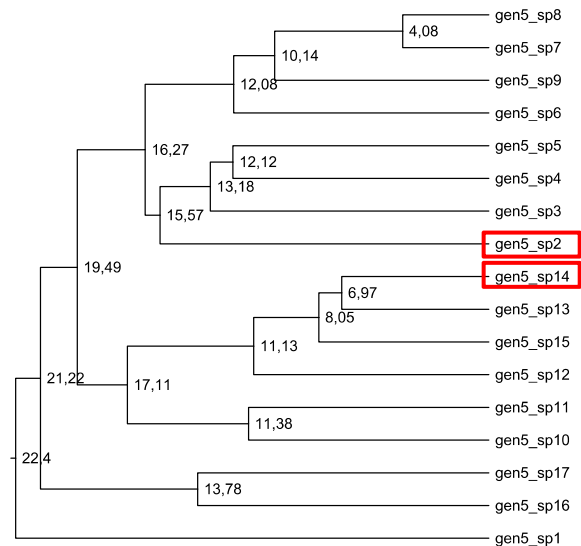


Tutorial

To study community assembly in your favourite group of organisms, you have sampled species presence/absence in 20 plots in each of 4 sites (`comm1.csv` ... `comm4.csv`). You want to conduct a simple analysis of phylogenetic community structure to obtain a hypothesis as to which mechanisms are responsible for local species co-occurrence in each site. Luckily, there is a dated phylogenetic tree covering most species in your community datasets (`phylo.tre`).

However, two species, `gen5_sp2` and `gen5_sp14`, are missing from your phylogenetic tree, but you can take the phylogenetic positions and divergence times of those species from another study of genus 5 (node labels are divergence times):

TASK 1: Add those two species to `phylo.tre`.



You have also measured the following data to improve your inference of assembly processes:

- One environmental variable for all the sites (`env.csv`). Columns 1-4 correspond to sites 1-4.
- A number of traits for all the species (`traits.csv`). You know a priori that characters C1 and C2 have something to do with your organisms' tolerance to the environmental factor measured in `env.csv`, while C3 and C4 have something to do with resource use.

Load the whole dataset into R.

TASK 2: Conduct a simple analysis of phylogenetic assemblage structure to infer in which of the sites local coexistence depends on environmental filtering or competition*. Use the traits and environmental variables to substantiate your inference.

Hint: Use the functions `ses.mpd`, `comdist`, and `multiPhylosignal` from the Picante package. See the Picante vignette (<http://cran.r-project.org/web/packages/picante/vignettes/picante-intro.pdf>) for additional examples.

* The communities have been simulated using those two assembly mechanisms. For real data, additional mechanisms have to be considered. See Cavender-Bares et al. 2009 *Ecol. Lett.* 12: 693–715