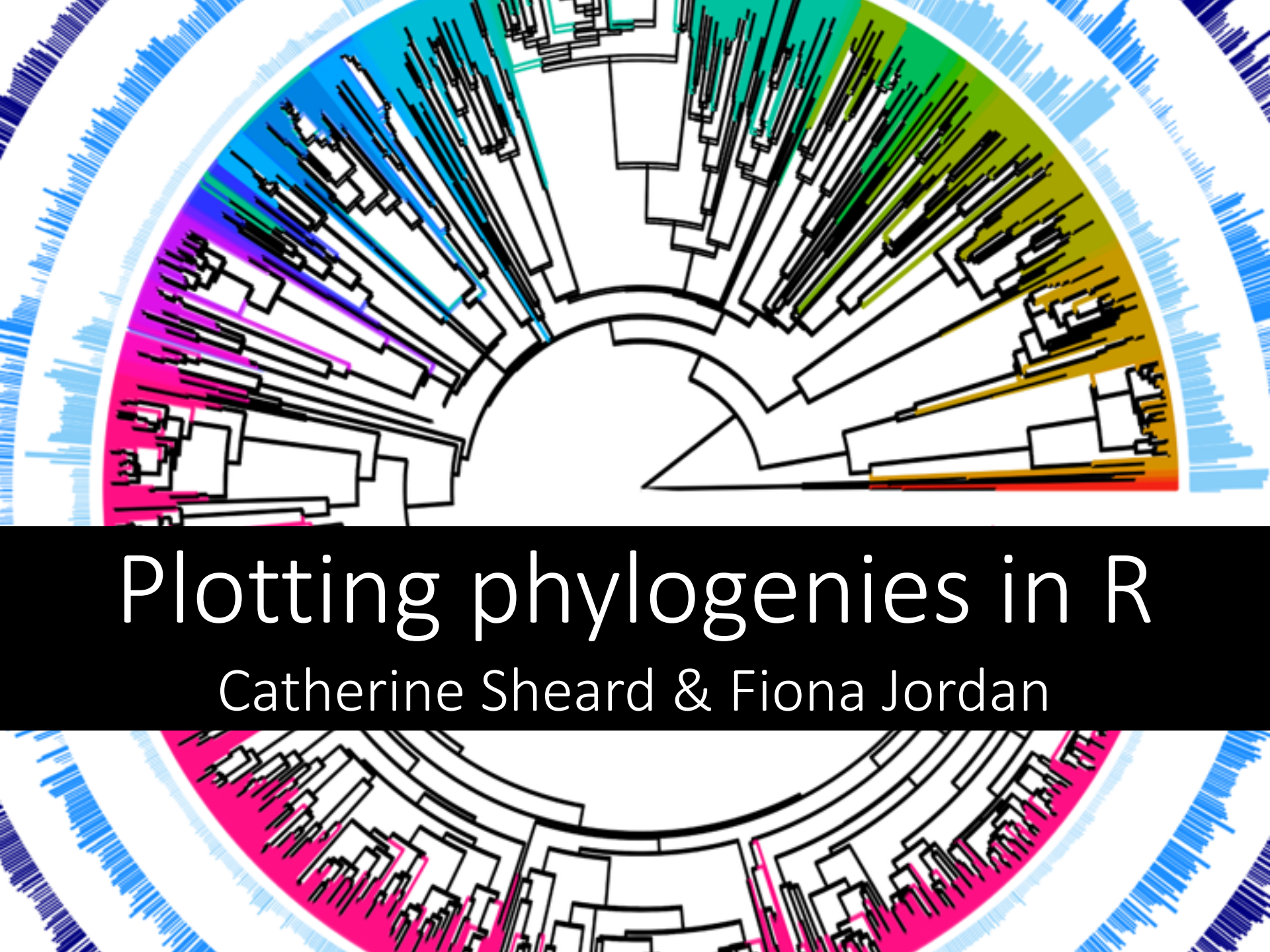
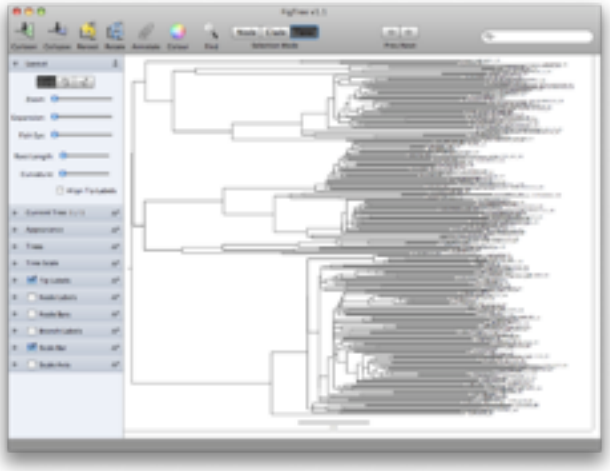


