

Synthetic Phylogeny of the Decapod Crustaceans

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WASHINGTON, DC



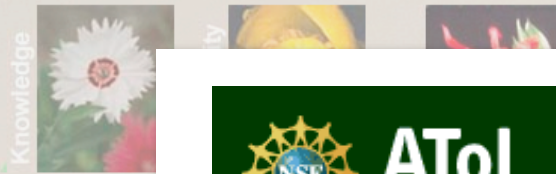
AmphibiaTree



Angiosperm Tree of Life Project

Resolving the trunk of the angiosperm tree and 12 of its thorniest branches

HOME | PAPERS | PIs | DATA | ACHIEVEMENTS | MEETINGS




Assembling the Tree of Life:

Early Bird



- introduction
- who's involved
- contacts



AToL

Assembling the Tree of Life

Assembling the Fungal Tree of Life

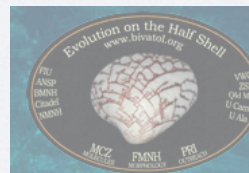


- about
- people
- participation
- resources
- data
- links

Mammal Tree of Life

Welcome

The **Mammal Tree of Life** project is a multi-institution collaboration sponsored by the National Science Foundation to build a phylogenetic tree for mammals using data from molecules, anatomy, behavior and physiology of both living and fossil mammals.



Assembling the Tree of Life:

The Bivalve Mollusks

Data Availability



High archival rate of sequence data



~4% of all published
phylogenetic trees



opentreeoflife.org

Karen Cranston, lead PI (Duke)

Gordon Burleigh (Florida)

Keith Crandall (GWU)

Karl Gude (MSU)

David Hibbett (Clark)

Mark Holder (Kansas)

Laura Katz (Smith)

Rick Ree (FMNH)

Stephen Smith (Michigan)

Doug Soltis (Florida)

Tiffani Williams (TAMU)



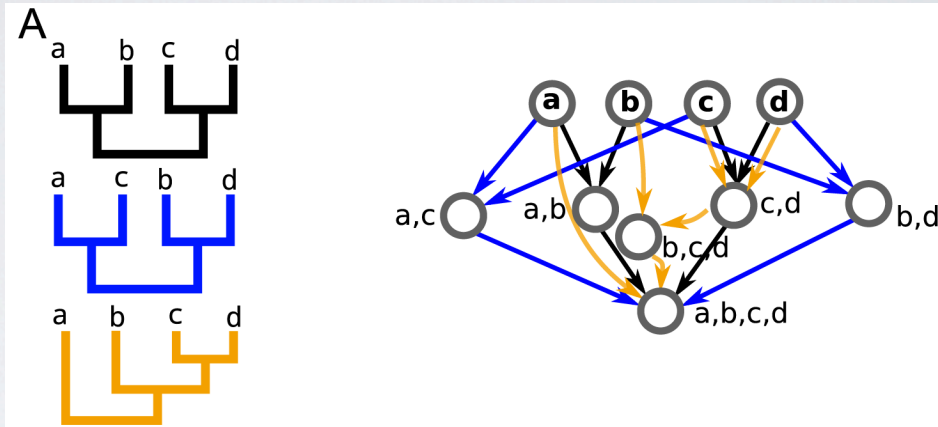
AVAToL: Assembling, Visualizing and Analysis of
the Tree of Life



