Open Tree and phylogenetic updating

Emily Jane McTavish

University of California, Merced
ejmctavish@ucmerced.edu, Twitter:@snacktavish

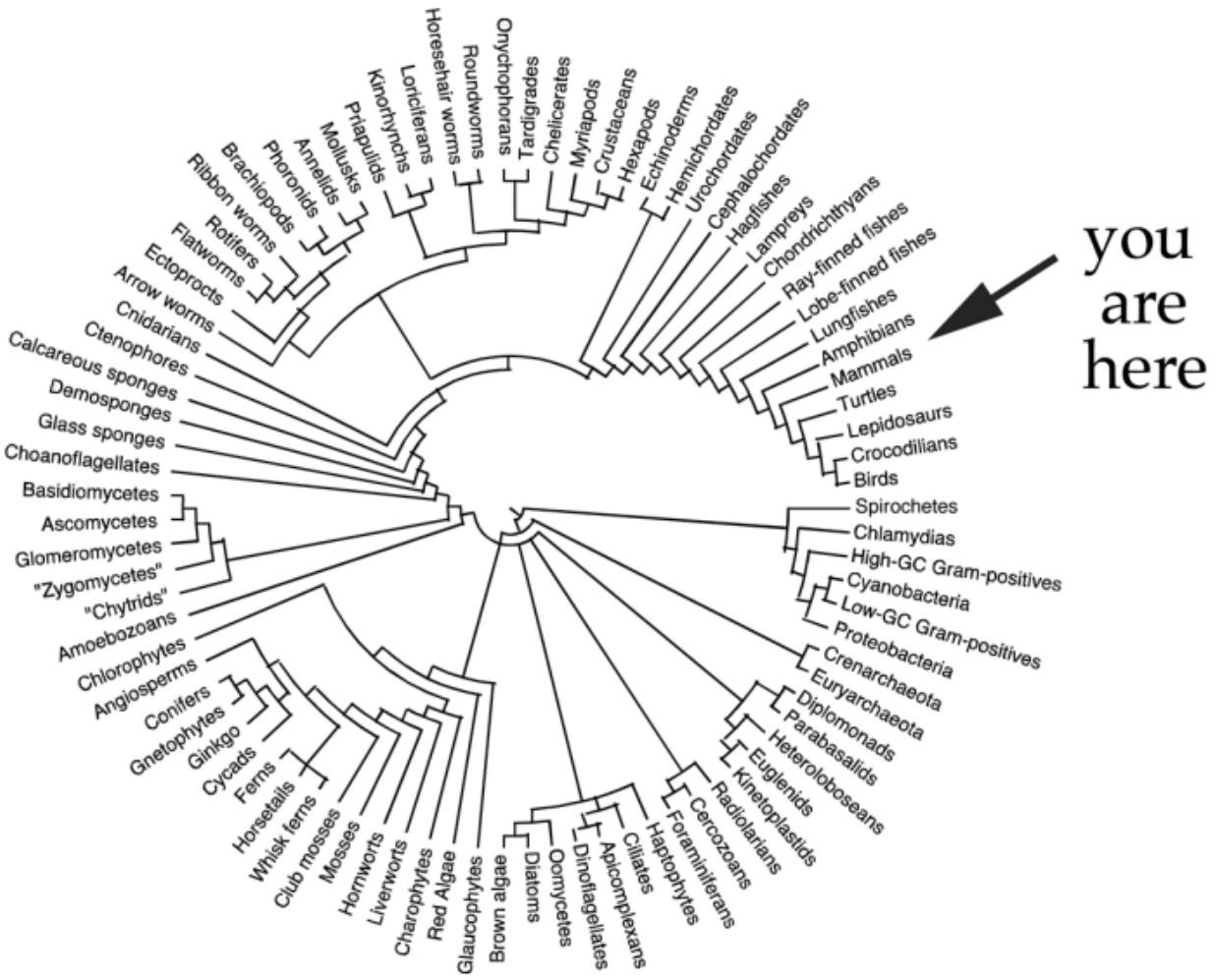


Image Ethan Hein

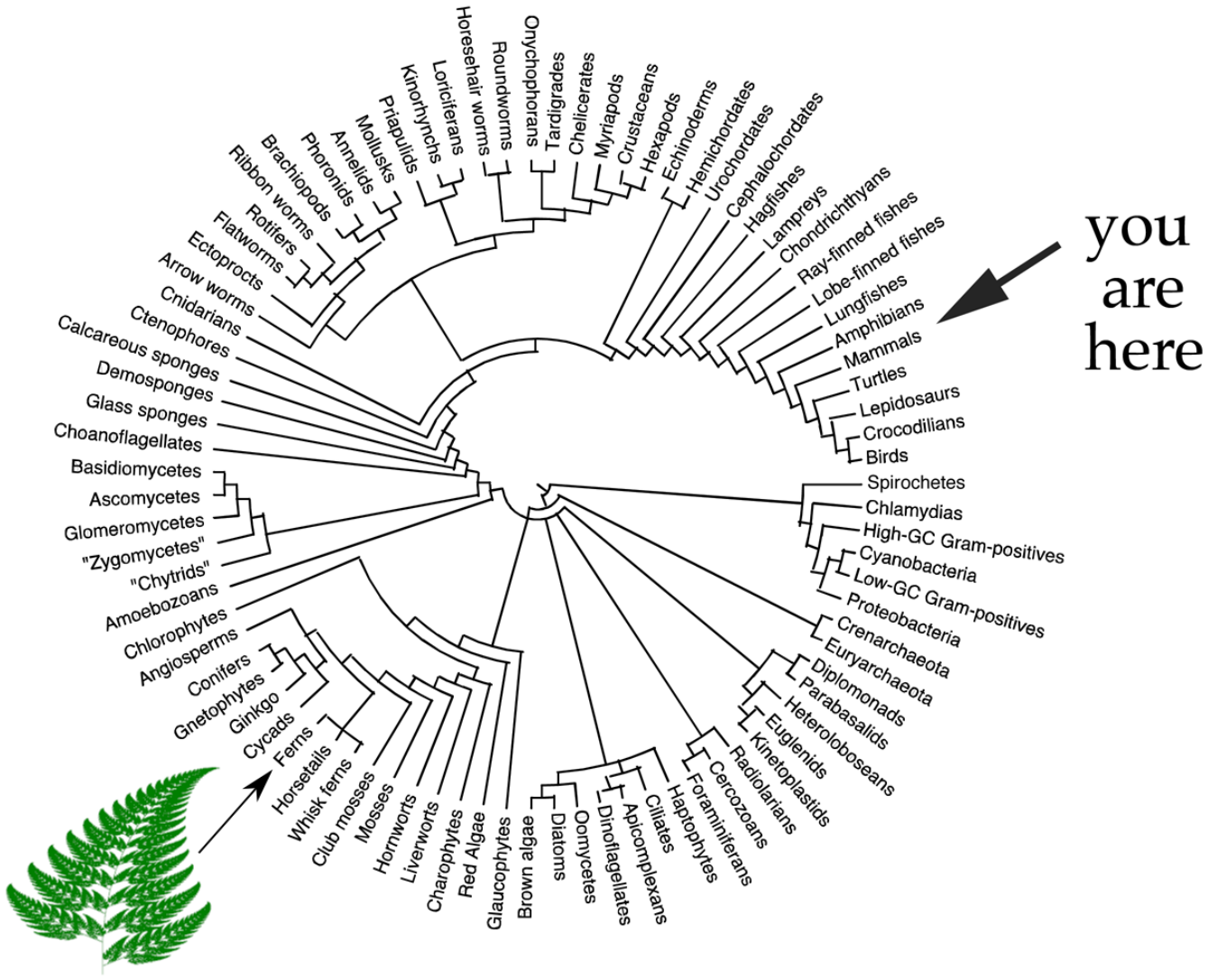


Image Ethan Hein

Why do we need phylogenies?

