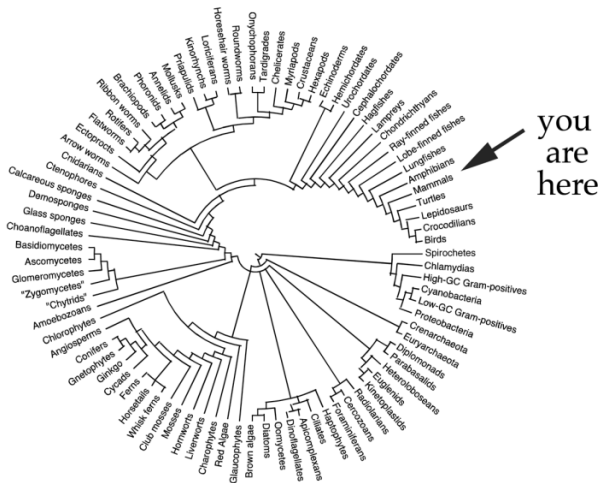# Open Tree of Life resources connect phylogenetic data

Emily Jane McTavish

University of California, Merced
ejmctavish@ucmerced.edu,

you
are
here

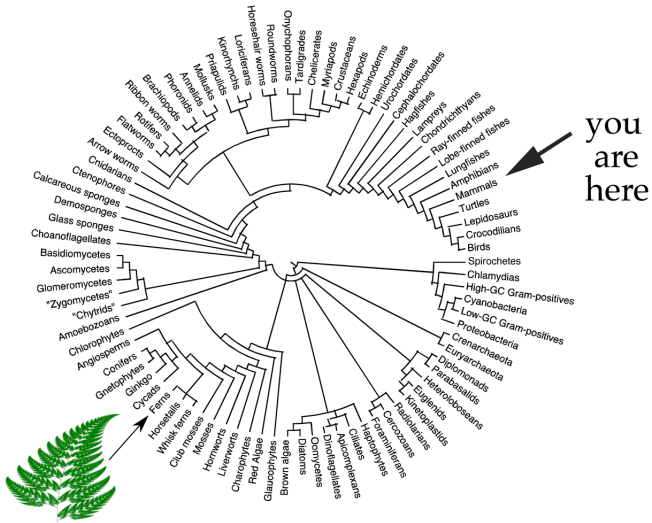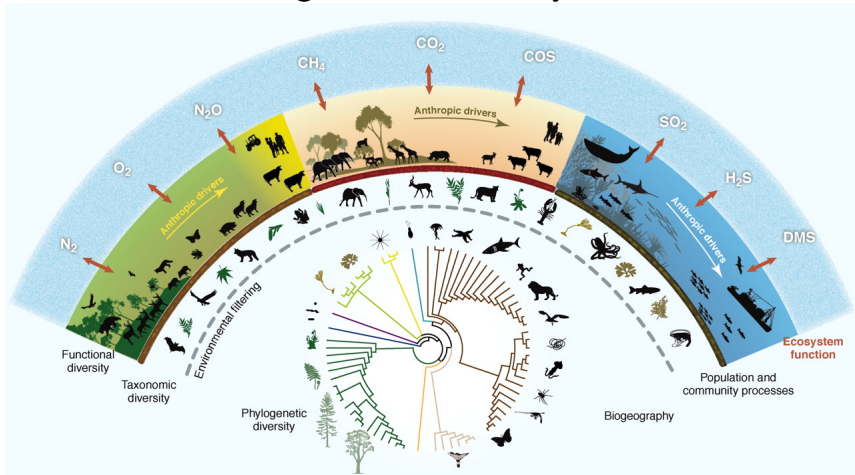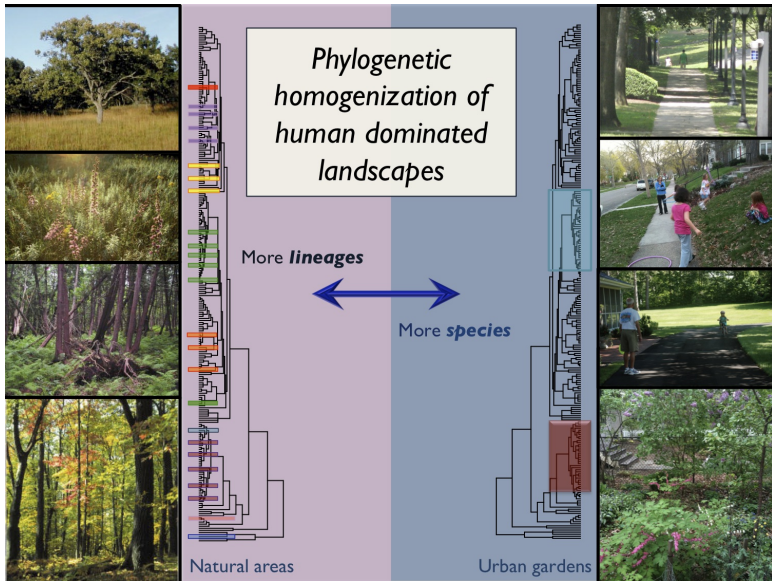Image Ethan Hein

