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AN R PACKAGE TO INTERACT WITH THE OPEN TREE OF LIFE

rotl an R package to interact with the Open Tree of Life Data

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Abstract.

1. While phylogenies have been getting easier to build, it has been difficult to re-use, combine, and synthesize the information they provide because published trees are often only available as image files, and taxonomic information is not standardized across studies.
2. The Open Tree of Life (OTL) project addresses these issues by providing a digital tree that encompasses all organisms, built by combining taxonomic information and published phylogenies. The project also provides tools and services to query and

download parts of this synthetic tree, as well as the source data used to build it.

Here, we present `rotl`, an R package to search and download data from the Open Tree of Life directly in R.

3. `rotl` uses common data structures allowing researchers to take advantage of the rich set of tools and methods that are available in R to manipulate, analyze, and visualize phylogenies. Here, and in the vignettes accompanying the package, we demonstrate how `rotl` can be used with other R packages to analyze biodiversity data.
4. As phylogenies are being used in a growing number of applications, `rotl` facilitates access to phylogenetic data, and allows their integration with statistical methods and data sources available in R.

Advances in sequencing and computing technologies have led to a revolution in systematic biology. The ability to routinely generate molecular datasets from any extant organism has allowed researchers to resolve long-standing taxonomic disputes and estimate phylogenies for previously understudied groups. In parallel, the ease with which phylogenies can be estimated has spurred the development of new phylogenetic comparative methods. These methods allow researchers to explore fundamental questions about the origin of biodiversity including the evolution of morphological and ecological traits, the spatio-temporal variation in speciation rates, or both (O’Meara 2012; Pennell and Harmon 2013).

Ideally, the ever increasing number of published phylogenies would contribute to a synthesis of phylogenetic knowledge, ultimately leading to a better understanding of the history of life while at the same time providing high-quality phylogenetic information for

use in comparative analyses. However, in practice, synthesizing phylogenetic data is a difficult task. Phylogenetic information is largely scattered, often only available as image files within publications, and the lack of standardization to store and represent phylogenetic data makes it difficult for researchers to access, synthesize, and integrate this information into their own research (Stoltzfus et al. 2012; Drew et al. 2013; Magee et al. 2014; but see Cranston et al. 2014 for suggestions of best practices).

The Open Tree of Life (OTL) project aims at assembling and synthesizing our current understanding of phylogenetic relationships across all organisms on Earth while providing tools and services that facilitate access to this information (Hinchliff et al. 2015). OTL combines taxonomic information that serves as the backbone for the phylogenetic relationships, and published phylogenies to elucidate relationships among taxa. This combination of information is used to structure the comprehensive synthetic tree. Studies can be contributed to the synthetic tree through a curator interface (<https://tree.opentreeoflife.org/curator>), allowing the synthetic tree to be continuously updated as relationships are elucidated or reevaluated. The current draft of the OTL synthetic tree contains 2.3 million tips. Beyond obvious applications across the life sciences to explore questions in evolution, biodiversity, and conservation, the resources OTL provides are useful for education and outreach (e.g., illustrating course material, or developing outreach activities to explore relationships among species).

The R programming language is a popular tool for phylogenetics and comparative analysis. The R packages `ape` (Paradis et al. 2004), `phylobase` (Bolker et al. 2015), `phangorn` (Schliep 2011), and `RNexML` (Boettiger et al. 2015b) each provide functions to import and manipulate trees within R and save the results in standard data formats. Additional packages including `phytools` (Revell 2012), `geiger` (Pennell et al. 2014), and `ggtree` (Yu et al. 2015), allow users to analyze and visualize data in a phylogenetic context (see <https://cran.r-project.org/web/views/Phylogenetics.html> for a comprehensive list of phylogenetics packages in R). In addition to packages for phylogenetic and

70 comparative analyses, a growing number of R packages allows users to query and access data from the web (e.g. `rFISHBASE` (Boettiger et al. 2012), `rAvis` (Varela et al. 2014), and `paleobioDB` (Varela et al. 2015)), such that data associated with taxa in a given phylogeny can be obtained directly in R.

In ecology, the development of the field of community phylogenetics (Webb et al. 75 2002) has created a need for researchers to have access to the evolutionary relationships of species making up communities. The relative contributions of the role of the environment (e.g., habitat filtering), and of biotic interactions (e.g., competitive exclusion), are inferred from the distribution of taxa on a phylogeny composed from species occurring at larger spatial scale. R packages and other software have been developed to generate phylogenies 80 from species lists using taxonomic information or DNA sequences (e.g., Webb et al. 2008; Pearse and Purvis 2013). These phylogenies can then be used for community phylogenetics analyses (e.g., Pearse et al. 2015; Kembel et al. 2010), but they are often incomplete or not resolved enough. As OTL becomes more comprehensive, and its taxonomic resolution increases, it could become a valuable resource for ecologists seeking to use phylogenetic 85 information in their research.

