Open Tree of Life resources connect phylogenetic data

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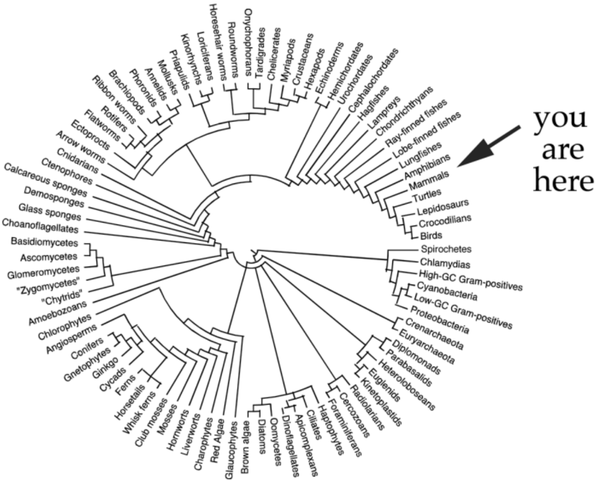


you
are
here

Image Ethan Hein

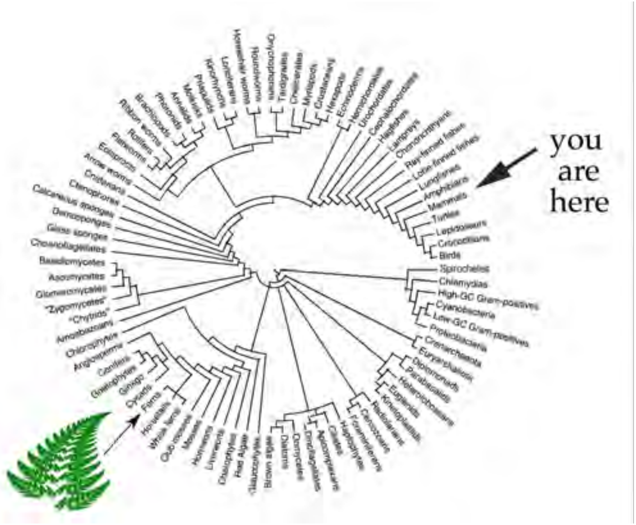
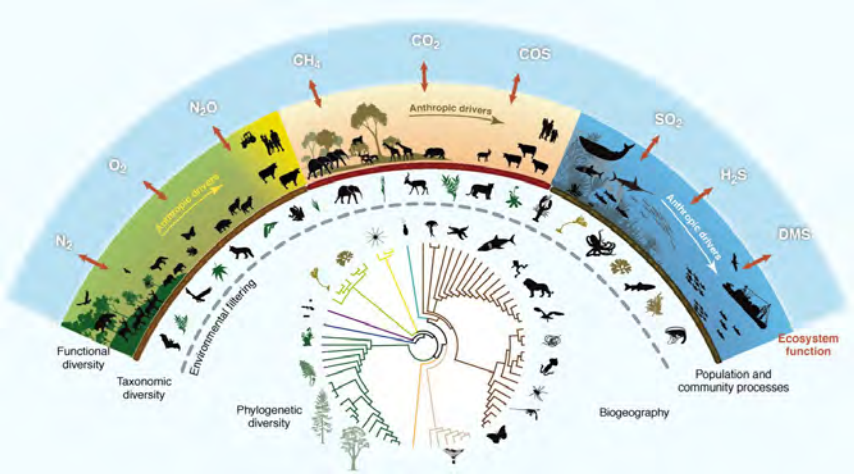
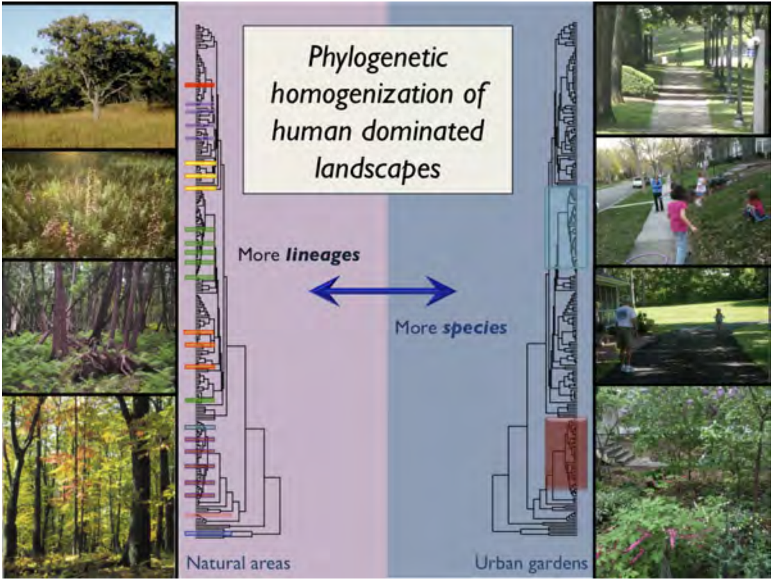


