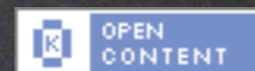
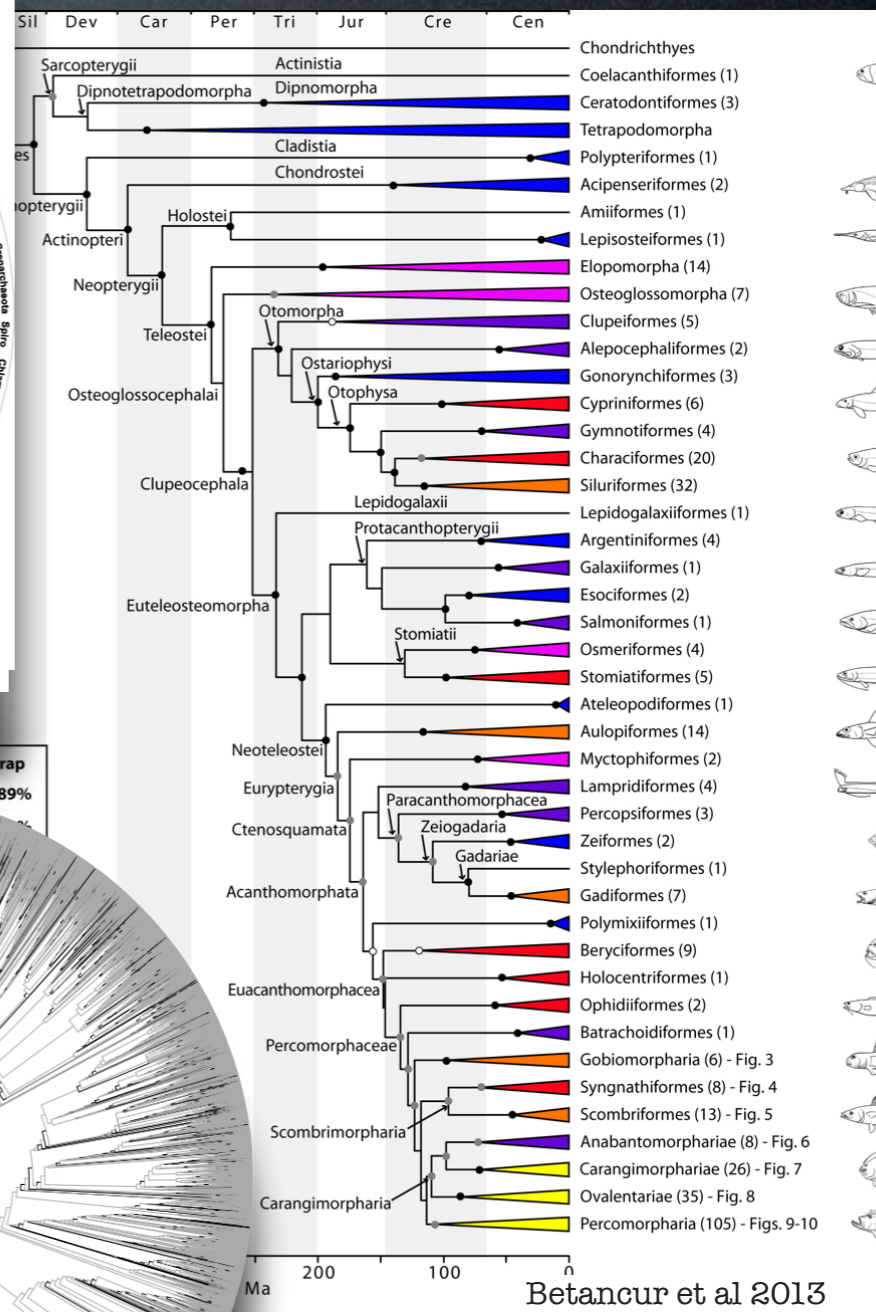