you
are
here

Horsehair worms
Roundworms
Onychophorans
Tardigrades
Chelicerates
Myriapods
Hexapods
Crustaceans
Echinoderms
Hemichordates
Urochordates
Cephalochordates
Hagfishes
Lampreys
Chondrichthyans
Ray-finned fishes
Lobe-finned fishes
Lungfishes
Amphibians
Mammals
Turtles
Lepidosaurs
Crocodilians
Birds

Loriciferans
Kinorhynchs
Priapulids
Mollusks
Annelids
Phoronids
Brachiopods
Ribbon worms
Rotifers
Flatworms
Ectoprocts
Arrow worms
Cnidarians
Ctenophores
Calcareous sponges
Demosponges
Glass sponges
Choanoflagellates
Basidiomycetes
Ascomycetes
Glomeromycetes
"Zygomycetes"
"Chytrids"
Amoebozoans
Chlorophytes
Angiosperms
Conifers
Gnetophytes
Ginkgo
Cycads
Ferns
Horsetails
Whisk ferns
Club mosses
Mosses
Hornworts
Liverworts
Charophytes
Red Algae
Glaucophytes
Brown algae
Diatoms
Oomycetes
Dinoflagellates
Apicomplexans
Ciliates
Haptophytes
Cercozoans
Forams
Radiolarians
Euglenids
Kinetoplastids
Heteroloboseans
Parabasalids
Diplomonads
Euryarchaeota
Crenarchaeota
Proteobacteria
Low-GC Gram-positives
Cyanobacteria
High-GC Gram-positives
Chlamydias
Spirochetes

Image Ethan Hein

Evolutionary context provides a framework for **understanding and conserving** global biodiversity

Naeem et al. (2012)

Phylogenetic homogenization of human dominated landscapes

More *lineages*

More *species*

Natural areas

Urban gardens

(example from the Cavender-Bares lab webpage)

Taxonomy is often used as a proxy for shared evolutionary history

at best taxonomy is a coarse representation of evolutionary history

at worst taxonomy is a mis-representation of evolutionary history

at worst taxonomy is a mis-representation of evolutionary history

RESEARCH ARTICLE

Traditional Taxonomic Groupings Mask Evolutionary History: A Molecular Phylogeny and New Classification of the Chromodorid Nudibranchs

Rebecca Fay Johnson, Terrence M. Gosliner

Johnson and Gosliner (2012)

Why do people use taxonomy as a proxy for shared evolutionary history?

Why do people use taxonomy as a proxy for shared evolutionary history?

Phylogenies:

> don't include all the species we are interested in,
>
> keep changing,
>
> are hard to access.

Goal: Build a tree of all life.

Goal: Build a tree of all life.

Every named species

Updated as new data becomes available

Freely and easily accessible

tree.opentreeoflife.org

phylogenies

taxonomy

unified tree of life
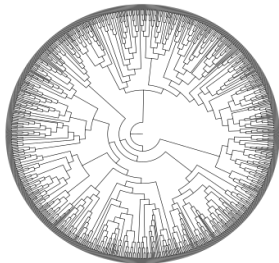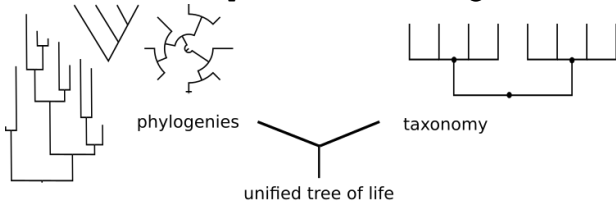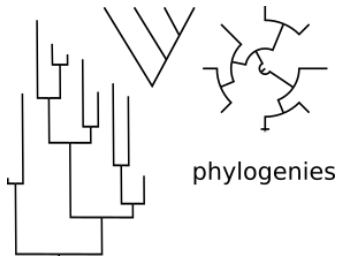
phylogenies
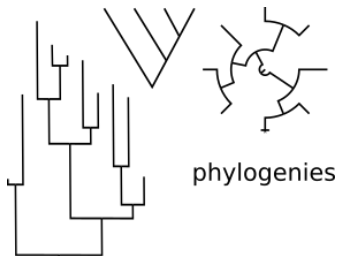
phylogenies

