Open Tree and phylogenetic updating

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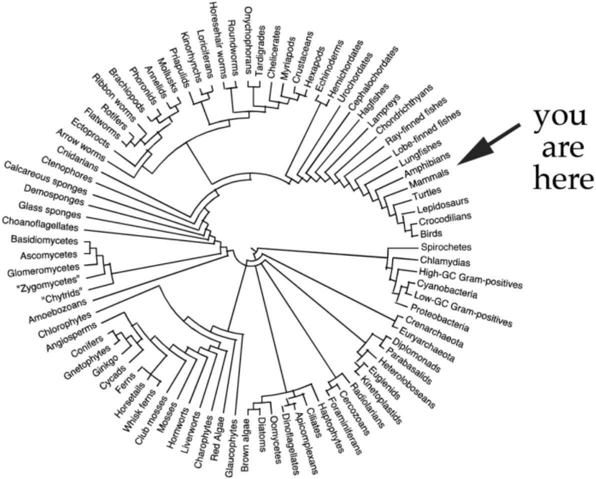


you
are
here

Image Ethan Hein

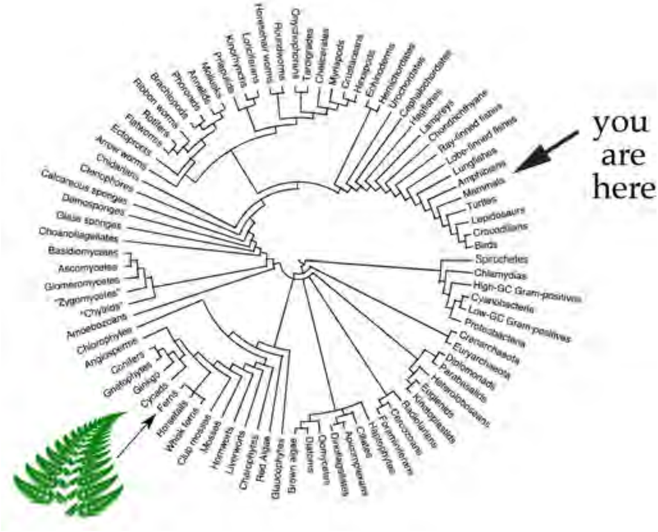


Image Ethan Hein

Why do we need phylogenies?

To understand the shared evolutionary history of life on earth

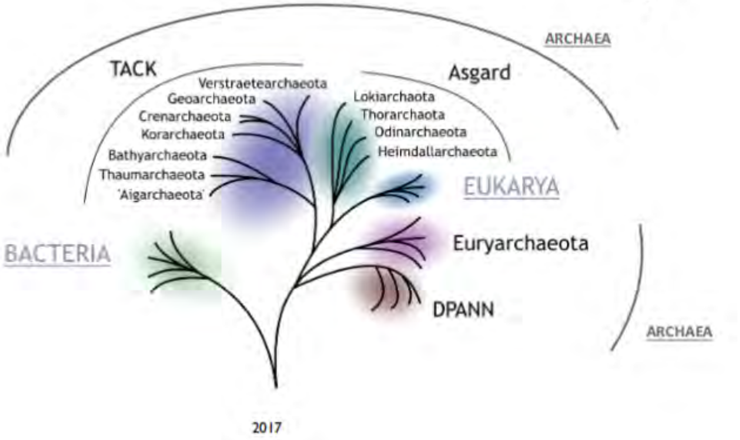
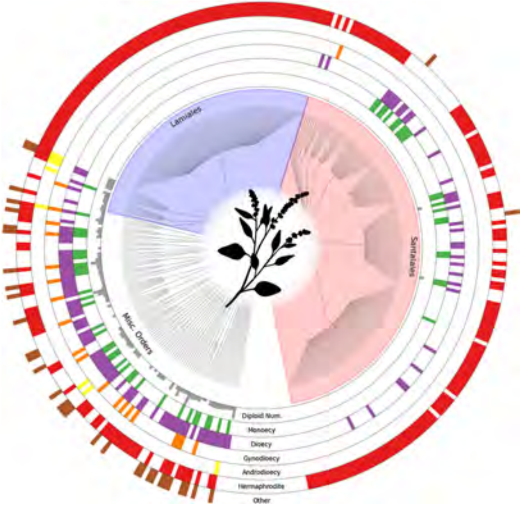