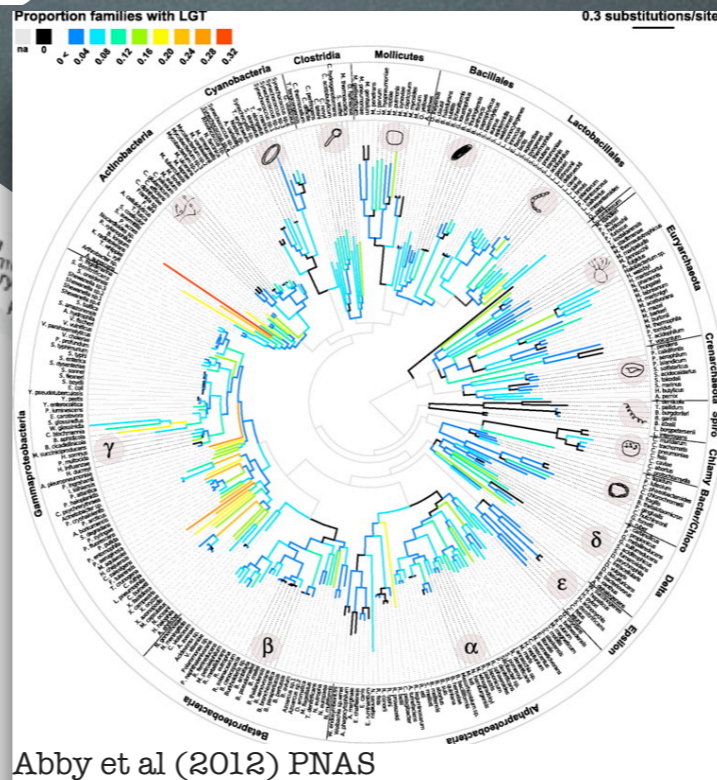
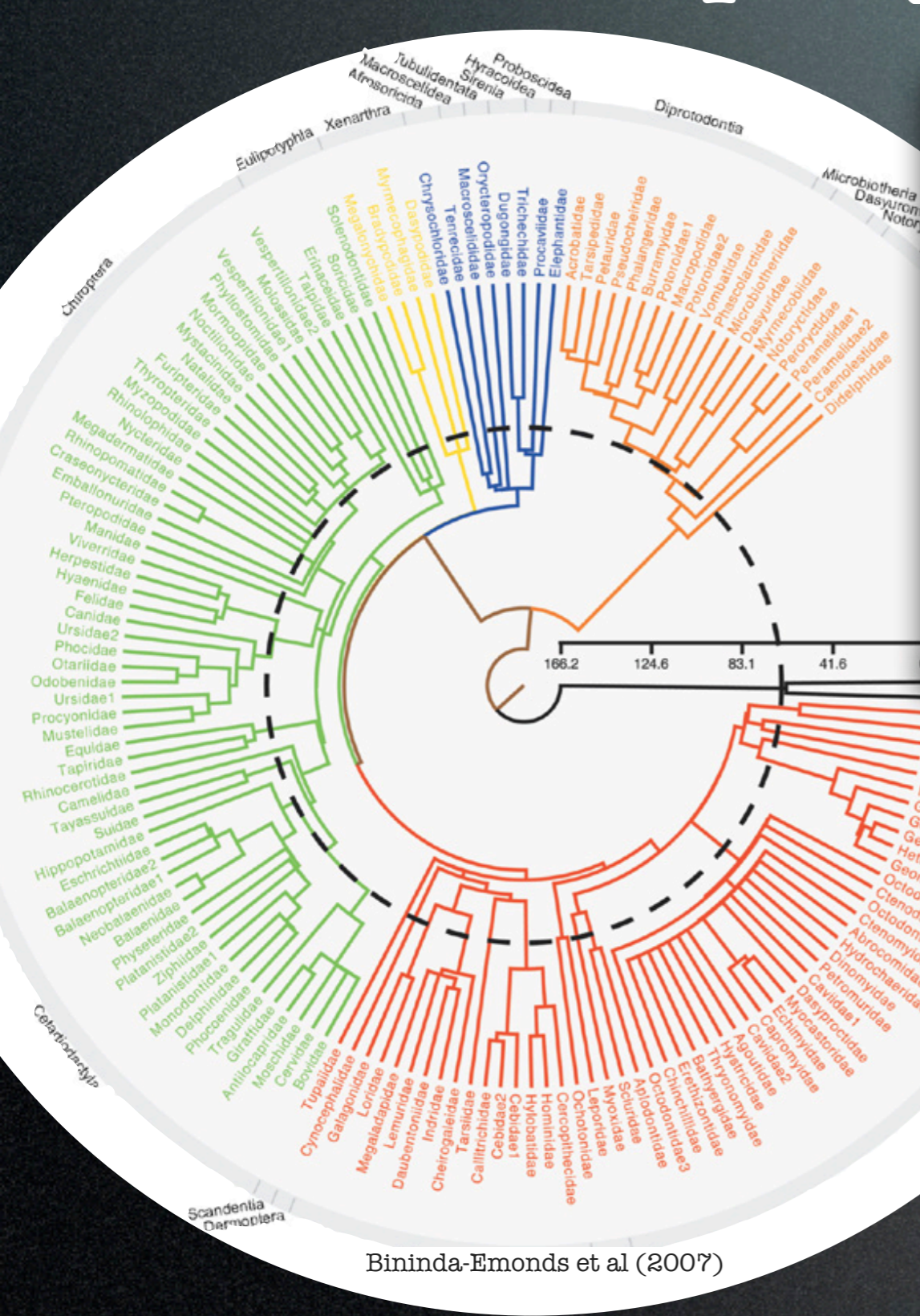