Image Ethan Hein

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



Naeem et al. (2012)



(example from the Cavender-Bares lab webpage)

Taxonomy is often used as a proxy for shared evolutionary history

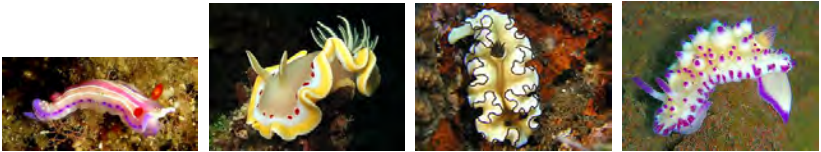
at best taxonomy is a coarse representation of evolutionary history

at worst taxonomy is a mis-representation of evolutionary history

at worst taxonomy is a mis-representation of evolutionary history

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.

OPEN
Tree of Life

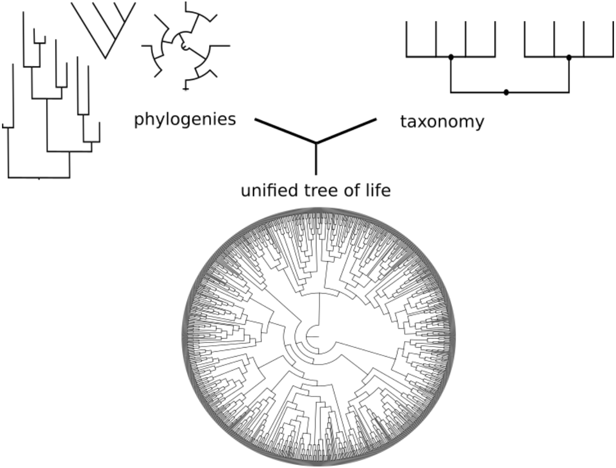
Goal: Build a tree of all life.

OPEN
Tree of Life

Goal: Build a tree of all life.

- Every named species
- Updated as new data becomes available
- Freely and easily accessible

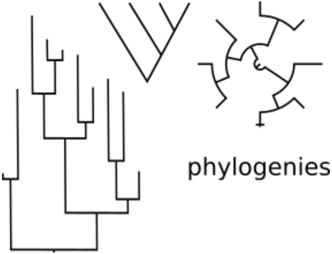
tree.opentreeoflife.org



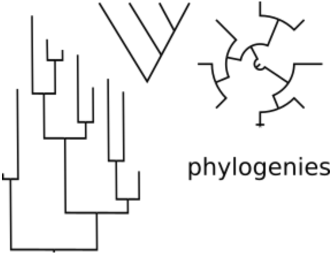
phylogenies

taxonomy

unified tree of life



phylogenies



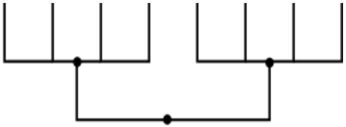
Current synthetic tree

1,331 representative phylogenies

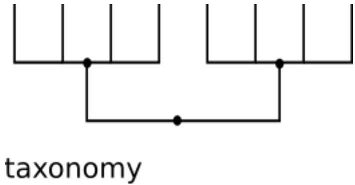
112,669 tips from phylogeny, 2,392,578 total tips.

Current draft posted Sept 2023, will be updated with more input trees regularly

Synthesis algorithm published in Redelings and Holder (2017), recent major speed improvements

