

Reuse

Open science

- **Document analysis code**
- Comments
- Consistent style
- ‘Drop-in’ data replacement
- Modular functions

```
26 registerDoParallel(clus)
25
24
23 # 2.1. Gather data #
22 # ----- #
21
20 # load tree, age, and cladistic data
19 # Hedman method does not always complete successfully so to get >100 trees we
18 # start by scaling 120
17 # NB the file `sample_trees.tre` contains 1000 trees from the posterior
16 # distribution of Moon (2018, J Syst Palaeontol)
15 trees <- ape::read.tree("data/sample_trees.tre")[1:120]
14 nexus_data <- ReadMorphNexus("data/matrix.nex")
13 full_ages <- read.table("data/ichthyosaur_occurrences.tsv",
12                       sep      = "\t",
11                       header    = TRUE,
10                       row.names = 1)
9 ages <- full_ages[match(trees[[1]]$tip.label, rownames(full_ages)), ]
8
7 # root, resolve, and ladderize trees
6 root_trees <- lapply(trees, function(x) {
5     ape::root(x,
4         outgroup = "Hupehsuchus_nanchangensis",
3         resolve.root = TRUE) %>%
2         ladderize
1     })
51 class(root_trees) <- "multiPhylo"
1
2 # write `root_trees` to Newick file and re-read:
3 # the Hedman method sometimes produces negative-length branches, but this
4 # seems
5 # to resolve that
```

NORMAL master 2-time_scaling.R utf-8 18% 51:1

20 >

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```

4 registerDoParallel(clus)
3
2
1 # 1.1. Gather data #
31 # ----- #
1
2 # get data
3 dist_data <- Claddis::ReadMorphNexus("data/matrix.nex") %>%
4   Claddis::MorphDistMatrixFast()
5
6 # get taxon ages
7 taxon_ages <- read.table("./data/ichthyosaur_occurrences.tsv",
8   header = TRUE,
9   row.names = 1,
10  sep = "\t")
11
12 # get bins
13 bins <- list(# bins corresponding to epochs
14   epochs = read.table("./data/epoch_bins.tsv",
15     header = TRUE,
16     row.names = 1,
17     sep = "\t"),
18   # 10 Ma bins aligned to the base of the Jurassic (201.3 Ma)
19   tenMa_bJ = data.frame(max_age = seq(251.3, 100, -10),
20     min_age = seq(241.3, 90, -10),
21     row.names = paste0("bin", seq(1, 16)))
22 )
23 # bin taxa and remove outgroup taxon Hupehsuchus_nanchangensis
24 outgroup <- "Hupehsuchus_nanchangensis"
25 bin_data <- lapply(bins, function(scheme) {
26   data <- list()
27   for (bin in seq_along(rownames(scheme))) {

```