PhyloCommons: Sharing, Annotating, and Reusing Phylogenies

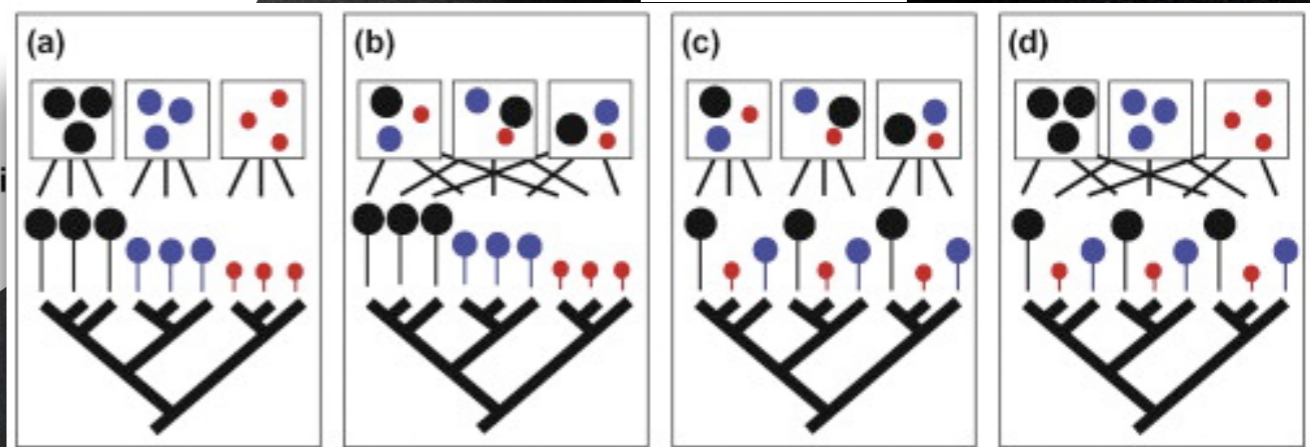
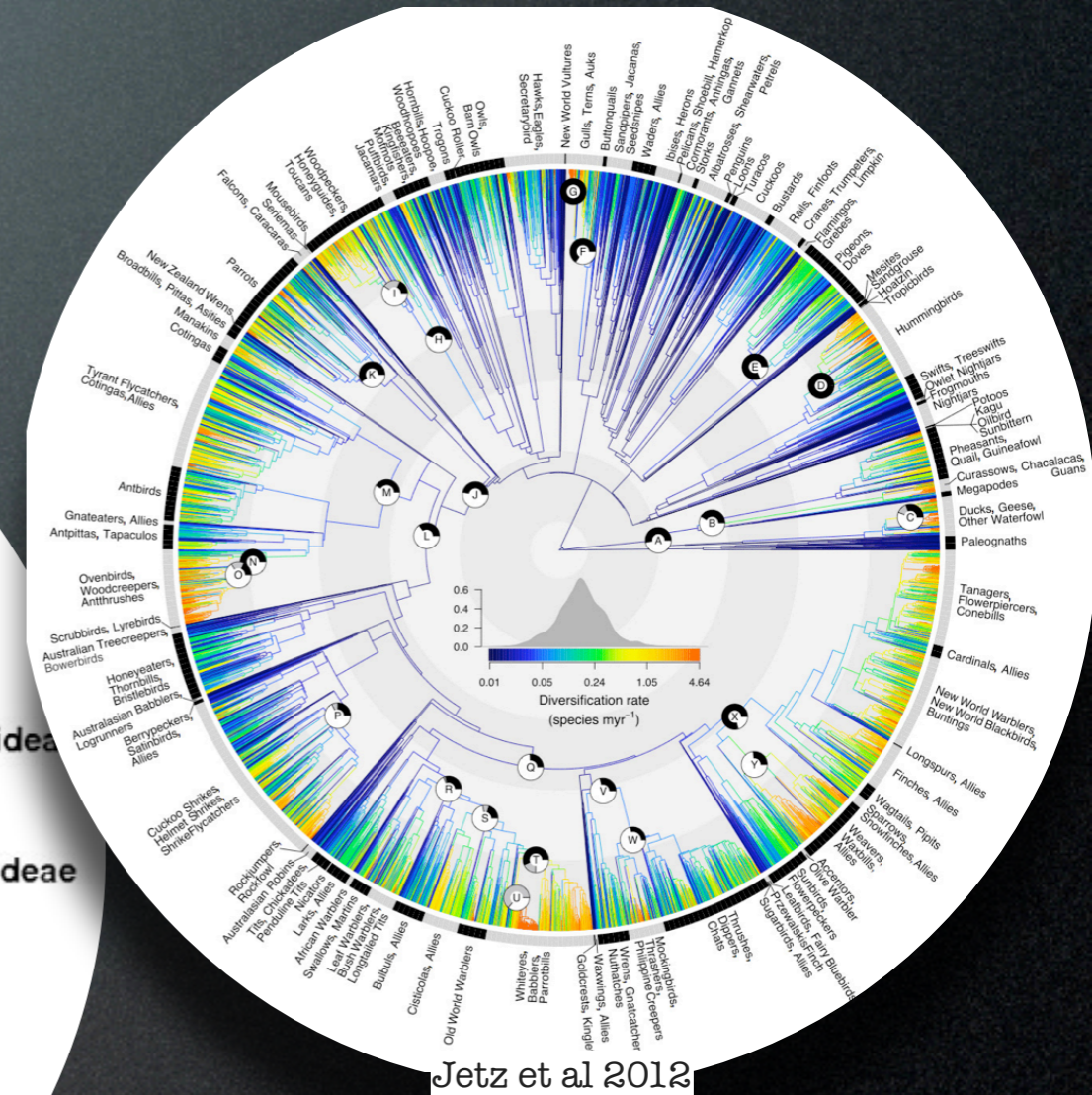