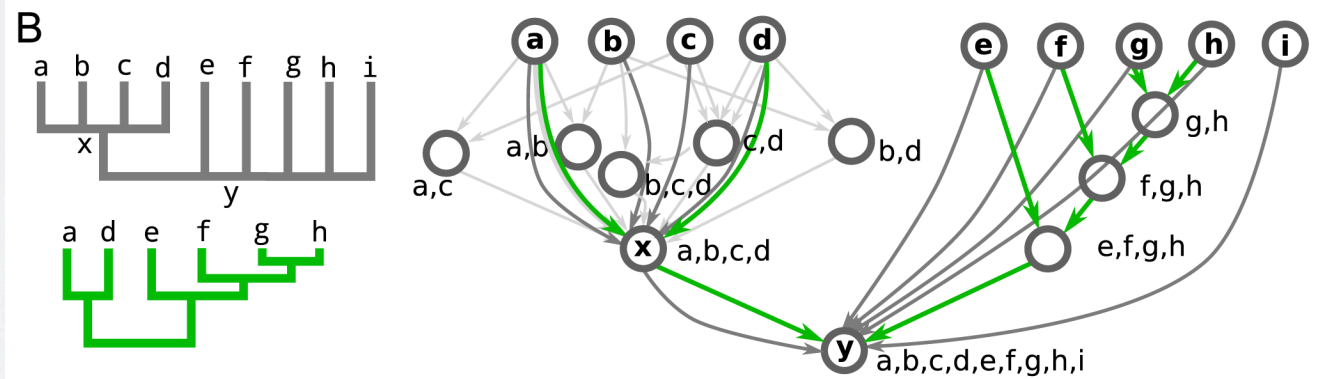
1. Build the **first complete draft tree** of life
2. Engage the community in **refinement and annotation**
3. Promote a **culture of data sharing** through software products
4. Develop **novel methods for phylogenetic synthesis**

Synthetic trees: description of the method

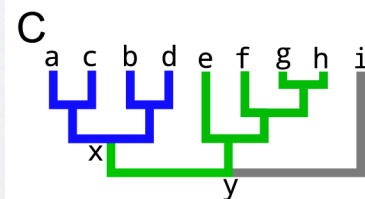
Input trees



Source tree +
taxonomy
(grey)



Synthesis



Smith et al. 2013
PLoS Comp. Biol.

