org/ontology/voc/TaxonName#">
	<tdwg_tn:TaxonName rdf:about="371873">
		<dc:identifier>371873</dc:identifier>
		<dc:creator rdf:resource="http://www.organismnames.com"/>
		<dc:Title>Pinnotheres atrinicola</dc:Title>
		<tdwg_tn:nameComplete>Pinnotheres atrinicola</tdwg_tn:nameComplete>
		<tdwg_tn:nomenclaturalCode rdf:resource="http://rs.tdwg.org/ontology/voc/TaxonName#ICZN"/>
		<tdwg_co:PublishedIn>Description of a new species of Pinnotheres, and redescription of P.
novaezelandiae (Brachyura: Pinnotheridae). New Zealand Journal of Zoology, 10(2) 1983: 151-162.  158
[Zoological Record Volume 120]</tdwg_co:PublishedIn>
		<tdwg_co:microreference>158</tdwg_co:microreference>
		<rdfs:seeAlso rdf:resource="http://www.organismnames.com/namedetails.htm?lsid=371873"/>
	</tdwg_tn:TaxonName>
</rdf:RDF>
```

Figure 3

Clustering taxonomic names

Graph depicting similarity between different authorship strings associated with the name "Rhacophorus". The components of this graph correspond to the name clusters recognised by BioNames.

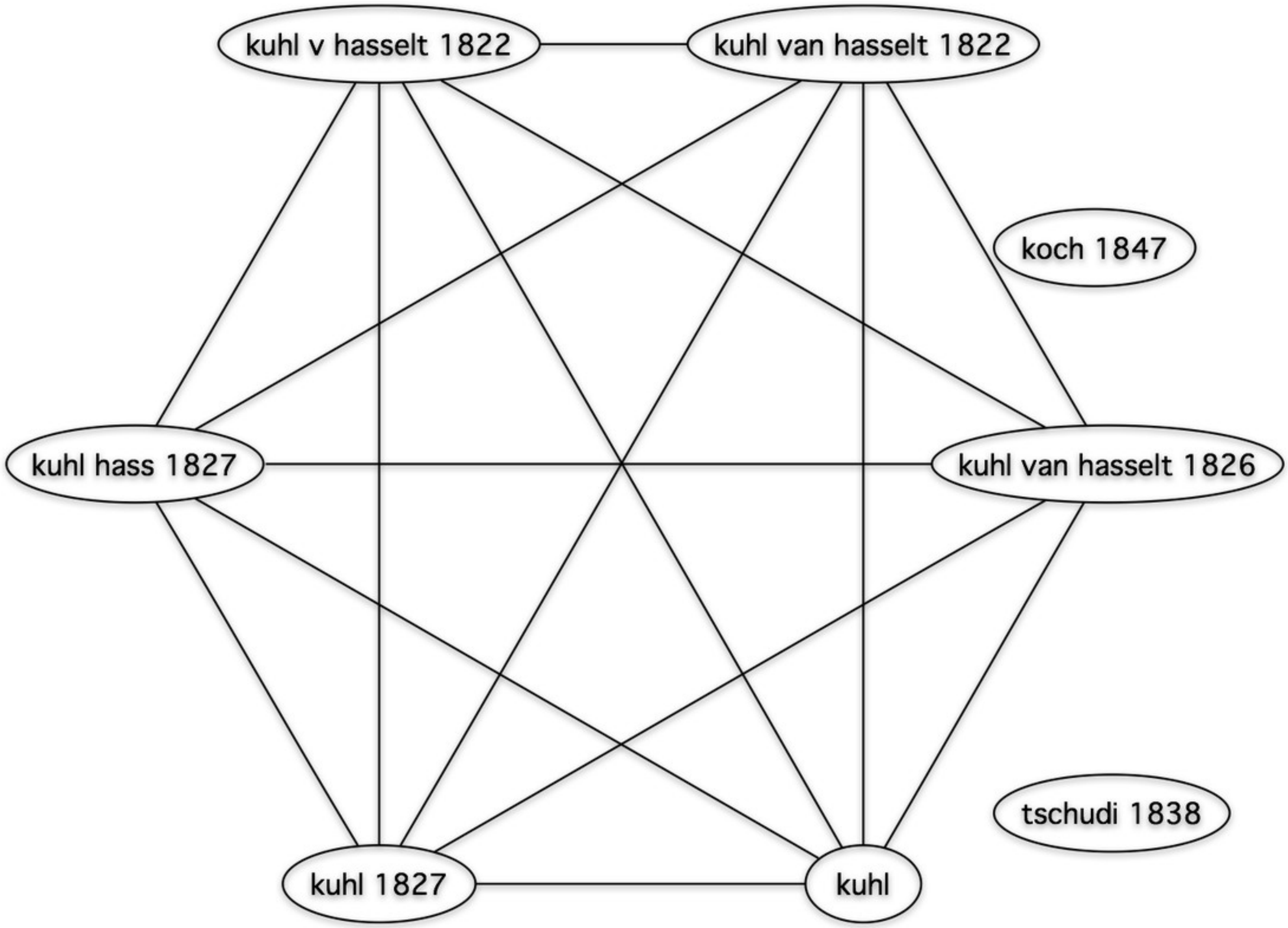

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Figure 4

Matching taxonomic names to taxa

Bipartite graph of string similarities between taxonomic names containing the string "Nystactes" in the ION and GBIF databases. Solid edges in the graph represent the maximum weighted bipartite matching, and define the mapping between ION and GBIF names.