Figure from Laura Eme

To understand rates and types of evolutionary transitions



The Tree of Sex Consortium,(2014) Scientific Data

OPEN
Tree of Life

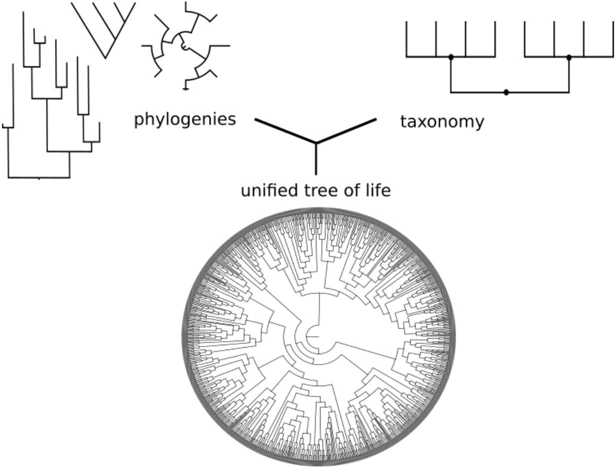
Goal: Build a tree of all life.

OPEN
Tree of Life

Goal: Build a tree of all life.

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

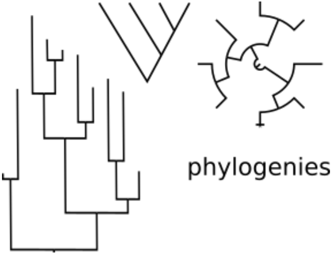
`tree.opentreeoflife.org`



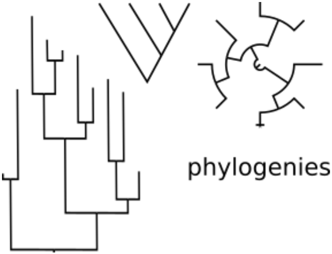
phylogenies

taxonomy

unified tree of life



phylogenies



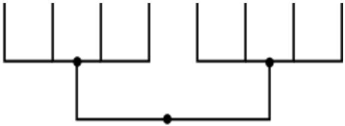
Current synthetic tree

987 representative phylogenies

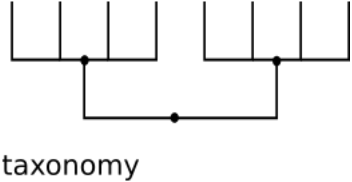
65,662 tips from phylogeny

New draft with more input trees every few months

Redelings and Holder, PeerJ 2017



taxonomy



2.7 million named taxa

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

Scaffold for combining ranked phylogenetic estimates

New drafts released as inputs change

Rees and Cranston, Biodiversity Data Journal 2017

Open Tree taxonomy: Metrosideros robusta

The current taxonomy version is ott3.0 (click for more information). See the OTT wiki for an explanation of the taxon flags used below, e.g., `extinct`

Taxon details

species **Metrosideros robusta** ncbi:101983 (gbif:3185294) (OTT id 284291)

View this taxon in the current synthetic tree

Synonym(s)