To understand the shared evolutionary history of life on earth

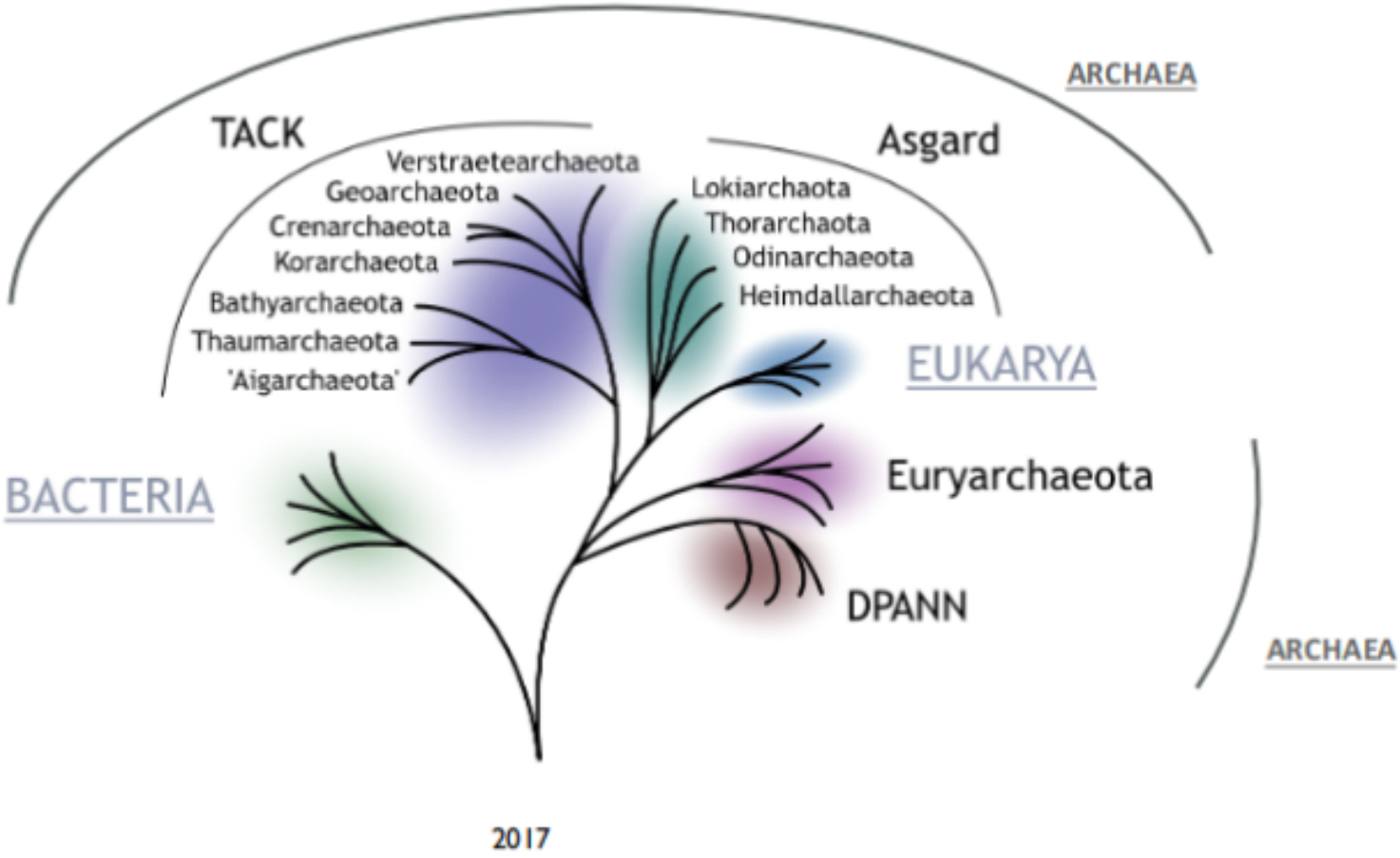
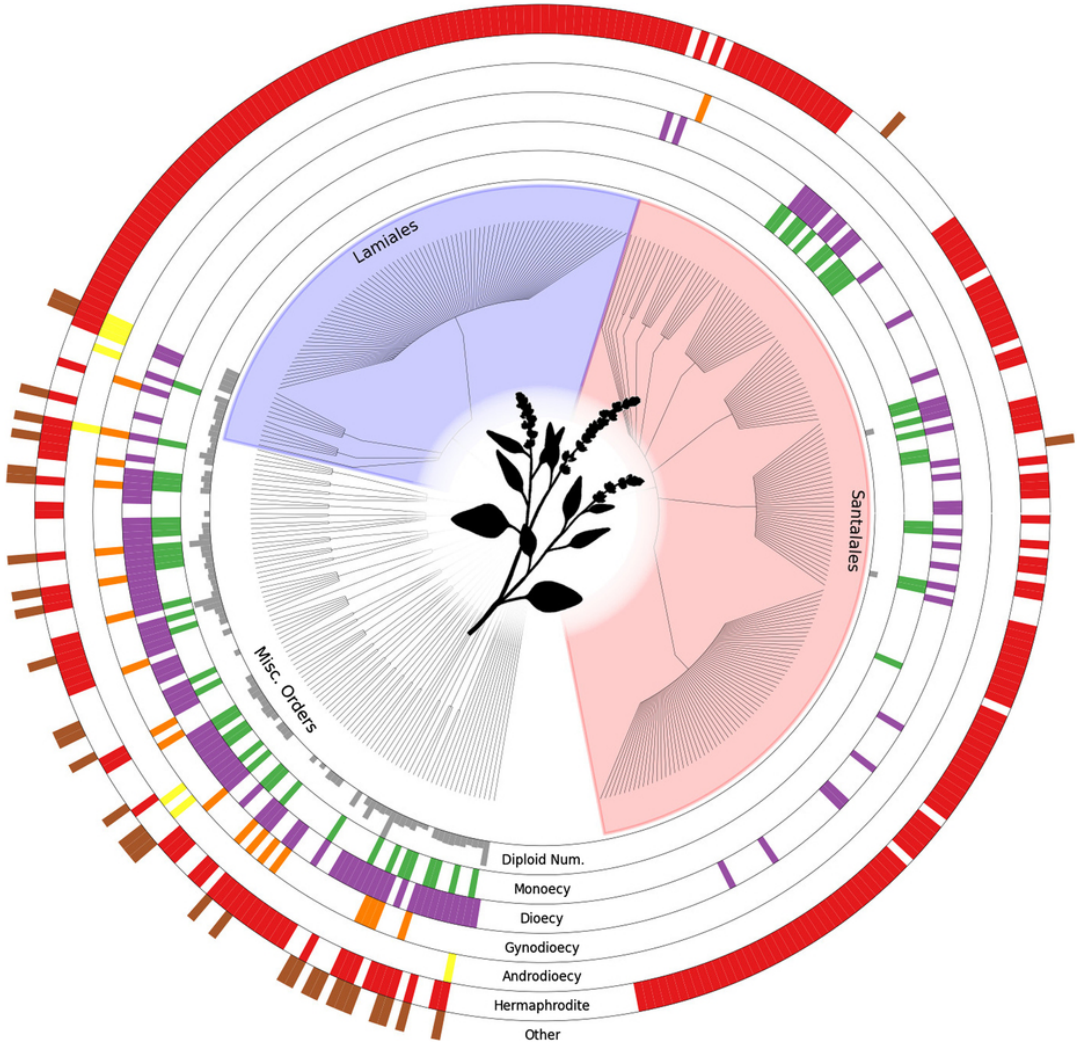


Figure from Laura Eme

To understand rates and types of evolutionary transitions



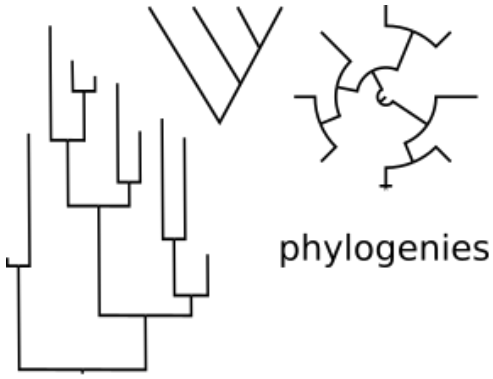
The Tree of Sex Consortium,(2014) Scientific Data

Goal: Build a tree of all life.

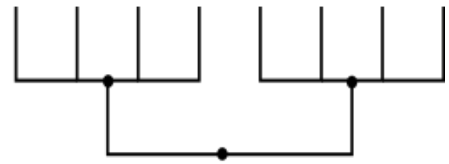
Goal: Build a tree of all life.