Plotting phylogenies in R

Catherine Sheard & Fiona Jordan

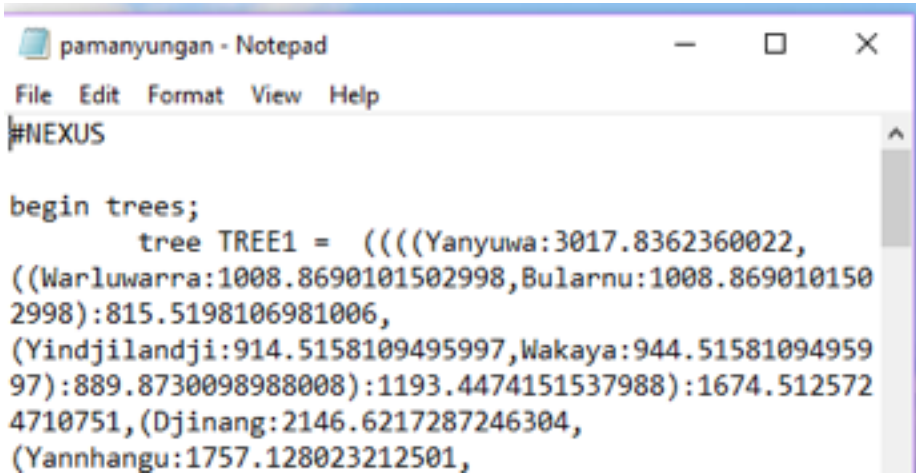
How do I plot a phylogeny?

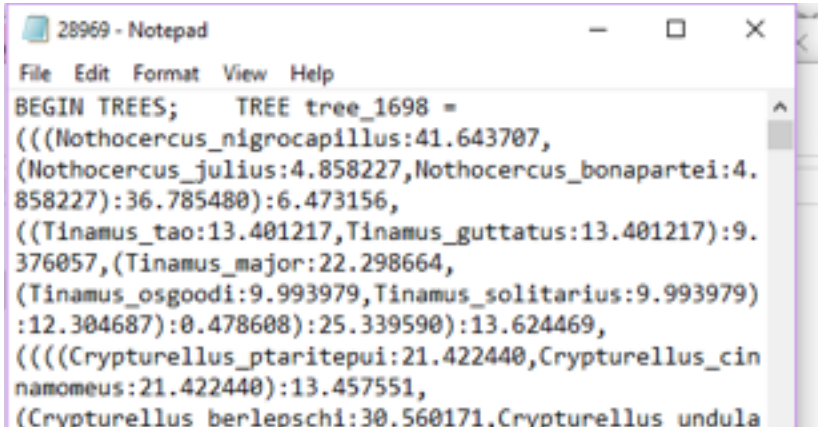
- Fig Tree:
  - Free.
  - Point-and-click (very easy to use!)
  - Not suitable for large phylogenies.
  - Not easily reproducible.
- Traditional R-based options:
  - *phytools* (Liam Revell)
  - *ape* (Emmanuel Paradis)
  - *geiger* (Luke Harmon)
  - Steep learning curve.
- New R-based option: ggtree.
- Many others!