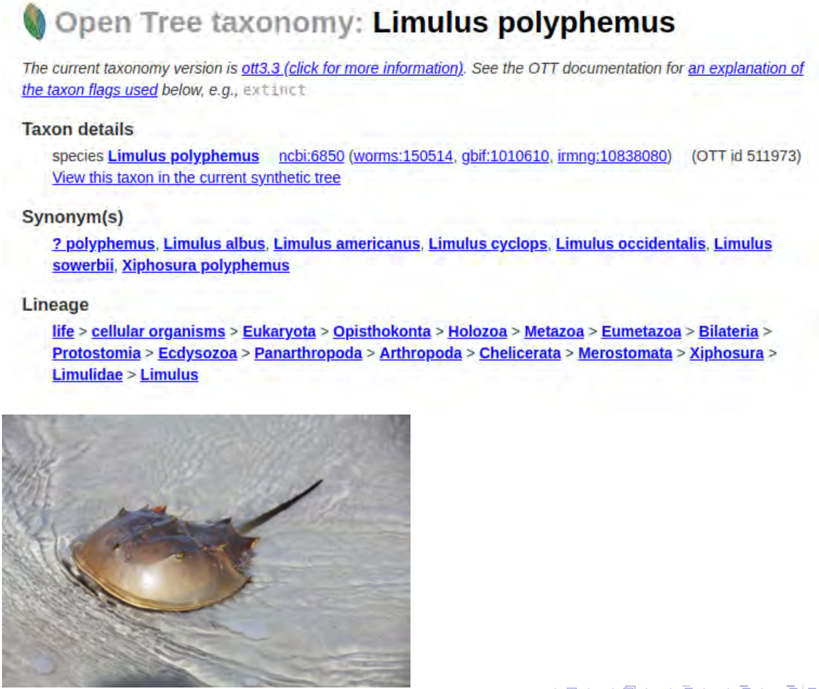


taxonomy



- 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**

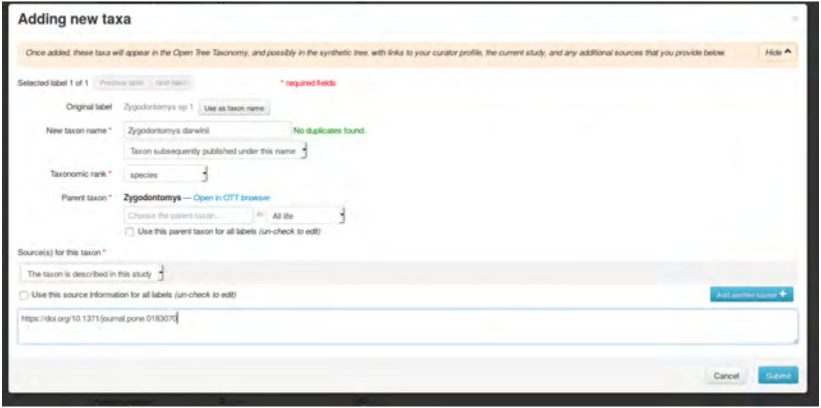
Lineage

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



Adding new taxa

Once added, these taxa will appear in the Open Tree Taxonomy, and possibly in the synthetic tree, with links to your curator profile, the current study, and any additional sources that you provide below.

Selected label 1 of 1

* required fields

Original label: Zygodontomys sp 1

New taxon name *: Zygodontomys darwinii — No duplicates found.

Taxon subsequently published under this name

Taxonomic rank *: species

Parent taxon *: **Zygodontomys** — Open in OTT browser

Choose the parent taxon... in All life

☐ Use this parent taxon for all labels *(un-check to edit)*

Source(s) for this taxon *

The taxon is described in this study

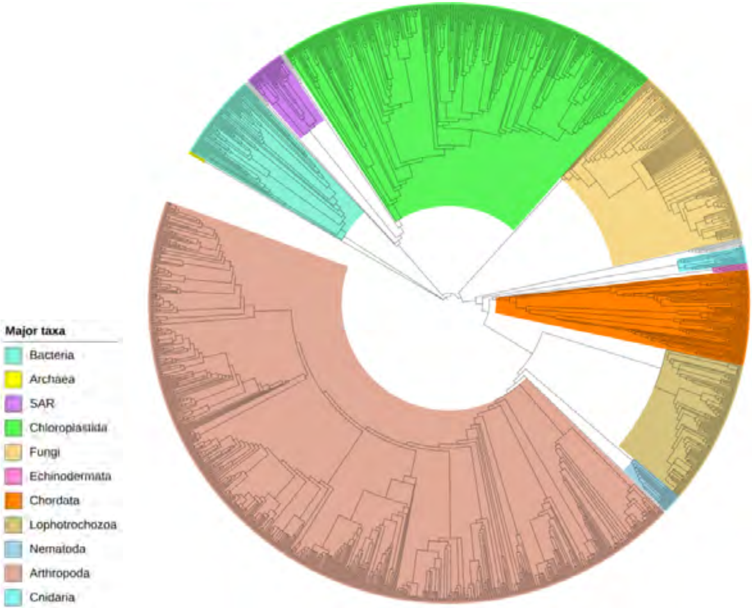
☐ Use this source information for all labels *(un-check to edit)*

https://doi.org/10.1371/journal.pone.0183070

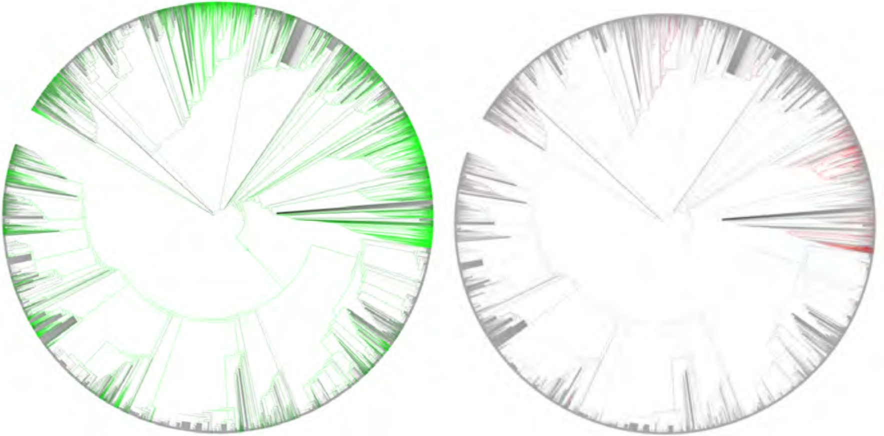
tree viewer demo

`https://tree.opentreeoflife.org/opentree/argus/opentree14.9@mrcaott30845ott82415/Amazonetta--Sibirionetta`