AVAToL: Open Tree of Life

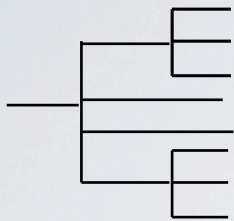
Published Taxonomies



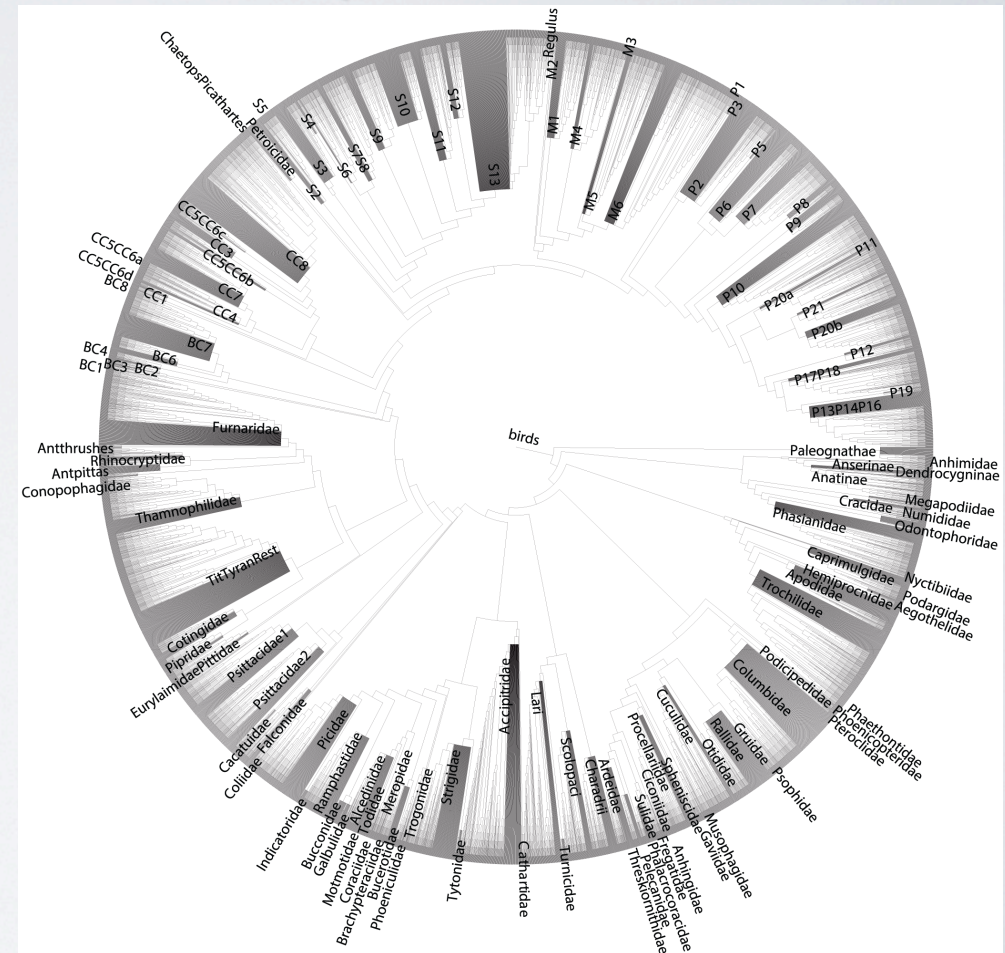
Published Phylogenies



www.opentreeoflife.org



- Phylogeny of all life
 - no new relationships
- Curated taxonomy
- Accessible to the public
- Add/Extract phylogenies
- Two additional AVAToL groups



The Tree of Life

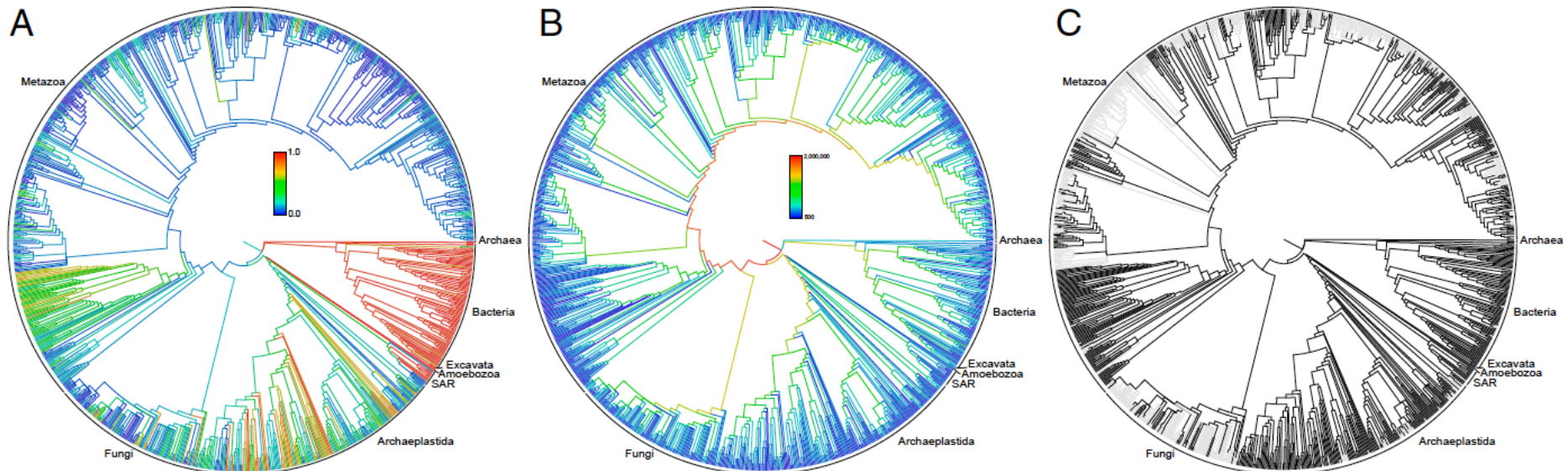
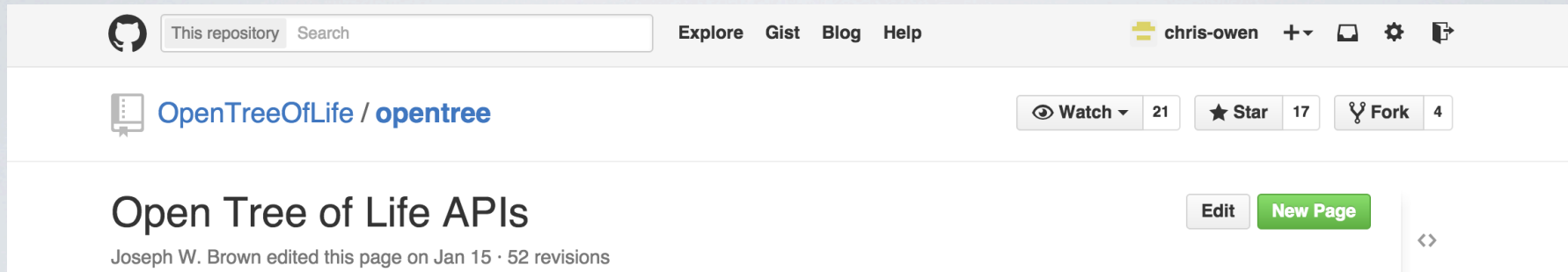