Nania robusta, **Metrosideros florida**

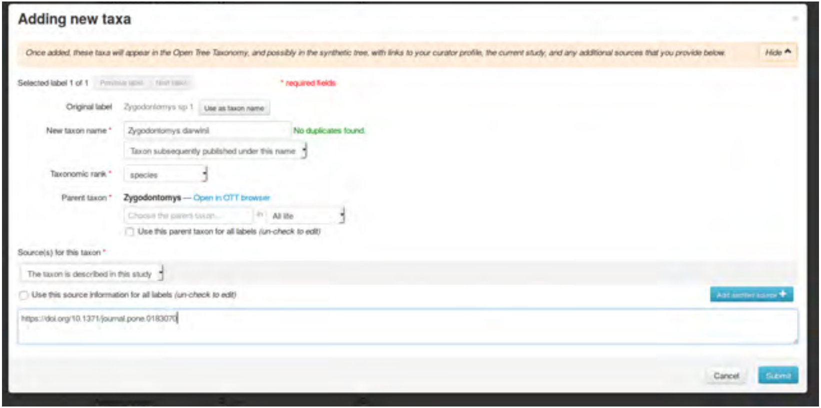
Lineage

life › **cellular organisms** › **Eukaryota** › **Archaeplastida** › **Chloroplastida** › **Streptophyta** › **Embryophyta** › **Tracheophyta** › **Euphyllophyta** › **Spermatophyta** › **Magnoliophyta** › **Mesangiospermae** › **eudicotyledons** › **Gunneridae** › **Pentapetalae** › **rosids** › **malvids** › **Myrtales** › **Myrtaceae** › **Myrtoideae** › **Metrosidereae** › **Metrosideros**

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)*

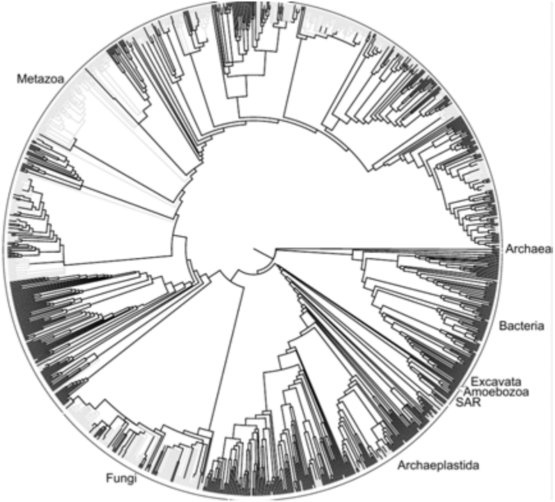
Source(s) for this taxon *: The taxon is described in this study

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

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

The synthetic tree (Hinchliff et al., PNAS 2015)

2.4 million species



Dark lineages have at least one representative in an input source tree

How will we fill in the gaps?

Need to build on existing phylogenetic information.

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. 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. PLoS Biology 2013

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

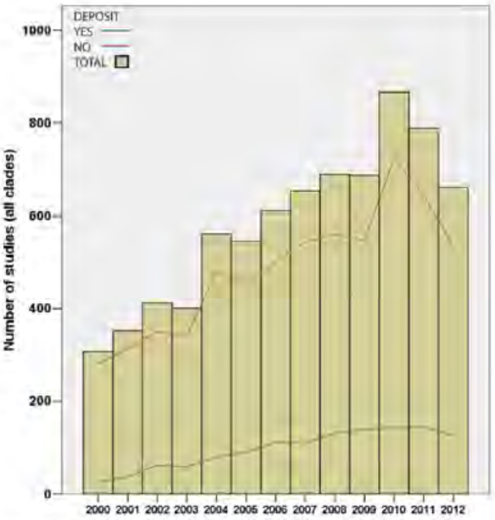


Figure 1. Overview of total number of publications surveyed from animal, fungus, seed plant, microbial eukaryote, archaea, and bacteria literature (indicated in red), and the number of those publications that archived their trees and alignments in either Dryad or TreeBASE (indicated in green).

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. BioEssays 2018)