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

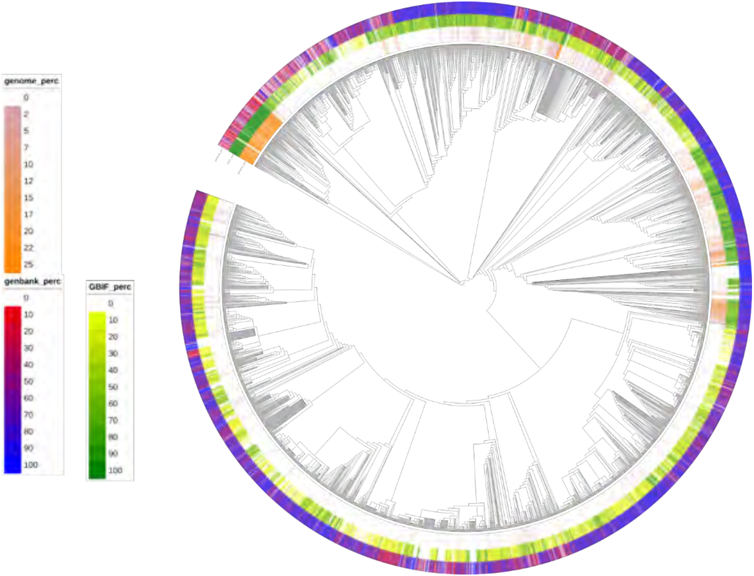


Phylogenetic information (green) and conflict (red) across the tree

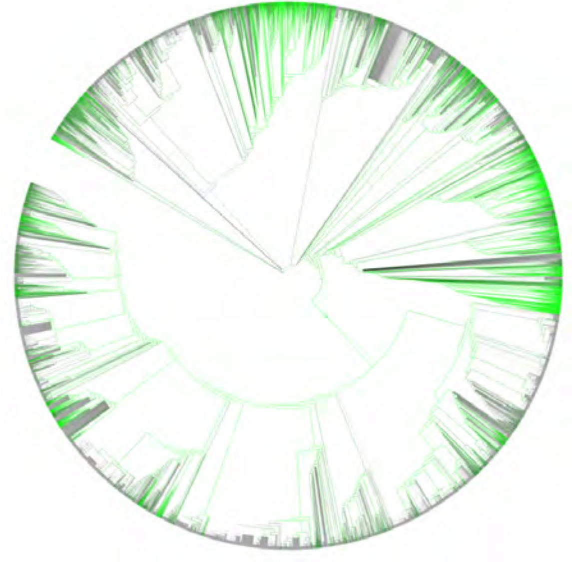


Annotated tree available at
`https://itol.embl.de/tree/10823010783159601596222895`

Cross-link data from other resources



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.

OPEN ACCESS Freely available online

PLOS | BIOLOGY

Perspective

Lost Branches on the Tree of Life

Bryan T. Drew[1]*, Romina Gazis[2], Patricia Cabezas[3,4], Kristen S. Switherss[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

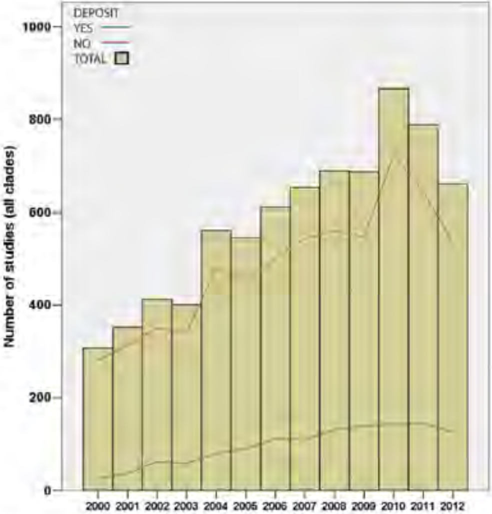


Figure 1. Overview of total number of publications surveyed from animal, fungus, seed plant, microbial eukaryote, archaea, and bacteria literature (indicated in red), and the number of those publications that archived their trees and alignments in either Dryad or TreeBASE (indicated in green).

doi:10.1371/journal.pbio.1001636.g001

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)