Fig. 1. Phylogenies representing the synthetic tree. The depicted tree is limited to lineages containing at least 500 descendants. (A) Colors represent proportion of lineages represented in NCBI databases. (B) Colors represent the amount of diversity measured by number of descendant tips. (C) Dark lineages have at least one representative in an input source tree.

- GenBank taxonomy has ~411,000 binomials (<5% of est.)
- AVAToL taxonomy = 2,227,481 terminals
- Tips represented by phylogenies = 49,487
- PNAS www.pnas.org/cgi/doi/10.1073/pnas.1423041112

Open Tree APIs



The screenshot shows the GitHub interface for the repository 'OpenTreeOfLife / opentree'. The repository name is displayed in blue. To the right, there are buttons for 'Watch' (21), 'Star' (17), and 'Fork' (4). Below the repository name, the title 'Open Tree of Life APIs' is shown in bold black text. Underneath the title, it says 'Joseph W. Brown edited this page on Jan 15 · 52 revisions'. To the right of the title, there are 'Edit' and 'New Page' buttons. The 'New Page' button is highlighted in green. At the far right, there is a code icon (<>).

- command-line access to versions of the Open Tree of Life
- access the Graph of Life
- taxonomic name resolution services
- taxonomy
- studies containing source tree
- <https://github.com/OpenTreeOfLife/opentree/wiki/Open-Tree-of-Life-APIs>

Open Tree Curator App

Open Tree of Life Curator Home Studies Login

Study Curator

This tool allows you to contribute studies and trees to our database for synthesis. Once your data is submitted, you can return and make improvements, share your data more widely, and watch for changes in your area of interest. Hide ▲

All data is stored as documents in [GitHub](#), a collaborative coding website. This curation tool makes it easy to edit and contribute data, but you'll need a (free) GitHub account to participate.

Once you've created an account on GitHub, just [login](#) using the link above. Once you've agreed to give access to the OpenTree tool, you can start adding data immediately.