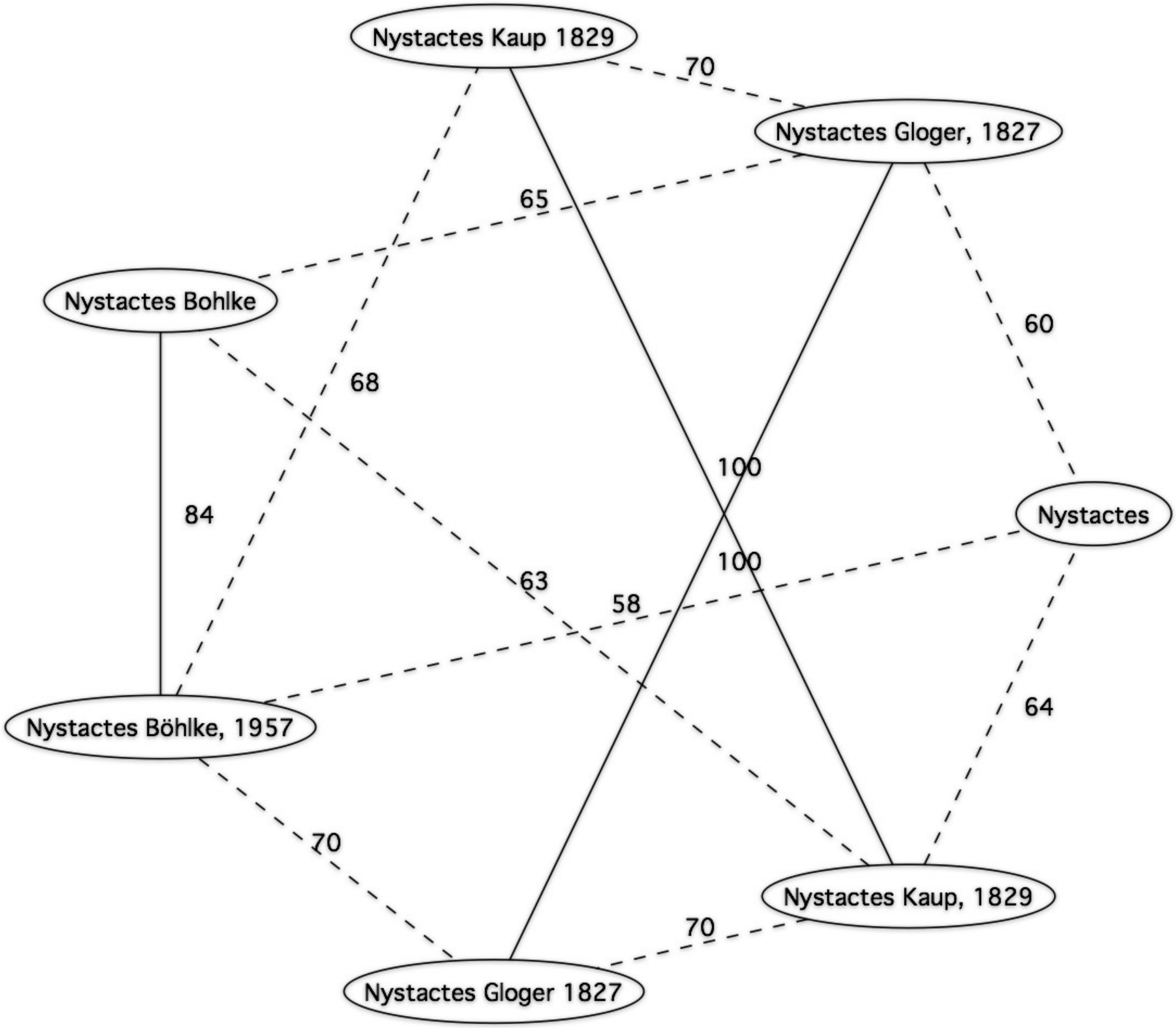

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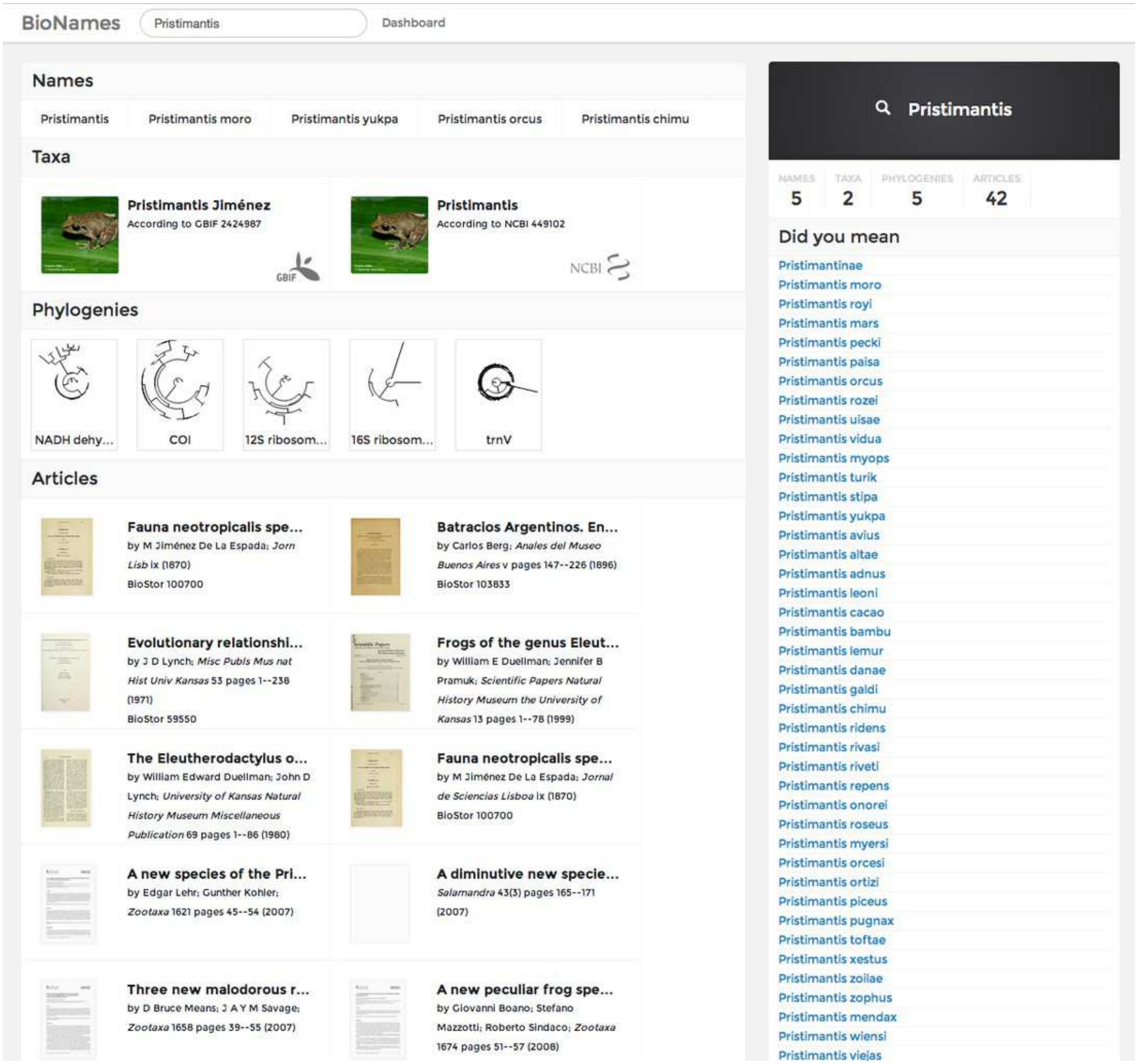
Figure 5

Search results

Screenshot of the search results for a query BioNames. The results include names that match the query, taxon concepts from GBIF and NCBI with thumbnail images from EOL, phylogenies containing members of the genus, and relevant taxonomic publications.



Names

Pristimantis | Pristimantis moro | Pristimantis yukpa | Pristimantis orcus | Pristimantis chimu

Taxa

Pristimantis Jiménez
According to GBIF 2424987

Pristimantis
According to NCBI 449102

Phylogenies

NADH dehy... | COI | 12S ribosom... | 16S ribosom... | trnV

Articles

Fauna neotropicalis spe...
by M Jiménez De La Espada; *Jorn Lisb* ix (1870)
BioStor 100700

Batracios Argentinos. En...
by Carlos Berg; *Anales del Museo Buenos Aires* v pages 147--226 (1896)
BioStor 103833

Evolutionary relationshi...
by J D Lynch; *Misc Publs Mus nat Hist Univ Kansas* 53 pages 1--238 (1971)
BioStor 59550

Frogs of the genus Eleut...
by William E Duellman; Jennifer B Pramuk; *Scientific Papers Natural History Museum the University of Kansas* 13 pages 1--78 (1999)

The Eleutherodactylus o...
by William Edward Duellman; John D Lynch; *University of Kansas Natural History Museum Miscellaneous Publication* 69 pages 1--86 (1980)

Fauna neotropicalis spe...
by M Jiménez De La Espada; *Jornal de Sciencias Lisboa* ix (1870)
BioStor 100700

A new species of the Pri...
by Edgar Lehr; Gunther Kohler; *Zootaxa* 1621 pages 45--54 (2007)

A diminutive new specie...
Salamandra 43(3) pages 165--171 (2007)

Three new malodorous r...
by D Bruce Means; J A Y M Savage; *Zootaxa* 1658 pages 39--55 (2007)

A new peculiar frog spe...