What types of phylogenetic trees can R cope with?

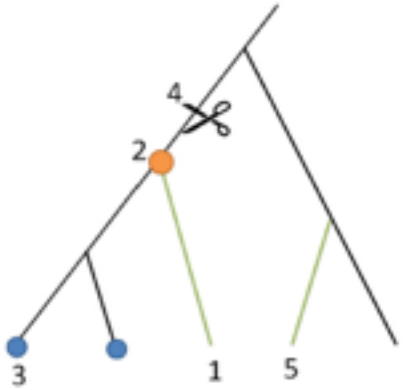
- NEXUS
  - read.nexus, write.nexus
  - From PAUP*, MrBayes, Mesquite, etc
- Newick
  - read.tree, write.tree
  - Named after Newick's restaurant in Dover, New Hampshire.
  - From PHYLIP, etc
- And others, probably.

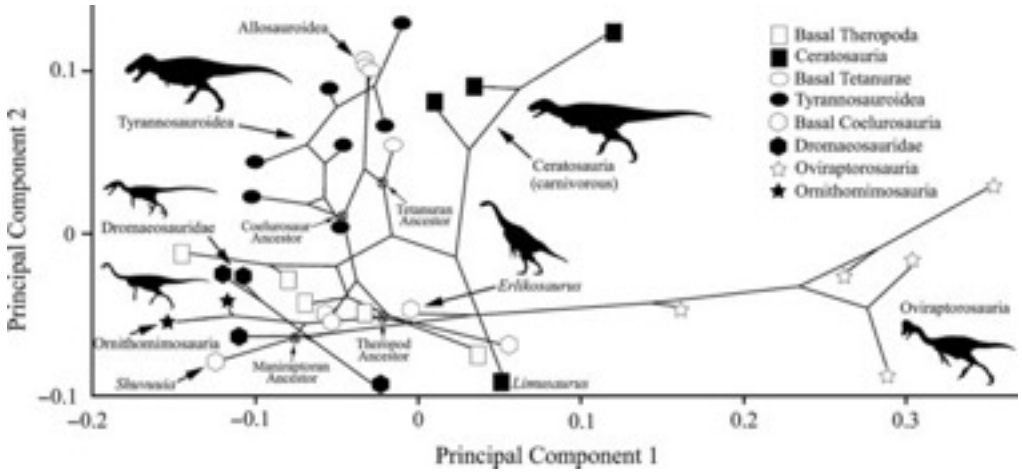


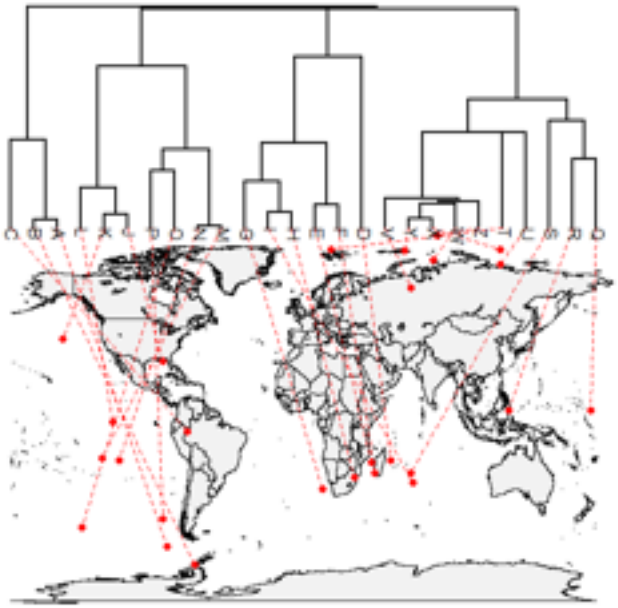


What sorts of things can I do in R?