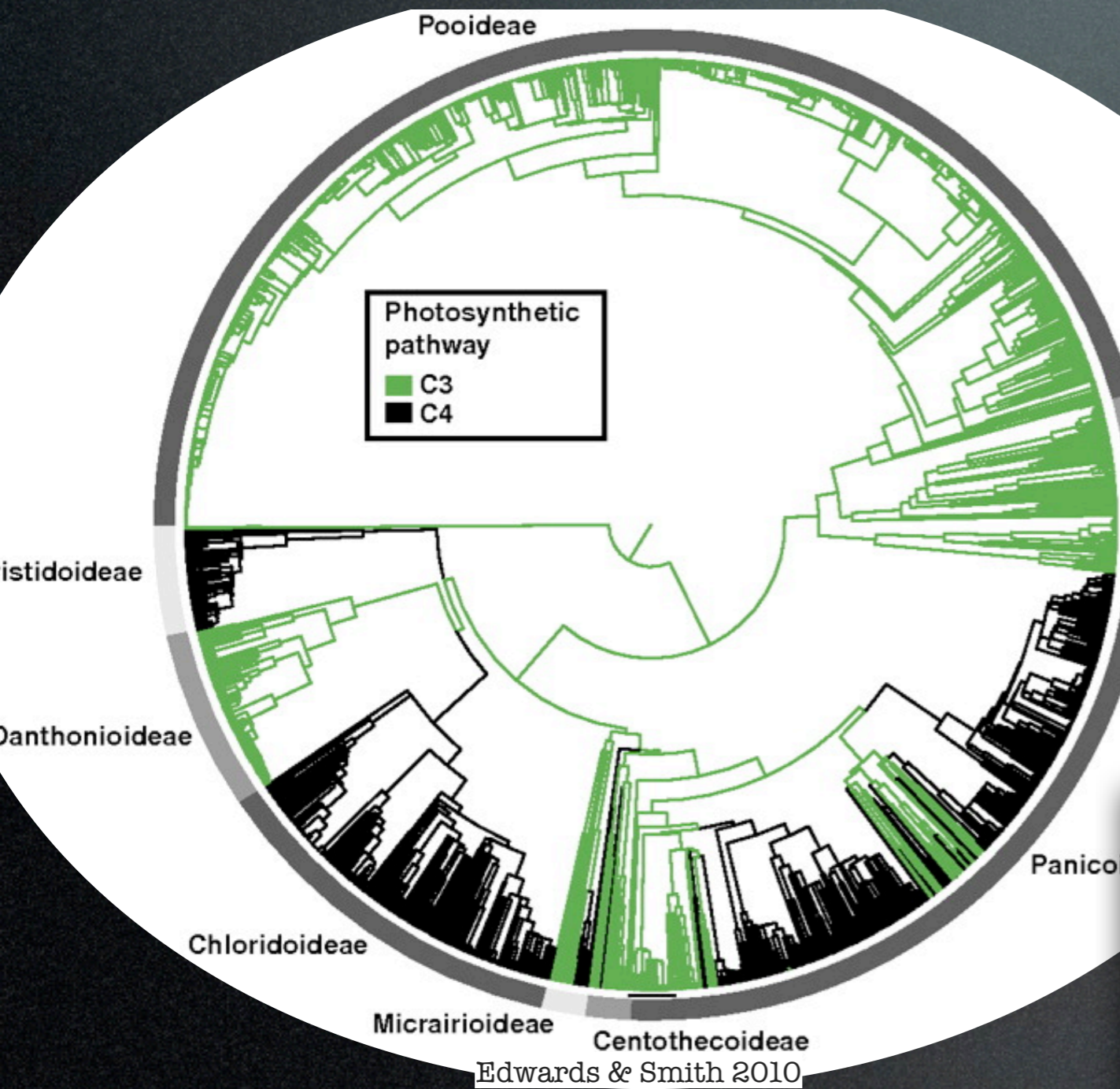
Ben Morris (University of North Carolina, Chapel Hill)
Hilmar Lapp (National Evolutionary Synthesis Center)