These packages, combined with the language's support for literate programming (Knuth 1984; Xie 2015), make R a comprehensive platform for reproducible research in phylogenetics and comparative biology, as they allow a complete record of the steps taken in gathering, processing, and analyzing a given data set to be produced.

90 Here we present `rot1`, an R package that allows users to download phylogenetic and taxonomic data from the OTL directly in R. `rot1` takes advantage of OTL's Application Programming Interfaces (APIs) to access sub-trees from the synthetic Open Tree, as well as the published source trees that contribute to the synthesis. By providing direct access to high quality phylogenetic data in R, `rot1` fills a key gap in typical comparative analysis 95 workflows, and extends the degree to which R supports reproducible research in phylogenetics and comparative biology.

API SERVICES PROVIDED BY OTL

The OTL project provides four resources that serve data to users through the APIs:

1. The *taxonomy* used as the backbone of the tree, the Open Tree Taxonomy (OTT);
- 100 2. The *studies* and their associated trees, some of which are chosen by curators to assemble the synthetic tree;
3. A *taxonomic name resolution service* (TNRS) used to match taxon names to the Open Tree Taxonomy identifiers;
4. The *synthetic tree* itself, the ‘Open Tree’.

105 `rotl` gives users access to the endpoints provided by version 3 of the APIs, and other versions of the APIs can be selected by the user as they become available.

Phylogenetic trees served by the API can be imported directly into R’s memory and are represented using the `ape` (Paradis et al. 2004) tree structure (objects of class `phylo`), or can be written to files in the Newick, NEXUS (Maddison et al. 1997), or NeXML (Vos
110 et al. 2012) file formats. This allows researchers to use these trees either directly with other R packages, or to be imported in other programs that make use of phylogenetic tree files.

Currently, the synthetic tree does not have any branch lengths associated with it, therefore parametric comparative methods cannot be used directly on the subtrees returned by OTL (although the OTL treestore contains the raw published source
115 phylogenies, complete with branch lengths and node annotations; see below). However, resources and methods are being developed to add branch lengths to these topological subtrees (e.g., Ksepka et al. 2015) or use topological trees to identify phylogenetically equivalent species to increase overlap between chronograms and species trait data (Pennell et al. 2015). Without branch lengths, these subtrees are nonetheless useful to illustrate
120 relationships among species, or to map traits on a phylogeny.

TECHNICAL INFORMATION ABOUT **rotl**

Phylogenetic information retrieved from OTL is converted into `phylo` objects by `rotl` using the NEXUS Class Library (NCL, Lewis 2003) as implemented in the `rnc1` package (<https://cran.r-project.org/package=rnc1>). Using NCL provides robust and efficient parsing of large trees that may contain singleton nodes labeled with taxonomic information (i.e., a monotypic taxon). Singleton nodes are collapsed after the tree has been parsed, making the resulting `phylo` object compatible with all functions from the `ape` package.

The package is well-documented, and includes three package vignettes (documents that demonstrate the use of the package and contain executable R code). There is also an extensive test-suite that covers both the internal functions that `rotl` uses to connect to OTL, and public functions that users apply to access and process data.

DEMONSTRATIONS

Getting relationships from a list of taxa

Before a researcher can use the Open Tree to retrieve relationships among a set of taxa, they first need to match the taxon names in their dataset with records in the Open Tree Taxonomy (OTT). OTL's taxonomic names resolution service (TNRS) combines information from multiple services (e.g., National Center for Biotechnology Information [NCBI], World Register for Marine Species [WoRMS], Global Biodiversity Information Facility [GBIF]) and allows users to search for taxon names, and retrieve identifiers for each matching taxon. We demonstrate the use of the TNRS within `rotl` by searching for taxonomic records associated with several model organisms.

```
taxa <- tnrs_match_names(names = c("Escherichia coli",  
                                  "Chlamydomonas reinhardtii",  
                                  "Drosophila melanogaster",  
                                  "Arabidopsis thaliana",  
                                  "Rattus norvegicus",  
                                  "Mus musculus",  
                                  "Cavia porcellus",  
                                  "Xenopus laevis",  
                                  "Saccharomyces cerevisiae",  
                                  "Danio rerio"))
```

The function `tnrs_match_names` returns a data frame that lists the Open Tree identifiers as well as other information to help users ensure that the taxa matched are the correct ones. Here, there is no ambiguity in the taxa matched; however, as OTT includes
145 taxa from bacteria, plants, and animals that are regulated by different nomenclatural codes (ICNP, ICN, and ICZN, respectively), both OTL and `rot1` provide tools to deal with names that may represent valid taxa in more than one code. The argument `context_name` can be used to limit potential matches to a taxonomic group such as “Animals” (see the
150 function `tnrs_contexts` for a complete list of possible options). When this strategy cannot be used (as in the present example, where the tree encompasses multiple domains), the function `inspect` lists alternative matches for a taxon name, and `update` replaces it in the results. An example of this approach is provided in the vignette “How to use `rot1`?” that accompanies the package.