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

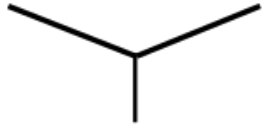
tree.opentreeoflife.org



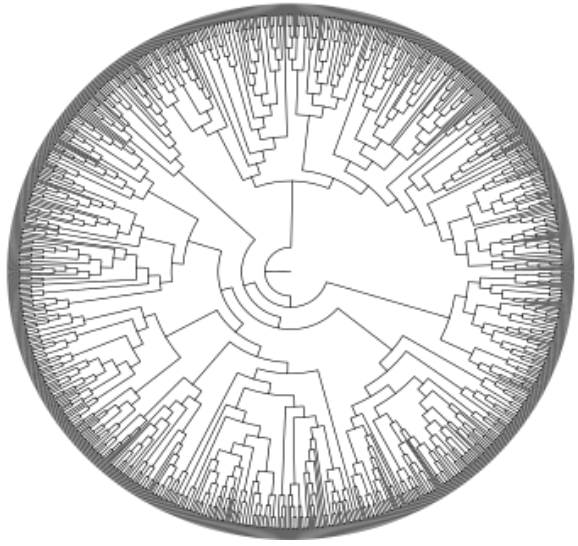
phylogenies

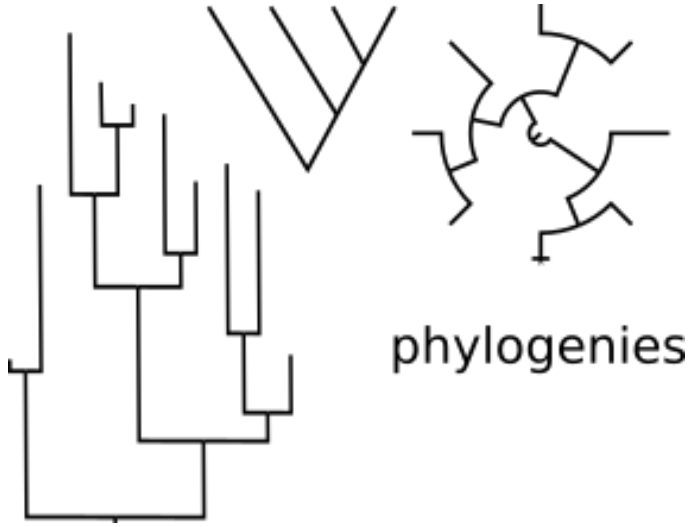


taxonomy

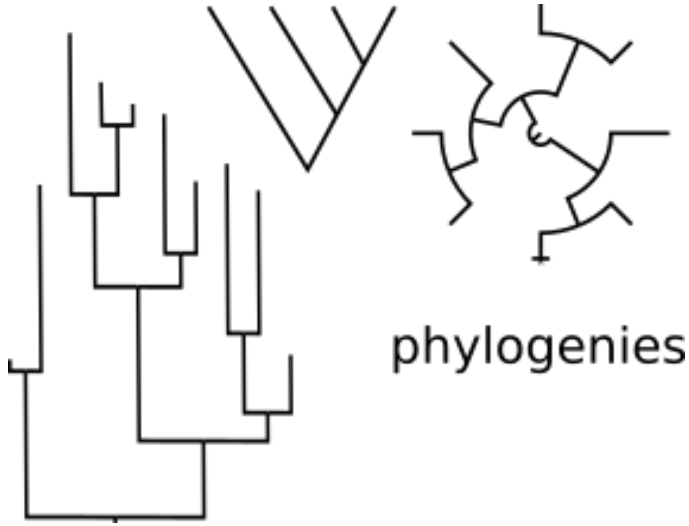


unified tree of life





phylogenies



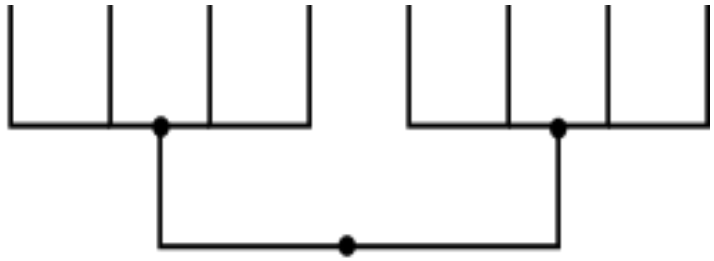
Current synthetic tree

987 representative phylogenies

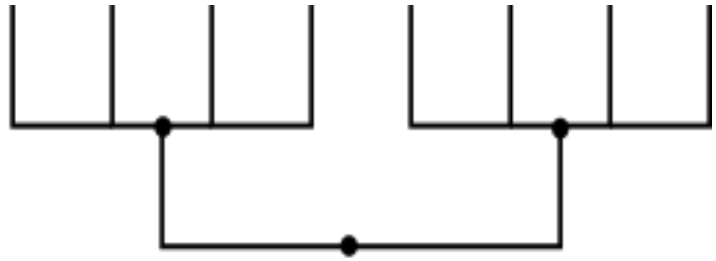
65,662 tips from phylogeny

New draft with more input trees every few months

Redelings and Holder, PeerJ 2017



taxonomy



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**

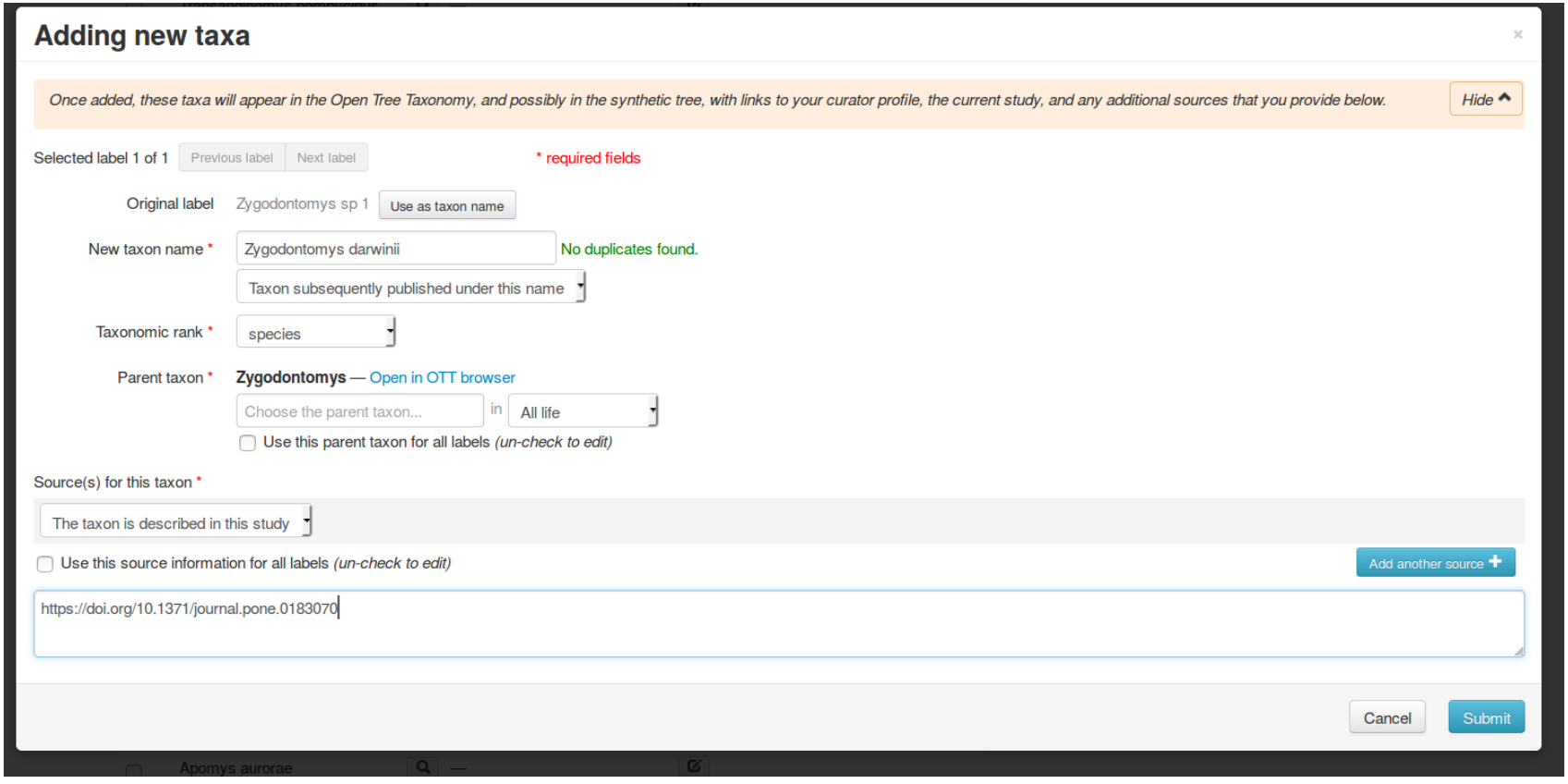