[Add new study](#)

Filter by reference text, DOI, tag, curator... Newest publication first

Reference (click to view study)	Focal clade	Curator
Coburn R.A., 2015 [show details]	—	redavids
Malysheva V.F., 2015 [show details]	—	isaacovercast
Dos Remedios, 2015 [show details]	—	Joseph W. Brown
Tan J., 2015 [show details]	—	MGNute
Dai S., 2015 [show details]	—	redavids
Pedro Selvatti, 2015 [show details]	Passeriformes	Joseph W. Brown
Shi J.J., 2015 [show details]	—	isaacovercast

Open Tree of Life Curator Home Studies

Viewing study ANDREAS ZWICK, 2011

<http://dx.doi.org/10.1111/j.1365-3113.2010.00543.x>

Study quality

Metadata **Trees 1** Files OTU Mapping Tools History

Filter by original or mapped label In all trees Unmapped OTUs first

Original name	Mapped to taxon
Apha aequalis AAEQ <input type="text"/>	Apha aequalis
Brahmaea certhia BHEAR <input type="text"/>	Brahmaea certhia
Carthaea saturnioides TB032177 <input type="text"/>	Carthaea saturnioides
Eupterote nr. naessigi EUPNN <input type="text"/>	Eupterote aff. naessigi JCR-2007
Apatelodes torrefacta ATOR <input type="text"/>	Apatelodes torrefacta
Prismosticta fenestrata PFENE <input type="text"/>	Prismosticta fenestrata
Hemaris diffinis HTHY <input type="text"/>	Hemaris diffinis
Malacosoma californicum MCALIFORN <input type="text"/>	Malacosoma californicum
Bombyx mandarina BMAND <input type="text"/>	Bombyx mandarina
Endromis versicolora EVERSICOL <input type="text"/>	Endromis versicolora
Gonometa rufobrunnea GRUFO <input type="text"/>	Gonometa rufobrunnea
Eutachyptera psidii EPSIDII <input type="text"/>	Eutachyptera psidii
Janiodes laverna nigripuncta JCKER <input type="text"/>	Janiodes laverna nigripuncta
Malacosoma americanum MAME2 <input type="text"/>	Malacosoma americanum
Oxytenis modestia OMOD <input type="text"/>	Oxytenis modestia
Colla glaucescens CGLA <input type="text"/>	Colla glaucescens
Poecilocampa populii PPOP <input type="text"/>	Poecilocampa populii
Sorocaba sp. ROLE <input type="text"/>	Sorocaba sp. Janzen01

Viewing study Tschopp A., 2013

<http://dx.doi.org/10.1186/1471-2148-13-74>

Study quality 92% (show details)

Metadata **Trees 1** Files OTU Mapping Tools History Return to study list Login to Edit Study

Publication reference **Tschopp A., Riedel M., Kropf C., Nentwig W., & Klopstein S. 2013. The evolution of host associations in the parasitic wasp genus Ichneumon (Hymenoptera: Ichneumonidae): convergent adaptations to host pupation sites. BMC Evolutionary Biology, 13: 74.**

Publication DOI (or URL) <http://dx.doi.org/10.1186/1471-2148-13-74>

Data deposit DOI/URL **Data for this study is archived as [Treebase study 13911](#)**

Study Year **2013**

Focal clade **Ichneumonidae**

Tags **None**

Submitted by **Chris Owen**

Waiver or license **None**

This study should contribute to synthesis.

This tool is a friendly visual editor for curating **NexSON** files. Like the NeXML and NEXUS formats from which it evolved, each NexSON file contains information about a single published study, with a particular focus on its trees and OTUs.

Each tab in this curation tool manages a different aspect of the study data. Watch for prompts—they look like **?**—in each tab that list areas ripe for improvement.

Here in the **Metadata** tab, we're primarily concerned with clearly identifying this study and making it easy to find using standard publication references, DOIs, and free-form tags.

Working with study data in other tools

You can **download this study** in several formats:

[NexSON](#) [NeXML](#) [NEXUS](#) [Trees as Newick](#)

You can also **use the Open Tree API** (the same one that powers this editor) to retrieve and make changes to study data.