155 By default, approximate matching is enabled when attempting to match taxonomic names to their OTT identifiers. Additionally, taxonomic synonyms are included in OTT, allowing researchers to match correct identifiers for taxon names that might include misspellings or synonyms. These features will facilitate the tedious data cleaning process

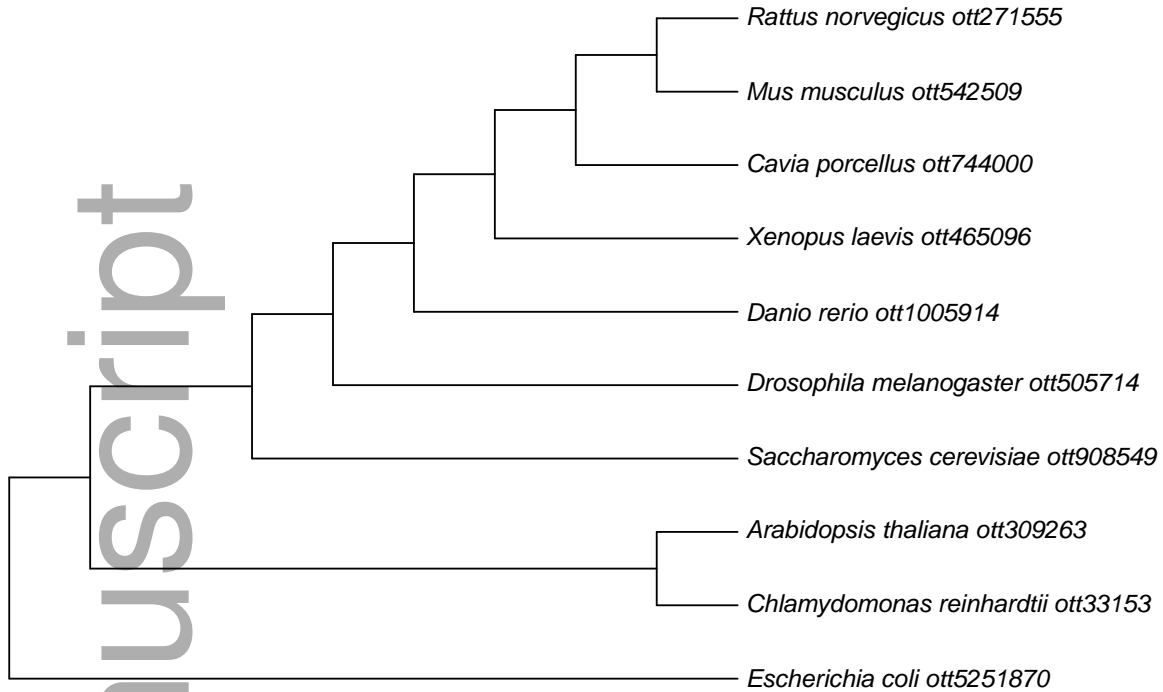


Figure 1: The phylogenetic tree returned by OTL for the list of model species used as an example.

often needed when mapping taxon names. In the example provided, both *Escherichia coli* and *Saccharomyces cerevisiae* are misspelled, but the OTL TNRS finds the correct match for these taxa.

Now that the taxon names are matched to the Open Tree identifiers, we can pass them to the function `tol_induced_subtree` to retrieve the relationships among these taxa. In turn, the tree can be plotted directly as it is returned as `phylo` object (Figure 1).

```
tree <- tol_induced_subtree(ott_ids = ott_id(taxa))
plot(tree, cex = .8, label.offset = .1, no.margin = TRUE)
```

Getting trees from studies

`rotl` can also be used to retrieve trees accompanying studies that have been submitted through the curator interface, and identify the trees that contribute to the synthetic tree. As of March 2016, the Open Tree of Life project stores 7755 trees from 3399

studies (each having between 0 and 61 trees), and 477 of these trees are used to assemble
170 the synthetic tree. These trees constitute a useful resource to reproduce or expand on a
previously published analysis, or to explore how the elucidation of relationships within a
clade has changed through time.

Criteria that can be used to search for studies or their associated trees are available
through the output of the function `studies_properties`. The meaning of these properties
175 is described at: <https://github.com/OpenTreeOfLife/phyloapi/wiki/NexSON>.
Typically, users will want to search for studies or trees based on taxon names (or their
OTT identifiers), but other criteria such as the title of the publication can be used. Here
we demonstrate how to look for and retrieve trees for studies focusing on the family Felidae
(Figure 2).

```
cat_studies <- studies_find_studies(property = "ot:focalCladeOTTTaxonName",  
                                   value = "Felidae", exact = TRUE)  
  
cat_studies  
  
##   study_ids n_trees tree_ids candidate study_year  
## 1   pg_1981      1 tree4052  tree4052      2006  
  
##                                     title  
## 1 The late Miocene radiation of modern Felidae: a genetic assessment  
  
##                               study_doi  
## 1 http://dx.doi.org/10.1126/science.1122277
```

180 Currently only one study focused on this family is available from OTL, and a single
tree is associated with it. We can then retrieve the study and tree identifiers, and pass
them to the function `get_study_tree` to have the tree in memory:

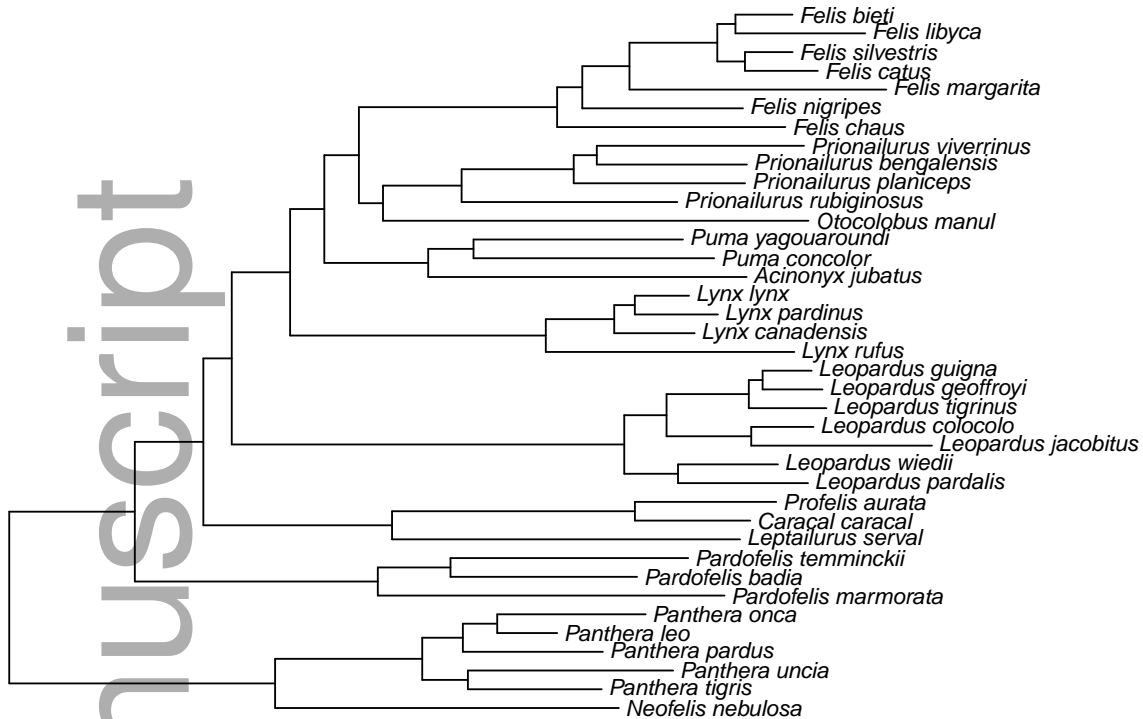


Figure 2: Phylogeny of the Felidae published in Johnson et al. 2006 and retrieved from OTL using rotl.

```
cat_tree <- get_study_tree(study_id = cat_studies[["study_ids"]][1],
                          tree_id = cat_studies[["tree_ids"]][1])
```

```
cat_tree
```

```
##
## Phylogenetic tree with 38 tips and 37 internal nodes.
##
## Tip labels:
## Neofelis_nebulosa, Panthera_tigris, Panthera_uncia, Panthera_pardus, ...
##
## Rooted; includes branch lengths.
```

When more than one tree is available for a given study, the function `list_trees` returns a list containing the tree identifiers for each study. Alternatively, the function

185 `get_study` returns all the trees (by default as `phylo` objects) associated with a particular study. Metadata about the study (e.g., citation information, information about the curator for the study, and other technical information regarding the import of this study) can be obtained using the functions `get_study_meta` and `study_external_IDs`.

■ *How does `rotl` fit into the R package ecosystem?*

190 In recent years, R has become an essential part of the toolbox of many researchers in evolutionary biology and ecology. R greatly facilitates the analysis of large datasets, and allows researchers to combine methods in novel ways because many methods for comparative analyses are implemented, and because it is a relatively easy to use programming language. Additionally, as more data are made available online and
205 accessible using web APIs, several packages have been developed to interact and download these datasets directly in R, thereby enabling direct and reproducible analyses. Notably, the organization rOpenSci (<https://ropensci.org>) has fostered a community of researchers who develop tools and methods to facilitate the use of open data as well broaden the adoption of open science practices in general (Boettiger et al. 2015a). For
200 instance, the rOpenSci-developed package `TreeBase` (Boettiger and Temple Lang 2012) allows users to access phylogenies stored in TreeBASE (<https://treebase.org>). `rotl` contributes to this initiative, and greatly extends the number of taxa for which phylogenetic data can be retrieved within R, while allowing the data from OTL to be combined with other sources easily.

205 Here we show how we can obtain a map of the occurrences for a subset of the cat species that were included in the phylogeny retrieved from the Felidae study above (genus *Lynx*). We extract the species names from the phylogeny, and use them to ask for the records for these species found in GBIF (Figure 3). We include the code to reproduce this figure in Appendix.