Lineage

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

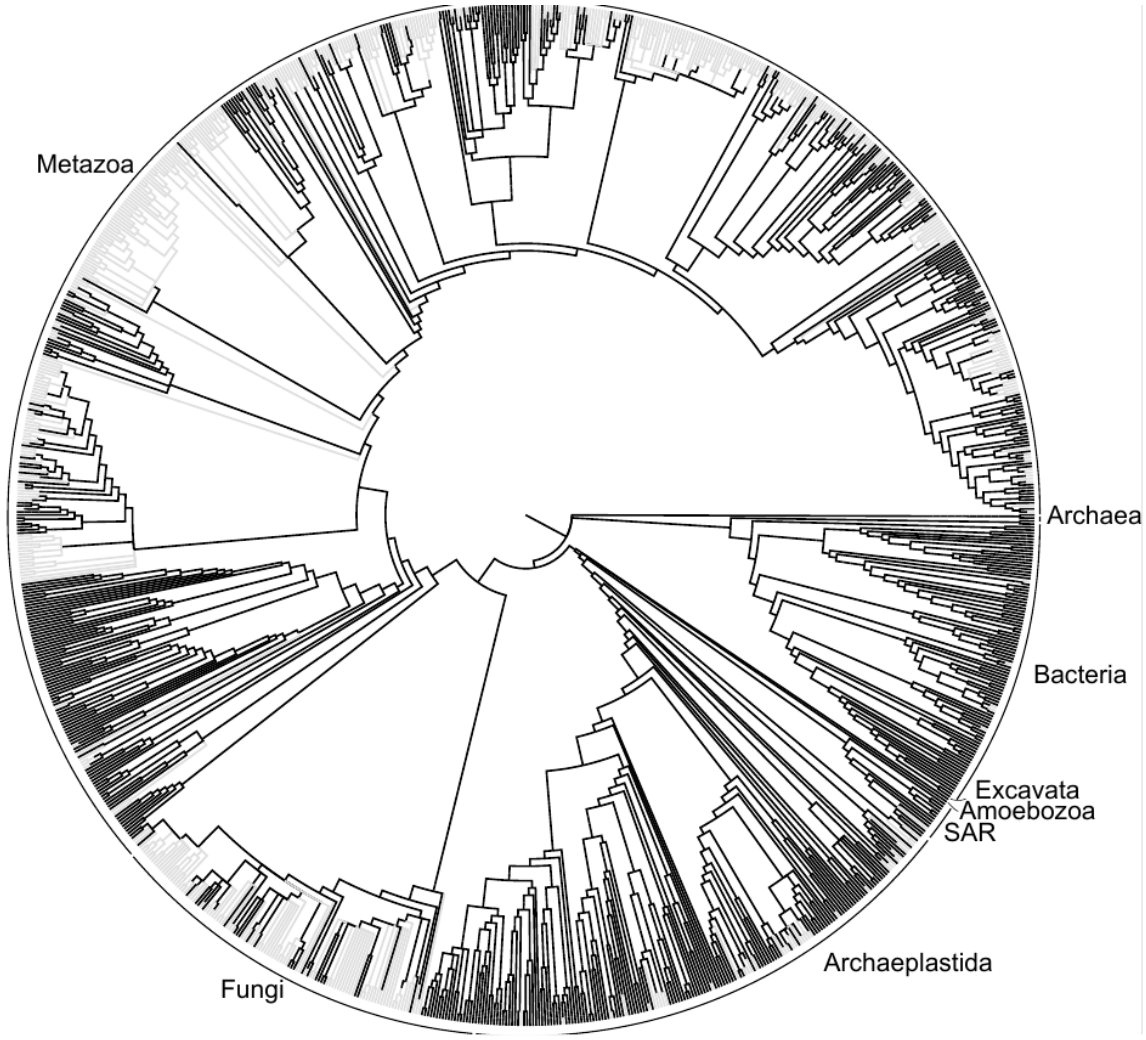
New taxa can be added from uploaded trees, and will be included in future synthetic trees

Opportunity to feed-back to input taxonomic resources



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

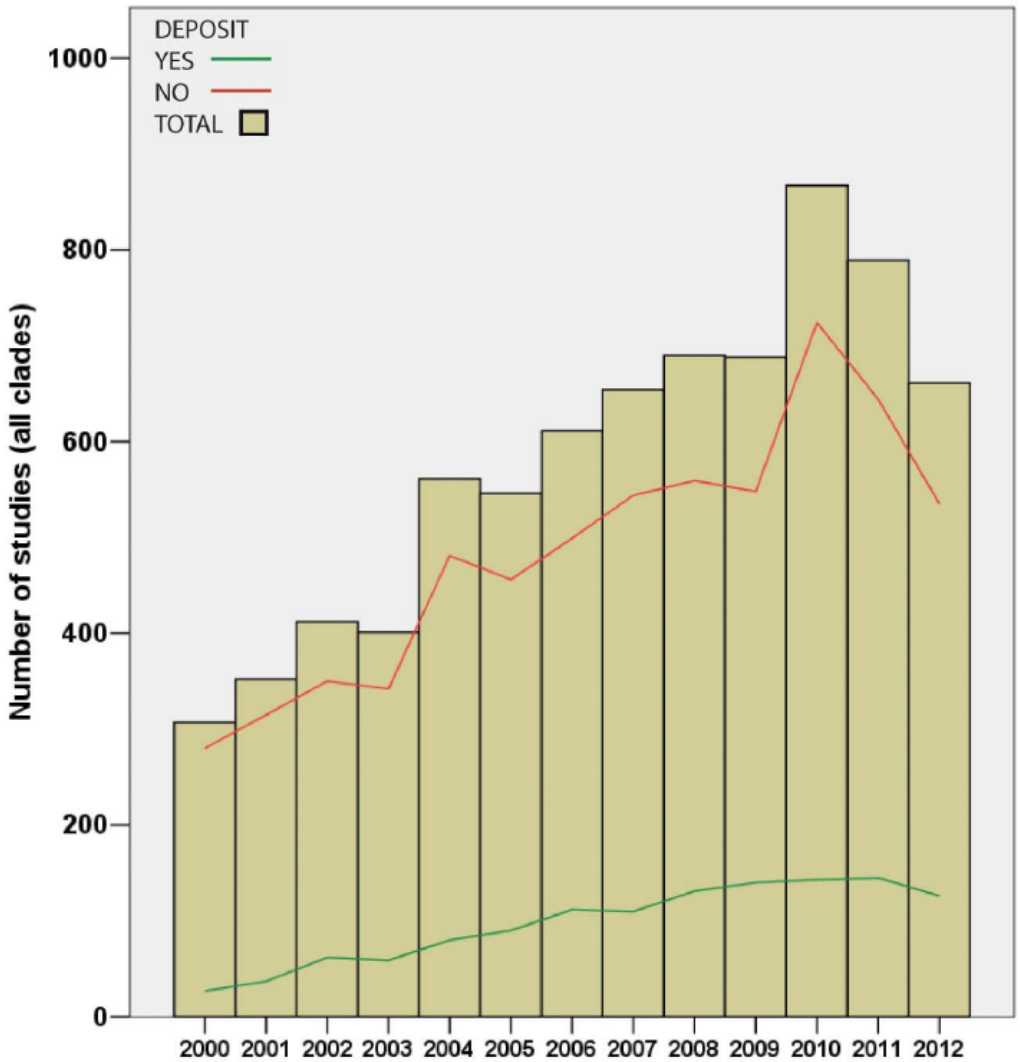


Figure 1. Overview of total number of publications surveyed from animal, fungus, seed plant, microbial eukaryote, archaea, and bacteria literature (indicated in red), and the number of those publications that archived their trees and alignments in either Dryad or TreeBASE (indicated in green).
doi:10.1371/journal.pbio.1001636.g001