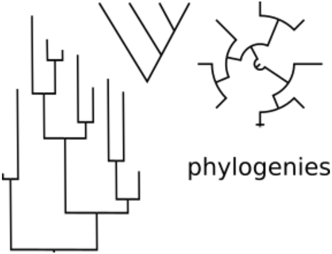
Community Curation

345 individual curators of 4,749 uploaded studies

Community Curation

345 individual curators of 4,749 uploaded studies

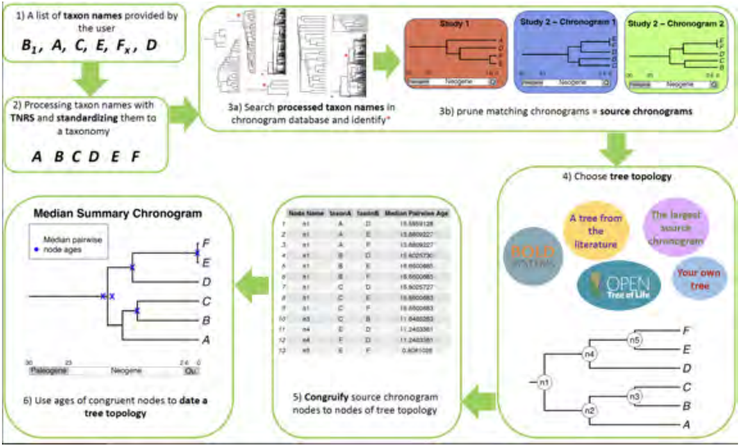
Currently a several month lag for incorporation into synthetic tree



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

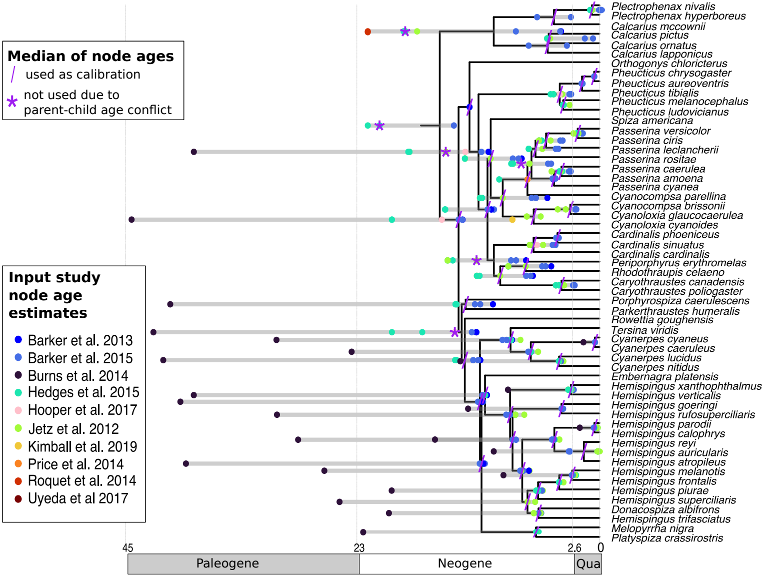
DATElife



Webserver at `datelife.opentreeoflife.org`

Sanchez-Reyes, McTavish, O'Meara, Systematic Biology, 2024

Dated finch tree - topology estimated based on 33 studies, dates from 11 studies

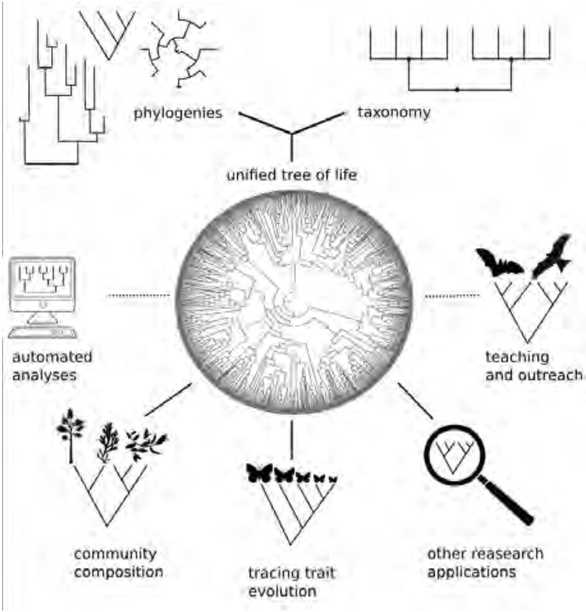


Sanchez-Reyes, McTavish, O'Meara, Systematic Biology, 2024

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`

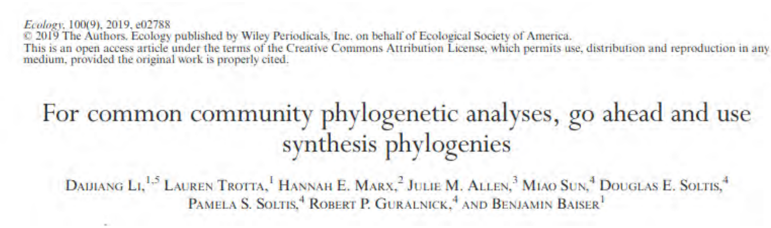


McTavish et al. (2017)

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) Michonneau et al. (2016)

Why would you need OpenTree if you can build your own trees?