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As trait databases are becoming increasingly more common, and interfaces to the data they contains are being developed as R packages (e.g., the package `traits` Chamberlain et al. 2016), `rot1` provides a way to easily retrieve phylogenetic information for species trait data that are available.

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In addition of an introduction on how to use the package, `rot1` includes two vignettes that demonstrate how to integrate a phylogeny and data associated with the taxa it represents. Specifically, the “Data mashups” vignette provides an example of how to retrieve a phylogeny for species a researcher may have data for, and visualize both the phylogeny and data associated with the species at the tips. The other vignette titled “Meta-analysis” demonstrates how a complete comparative method analysis, including the gathering of data and a phylogeny, can be performed in a single R session. We reproduce a published meta-analysis testing for differential investment in male and female offsprings among 51 species of birds. As new versions of the OTL API and `rot1` are released, these vignettes will be kept up-to-date.

220

CONCLUDING REMARKS

225

The recognition of the importance of phylogenies to account for the statistical non-independence of species in comparative methods, the recent development of methods to explore trait evolution or changes in diversification rates, and attempts to incorporate the evolutionary history of species forming ecological communities, have driven the need for accurate phylogenies. However, there is often a discrepancy between taxa targeted by studies wanting to use phylogenetic information, and taxa for which phylogenies are available. Typically, the latter result from focused studies of taxonomic groups, while the former encompass species found in a given geographical location or ecosystem. We believe that by providing an easy-to-use interface to obtain phylogenies for an arbitrary set of taxa directly in R, `rot1` will be useful in a wide variety of contexts.

230

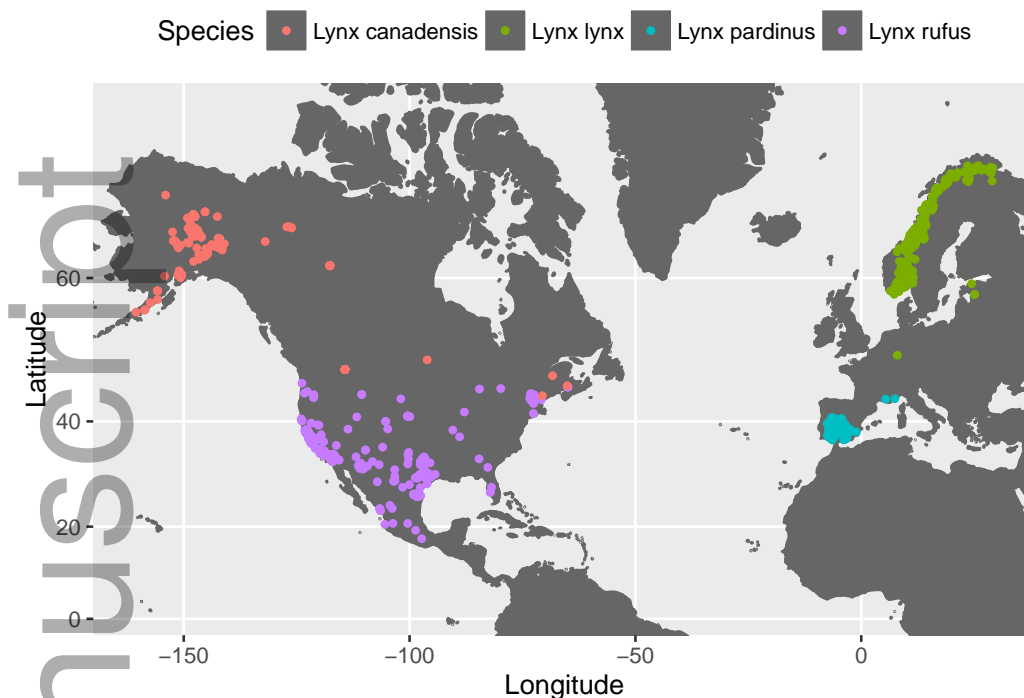


Figure 3: GBIF records for the species in *Lynx* included in the phylogeny associated with the study by Johnson et al. 2006.

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The accuracy and usefulness of the data provided by OTL relies on the community to make generated phylogenies (and their metadata) digitally available as tree files (i.e., Newick, NEXUS or NeXML). We strongly encourage researchers to submit their published phylogenies to OTL using the curator interface

(<https://tree.opentreeoflife.org/curator>). By facilitating the discovery and re-use

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of published trees and of the synthetic Open Tree, we hope `rot1` will contribute to the wider adoption of best practices to make phylogenetic information available and re-usable.

AVAILABILITY

`rot1` is free, open source, and released under a Simplified BSD license. Stable versions are available from the CRAN repository

245

(<https://cran.r-project.org/package=rot1>), and development versions are available from GitHub (<https://github.com/ropensci/rot1>). This manuscript was built using

rotl 3.0.0 (<https://github.com/ropensci/rotl/tree/v3.0.0>). The package is under active development, and authors welcome bug reports or feature requests via the GitHub repository. The source for this manuscript is available on GitHub

250 (<https://github.com/fmichonneau/rotl-ms>).