Current synthetic tree

- 1,330 representative phylogenies
- 112,890 tips from phylogeny
- Current draft posted June 2023, will be updated with more input trees regularly
- Synthesis algorithm published in Redelings and Holder (2017), recent major speed improvements
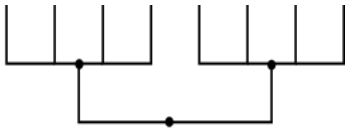
taxonomy
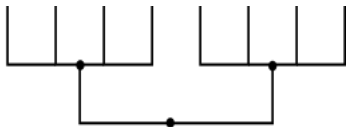
taxonomy

4.5 million named taxa, around 2.4 million tips

Merges NCBI, Index fungorum, Silva, IRMNG, GBIF and other taxonomies

Scaffold for combining ranked phylogenetic estimates

New drafts released as inputs change, most recent update June 2023

Rees and Cranston (2017)

🍃 Open Tree taxonomy: **Limulus polyphemus**

The current taxonomy version is [ott3.3 (click for more information)](#). See the OTT documentation for [an explanation of the taxon flags used](#) below, e.g., `extinct`

Taxon details

species **Limulus polyphemus**   [ncbi:6850](#) ([worms:150514](#), [gbif:1010610](#), [irmng:10838080](#))   (OTT id 511973)

[View this taxon in the current synthetic tree](#)

Synonym(s)

[? polyphemus](#), [Limulus albus](#), [Limulus americanus](#), [Limulus cyclops](#), [Limulus occidentalis](#), [Limulus sowerbii](#), [Xiphosura polyphemus](#)

Lineage

[life](#) > [cellular organisms](#) > [Eukaryota](#) > [Opisthokonta](#) > [Holozoa](#) > [Metazoa](#) > [Eumetazoa](#) > [Bilateria](#) > [Protostomia](#) > [Ecdysozoa](#) > [Panarthropoda](#) > [Arthropoda](#) > [Chelicerata](#) > [Merostomata](#) > [Xiphosura](#) > [Limulidae](#) > [Limulus](#)

Taxonomic amendments

New taxa can be added from uploaded trees, and will be included in future synthetic trees
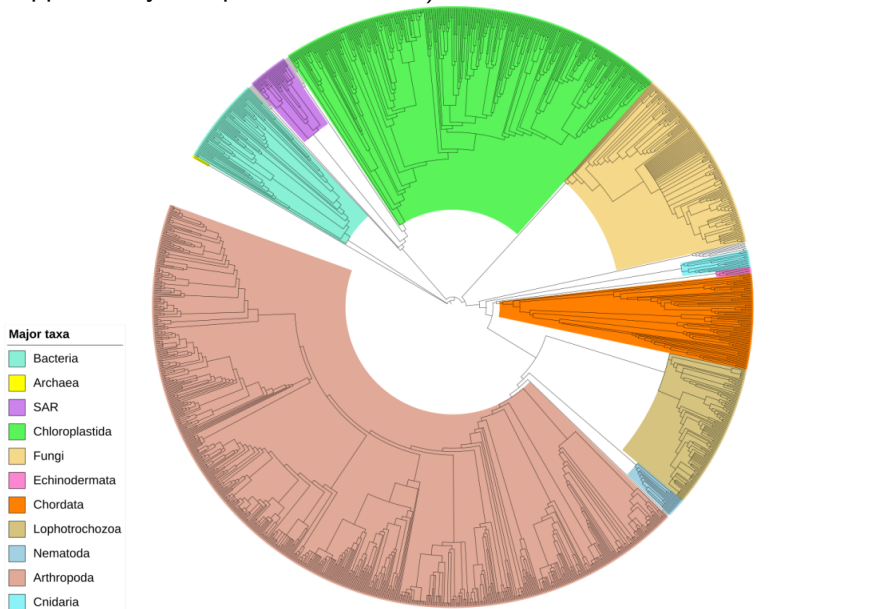
Opportunity to feed-back to input taxonomic resources
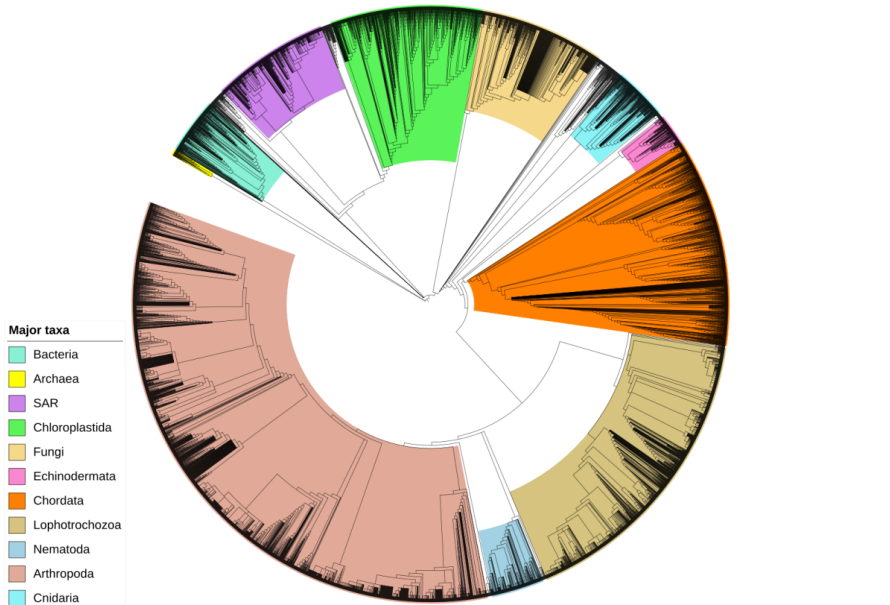
tree viewer demo
https:
//tree.opentreeoflife.org/opentree/argus/opentree14.7@
mrcaott30845ott82415/Amazonetta--Sibirionetta