Ecology, 100(9), 2019, e02788

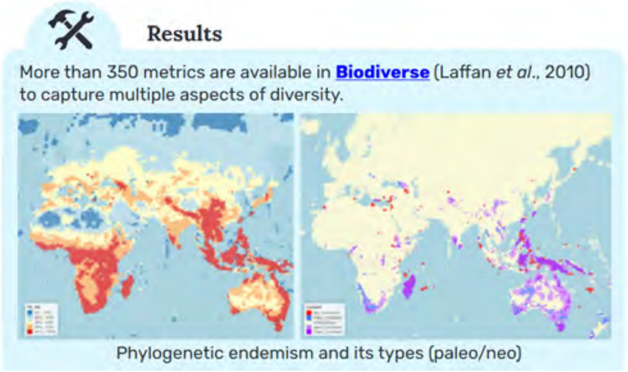
For common community phylogenetic analyses, go ahead and use synthesis phylogenies

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)

Assess phylogenetic diversity at large scales

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



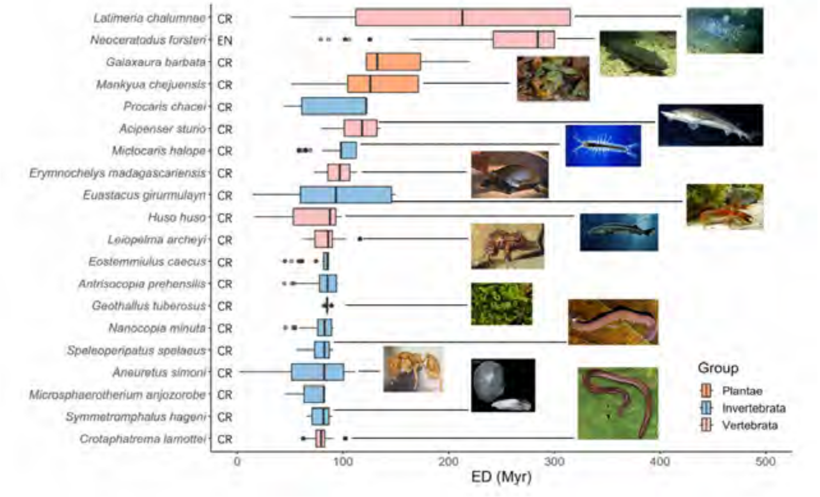
Results

More than 350 metrics are available in **Biodiverse** (Laffan *et al.*, 2010) to capture multiple aspects of diversity.

Phylogenetic endemism and its types (paleo/neo)

(Mikryukov et. al, in press, BMC Ecology and Evolution)

Measure potential for phylogenetic diversity loss due to extinctions



Species at risk of extinction (per IUCN red list) which could result in greatest loss of evolutionary distinct history

(Guo, McTavish, Rosindell, preprint at `https://www.researchsquare.com/article/rs-4397985/v1`)

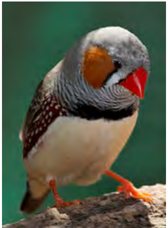
Easily get accurate relationships (and citations!) for arbitrary sets of species

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 ROpenSci

Michonneau et al. (2016))

Access OPEN Tree of Life via `rotl` package from ROpenSci

Michonneau et al. (2016))

```
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)
```

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Michonneau et al. (2016))

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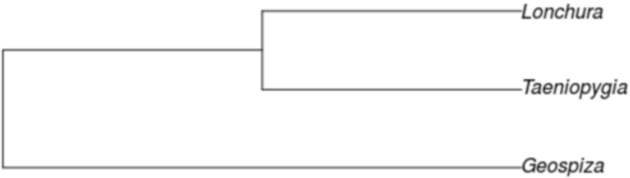
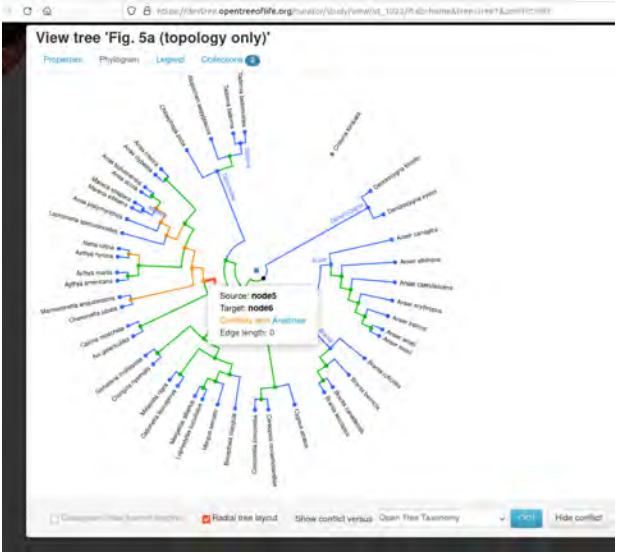


Use the zebra finch as reference!