Python (<https://github.com/OpenTreeOfLife/pyopentree>) and Ruby (<https://github.com/SpeciesFileGroup/bark>) libraries to interact with the OTL APIs are also available.

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*

References

Boettiger, C., S. Chamberlain, E. Hart, and K. Ram. 2015a. Building Software, Building Community: Lessons from the rOpenSci Project. *Journal of Open Research Software* 3.

- 270 Boettiger, C., S. Chamberlain, R. Vos, and H. Lapp. 2015b. RNeXML: a package for reading and writing richly annotated phylogenetic, character, and trait data in R. *Methods in Ecology and Evolution* Pages n/a–n/a.
- Boettiger, C., D. T. Lang, and P. C. Wainwright. 2012. Rfishbase: Exploring, manipulating and visualizing FishBase data from R. *Journal of Fish Biology* 81:2030–2039.
- 275 Boettiger, C. and D. Temple Lang. 2012. Treebase: an R package for discovery, access and manipulation of online phylogenies. *Methods in Ecology and Evolution* 3:1060–1066.
- Bolker, B., M. Butler, P. Cowan, D. de Vienne, D. Eddelbuettel, M. Holder, T. Jombart, S. Kembel, F. Michonneau, D. Orme, B. O’Meara, E. Paradis, J. Regetz, and D. Zwickl. 2015. phylobase: Base Package for Phylogenetic Structures and Comparative Data.
- 280 Chamberlain, S., Z. Foster, I. Bartomeus, D. LeBauer, and D. Harris. 2016. traits: Species Trait Data from Around the Web.
- Cranston, K., L. J. Harmon, M. A. O’Leary, and C. Lisle. 2014. Best practices for data sharing in phylogenetic research. *PLoS currents* 6:1–8.
- Drew, B. T., R. Gazis, P. Cabezas, K. S. Swithers, J. Deng, R. Rodriguez, L. A. Katz, 285 K. A. Crandall, D. S. Hibbett, and D. E. Soltis. 2013. Lost Branches on the Tree of Life. *PLoS Biology* 11.
- Hinchliff, C. E., S. A. Smith, J. F. Allman, J. G. Burleigh, R. Chaudhary, L. M. Coghill, K. A. Crandall, J. Deng, B. T. Drew, R. Gazis, K. Gude, D. S. Hibbett, L. A. Katz, H. D. Laughinghouse, E. J. McTavish, P. E. Midford, C. L. Owen, R. H. Ree, J. A. Rees, 290 D. E. Soltis, T. Williams, and K. A. Cranston. 2015. Synthesis of phylogeny and taxonomy into a comprehensive tree of life. *Proceedings of the National Academy of Sciences* 112:12764–12769.

- Johnson, W. E., E. Eizirik, J. Pecon-Slattery, W. J. Murphy, A. Antunes, E. Teeling, and
S. J. O'Brien. 2006. The Late Miocene Radiation of Modern Felidae: A Genetic
295 Assessment. *Science* 311:73–77.
- Kembel, S. W., P. D. Cowan, M. R. Helmus, W. K. Cornwell, H. Morlon, D. D. Ackerly,
S. P. Blomberg, and C. O. Webb. 2010. Picante: R tools for integrating phylogenies and
ecology. *Bioinformatics* 26:1463–1464.
- Knuth, D. E. 1984. Literate programming. *The Computer Journal (British Computer*
300 *Society)* 27:97–111.
- Ksepka, D. T., J. F. Parham, J. F. Allman, M. J. Benton, M. T. Carrano, K. A. Cranston,
P. C. J. Donoghue, J. J. Head, E. J. Hermsen, R. B. Irmis, W. G. Joyce, M. Kohli, K. D.
Lamm, D. Leehr, J. L. Patané, P. D. Polly, M. J. Phillips, N. A. Smith, N. D. Smith,
M. Van Tuinen, J. L. Ware, and R. C. M. Warnock. 2015. The Fossil Calibration
305 Database: A New Resource for Divergence Dating. *Systematic Biology* 64:853–859.
- Lewis, P. O. 2003. NCL: A C++ class library for interpreting data files in NEXUS format.
Bioinformatics 19:2330–2331.
- Maddison, D. R., D. L. Swofford, and W. P. Maddison. 1997. NEXUS: an extensible file
format for systematic information. *Systematic biology* 46:590–621.
- 310 Magee, A. F., M. R. May, and B. R. Moore. 2014. The dawn of open access to phylogenetic
data.
- O'Meara, B. C. 2012. Evolutionary Inferences from Phylogenies: A Review of Methods.
Annual Review of Ecology, Evolution, and Systematics 43:267–285.
- Paradis, E., J. Claude, and K. Strimmer. 2004. APE: Analyses of Phylogenetics and
315 Evolution in R language. *Bioinformatics* 20:289–290.

Pearse, W. D., M. W. Cadotte, J. Cavender-Bares, A. R. Ives, C. M. Tucker, S. C. Walker, and M. R. Helmus. 2015. Pez: Phylogenetics for the environmental sciences. *Bioinformatics* 31:2888–2890.