Phylogenetic trees are published at a rapidly increasing rate



Phylogenies are key to many biological questions



Emerson & Gillespie, 2008

Reuse of phylogenies is nonetheless rare

DATA NOTE

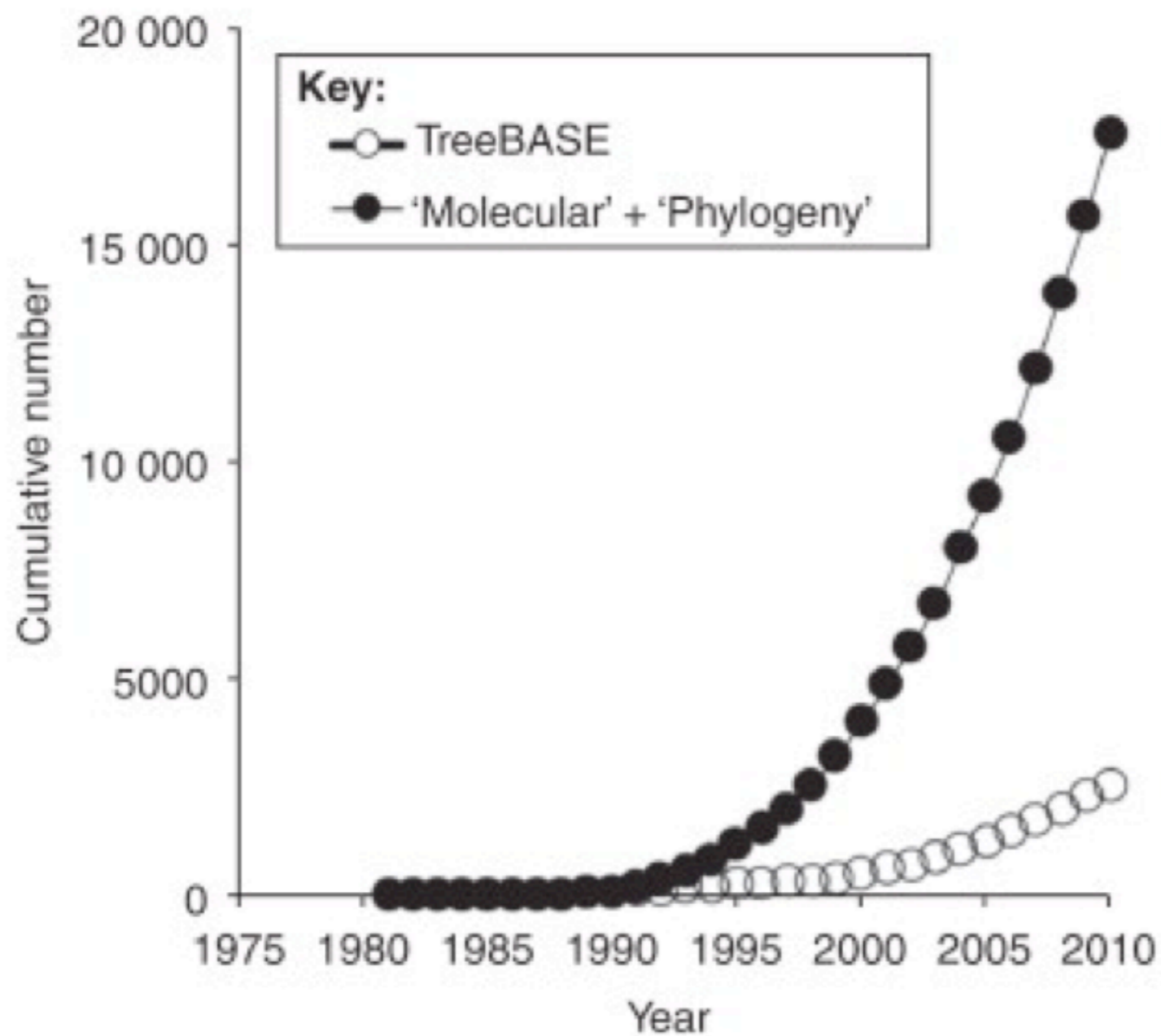
Open Access

Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis

Arlin Stoltzfus^{1*}, Brian O'Meara², Jamie Whitacre³, Ross Mounce⁴, Emily L Gillespie⁵, Sudhir Kumar⁶, Dan F Rosauer⁷ and Rutger A Vos⁸



“Most attempts at phylogenetic data reuse seem to end in disappointment.”

Digital archival lags behind



Stoltzfus et al (2012):
<4% of published
phylogenies archived

Files in this package

To the extent possible under law, the authors have waived all copyright and related or neighboring rights to this data.  

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Downloaded	116 times
Description	Contained within this archive are the phylogenetic matrices and trees generated for this study. NOTE: Please use revised_phylo.tar.gz, an updated version of the data file that was added on 2012-11-15.
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Title	Assembled data generated for study
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Lack of archival is not the only barrier to reuse

Science

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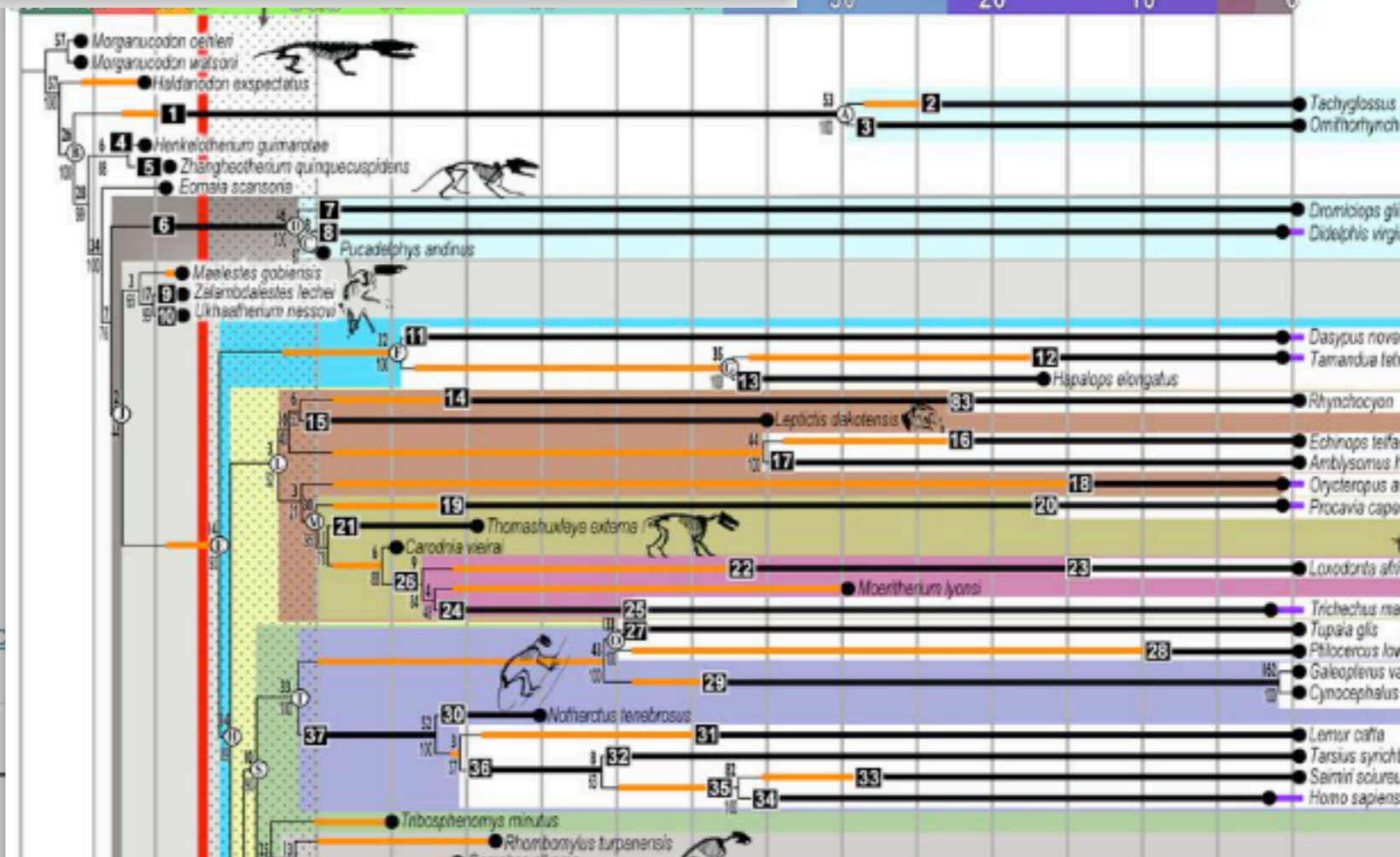
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THE PLACENTAL MAMMAL ANCESTOR AND THE POST-K-PLEISTOCENE

To discover interordinal relationships of living and fossil placental mammals and the time of origin of placentals relative to the Cretaceous-Paleogene (K-Pg) boundary, we scored 4541 phenomic





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PhyloCommons is a community-edited, annotated repository of phylogenetic trees. It simplifies the reuse of published trees and aggregates knowledge about each tree that can be used to inform evolutionary analyses.

