

A phylogenetic view on aggregated biodiversity data



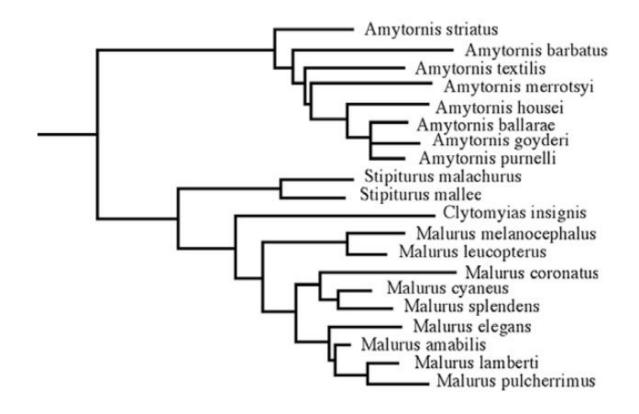
Rebecca Pirzl¹, Dan Rosauer², Joe Miller³, Garry Jolley-Rogers⁴, Temi Varghese¹

¹Atlas of Living Australia CSIRO, ²Australian National University, ³National Science Foundation, ⁴CSIRO Taxonomic Research Network

Phylogenies



 hypotheses about the evolutionary relationships between organisms

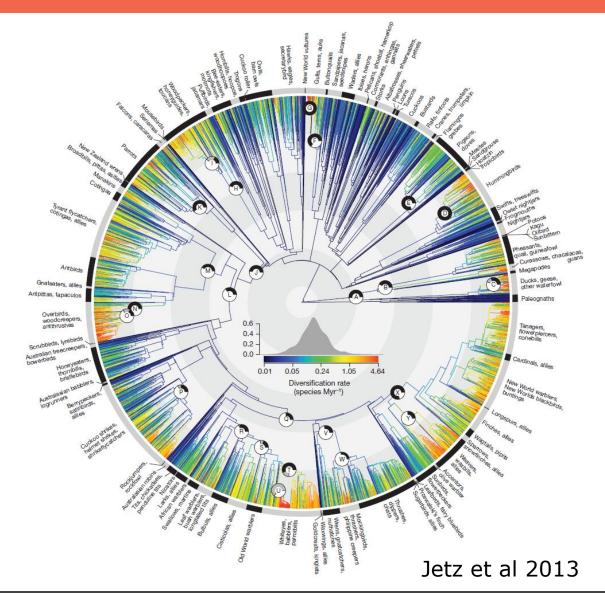


Gardner et al 2010

Phylogenies



- many depictions
- many levels
- multiple phylogenies





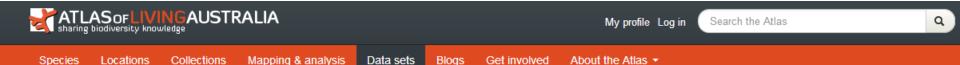
Relevance of a phylogenetic view

Evolutionary context can provide a deeper understanding of biodiversity

- Acquire insights into the evolution of diversity
- Make predictions about poorly studied species
- Expose data below species level
- Assist conservation decisions

phylojive.ala.org.au





Home → Phylojive

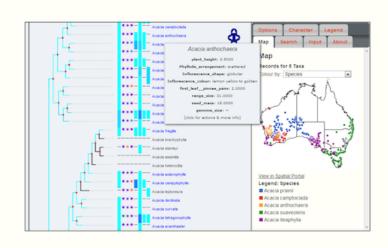
Phylojive

PhyloJive (<u>Phylogeny Javascript Information Visualiser and Explorer</u>) is a web based application that places biodiversity information aggregated from many sources onto compact phylogenetic trees.

The project is the brainchild of Garry Jolley-Rogers and Joe Miller and was developed by Temi Varghese and Garry Jolley-Rogers as part of the Taxonomy Research & Information Network (TRIN) – see the original project page, original code repository and ALA code repository. The ALA has contributed to the PhyloJive codebase to integrate a number of web services: occurrence data, maps and character data from Identify Life. This work has been undertaken with help and advice from Joe Miller.

The getting started page outlines the steps for creating a new phylogenetic tree and contains demo data sets that can be used to get up and running.