by Giovanni Boano; Stefano Mazzotti; Roberto Sindaco; *Zootaxa* 1674 pages 51--57 (2008)

Pristimantis

NAMES	TAXA	PHYLOGENIES	ARTICLES
5	2	5	42

Did you mean

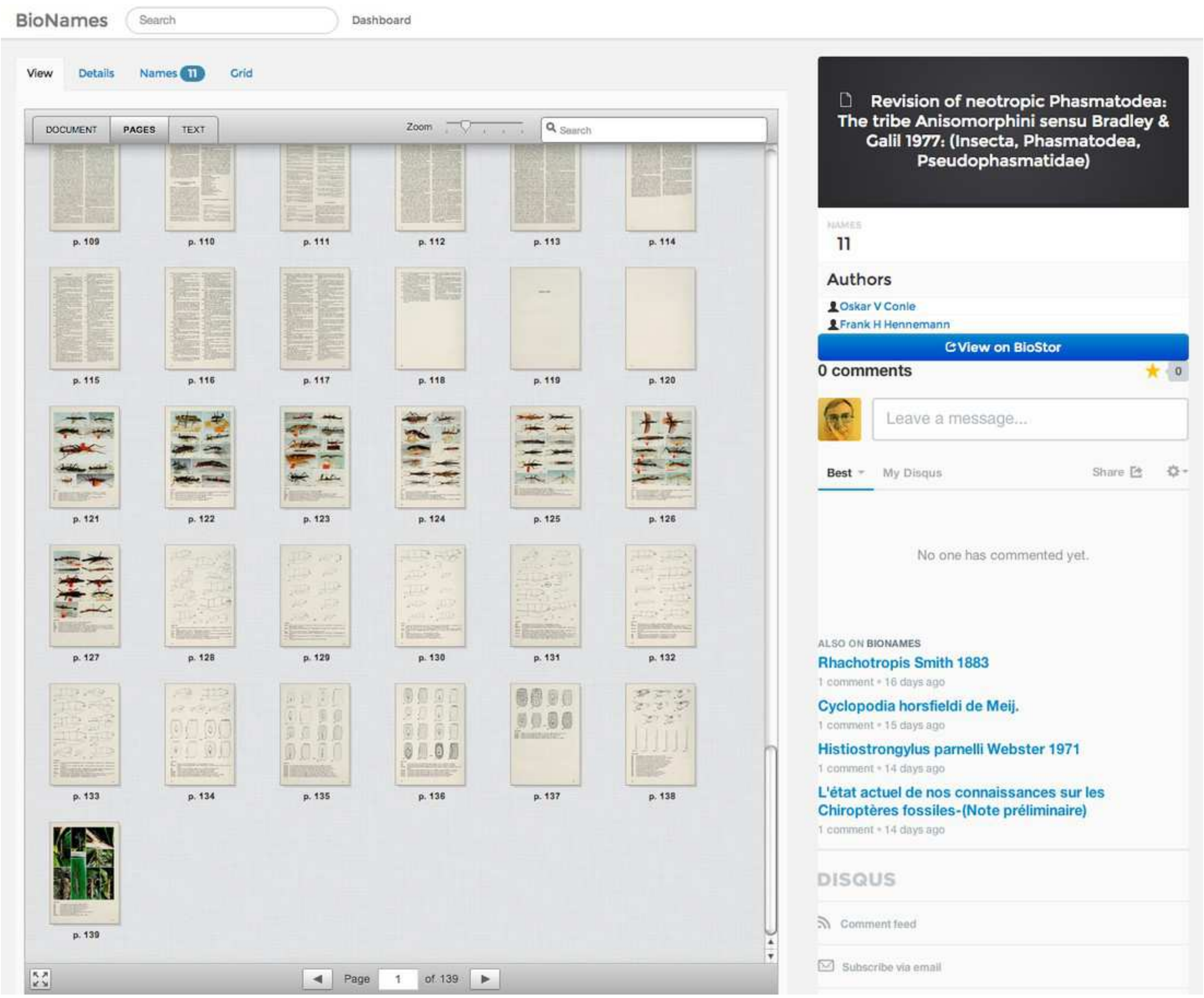
- Pristimantinae
- Pristimantis moro
- Pristimantis royi
- Pristimantis mars
- Pristimantis pecki
- Pristimantis paisa
- Pristimantis orcus
- Pristimantis rozei
- Pristimantis uisae
- Pristimantis vidua
- Pristimantis myops
- Pristimantis turik
- Pristimantis stipa
- Pristimantis yukpa
- Pristimantis avius
- Pristimantis altae
- Pristimantis adnus
- Pristimantis leoni
- Pristimantis cacao
- Pristimantis bambu
- Pristimantis lemur
- Pristimantis danae
- Pristimantis galdi
- Pristimantis chimu
- Pristimantis ridens
- Pristimantis rivasi
- Pristimantis riveti
- Pristimantis repens
- Pristimantis onorei
- Pristimantis roseus
- Pristimantis myersi
- Pristimantis orcesi
- Pristimantis ortizi
- Pristimantis piceus
- Pristimantis pugnax
- Pristimantis toftae
- Pristimantis xestus
- Pristimantis zoilae
- Pristimantis zophus
- Pristimantis mendax
- Pristimantis wiensi
- Pristimantis viejas

Figure 6

Displaying an article

Screenshot of BioNames displaying a document from BioStor (Conle and Hennemann 2002).

The document viewer can display page images, thumbnails, and (where available) text.



Revision of neotropic Phasmatodea: The tribe Anisomorphini sensu Bradley & Galil 1977: (Insecta, Phasmatodea, Pseudophasmatidae)

NAMES
11

Authors
Oskar V Conle
Frank H Hennemann

0 comments ★ 0

Leave a message...

No one has commented yet.

ALSO ON BIONAMES

Rhachotropis Smith 1883
1 comment • 16 days ago

Cyclopodia horsfieldi de Meij.