320 Pearse, W. D. and A. Purvis. 2013. phyloGenerator: An automated phylogeny generation tool for ecologists. *Methods in Ecology and Evolution* 4:692–698.

Pennell, M. W., J. M. Eastman, G. J. Slater, J. W. Brown, J. C. Uyeda, R. G. FitzJohn, M. E. Alfaro, and L. J. Harmon. 2014. Geiger V2.0: an Expanded Suite of Methods for Fitting Macroevolutionary Models To Phylogenetic Trees. *Bioinformatics* 30:2216–2218.

325 Pennell, M. W., R. G. FitzJohn, and W. K. Cornell. 2015. A simple approach for maximizing the overlap of phylogenetic and comparative data. *Methods in Ecology and Evolution* .

Pennell, M. W. and L. J. Harmon. 2013. An integrative view of phylogenetic comparative methods: connections to population genetics, community ecology, and paleobiology. *Annals of the New York Academy of Sciences* 1289:90–105.

330 Revell, L. J. 2012. phytools: an R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217–223.

Schliep, K. P. 2011. phangorn: Phylogenetic analysis in R. *Bioinformatics* 27:592–593.

335 Stoltzfus, A., B. O’Meara, J. Whitacre, R. Mounce, E. L. Gillespie, S. Kumar, D. F. Rosauer, and R. a. Vos. 2012. Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. *BMC Research Notes* 5:574.

Varela, S., J. González-Hernández, E. Casabella, and R. Barrientos. 2014. rAvis: An R-package for downloading information stored in proyecto AVIS, a citizen science bird project. *PLoS ONE* 9.

- Varela, S., J. Gonzalez-Hernandez, L. F. Sgarbi, C. Marshall, M. D. Uhen, S. Peters, and
340 M. McClennen. 2015. paleobioDB: An R package for downloading, visualizing and
processing data from the Paleobiology Database. *Ecography* 38:419–425.
- Vos, R. A., J. P. Balhoff, J. A. Caravas, M. T. Holder, H. Lapp, W. P. Maddison, P. E.
Midford, A. Priyam, J. Sukumaran, X. Xia, and A. Stoltzfus. 2012. NeXML: Rich,
extensible, and verifiable representation of comparative data and metadata. *Systematic*
345 *Biology* 61:675–689.
- Webb, C. O., D. D. Ackerly, and S. W. Kembel. 2008. Phylocom: Software for the analysis
of phylogenetic community structure and trait evolution. *Bioinformatics* 24:2098–2100.
- Webb, C. O., D. D. Ackerly, M. A. McPeck, and M. J. Donoghue. 2002. Phylogenies and
Community Ecology. *Annual Review of Ecology and Systematics* 33:475–505.
- 350 Xie, Y. 2015. *Dynamic Documents with R and knitr*. 2nd ed. Chapman and Hall/CRC,
Boca Raton, Florida.
- Yu, G., D. Smith, H. Zhu, Y. Guan, and T. T.-Y. Lam. 2015. ggtree: an R package for
visualization and annotation of phylogenetic tree with different types of meta-data.
Methods in Ecology and Evolution submitted.

355 SUPPLEMENTARY INFORMATION

Appendix: Source code used to generate Figure 3.