Adding phylogenetic data

- 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. Bioinformatics 2015

Community Curation

253 individual curators of 4,431 uploaded studies

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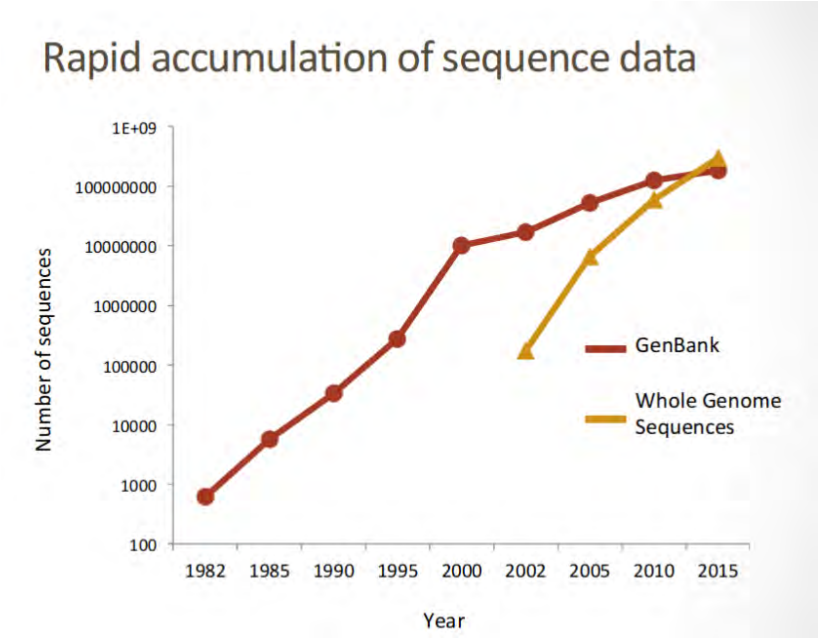
Rapid curation progress at taxon focused in-person working groups, in collaboration with FuturePhy

Community Curation

- 253 individual curators of 4,431 uploaded studies
- Rapid curation progress at taxon focused in-person working groups, in collaboration with FuturePhy
- Currently a several month lag for incorporation into synthetic tree, will begin daily builds in the next year

Automated tree updating



Rapid accumulation of sequence data

Figure from Belinda Chang

Often time lag of months to years between sequencing and inclusion in phylogenetic estimates!

Streamlining the process

Inputs: An existing alignment and phylogeny, and a database of sequences or reads

Output: A maximum likelihood phylogenetic estimate including new taxa

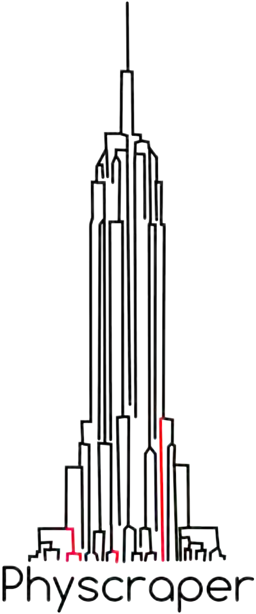
Problems with automated phylogenetics

Homology/paralogy

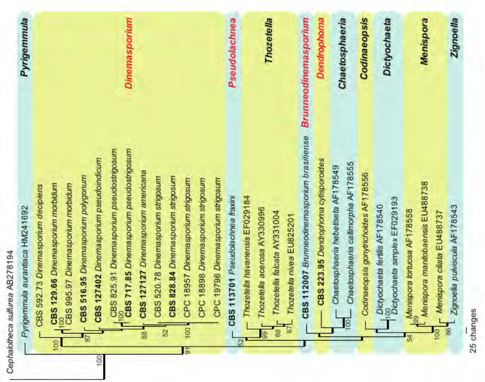
Data collection and assembly

Alignment

Physcraper
Automated updating of existing phylogenies
https://github.com/McTavishLab/physcraper



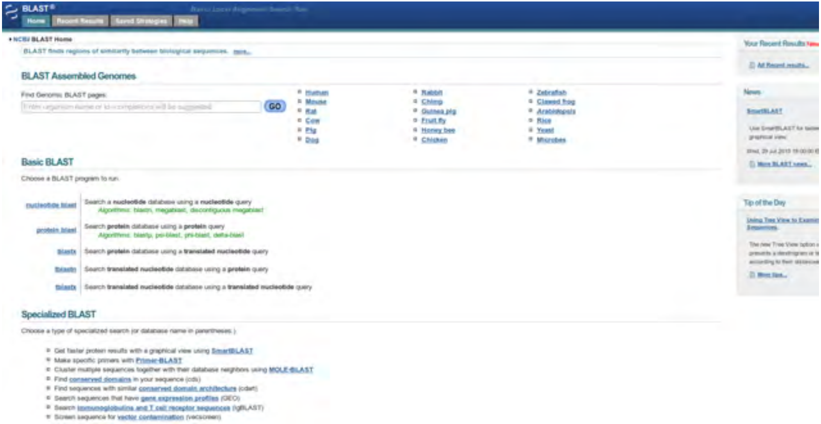
Restrict taxon addition to in-group
Uses loci that have been developed by taxon experts



e.g. using ITS to understand relationships within ascomycota
Crous et al. 2012 Persoonia

Data collection and assembly

Blast existing loci for assembled sequences and use their NCBI taxon id as label



NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. more...

