

Open science

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

```

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))) {

```

Reach

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- **Open Access publication**
 - *Communications Biology*
 - DOI: [10.1038/s42003-020-0779-6](https://doi.org/10.1038/s42003-020-0779-6)
- **Open review**
- Press release
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 - Popular in Japan