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

Community Curation

253 individual curators of 4,431 uploaded studies

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

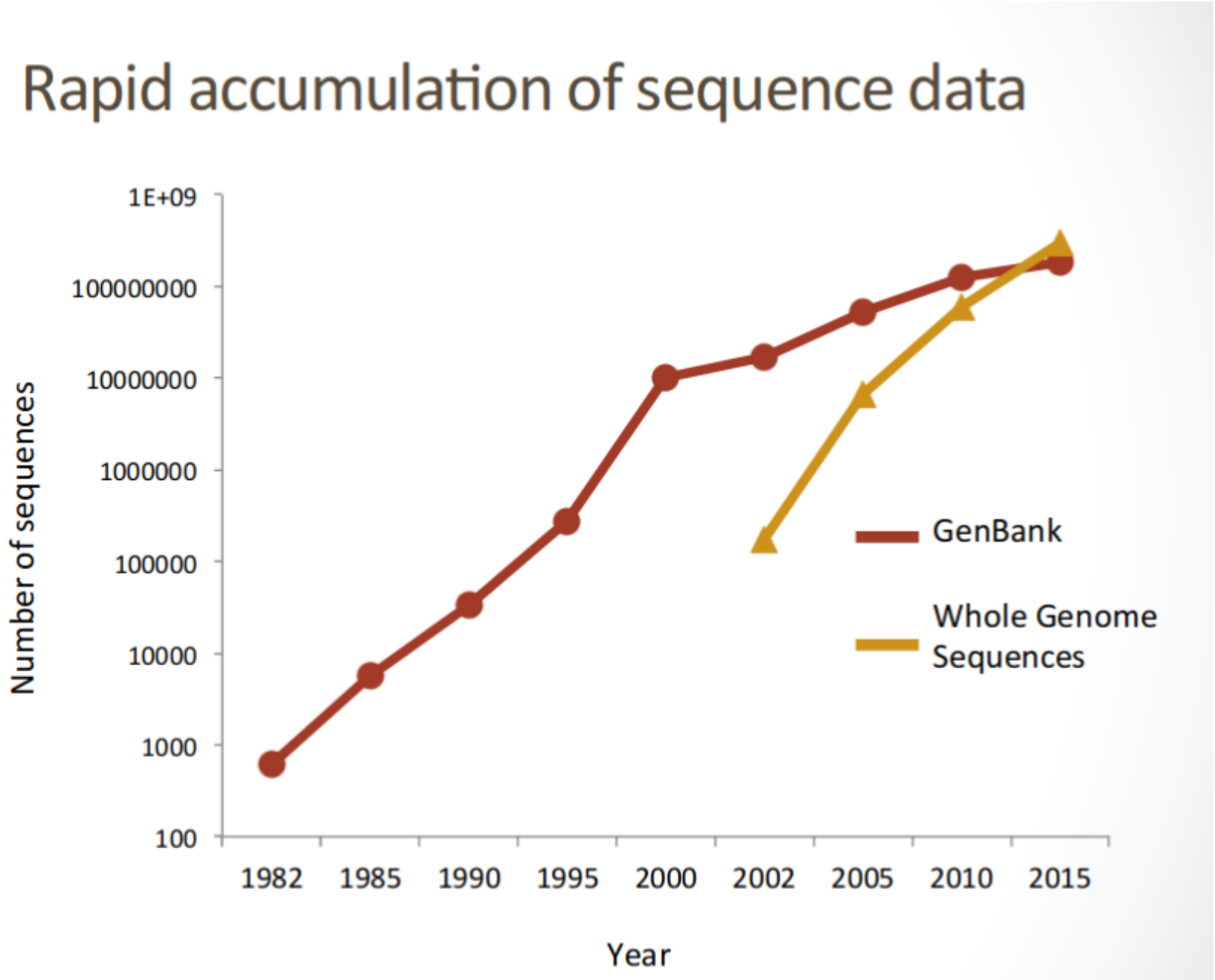


Figure from Belinda Chang

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

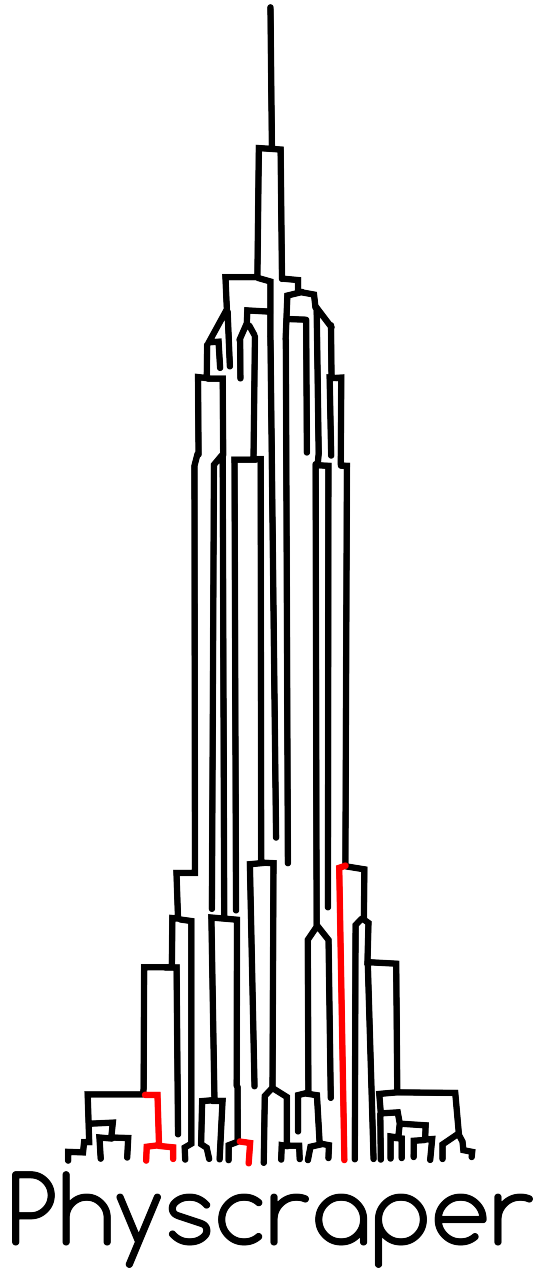
Problems with automated phylogenetics

- Homology/paralogy
- Data collection and assembly
- Alignment

Physcraper

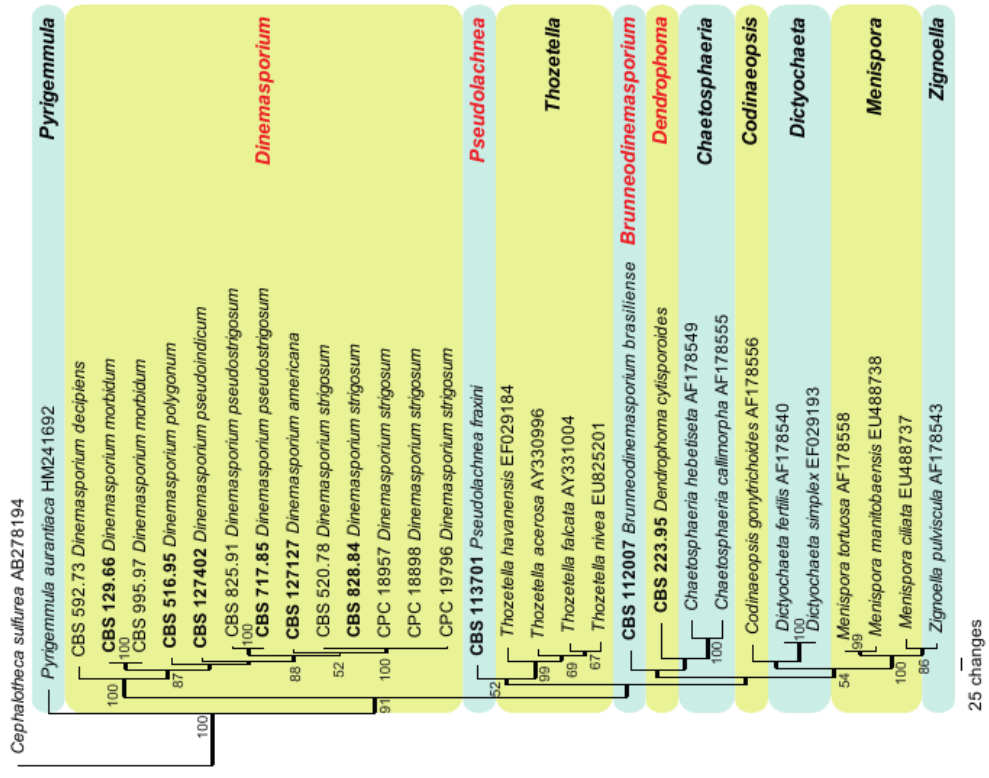
Automated updating of existing phylogenies