BLAST Assembled Genomes

Find Genomic BLAST pages:

- Human
- Mouse
- Rat
- Cow
- Pig
- Dog
- Rabbit
- Chimp
- Guinea pig
- Fruit fly
- Honey bee
- Chicken
- Zebrafish
- Clawed frog
- Arabidopsis
- Rice
- Yeast
- Microbes

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query Algorithms: blastn, megablast, discontiguous megablast
protein blast	Search **protein** database using a **protein** query Algorithms: blastp, psi-blast, phi-blast, delta-blast
blastx	Search **protein** database using a **translated nucleotide** query
tblastn	Search **translated nucleotide** database using a **protein** query
tblastx	Search **translated nucleotide** database using a **translated nucleotide** query

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

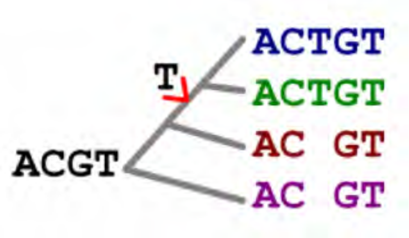
- Get faster protein results with a graphical view using SmartBLAST
- Make specific primers with Primer-BLAST
- Cluster multiple sequences together with their database neighbors using MOLE-BLAST
- Find conserved domains in your sequence (cds)
- Find sequences with similar conserved domain architecture (cdart)
- Search sequences that have gene expression profiles (GEO)
- Search immunoglobulins and T cell receptor sequences (IgBLAST)
- Screen sequence for vector contamination (vecscreen)

Data collection and assembly

Alternately, use aligned sequences to directly assemble loci of interest from whole genome sequencing reads.

- Decreases bias due to selection of reference
- Whole genome assembly is computationally expensive, and results in data being discarded
- Captures read quality and polymorphism

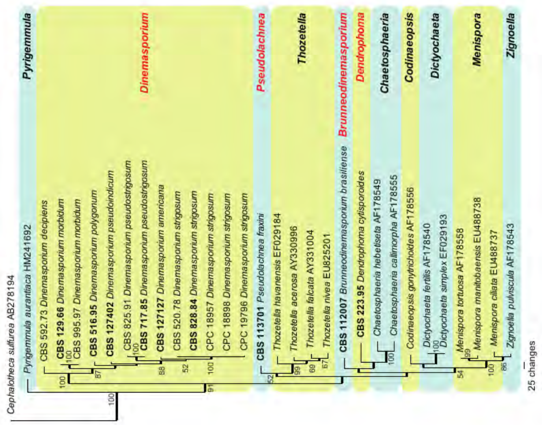
Using existing phylogeny as a guide tree can inform multiple sequence alignment