- Manipulate trees
- Plot traits & ancestral states on trees
- Plot trees into morphospace
- Plot trees on maps





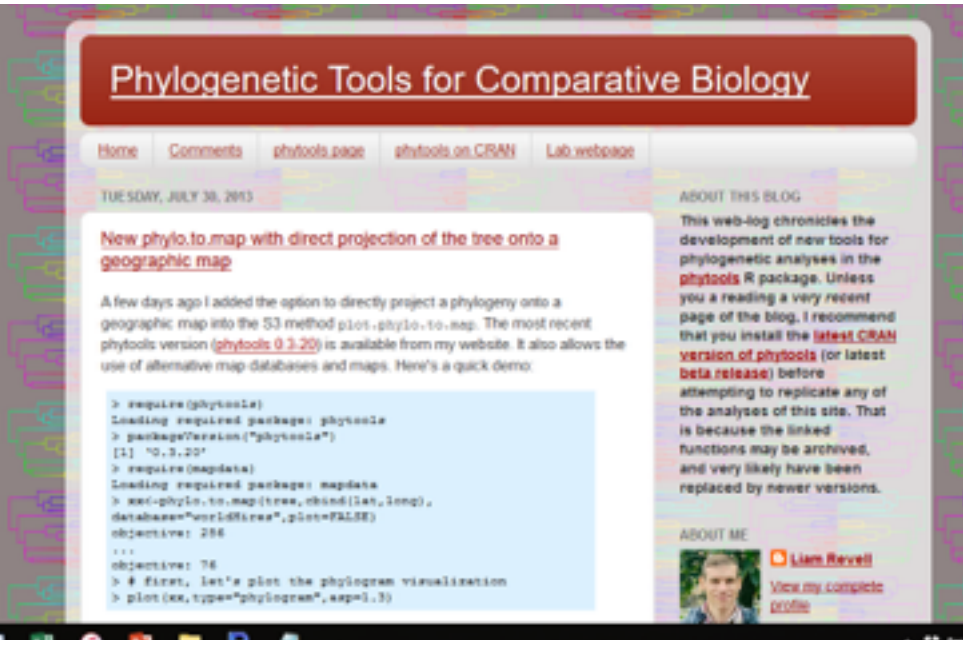


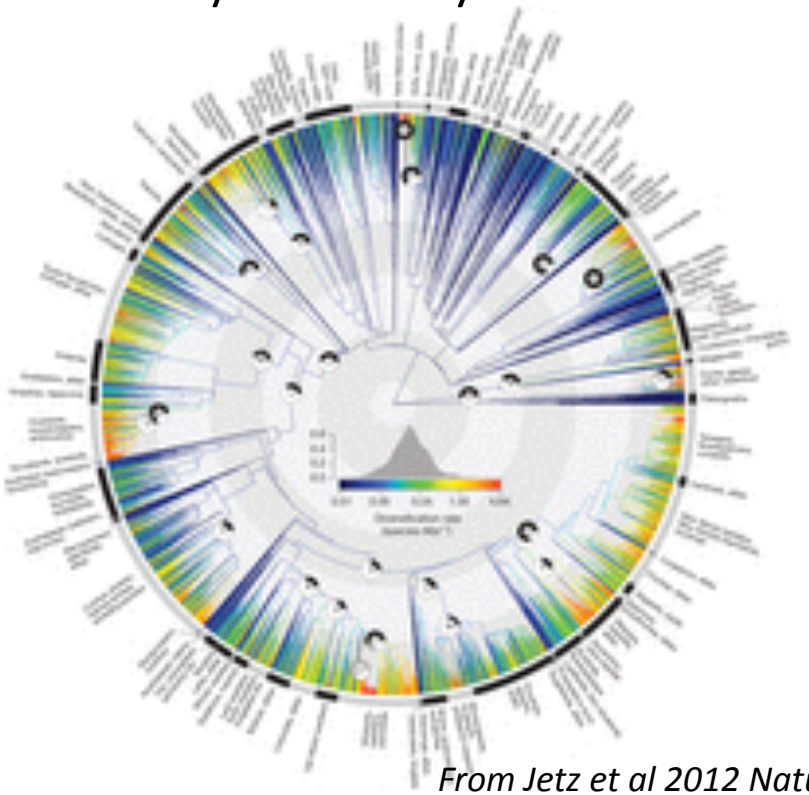
Brusatte et al 2011. The evolution of cranial form and function in theropod dinosaurs JEB