`https://github.com/McTavishLab/physcraper`



Restrict taxon addition to in-group

Uses loci that have been developed by taxon experts

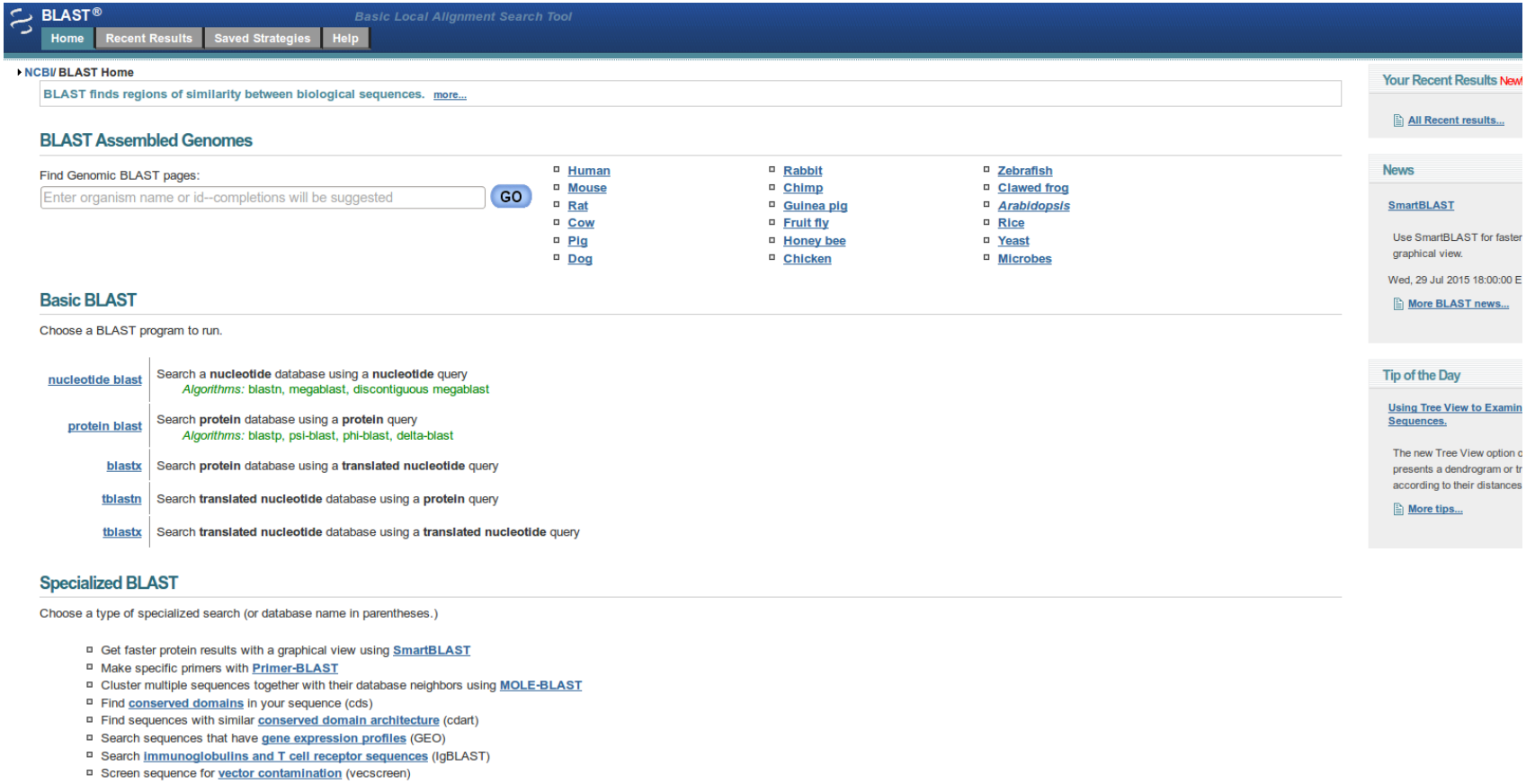


e.g. using ITS to understand relationships within ascomycota

Crous et al. 2012 Persoonia

Data collection and assembly

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

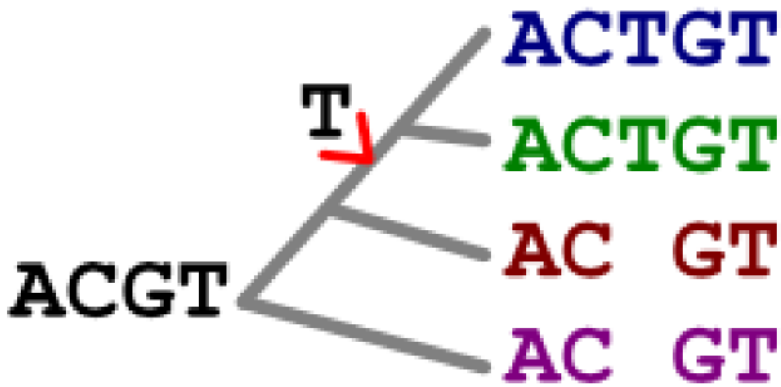


Data collection and assembly

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

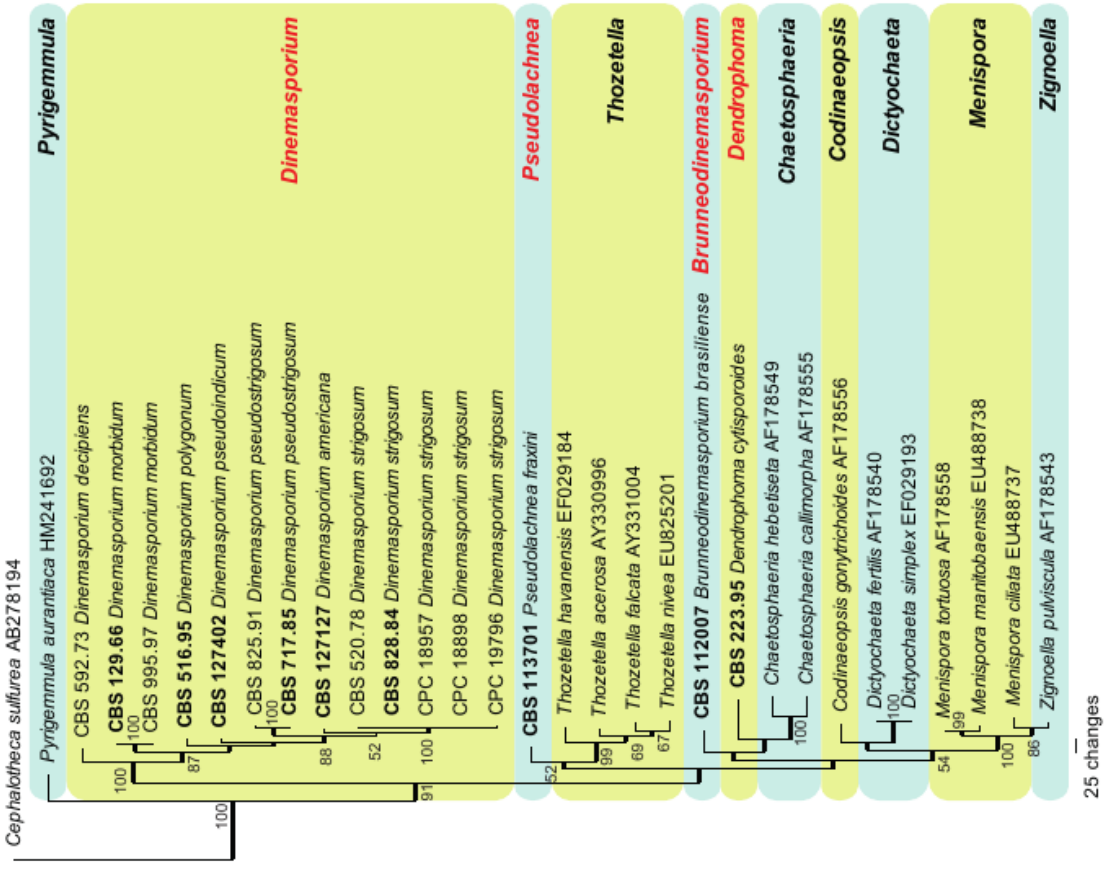
Using existing phylogeny as a guide tree can inform multiple sequence alignment



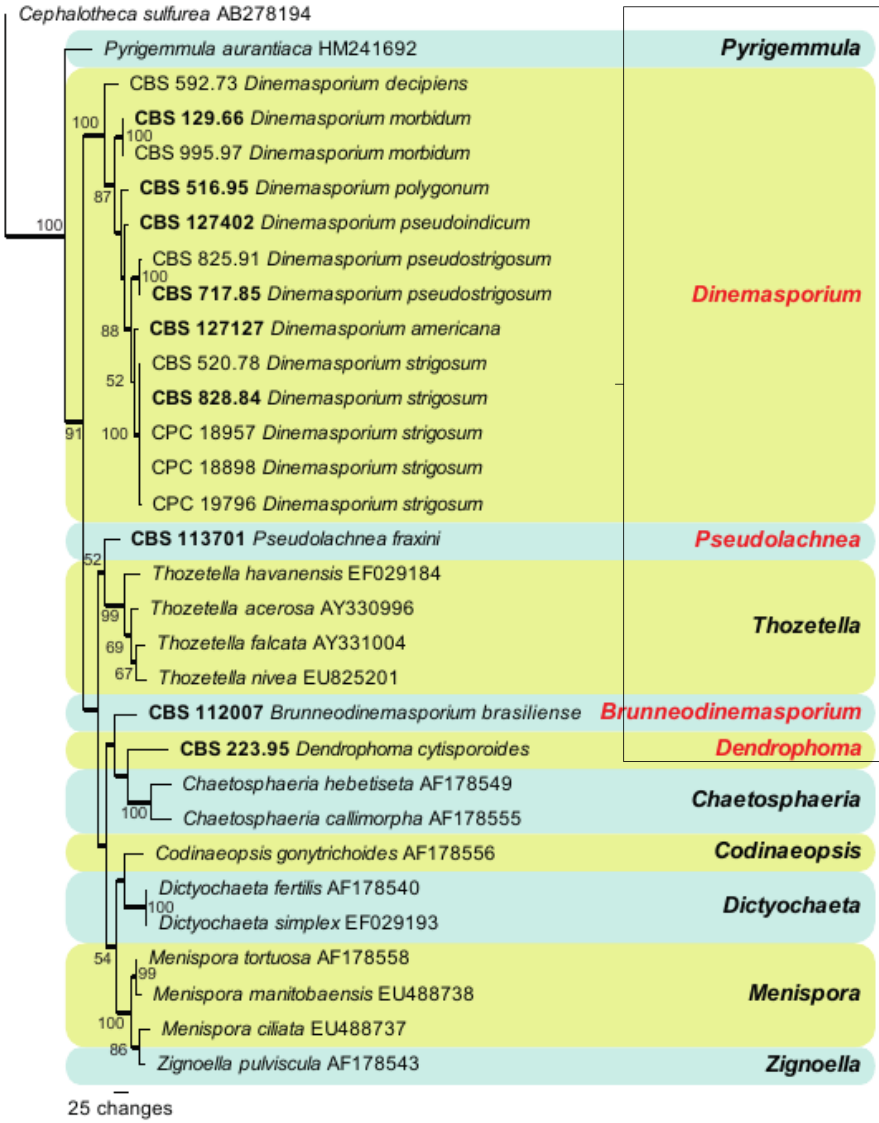
http://www.ebi.ac.uk/goldman-srv/prank/differences/