# Tree of tips with 500 or more descendants in OpenTree (1,408 tips, supported by 442 published studies)

Major taxa

- Bacteria
- Archaea
- SAR
- Chloroplastida
- Fungi
- Echinodermata
- Chordata
- Lophotrochozoa
- Nematoda
- Arthropoda
- Cnidaria

Tree of all families in OpenTree (9,306 tips, supported by 455 published studies)

Phylogenetic information (green) and conflict (red) across the tree

Annotated tree available at
https://itol.embl.de/tree/10823010783159601596222895
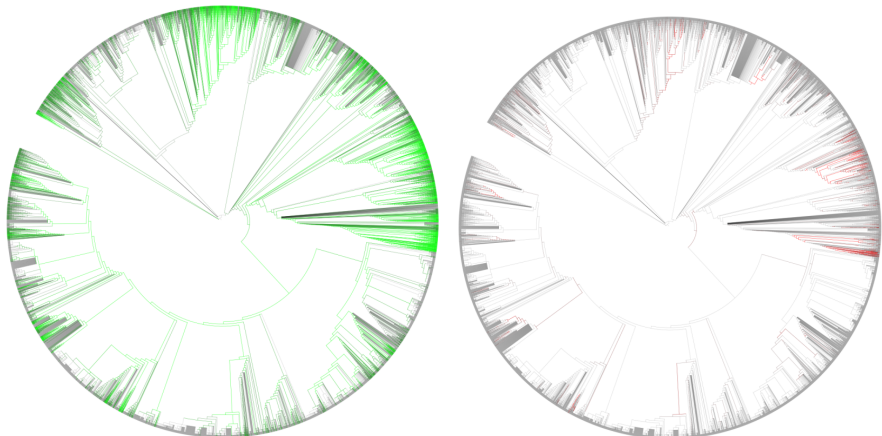
Cross-link data from other resources
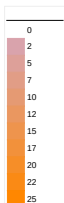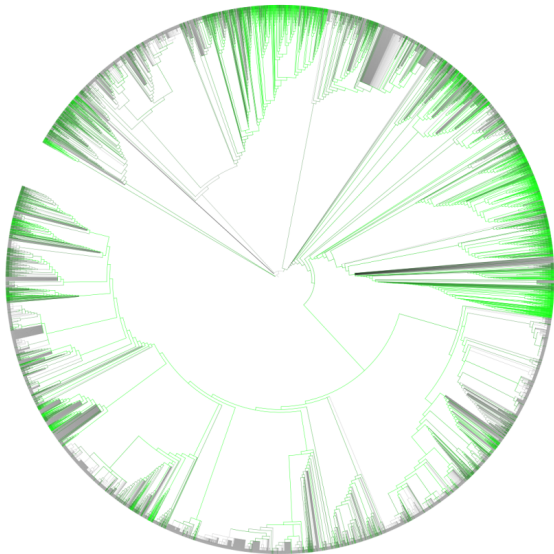
Proportion of lineages with data:
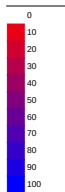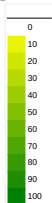
GenBank **GBIF** **Genome**
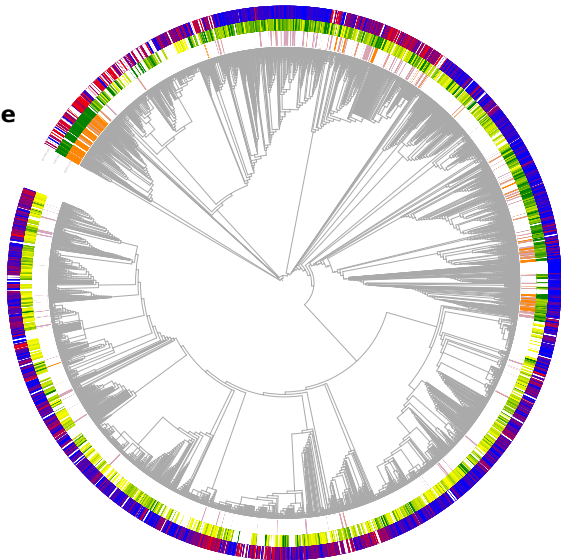
We are missing phylogenetic data for many lineages.
How will we fill in the gaps?