Create a new tree



Trees with character data

- · quantitative characters
- · kimberley land snails3
- · Joe's acacia
- Damien

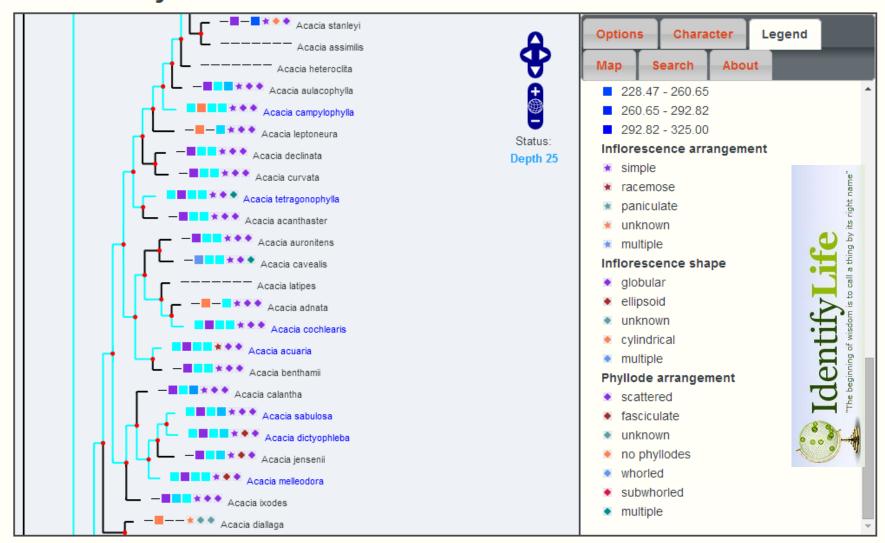
"Bare" Trees

- · Molluscsa-tree of life
- · amphibia frogs, salamanders and caecilians
- Damien
- · Bird super tree

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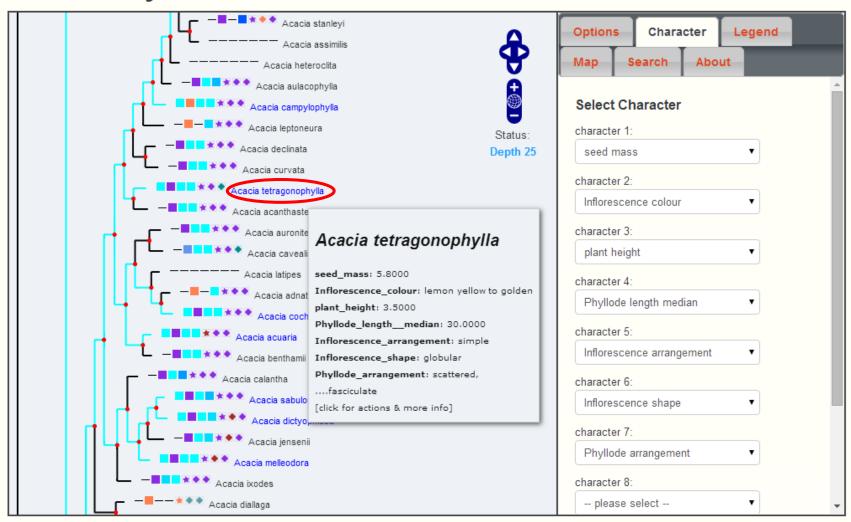