Perform a full maximum likelihood tree search

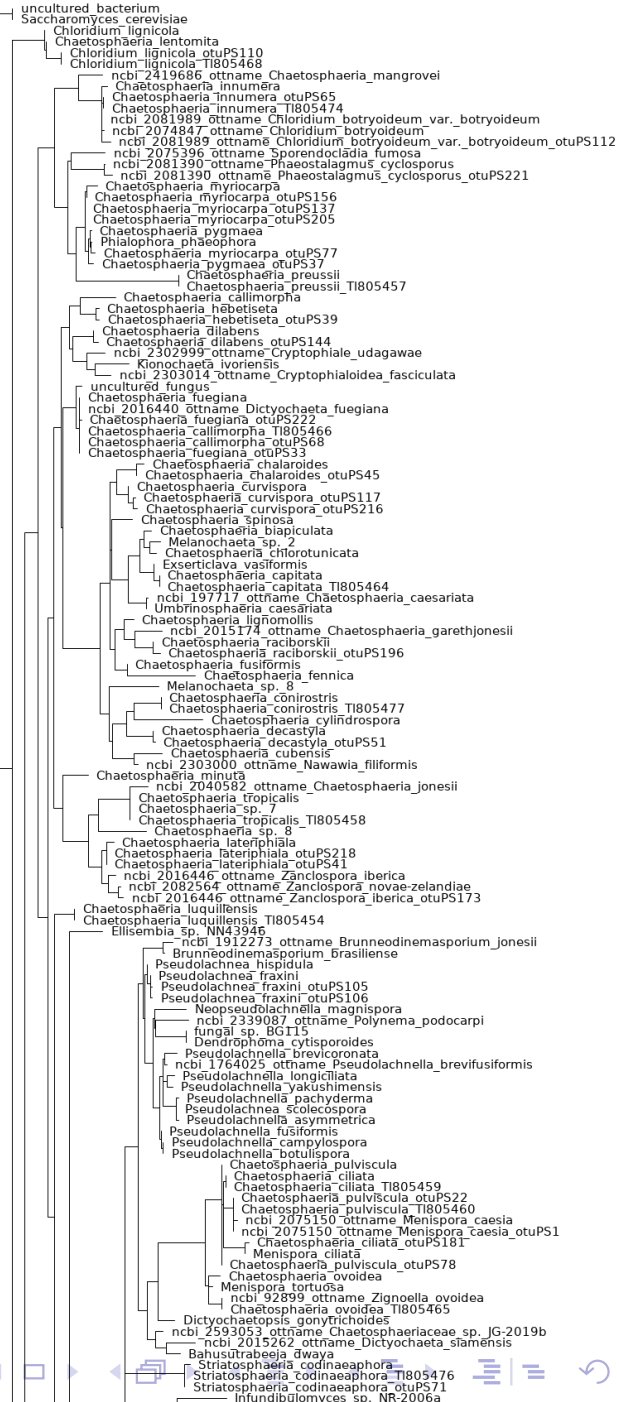
Improve convergence using previous estimate as starting tree



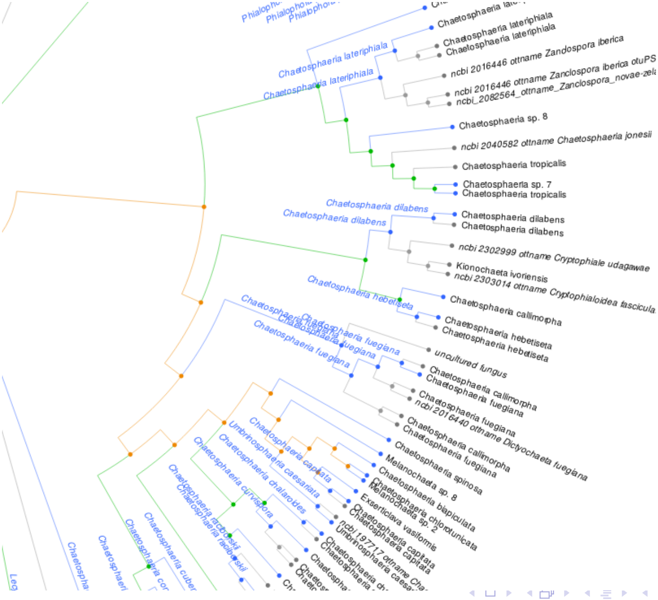
Original tree (36 taxa)



Updated tree (100 taxa)



This is exploratory!
but can flag potential areas of interest.
e.g.