We need to build on existing phylogenetic information.

We need to build on existing phylogenetic information.

Perspective

Lost Branches on the Tree of Life

Bryan T. Drew[1]*, Romina Gazis[2], Patricia Cabezas[3,4], Kristen S. Swithers[5], Jiabin Deng[1], Roseana Rodriguez[1], Laura A. Katz[5], Keith A. Crandall[4], David S. Hibbett[2], Douglas E. Soltis[1,6]

[1] University of Florida, Gainesville, Florida, United States of America, [2] Clark University, Worcester, Massachusetts, United States of America, [3] Brigham Young University, Provo, Utah, United States of America, [4] George Washington University, Washington, DC, United States of America, [5] Smith College, Northampton, Massachusetts, United States of America, [6] Florida Museum of Natural History, Gainesville, Florida, United States of America

Drew et al. (2013)

only 16% of phylogenies published 2000-2013 are digitally available Drew et al. PLoS Biology 2013
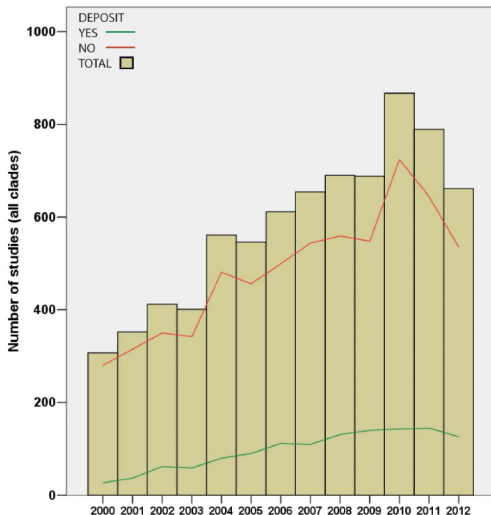

Figure 1. Overview of total number of publications surveyed from animal, fungus, seed plant, microbial eukaryote, archaea, and bacteria literature (indicated in red), and the number of those publications that archived their trees and alignments in either Dryad or TreeBASE (indicated in green).

only 16% of phylogenies published 2000-2013 are digitally available (Drew et al. PLoS Biology 2013)

20% of phylogenies published 2013-2018

McTavish et al. (2017)

Recent multi-month outage of treebase makes future of phylogenetic data sharing even more concerning

Adding phylogenetic data to OpenTree data store

- Trees can be uploaded from any source, does not have to be own data.

- Easy to use browser based interface

- Track curation attribution by name or pseudonym

- Files are json representation of NeXML phylogenetic data format

- Data store is hosted publicly on GitHub

github.com/OpenTreeOfLife/phylesystem-1
McTavish et al. (2015)

Community Curation

311 individual curators of 4,676 uploaded studies

Community Curation

    311 individual curators of 4,676 uploaded studies

    Currently a several month lag for incorporation into synthetic
    tree, will begin monthly builds in the next year

Date estimates

- The synthetic tree does not currently have any branch lengths (when combining across DNA, morphology and taxonomy, branch lengths are not obvious!!)

- However! We can translate dates from input trees to the synthetic tree
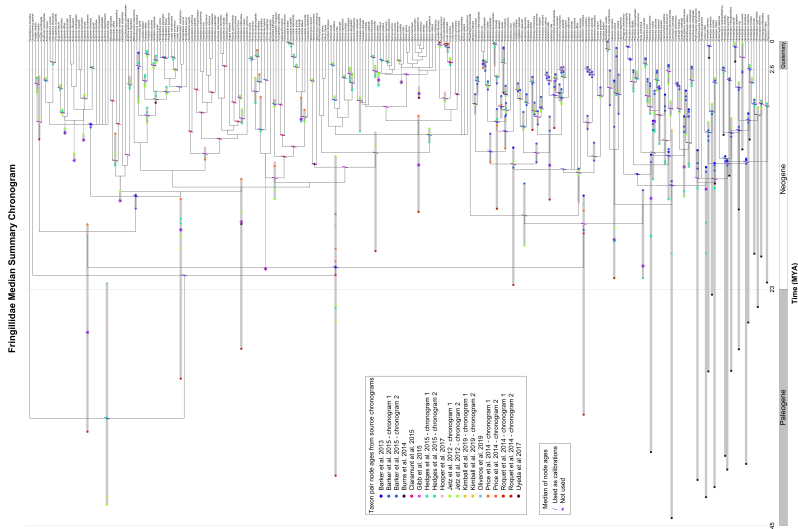
Webserver at datelife.opentreeoflife.org