1 comment • 15 days ago

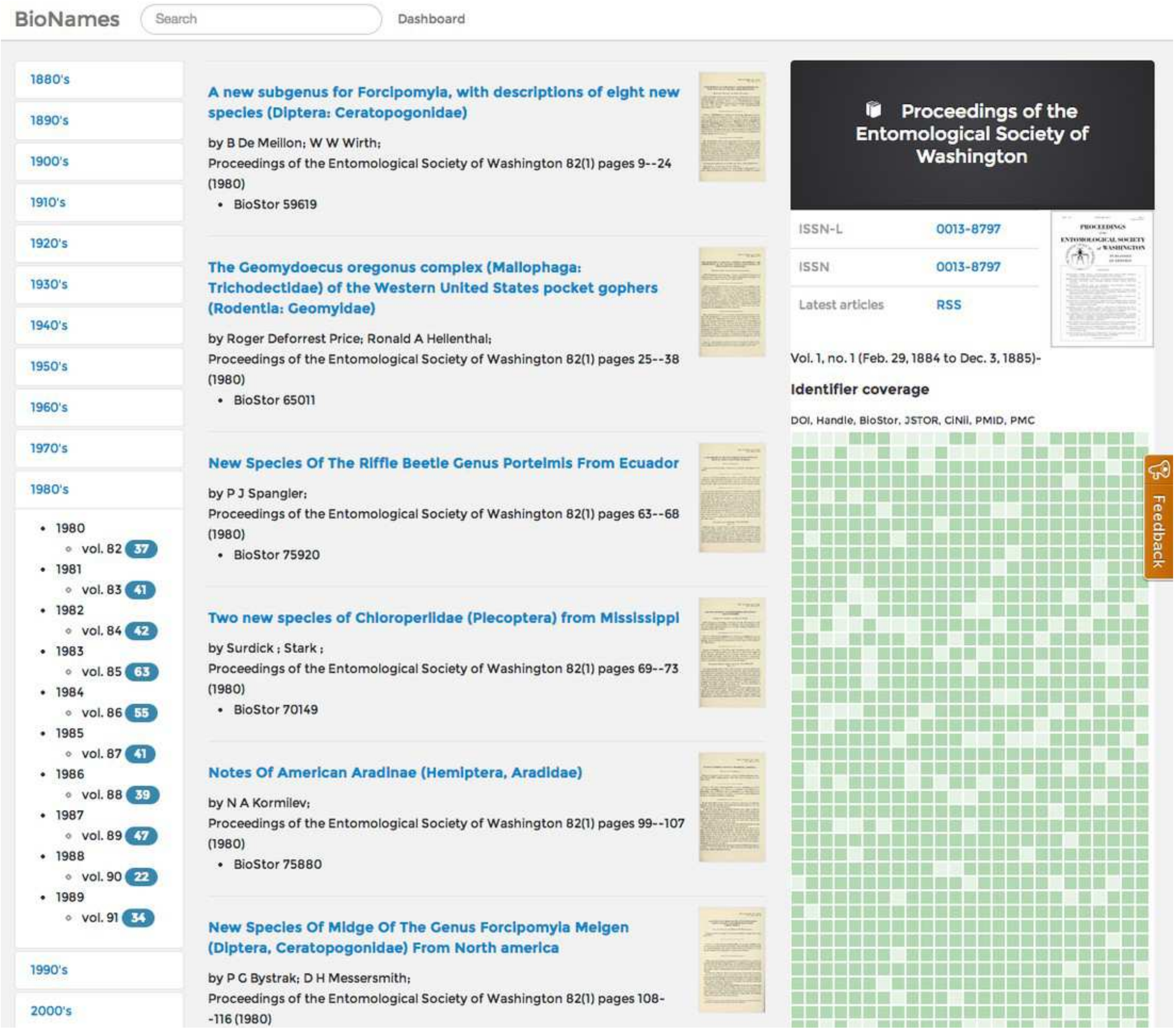
Histiostrongylus parnelli Webster 1971
1 comment • 14 days ago

L'état actuel de nos connaissances sur les Chiroptères fossiles-(Note préliminaire)
1 comment • 14 days ago

Figure 7

Displaying a journal

Screenshot of the page in BioNames for the journal *Proceedings of the Entomological Society of Washington* (ISSN 0013-8797). The centre column lists the articles in a volume selected by the user using the index on the left. The right hand column displays basic data about the journal, and a graphical display of how many articles have been mapped to a globally unique identifier.



- 1980
    - vol. 82 37
- 1981
    - vol. 83 41
- 1982
    - vol. 84 42
- 1983
    - vol. 85 63
- 1984
    - vol. 86 55
- 1985
    - vol. 87 41
- 1986
    - vol. 88 39
- 1987
    - vol. 89 47
- 1988
    - vol. 90 22
- 1989
    - vol. 91 34

A new subgenus for Forcipomyia, with descriptions of eight new species (Diptera: Ceratopogonidae)

by B De Meillon; W W Wirth;
Proceedings of the Entomological Society of Washington 82(1) pages 9--24 (1980)

- BioStor 59619

The Geomydoecus oregonus complex (Mallophaga: Trichodectidae) of the Western United States pocket gophers (Rodentia: Geomyidae)

by Roger Deforrest Price; Ronald A Hellenthal;
Proceedings of the Entomological Society of Washington 82(1) pages 25--38 (1980)

- BioStor 65011

New Species Of The Riffle Beetle Genus Portelmis From Ecuador

by P J Spangler;
Proceedings of the Entomological Society of Washington 82(1) pages 63--68 (1980)