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

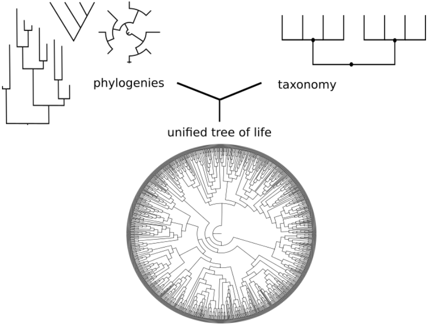


View tree 'Fig. 5a (topology only)'

Source: **node5**
Target: **node6**
Conflicts with Anatinae
Edge length: 0

https://tree.opentreeoflife.org/curator/study/view/ot_1022/?tab=home&tree=tree1&conflict=ott
https://tree.opentreeoflife.org/curator/study/view/ot_500/?tab=home&tree=tree1&conflict=pg_420@tree522

Generate a custom synthetic tree for your taxa



Synthesis on demand

Personal phylogeny rankings

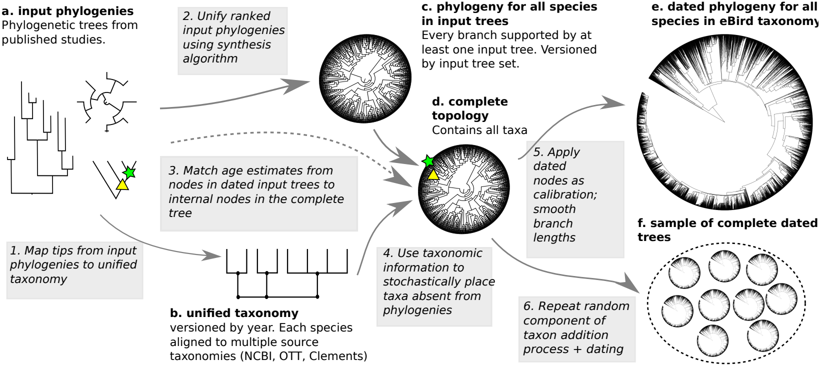
Any root node

Synthesis phylogeny of all birds

- 262 phylogenetic inputs
- Custom taxonomic translation table to match eBird data
- Phylogenetic information for 9239 of the 10824 species (85%)
- Dates estimated from 88 input trees provide estimates for 6874 internal nodes

Collaboration with Eliot Miller and others at Cornell Lab of Ornithology

Synthesis phylogeny of all birds



a. input phylogenies
Phylogenetic trees from published studies.

2. Unify ranked input phylogenies using synthesis algorithm

c. phylogeny for all species in input trees
Every branch supported by at least one input tree. Versioned by input tree set.

e. dated phylogeny for all species in eBird taxonomy

d. complete topology
Contains all taxa

3. Match age estimates from nodes in dated input trees to internal nodes in the complete tree

5. Apply dated nodes as calibration; smooth branch lengths

f. sample of complete dated trees

1. Map tips from input phylogenies to unified taxonomy

4. Use taxonomic information to stochastically place taxa absent from phylogenies

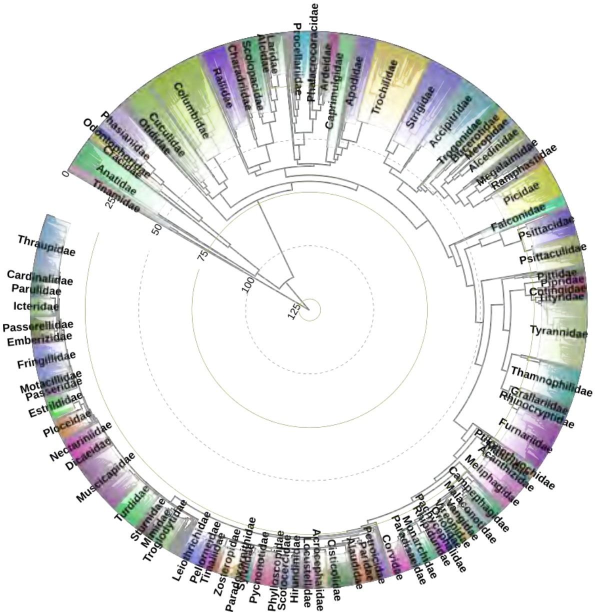
6. Repeat random component of taxon addition process + dating

b. unified taxonomy
versioned by year. Each species aligned to multiple source taxonomies (NCBI, OTT, Clements)