http://www.ebi.ac.uk/goldman-srv/prank/differences/

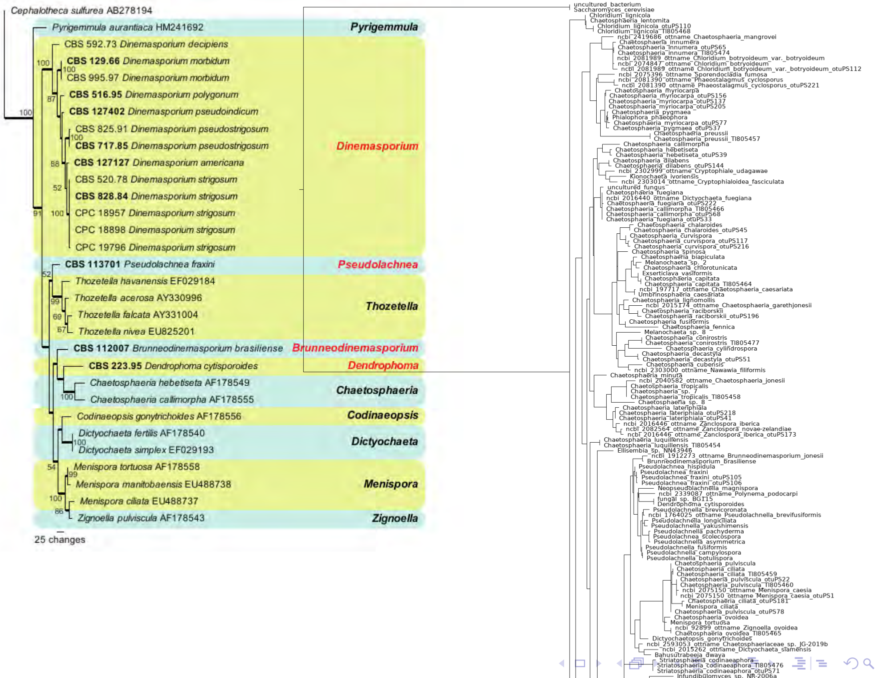
Perform a full maximum likelihood tree search

Improve convergence using previous estimate as starting tree



Original tree (36 taxa)

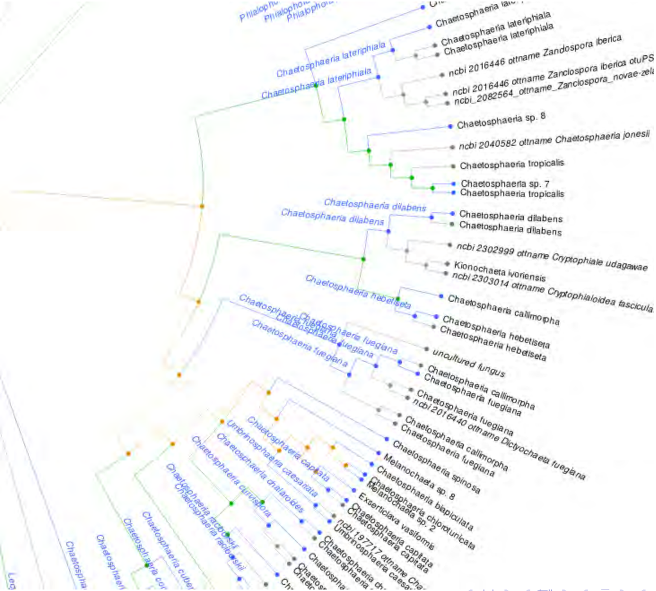
Updated tree (100 taxa)



This is exploratory!

but can flag potential areas of interest.

e.g.



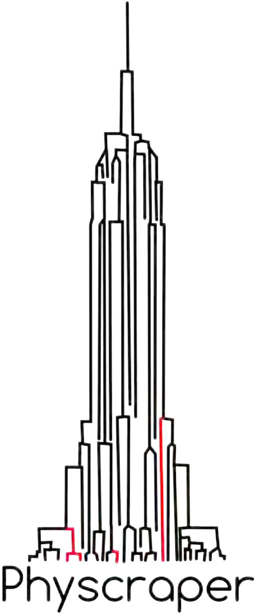
Advantages

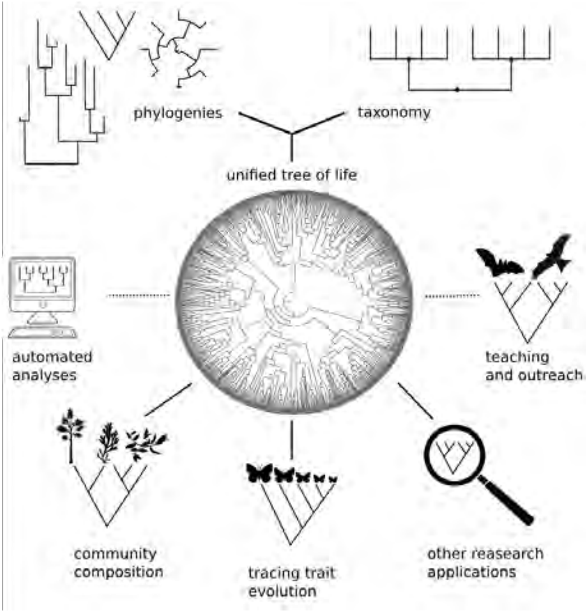
- Rapid data-to-phylogeny loop
- Prioritize further data collection
- Apply data collected for other projects
- Minimize researcher time input
- Stream taxa into draft of synthetic tree