- BioStor 75920

Two new species of Chloroperlidae (Plecoptera) from Mississippi

by Surdick ; Stark ;
Proceedings of the Entomological Society of Washington 82(1) pages 69--73 (1980)

- BioStor 70149

Notes Of American Aradinae (Hemiptera, Aradidae)

by N A Kormilev;
Proceedings of the Entomological Society of Washington 82(1) pages 99--107 (1980)

- BioStor 75880

New Species Of Midge Of The Genus Forcipomyia Meigen (Diptera, Ceratopogonidae) From North america

by P G Bystrak; D H Messersmith;
Proceedings of the Entomological Society of Washington 82(1) pages 108--116 (1980)

Proceedings of the Entomological Society of Washington

ISSN-L	0013-8797
ISSN	0013-8797
Latest articles	RSS

Vol. 1, no. 1 (Feb. 29, 1884 to Dec. 3, 1885)-

Identifier coverage

DOI, Handle, BioStor, JSTOR, CiNii, PMID, PMC

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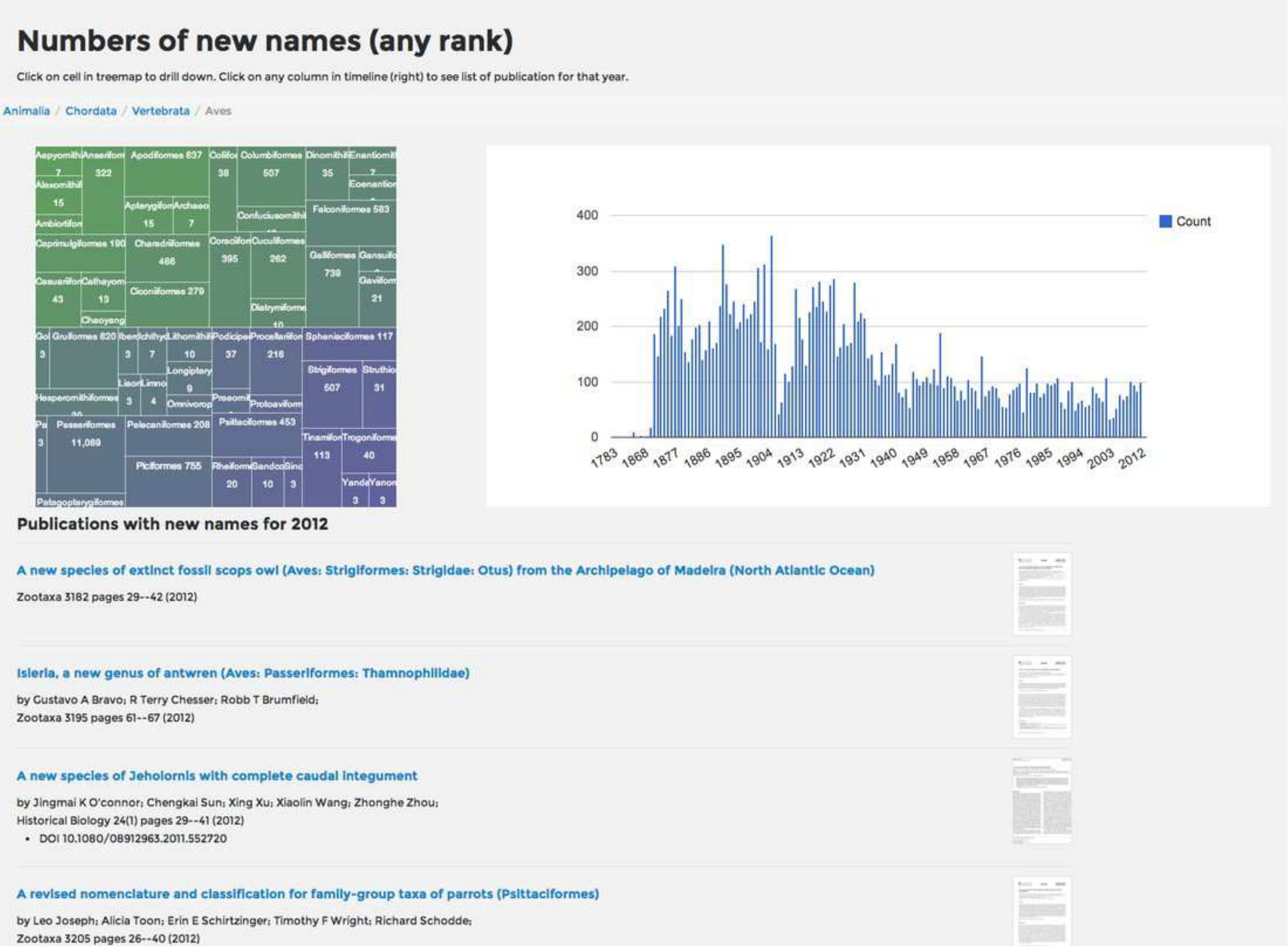
Figure 8

Timeline of taxonomic names for birds

Screenshot of the distribution overtime of publications of new names for birds (Aves). The treemap on the left displays taxa below Aves in the taxonomic hierarchy, the chart on the right displays the number of publications in each year that publish a new bird name. The user has clicked on "2012", resulting in a list of the papers published in that year appearing below the timeline.



Numbers of new names (any rank)

Click on cell in treemap to drill down. Click on any column in timeline (right) to see list of publication for that year.