Impacts

- Benchmark for current state of phylogenetic knowledge
- Increasing rate of data archive
- Placing “dark taxa” in global informatics framework
- Phylogenies for any set of species easily available for conservation and ecological studies

Maximizing Outreach



Encyclopedia of Life

OpenTree of Life blog

Public Tree Videos

Mouse around to
Explore, play, learn

What is the Tree of Life?

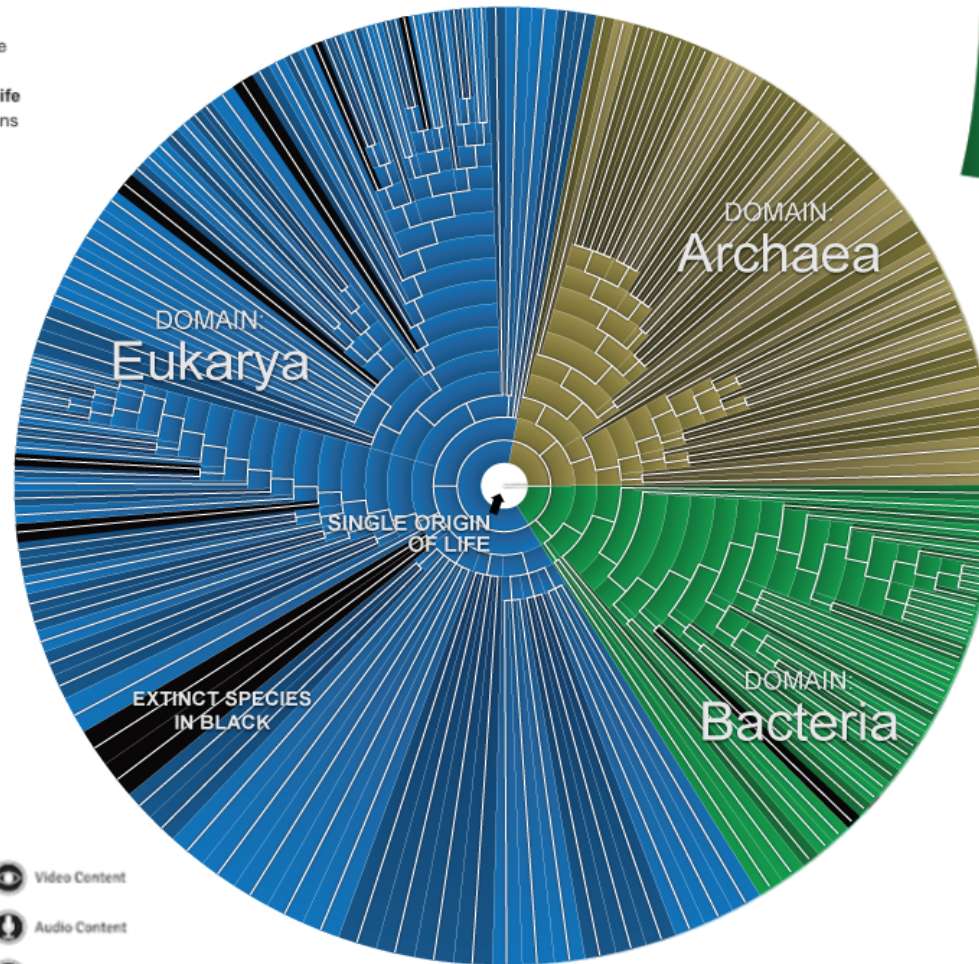
The 'tree' is an imaginary branching, tree-like structure representing the evolutionary divergence of all living creatures, or species, on Earth. The **Public Tree of Life** is a small representation showing only 200 of the millions of species that exist on the planet.

- [Click here](#) to watch a short video explaining this tree
- [Click here](#) to watch a short video explaining the common ancestry.
- [Click here](#) to watch a short video explaining the common ancestry.