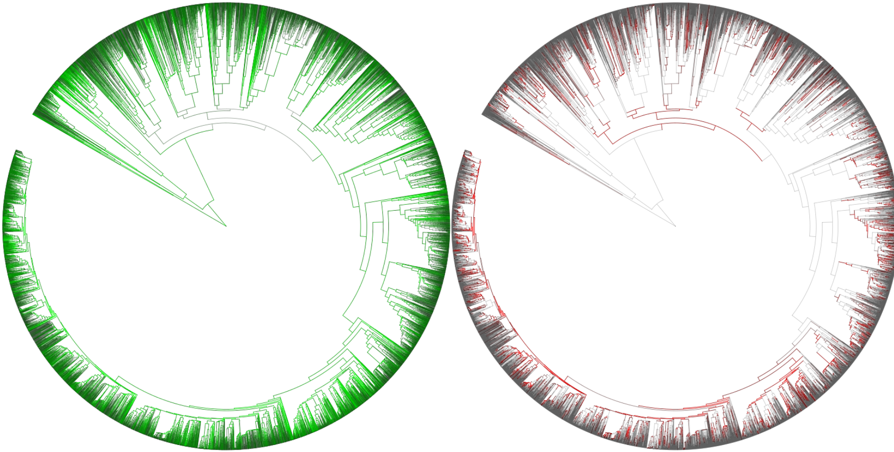
Preprint “A complete and dynamic tree of birds” at `https://www.biorxiv.org/content/10.1101/2024.05.20.595017v1`

Data products in `https://github.com/McTavishLab/AvesData`

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/1692367824176071715799973`

CC0 license provides fully open access for downstream re-usability

CC0 license provides fully open access for downstream re-usability

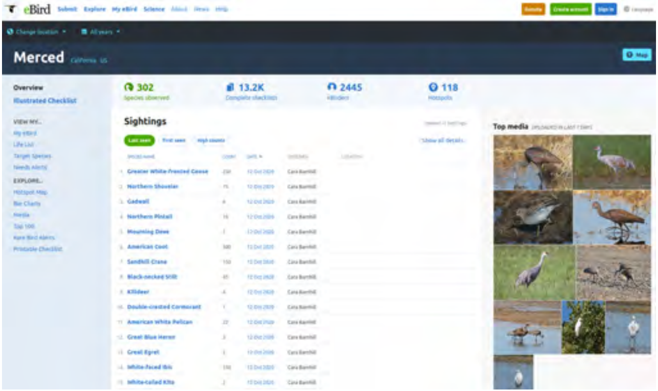
Open Tree provides the tree backend for:

PHYLOtastic

Lifemap OPEN Tree of Life

DATElife

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



Merced California, US

302 Species observed

13.2K Complete checklists

2445 eBirders

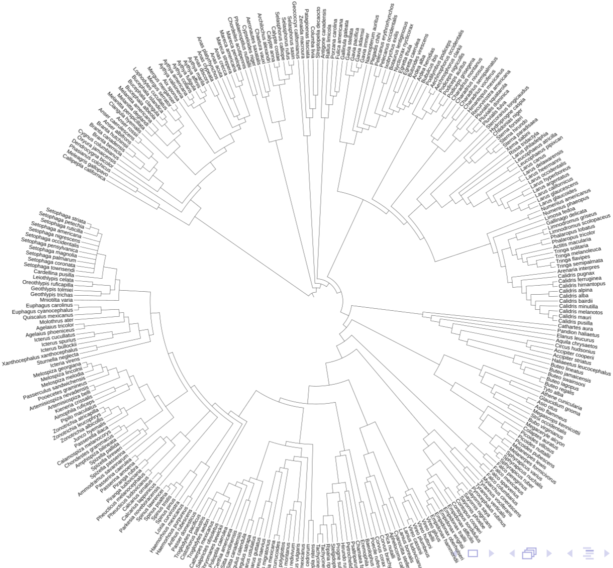
118 Hotspots

Sightings

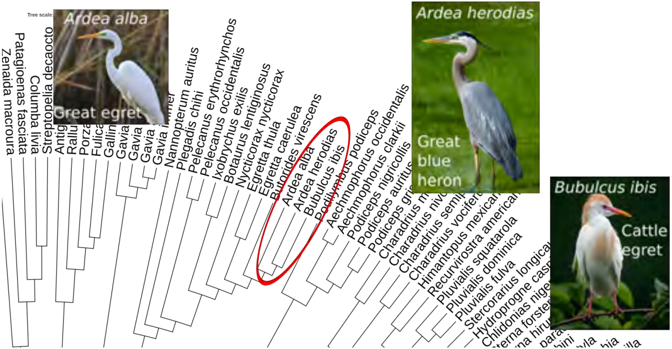
1. Greater White-fronted Goose
2. Northern Shoveler
3. Gadwall
4. Northern Pintail
5. Mourning Dove
6. American Coot
7. Sandhill Crane
8. Black-necked Stilt
9. Killdeer
10. Double-crested Cormorant
11. American White Pelican
12. Great Blue Heron
13. Great Egret
14. White-faced Ibis
15. White-tailed Kite

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

OPEN
Tree of Life

NSF ABI 1759846
Mark Holder
Karen Cranston
Ben Redelings

NSF

NSF AVATOL 1208809
AVATOL PI'S: Burleigh, Crandall, Cranston, Gude, Hibbett, Holder, Katz, Ree, Smith, Soltis, Williams

Dendropy Jeet Sukumaran

Developer team:
Luna Luisa Sanchez Reyes
Ben Redelings
Jim Allman

UNIVERSITY OF CALIFORNIA
UCMERCED

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).

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