Future directions

- Test effect of new data on alignment
- Develop new tree search algorithms that leverage previous search results
- Use placements to inform a divide-and-conquer approach

Phylogenetic updating code available at:
`https://github.com/McTavishLab/physcraper` (searches GenBank for homologous loci)
`https://github.com/McTavishLab/phycorder` (assembles homologous loci from short read data)





(McTavish et al. Bioessays 2017)

Open Tree resources are available via a range of implementations

- Browser interface, `tree.opentreeoflife.org`
- Open Tree of Life API
- Peyotl python wrapper
- R Open Tree of Life (rotl) ROpenSci

CC0 license provides fully open access for downstream re-usability

CC0 license provides fully open access for downstream re-usability

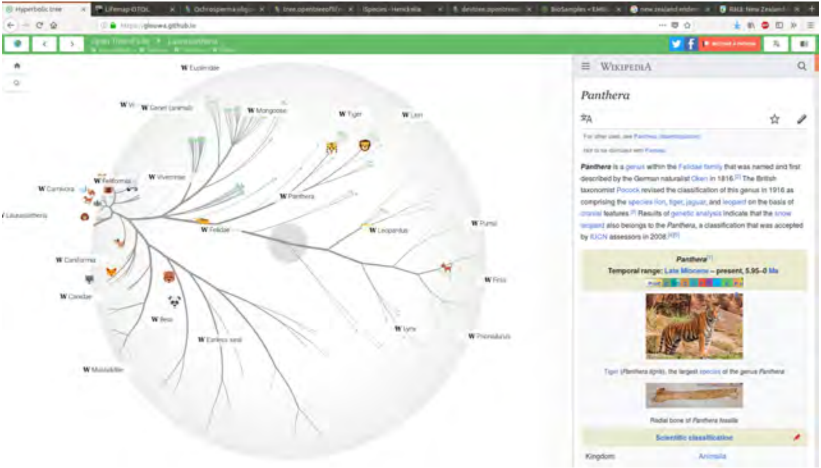
Open Tree provides the tree backend for:

PHYLO tastic

Lifemap
OPEN Tree of Life

DATE life

New this year! https://glouwa.github.io/



Panthera

Panthera is a genus within the Felidae family that was named and first described by the German naturalist Oken in 1816.[2] The British taxonomist Pocock revised the classification of this genus in 1916 as comprising the species lion, tiger, jaguar, and leopard on the basis of cranial features.[3] Results of genetic analysis indicate that the snow leopard also belongs to the *Panthera*, a classification that was accepted by IUCN assessors in 2008.[4][5]

Panthera[1]

Temporal range: Late Miocene – present, 5.95–0 Ma

Tiger (*Panthera tigris*), the largest species of the genus *Panthera*

Radial bone of *Panthera fossilis*

Scientific classification

Kingdom: Animalia

Coming soon!

- Automated updating with new genetic data
- Branch lengths / Node ages
- Private data stores
- Custom synthesis
- Infrastructure improvements

Holder, McTavish NSF ABI
Cranston 🇨🇦

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

Lab today:

- Browser interface, `tree.opentreeoflife.org`
- Standardizing taxon names
- Getting existing trees for arbitrary sets of taxa
- Visualizing conflict between estimates, by uploading to OpenTree
- Updating an existing phylogeny with new data from GenBank

Contribute your knowledge!

`tree.opentreeoflife.org/curator`

OPEN
Tree of Life

Thank You

OPEN Tree of Life

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