

# 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
  - Twitter
  - Popular in Japan