Animalia / Chordata / Vertebrata / Aves

Publications with new names for 2012

A new species of extinct fossil scops owl (Aves: Strigiformes: Strigidae: Otus) from the Archipelago of Madeira (North Atlantic Ocean)

Zootaxa 3182 pages 29--42 (2012)

Isleria, a new genus of antwren (Aves: Passeriformes: Thamnophilidae)

by Gustavo A Bravo; R Terry Chesser; Robb T Brumfield;
Zootaxa 3195 pages 61--67 (2012)

A new species of Jeholornis with complete caudal integument

by Jingmai K O'connor; Chengkai Sun; Xing Xu; Xiaolin Wang; Zhonghe Zhou;
Historical Biology 24(1) pages 29--41 (2012)

- DOI 10.1080/08912963.2011.552720

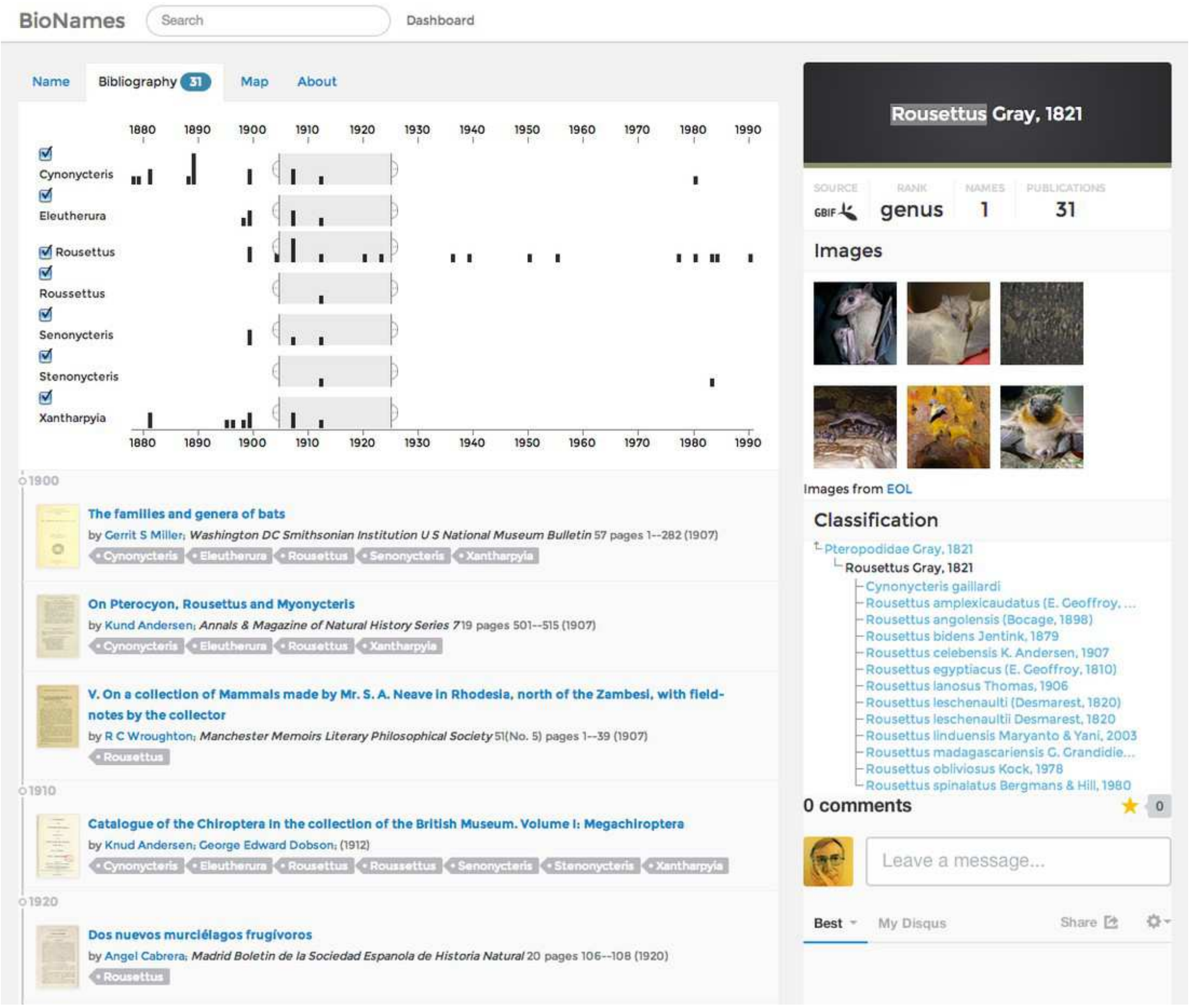
A revised nomenclature and classification for family-group taxa of parrots (Psittaciformes)

by Leo Joseph; Alicia Toon; Erin E Schirtzinger; Timothy F Wright; Richard Schodde;
Zootaxa 3205 pages 26--40 (2012)

Figure 9

Bibliography for a taxon

Screenshot of the bibliography tab on a taxon page in BioNames. This example shows the publications relevant to the bat genus *Rousettus*, including those for synonyms. The user can select publications from a given time slice and/or combination of synonyms.



