

### Exercises, part 2:

1. Read in the data `phelsuma.csv`. Describe the data set. How many species are included? How many variables?
2. Read in the tree `phelsuma.phy`. Plot the tree. Is it ultrametric?
3. Do the names match in the two data sets? If not, make a tree and data set that do match using `treedata()`.
4. Reroot the tree using the species “ornata” as an outgroup.

### Exercises, part 3:

5. Carry out a test for phylogenetic signal in  $\ln(\text{svl})$  for the gecko species.
6. Is there a correlation between  $\ln(\text{SVL})$  and  $\ln(\text{jaw})$  across these species?