Sanchez-Reyes, McTavish, O'Meara, Accepted, Syst Bio

Dated finch tree - topology estimated based on 33 studies, dates from 13 studies

OpenTree Dates API

- Match internal nodes of dated inputs to nodes in the synthetic tree (phyloreferenceing approach)
- Apply dates to nodes induced subtree
- Smooth undated nodes using bladj (Webb et al. (2008))
- Beta functionality available at dates.opentreeoflife.org
- Date estimates for 46,639 internal nodes from 320 input chronograms

https://github.com/OpenTreeOfLife/ChronoSynth
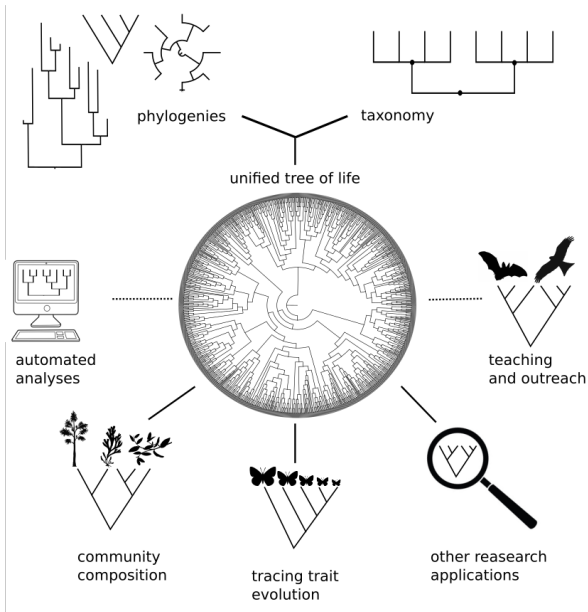
McTavish et al. (2017)

Open Tree resources are available via a range of implementations

- Browser interface, `tree.opentreeoflife.org`
- Open Tree of Life API
- Python-opentree python wrapper McTavish et al. (2021)
- R Open Tree of Life (rotl) **R**OpenSci Michonneau et al. (2016)

Why would you need OpenTree if you can build your own trees?
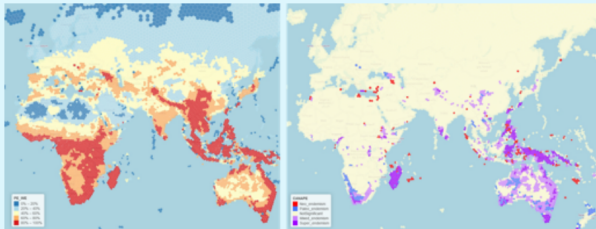
Assess phylogenetic diversity at large scales

Assess phylogenetic diversity at large scales

PhyloNext: a pipeline for phylogenetic diversity analysis of GBIF-mediated data in the cloud:

Phylogenetic endemism and its types (paleo/neo)

Work in progress with Mikryukov, Laffan, Miller and others (Mikryukov et al. (2023))

For common community phylogenetic analyses, go ahead and use synthesis phylogenies

DAIJIANG LI,[1,5] LAUREN TROTTA,[1] HANNAH E. MARX,[2] JULIE M. ALLEN,[3] MIAO SUN,[4] DOUGLAS E. SOLTIS,[4] PAMELA S. SOLTIS,[4] ROBERT P. GURALNICK,[4] AND BENJAMIN BAISER[1]

"our results justify taking advantage of recently developed and continuously improving synthesis trees, especially the Open Tree of Life." Li et al. (2019)

Easily get accurate relationships (and citations!) for arbitrary sets of species

Easily get accurate relationships (and citations!) for arbitrary sets of species

Which species with an existing reference genome is most closely related to the Society finch?