http://blog.phytools.org/2013/07/

Where do I go for help?

- The internet is amazing.
  - Liam Revell's blog (author of phytools) is particularly good.
- R-sig-phylo mailing list. We're really friendly!





From Jetz et al 2012 Nature

Tutorial: Pama-Nyungan phylogeny from Bowern and Atkinson 2012

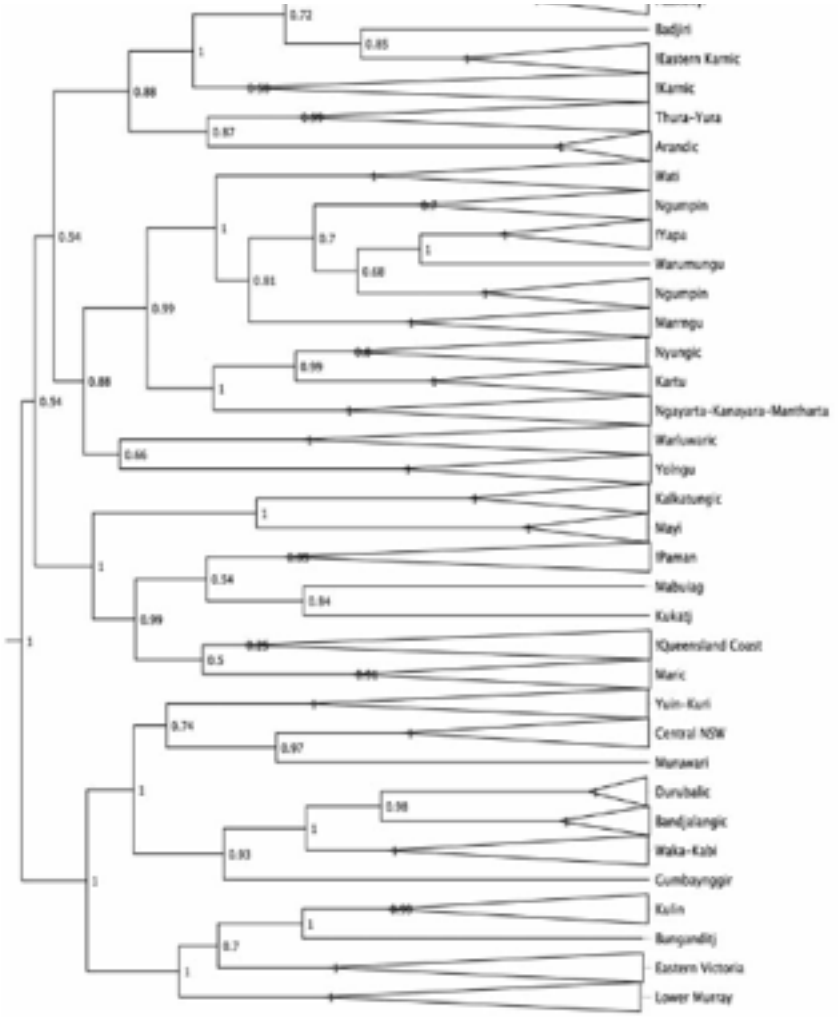


FIGURE 4. Languages included in the sample.

Bowern, C, and Atkinson, Q. (2012) Computational phylogenetics and the internal structure of Pama-Nyungan. Language 88, 817-845.