Click on any species to learn about a species

	Common Sea Otter <i>Otternicus Gerfunct</i>	
	Bald Eagle <i>Americus Yesicus</i>	
	Stick Bug <i>Awkwardus Walkicus</i>	
	Human <i>Homo Sapiens</i>	
	Peat Moss <i>Peaty Mossiti</i>	
	Common Cold <i>Whaticus Thisicus</i>	
	Spicy Archaea <i>Archaeas Salsicus</i>	

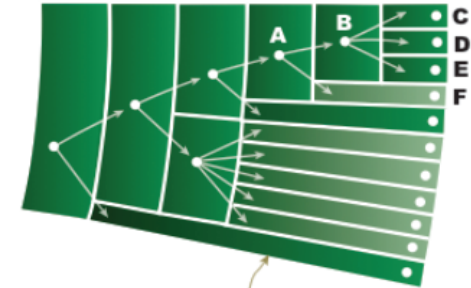
- Video Content
- Audio Content
- Picture Content



Species **A** is the common ancestor to species **B** and **F**

Species **B** is the common ancestor to species **C, D** and **E**

Species alive today
(Extinct species in black)



Why these long shapes? With only 200 species shown here, many common ancestors are omitted from this tree, which results in these long shapes that go back to until they find an ancestor.

How to Read the Wheel

Each rectangle, regardless of size or shape, represents a **species** (also illustrated below as a white dot). All species evolved from another species that lived before it (their **ancestor**). All species share some common ancestor, the most recent ancestral form or species from which two or more different species evolved. For example, humans didn't evolve from chimps, but both humans and chimps evolved from a common ancestor long ago.

OPEN Tree of Life Link here to the the AvaToL Tree of Life tool, etc. Something here about the the AvaToL

Link here to the Encyclopedia of Life link etc. Attribution, etc. Encyclopedia

Link here to the NSF AvaToL project and attribution etc. etc. etc.

Future work: automatic updating

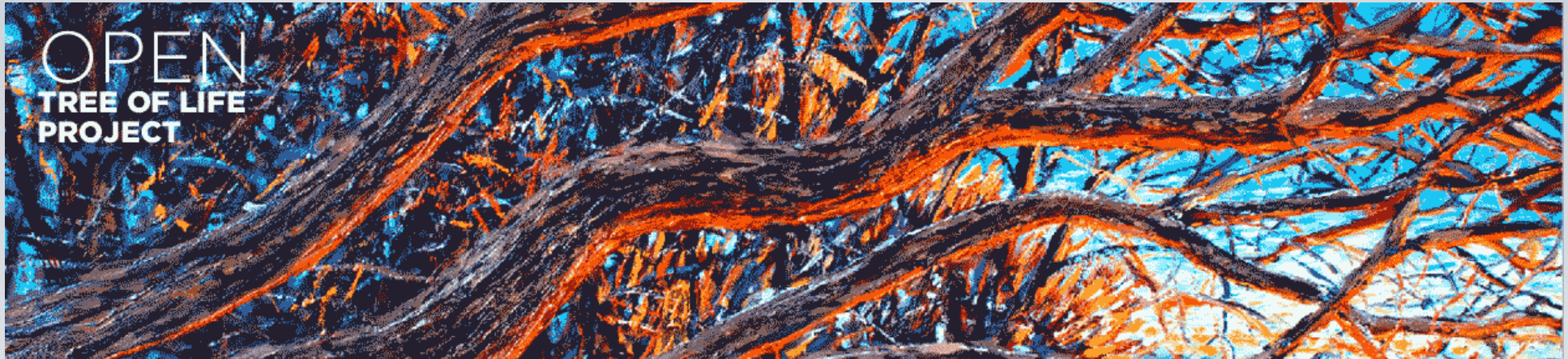


*update trees
with new
sequence data*



*detect and incorporate newly
published trees*





“OPEN” TREE OF LIFE

<http://opentreeoflife.org>



National Science Foundation
WHERE DISCOVERIES BEGIN