Rattus norvegicus ott271555

Mus musculus ott542509

Cavia porcellus ott744000

Xenopus laevis ott465096

Danio rerio ott1005914

Drosophila melanogaster ott505714

Saccharomyces cerevisiae ott908549

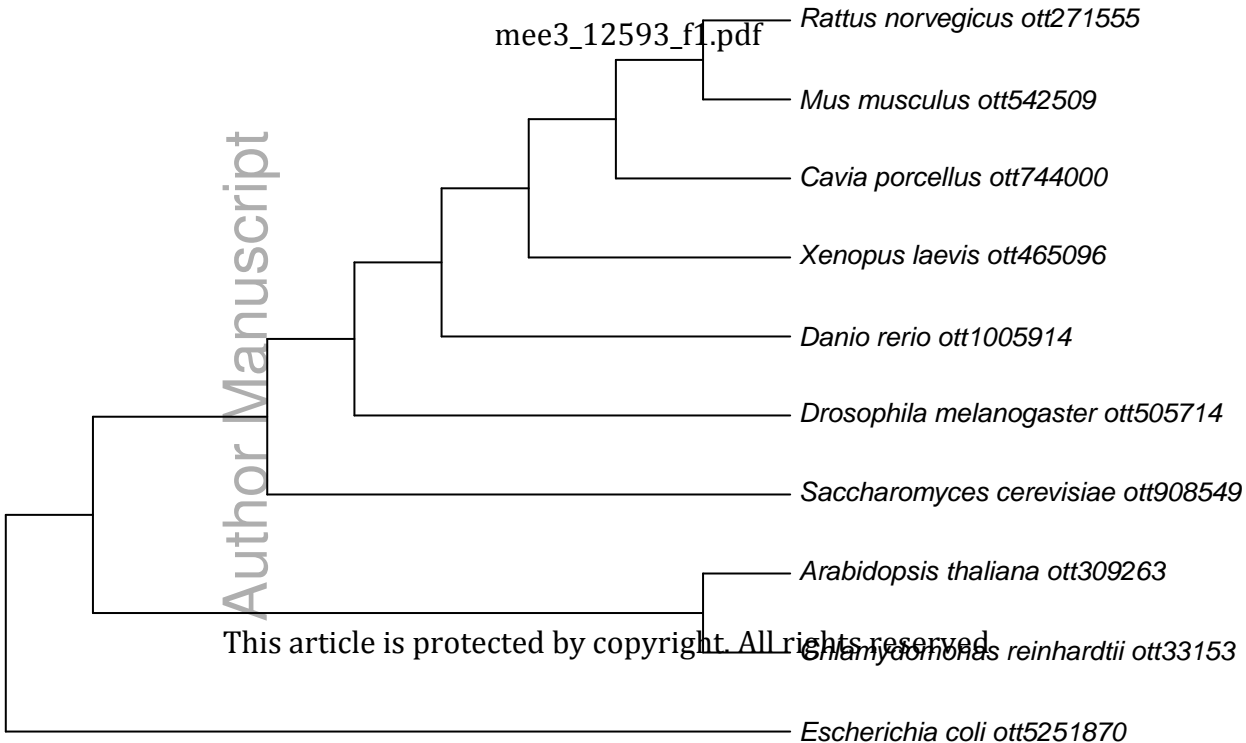
Arabidopsis thaliana ott309263

Glycine max ott33153

Escherichia coli ott5251870

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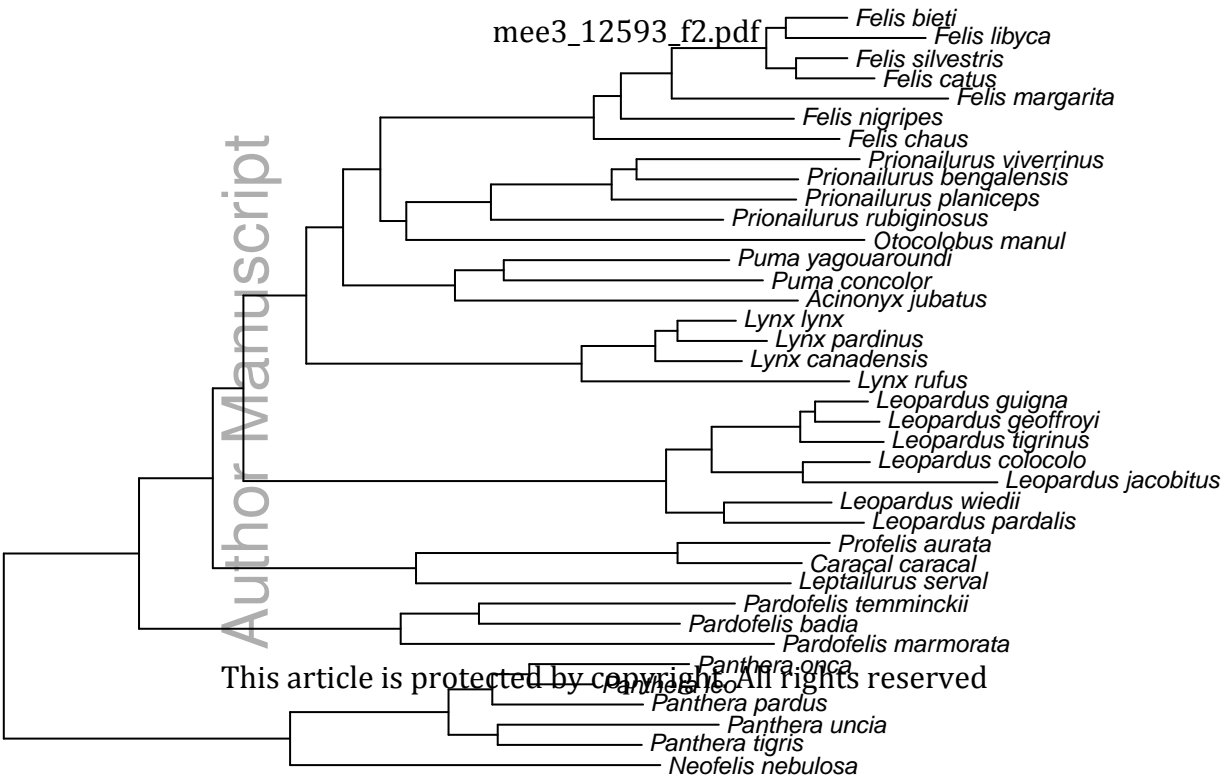
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mee3_12593_f2.pdf

- Felis bieti*
- Felis libyca*
- Felis silvestris*
- Felis catus*
- Felis margarita*

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Species ● Lynx canadensis ● Lynx lynx ● Lynx pardinus ● Lynx rufus