Lonchura striata domestica

Zebra finch
(*Taeniopygia guttata*)

Ground finch
(*Geospiza fortis*)

Access **OPEN Tree of Life** via `rotl` package from **R OpenSci**

Michonneau et al. (2016))

Access ![OPEN Tree of Life] via `rotl` package from ![R OpenSci]

```
install.packages("rotl")
library(rotl)
spp <- c("Geospiza", "Taeniopygia", "Lonchura")
taxa <- tnrs_match_names(spp, context="Animals")
tr <- tol_induced_subtree(ott_id(taxa), label="name")
plot(tr)
```

Access OPEN Tree of Life via rotl package from R OpenSci

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install.packages("rotl")
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```
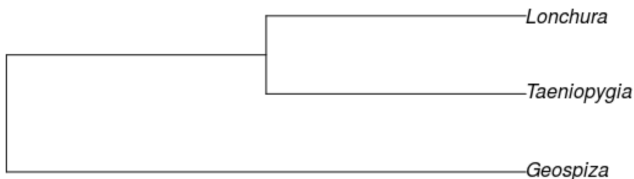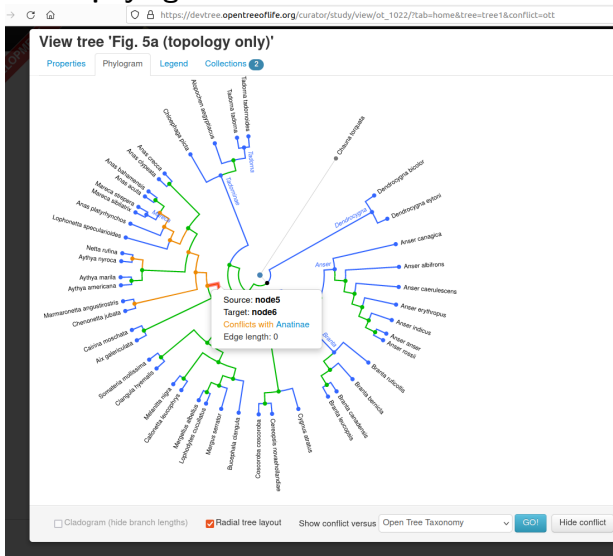

Use the zebra finch as reference!
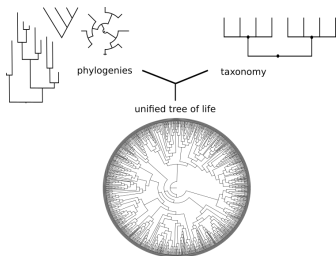Phylogenies generating subtree:

(Barker et al. 2004 PNAS; Selvatti et al. 2015 MPE; Burns et al. 2014 MPE; Barker et al. 2015 The Auk)

Compare new phylogenetic estimates to taxonomy, synthetic tree, or other phylogeneies

https://tree.opentreeoflife.org/curator/study/view/ot_1022/?tab=home&tree=tree1&conflict=ott

Generate a custom synthetic tree for your taxa


Synthesis on demand

Personal phylogeny rankings

Any root node

Synthesis phylogeny of all birds

- 276 phylogenetic inputs
- Custom taxonomic translation table to match eBird data
- Phylogenetic information for 9261 of the 10824 species (85%)
- 8785 of 9006 internal nodes (90%) are directly supported by phylogentic information (the rest are from taxonomy)
- Dates estimated from 88 input trees provide estimates for 6874 internal nodes

Collaboration with Eliot Miller and others at Cornell Lab of Ornithology

Custom synthesis phylogeny of all birds
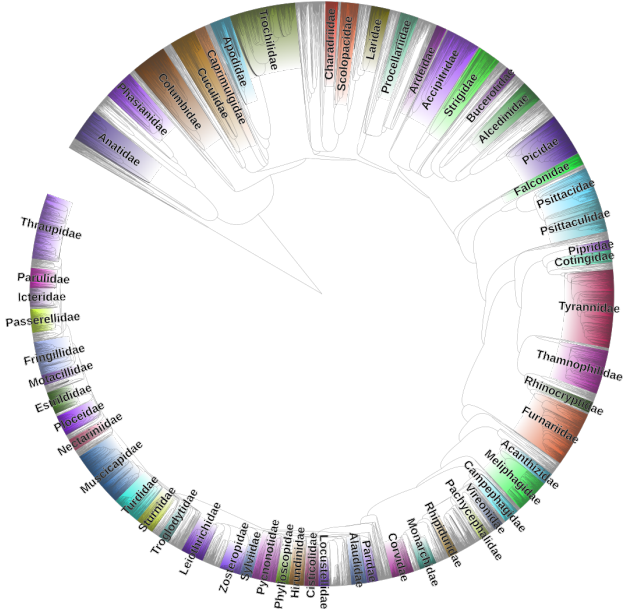
Phylogenetic information (green) and conflict (red) across the bird tree
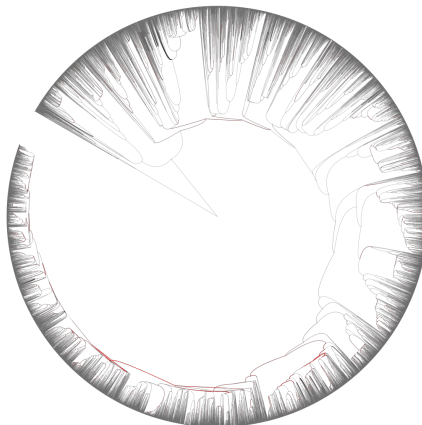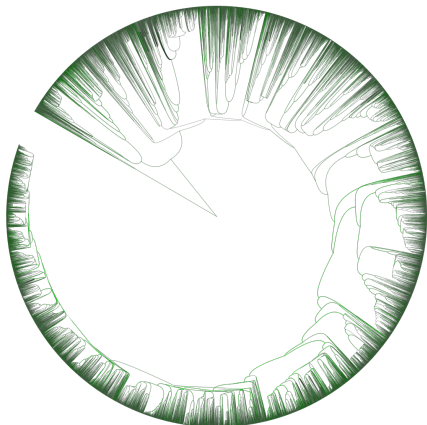
Annotated tree available at
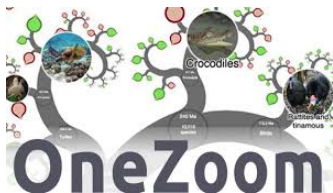https://itol.embl.de/tree/169236782449141167829549