This is an alpha release; PhyloCommons may change rapidly before a stable version is released.

PhyloCommons uses semantic web technologies including RDF to enable quick, efficient reuse of trees. PhyloCommons leverages the open source [BioPython project](#) to convert trees in various formats into RDF. These trees are then stored in Virtuoso, a database optimized for RDF storage. This makes common tasks such as querying for specific trees based on metadata (year published, reconstruction method) or creating subtrees from a list of taxa very efficient.

Make PhyloCommons better - you can contribute to PhyloCommons by:

- [Submitting new trees](#)
- [Adding or correcting metadata on existing trees](#)
- [Suggesting enhancements or reporting bugs](#)
- [Forking PhyloCommons on GitHub, adding new features, and submitting a pull request](#)

PhyloCommons builds on tools that were developed at two [Phylotastic](#) hackathons.

View the list of [contributors](#).

PhyloCommons is open source and is available on [GitHub](#).

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Taxa [?](#)

Enter a comma-separated list of taxa (e.g. Homo sapiens, Pan troglodytes, Pan paniscus, Gorilla gorilla, Pongo pygmaeus) to build a tree containing those taxa

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Tree	Matches	
TB2_Tr57779	5/5	Get tree
TB2_Tr61622	5/5	Get tree
bininda-emonds_mammals	5/5	Get tree
itis_taxonomy	5/5	Get tree
ncbi_taxonomy	5/5	Get tree
TB2_Tr1222	4/5	Get tree
TB2_Tr1783	4/5	Get tree
TB2_Tr47029	4/5	Get tree
TB2_Tr1781	3/5	Get tree
TB2_Tr1784	3/5	Get tree

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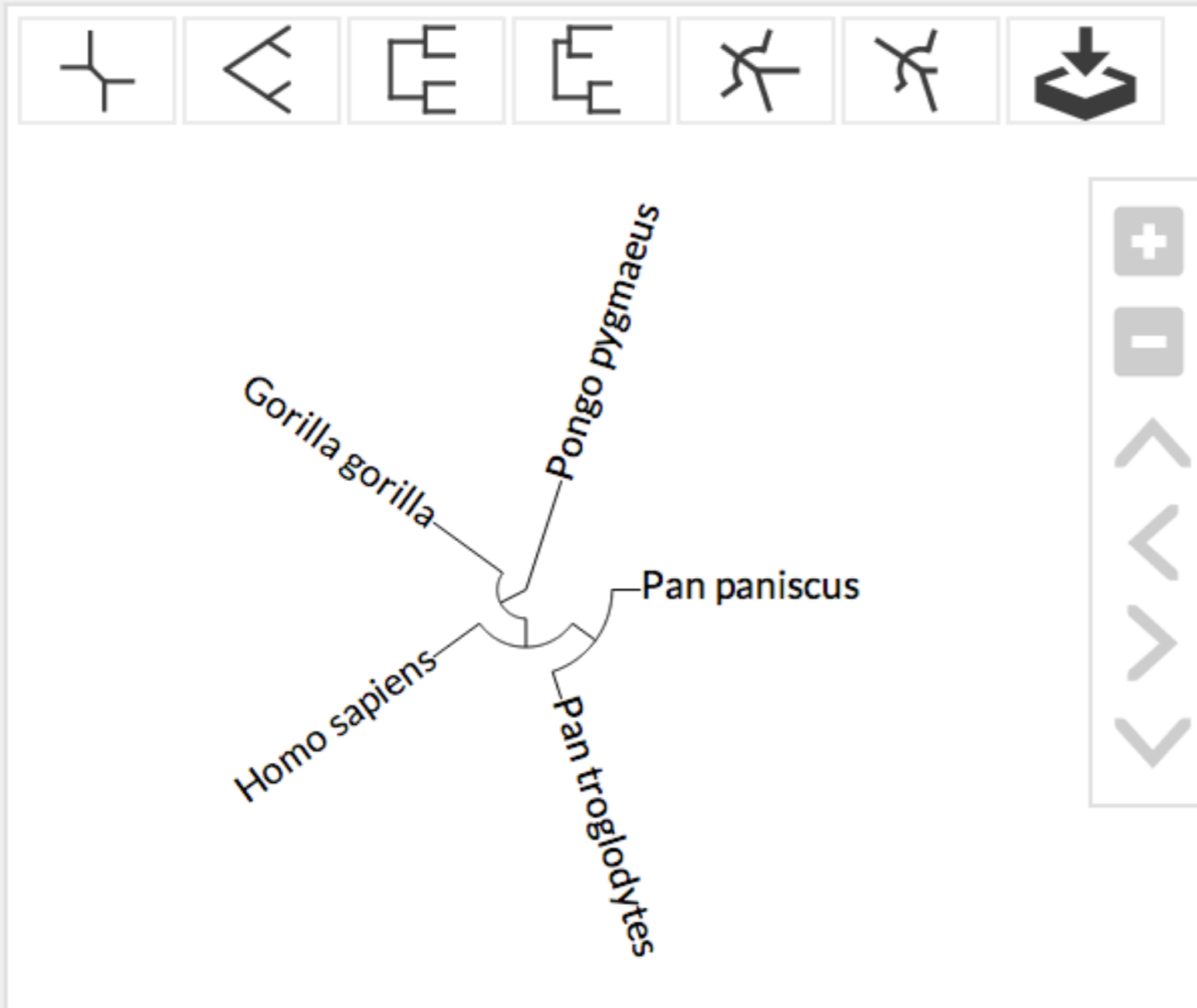
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From tree [bininda-emonds_mammals](#)