1900

The families and genera of bats
by Gerrit S Miller; *Washington DC Smithsonian Institution U S National Museum Bulletin* 57 pages 1--282 (1907)
• Cynonycteris • Eleutherura • Rousettus • Senonycteris • Xantharpyia

On Pterocyon, Rousettus and Myonycteris
by Kund Andersen; *Annals & Magazine of Natural History Series 7* 19 pages 501--515 (1907)
• Cynonycteris • Eleutherura • Rousettus • Xantharpyia

V. On a collection of Mammals made by Mr. S. A. Neave in Rhodesia, north of the Zambesi, with field-notes by the collector
by R C Wroughton; *Manchester Memoirs Literary Philosophical Society* 51(No. 5) pages 1--39 (1907)
• Rousettus

1910

Catalogue of the Chiroptera in the collection of the British Museum. Volume I: Megachiroptera
by Knud Andersen; George Edward Dobson; (1912)
• Cynonycteris • Eleutherura • Rousettus • Roussettus • Senonycteris • Stenonycteris • Xantharpyia

1920

Dos nuevos murciélagos frugívoros
by Angel Cabrera; *Madrid Boletin de la Sociedad Espanola de Historia Natural* 20 pages 106--108 (1920)
• Rousettus

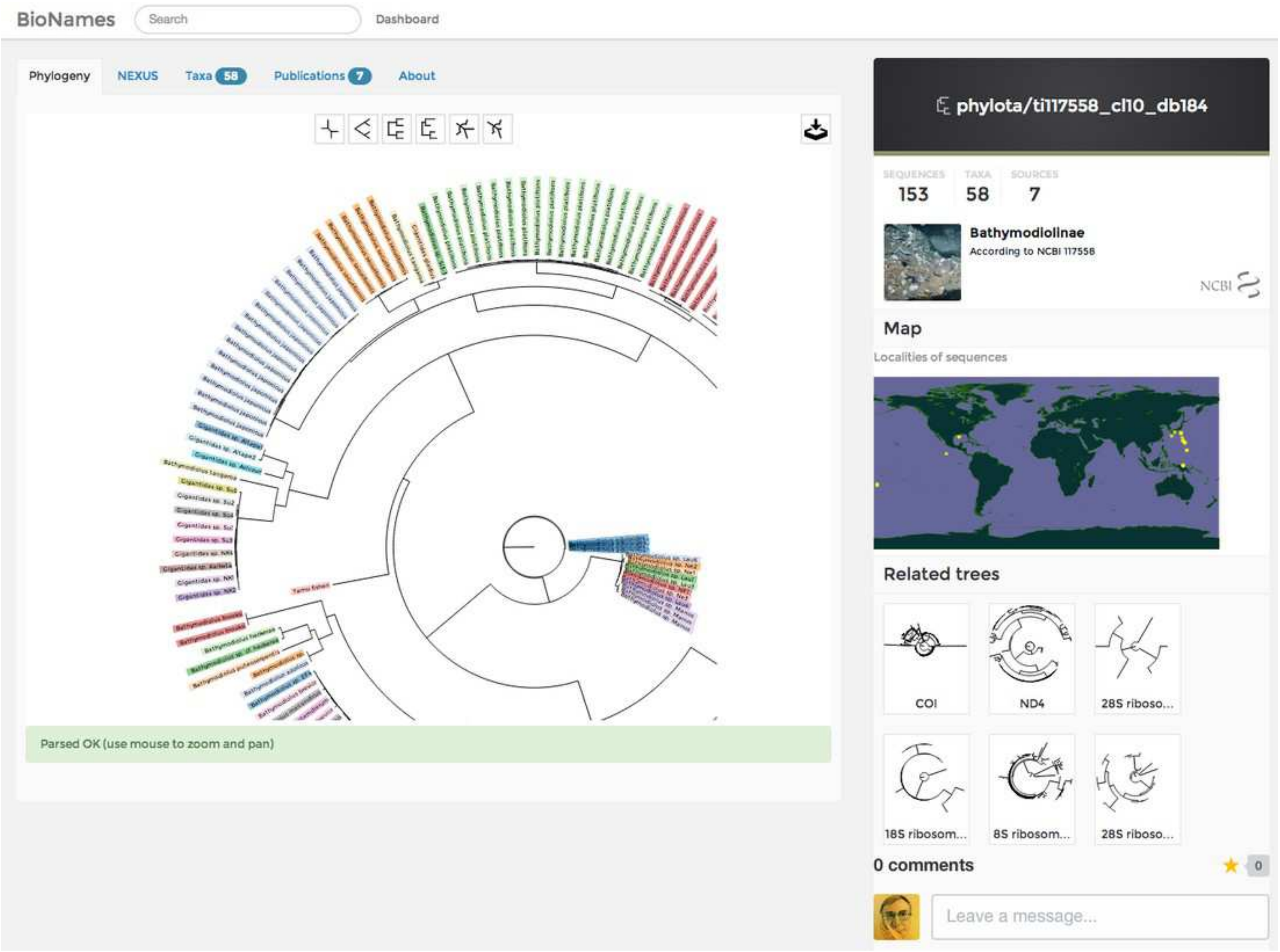
Classification

- Pteropodidae Gray, 1821
  - Rousettus Gray, 1821
    - Cynonycteris gaillardi
    - Rousettus amplexicaudatus (E. Geoffroy, ...
    - Rousettus angolensis (Bocage, 1898)
    - Rousettus bidens Jentink, 1879
    - Rousettus celebensis K. Andersen, 1907
    - Rousettus egyptiacus (E. Geoffroy, 1810)
    - Rousettus lanosus Thomas, 1906
    - Rousettus leschenaulti (Desmarest, 1820)
    - Rousettus leschenaultii Desmarest, 1820
    - Rousettus linduensis Maryanto & Yani, 2003
    - Rousettus madagascariensis G. Grandidie...
    - Rousettus obliviosus Kock, 1978
    - Rousettus spinalatus Bergmans & Hill, 1980

Figure 10

Phylogeny viewer

Screenshot of phylogeny from PhyLoTA as displayed in BioNames. The user can zoom in and out and pan, as well as change the layout of the tree.



SEQUENCES 153 TAXA 58 SOURCES 7

Bathymodiolinae
According to NCBI 117558

Parsed OK (use mouse to zoom and pan)

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Figure 11

Relative importance of different publishers of taxonomic literature

Bubble chart showing relative numbers of taxonomic articles made available online by different publishers.