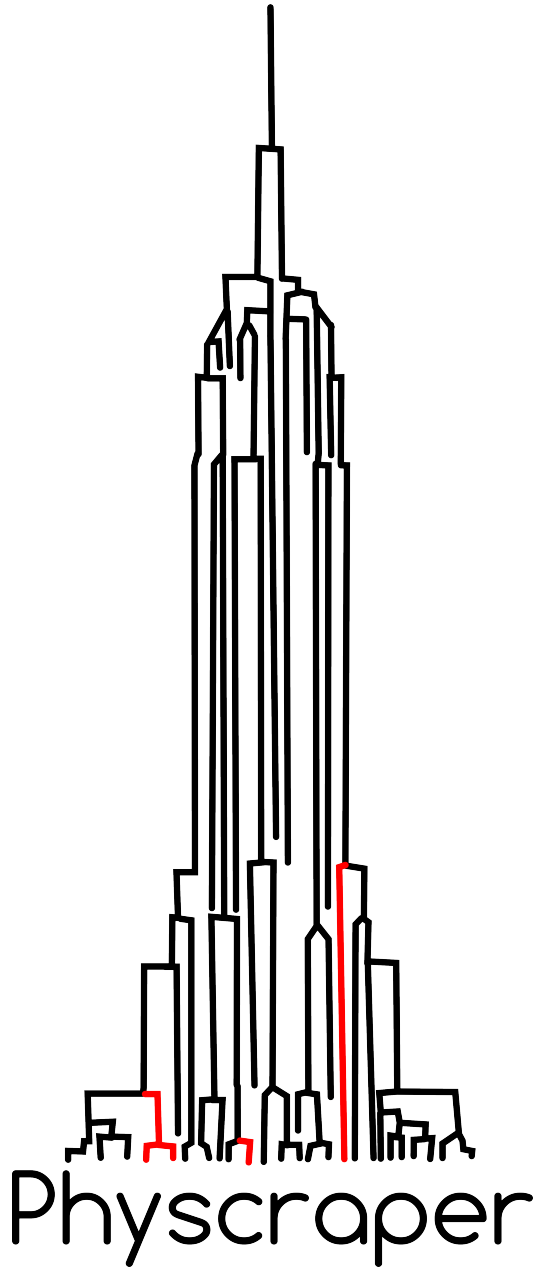
Advantages

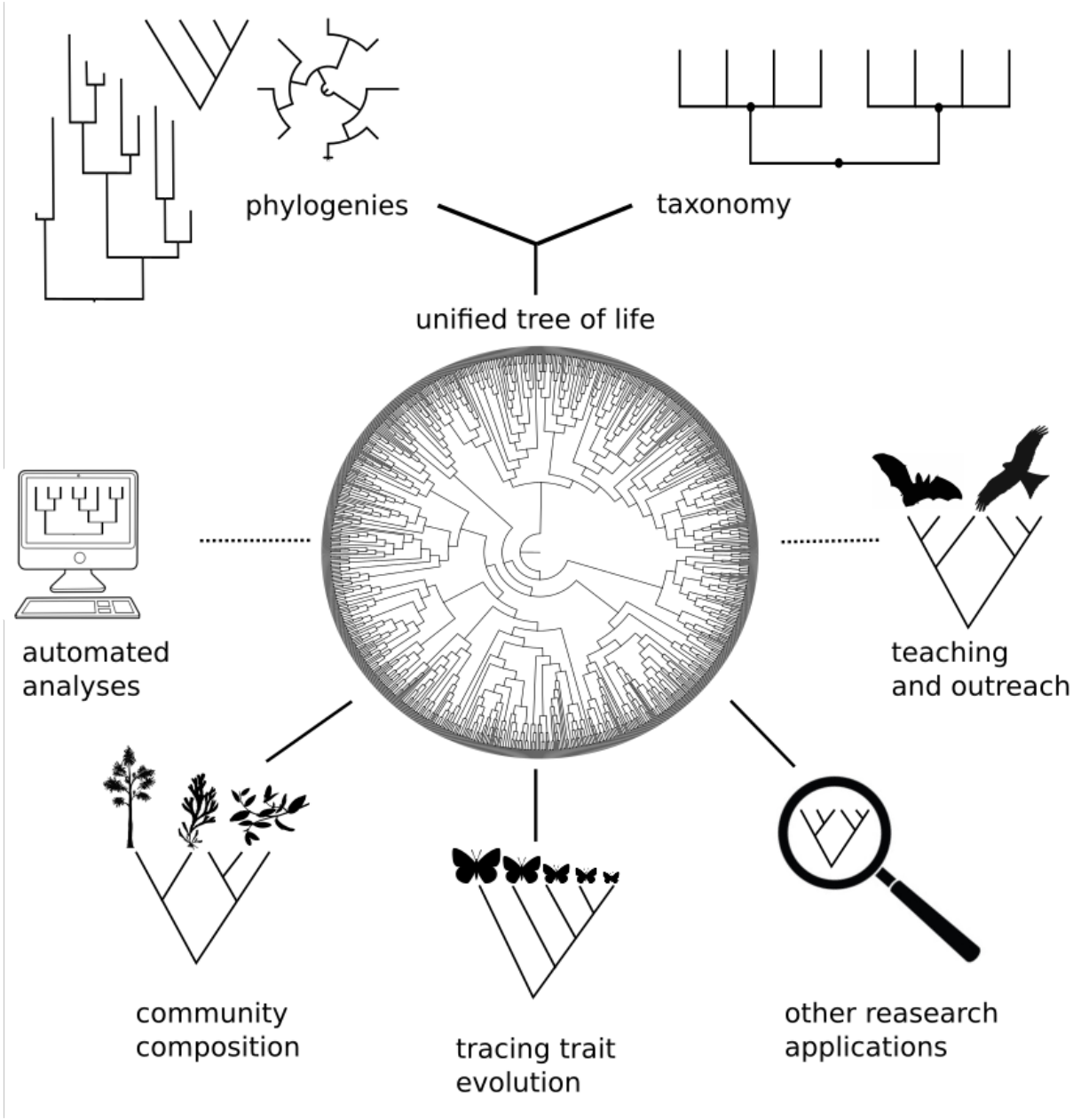
- Rapid data-to-phylogeny loop
- Prioritize further data collection
- Apply data collected for other projects
- Minimize researcher time input
- Stream taxa into draft of synthetic tree

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

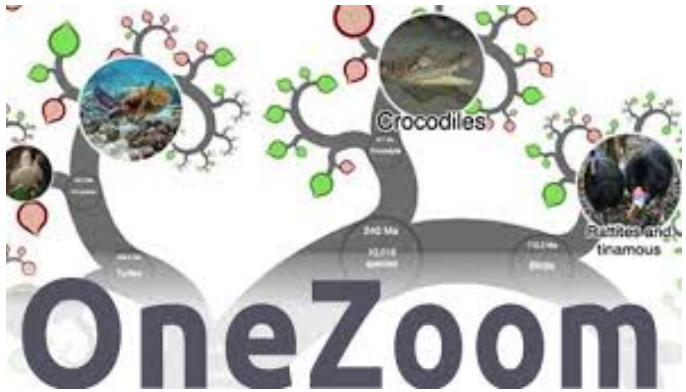
Open Tree provides the tree backend for:

PHYLOtastic

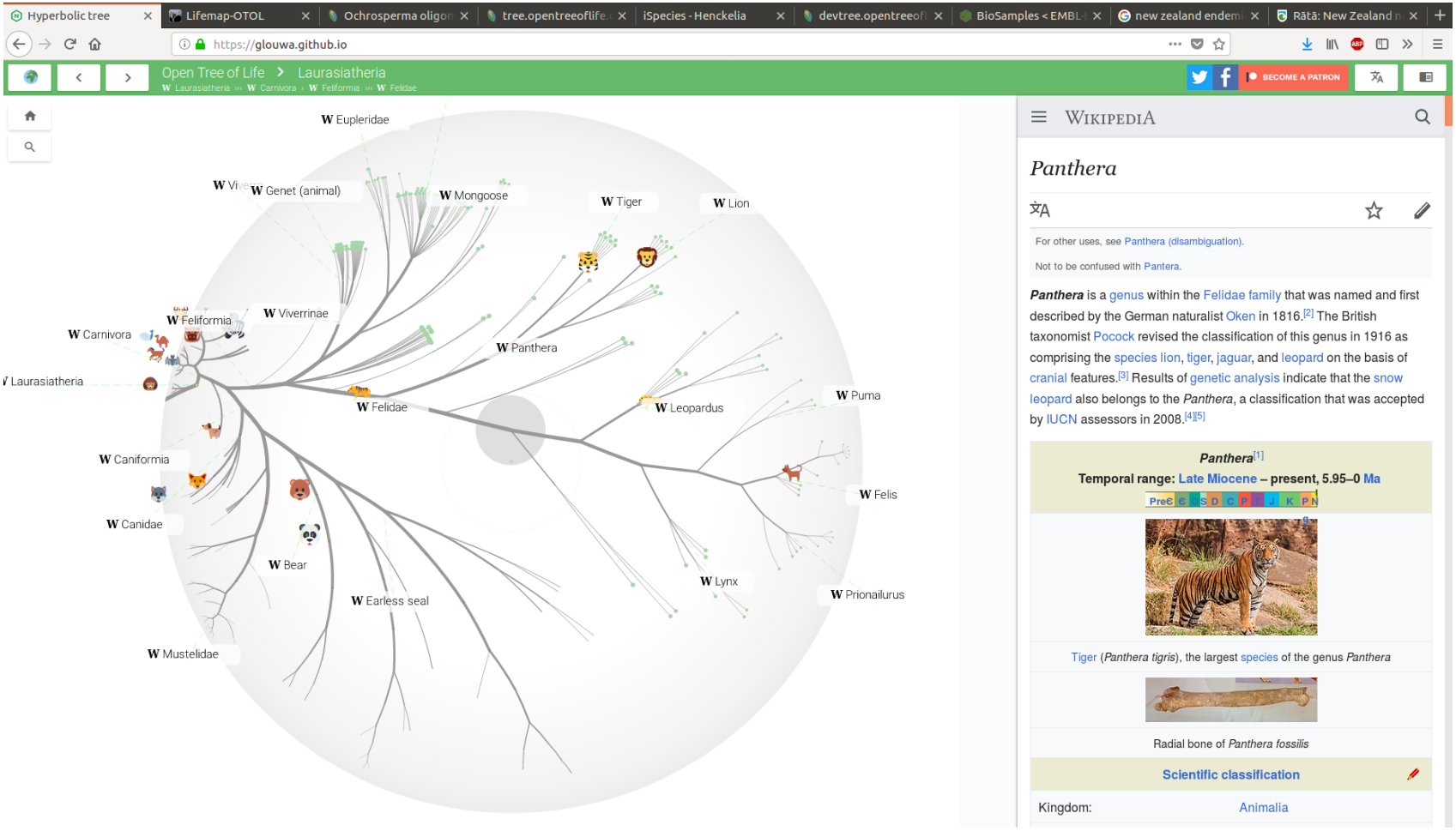
DATElife

Lifemap

OPEN Tree of Life



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



Coming soon!

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

Holder, McTavish  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`

Thank You

NSF ABI 1759846
Mark Holder
Karen Cranston

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

Dendropy Jeet Sukumaran

Lab group:
Martha Kandziora
Luna Luisa Sanches Reyes
Lesly Lopez Fang
Jasper Toscani-Field