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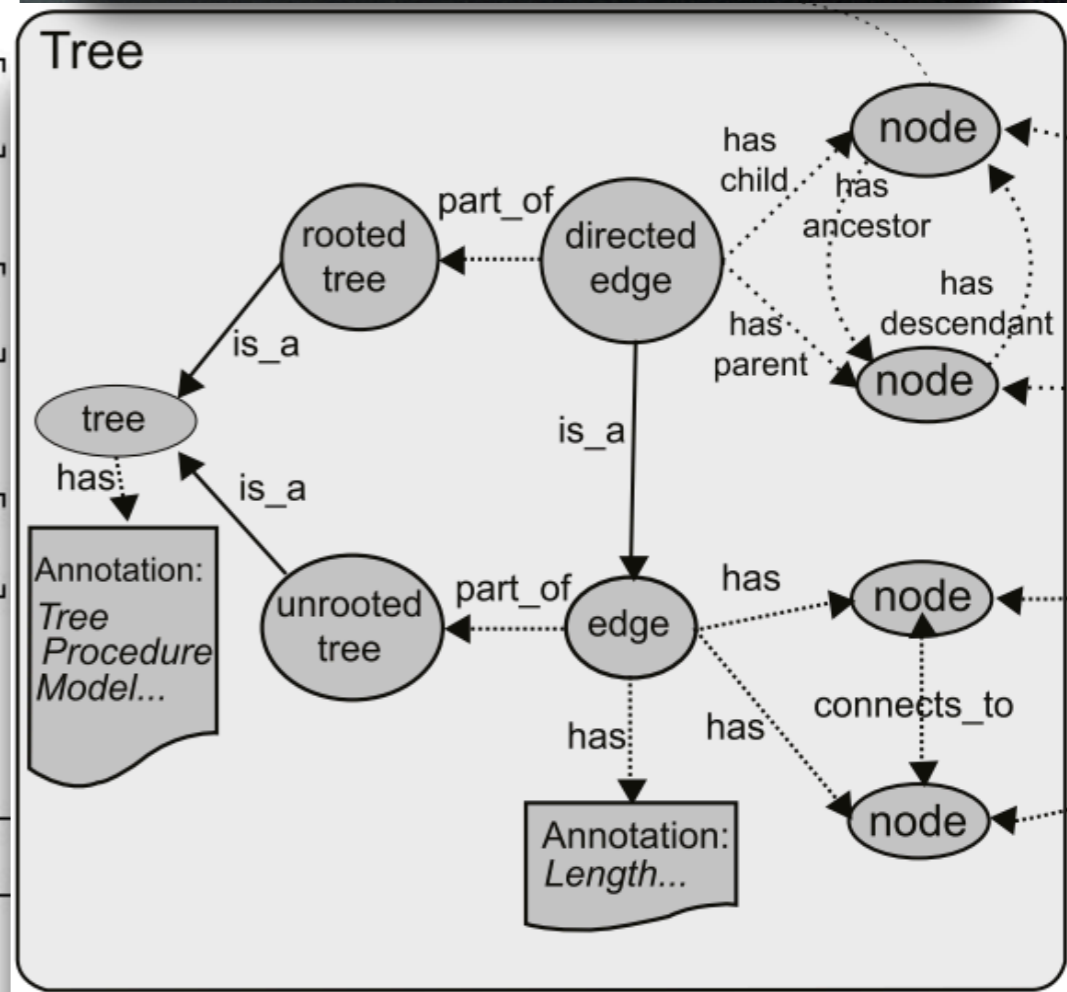
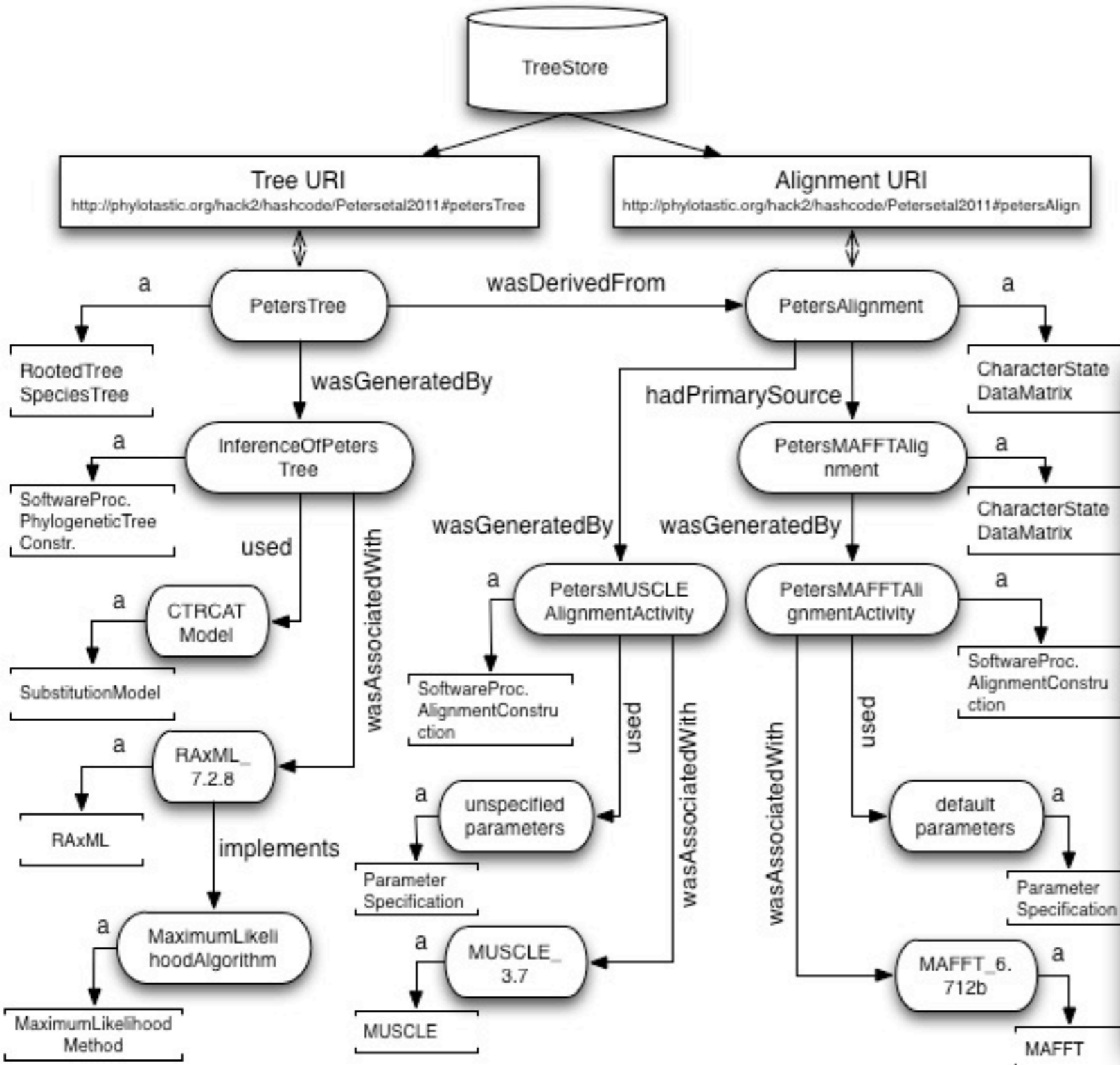
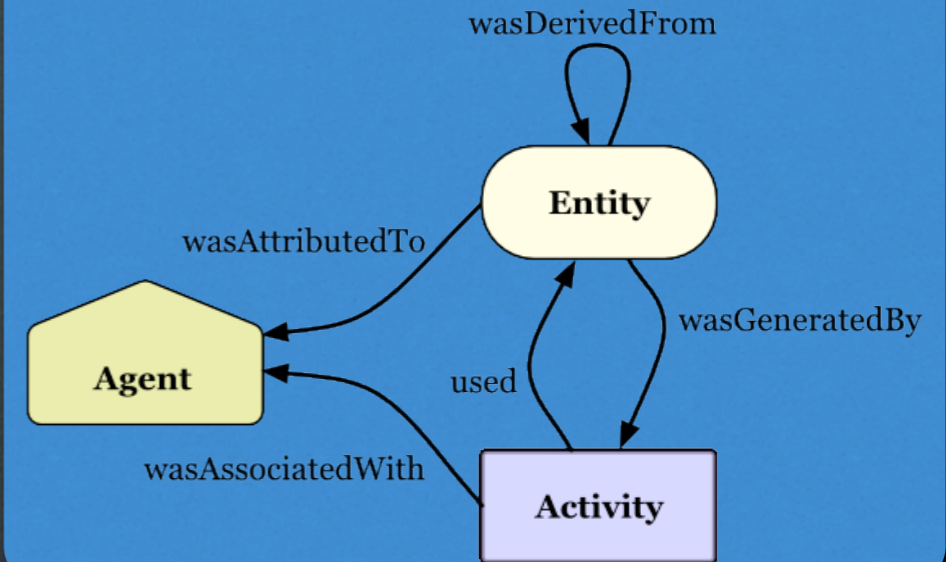
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Data annotation using ontologies

W3C[®] PROV Model



An example use-case

- Ben is an ecologist assessing phylogenetic community patterns in birds, using the North American Breeding Bird Survey (BBS).
- There are a total of 601 fully identified species in the BBS from 2006-2010. I need to know how these are related.

Example use-case: naïve approach

- Manually or with scripting match names from the BBS to the Jetz et al. (2012) bird supertree.
- Manually prune out unwanted taxa.
- Results in successfully locating 478 BBS species (80%) in the Jetz et al. tree.

Example use-case: using PhyloCommons

- With synonym matching, simply paste in unaltered list of species names
- Receive a phylogeny in any desired format containing 575 species (96%)
- Can also filter by additional criteria which trees will be searched
- Disambiguation step shows potential matches, select one to complete the query.

Acknowledgements

- HIP Leadership Team (organizers of the 2012 and 2013 Phylotastic Hackathons)
- Phylotastic Hackathon sponsors: NESCent, Biodiversity Synthesis Center, iPlant Collaborative

Try it out, and contribute

- Working instance:
<http://www.phylocommons.org>
- Source code:
<http://github.com/bendmorris/phylocommons>
- MIT licensed