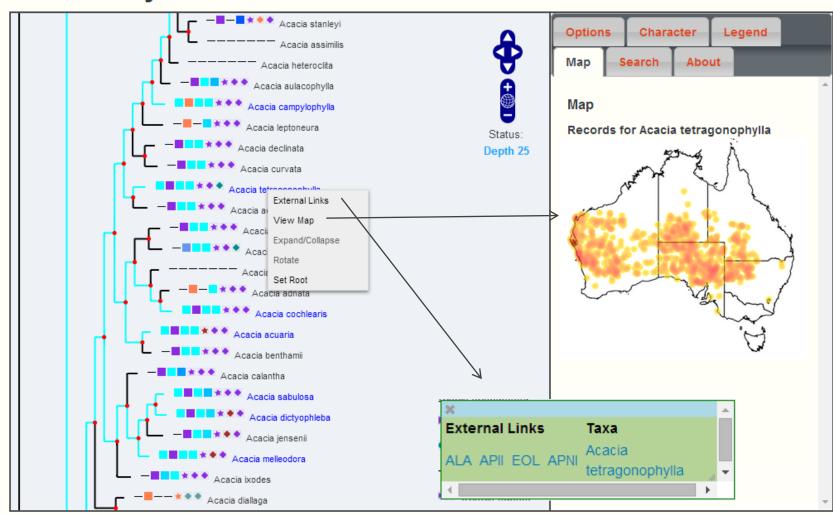






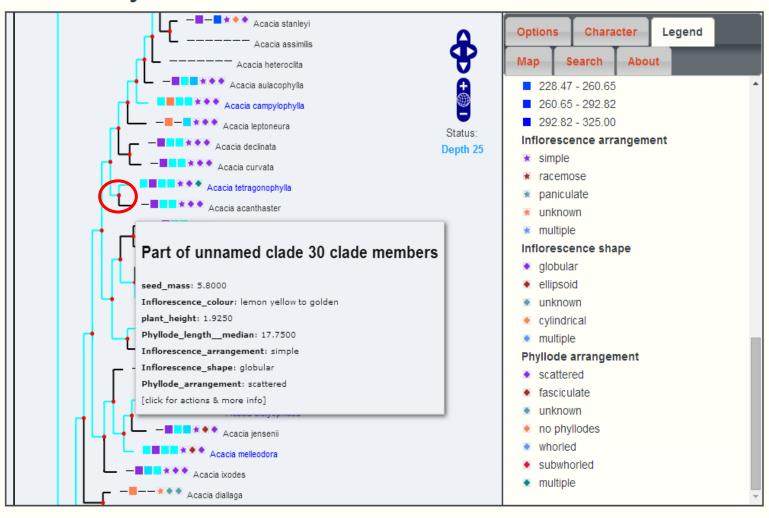


View maps and link externally



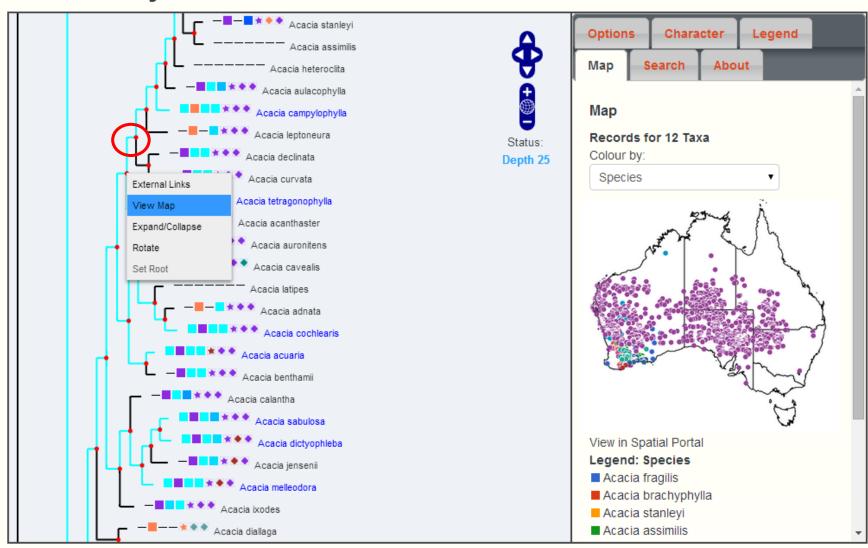


Reconstruct ancestral state



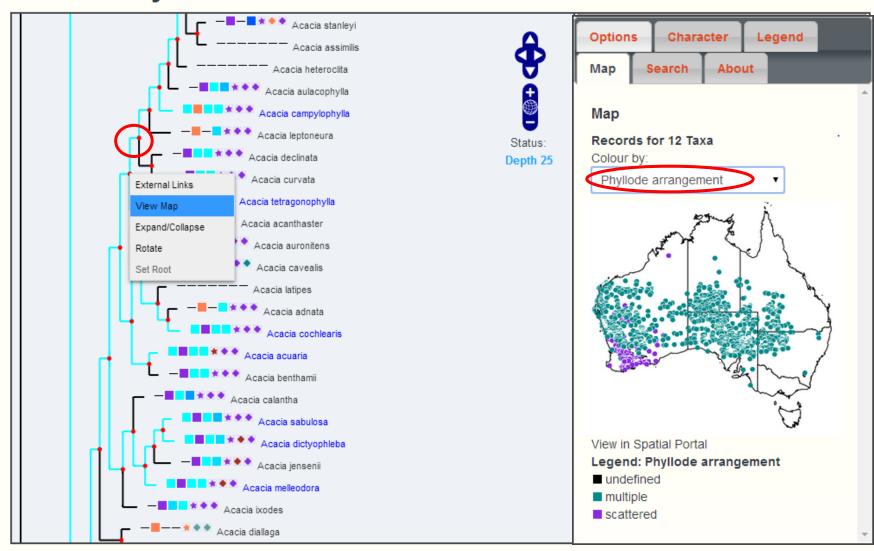


Map records – by taxon



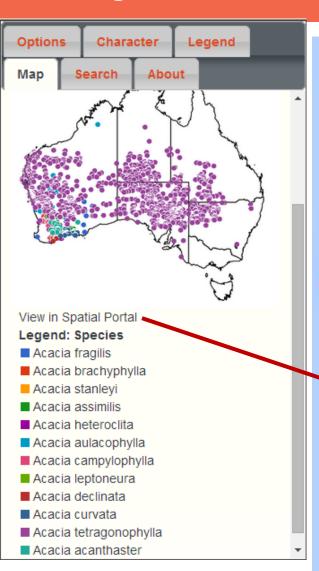


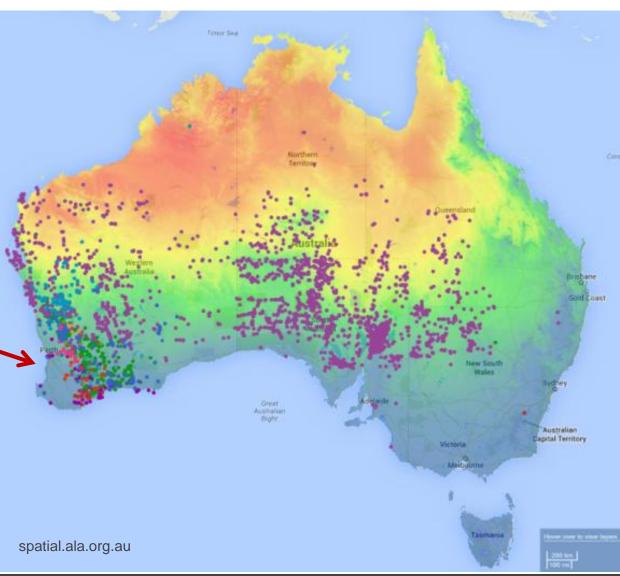
Map records – by character state





Integrate with ALA spatial portal







- sourcing trees
- organising and searching trees





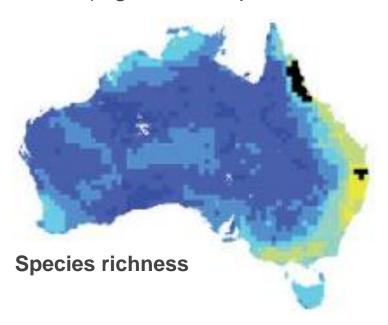
treebase.org

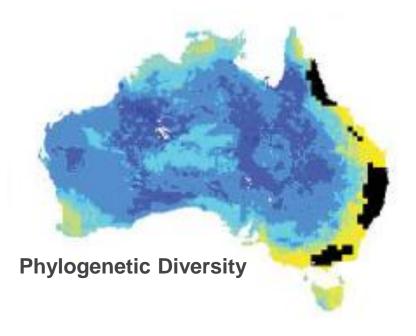
blog.opentreeoflife.org

navigating Atlas pages via phylogenies



- calculate phylogenetic measures e.g. phylogenetic diversity
 - compare to measures generated from non-phylogenetic approaches (e.g. PD and species richness)





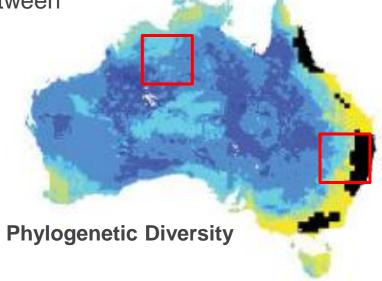
Marsupial diversity – black indicates hotspots

Amboni & Laffan 2010



- calculate phylogenetic measures e.g. phylogenetic diversity
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compare phylogenetic measures between user defined areas





- calculate phylogenetic measures e.g. phylogenetic diversity
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 - compare phylogenetic measures between user defined areas

 generate environmental distributions for clades using ALA occurrence records and environmental layers



Stimulating other assessments...

Other analyses using phylogenetic views of aggregated biodiversity data:

- risk analyses to understand the impact of species loss on biodiversity
- anticipating the effects of climate change





































National Collaborative Research Infrastructure Strategy



Australian Government

Department of Agriculture, Fisheries and Forestry