CC0 license provides fully open access for downstream re-usability

CC0 license provides fully open access for downstream re-usability

Open Tree provides the tree backend for:

Case study: What is the phylogeny of all bird species observed in Merced?

Undated tree:

    TNRS on species names to match to unique identifiers

    Request induced subtree from OpenTree APIs

    Tree with 302 tips, informed by 102 published studies

Taxonomy lags behind phylogeny (e.g. *Ardea*)

https://itol.embl.de/tree/1082301078373711602860218

Conclusions

Phylogenetic estimates should be freely accessible and reusable

Open Tree cross-links phylogenetic and taxonomic information

A variety of tools and approaches provides wide access to Open Tree resources

Contribute your knowledge!
`tree.opentreeoflife.org/curator`

Try it out! A variety of tutorials are available at:
`https://opentreeoflife.github.io/use`

Ask for help on our gitter chat:
`https://gitter.im/OpenTreeOfLife/public`

Thank You

Drew, B. T., Gazis, R., Cabezas, P., Swithers, K. S., Deng, J., Rodriguez, R., Katz, L. A., Crandall, K. A., Hibbett, D. S., and Soltis, D. E. (2013). Lost Branches on the Tree of Life. *PLoS Biology*, 11(9):e1001636. Number: 9.

Johnson, R. F. and Gosliner, T. M. (2012). Traditional Taxonomic Groupings Mask Evolutionary History: A Molecular Phylogeny and New Classification of the Chromodorid Nudibranchs. *PLOS ONE*, 7(4):e33479.

Li, D., Trotta, L., Marx, H. E., Allen, J. M., Sun, M., Soltis, D. E., Soltis, P. S., Guralnick, R. P., and Baiser, B. (2019). For common community phylogenetic analyses, go ahead and use synthesis phylogenies. *Ecology*, 100(9).

McTavish, E. J., Drew, B. T., Redelings, B., and Cranston, K. A. (2017). How and Why to Build a Unified Tree of Life. *BioEssays*, 39(11).

McTavish, E. J., Hinchliff, C. E., Allman, J. F., Brown, J. W., Cranston, K. A., Holder, M. T., Rees, J. A., and Smith, S. A. (2015). Phylesystem: a git-based data store for community-curated phylogenetic estimates. *Bioinformatics*, 31(17):2794–2800.

McTavish, E. J., Sánchez-Reyes, L. L., and Holder, M. T. (2021). OpenTree: A Python Package for Accessing and Analyzing Data from the Open Tree of Life. *Systematic Biology*, 70(6):1295–1301.

Michonneau, F., Brown, J. W., and Winter, D. J. (2016). rotl: an R package to interact with the Open Tree of Life data. *Methods in Ecology and Evolution*, pages n/a–n/a.

Mikryukov, Abarenkov, Laffan, Robertson, McTavish, Waller, and Miller (2023). PhyloNext: a pipeline for phylogenetic diversity analysis of GBIF-mediated data in the cloud.

Naeem, S., Duffy, J. E., and Zavaleta, E. (2012). The Functions of Biological Diversity in an Age of Extinction. *Science*, 336(6087):1401–1406.

Redelings, B. D. and Holder, M. T. (2017). A supertree pipeline for summarizing phylogenetic and taxonomic information for millions of species. *PeerJ*, 5:e3058.

Rees, J. A. and Cranston, K. (2017). Automated assembly of a reference taxonomy for phylogenetic data synthesis. *Biodiversity Data Journal*.

Webb, C. O., Ackerly, D. D., and Kembel, S. W. (2008). Phylocom: software for the analysis of phylogenetic community structure and trait evolution. *Bioinformatics*, 24(18):2098–2100.