Reuse

Open science

- Document analysis code
 - Comments
 - Consistent style
- 'Drop-in' data replacement
 - Modular functions

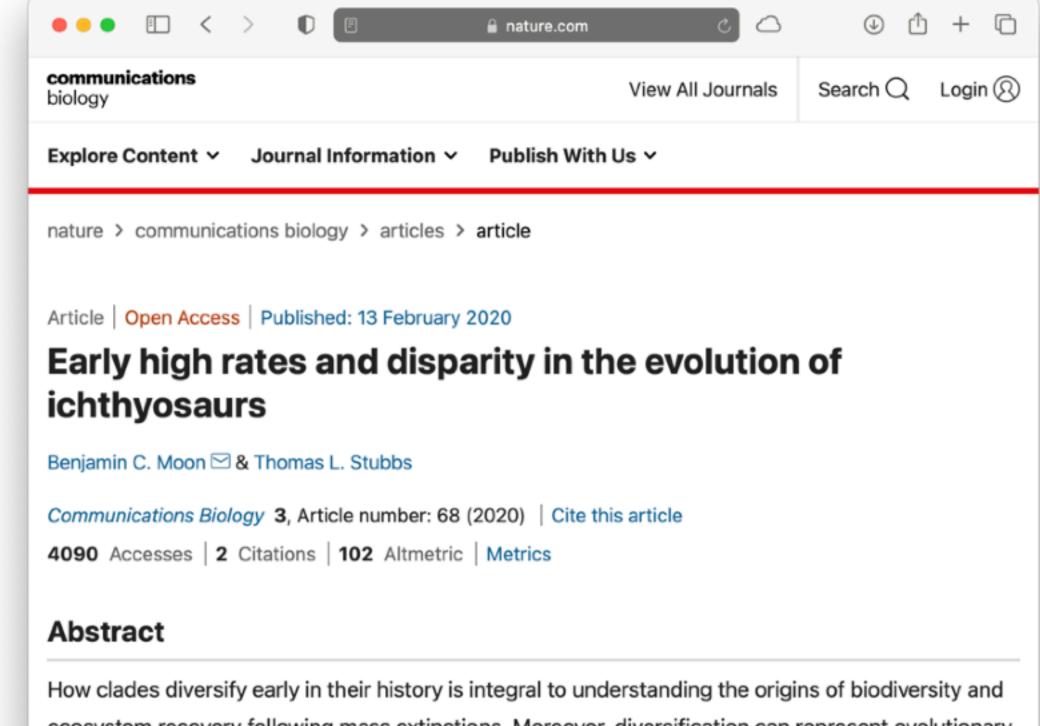
```
4 registerDoParallel(clus)
    1 # 1.1. Gather data #
    2 # get data
    3 dist_data <- Claddis::ReadMorphNexus("data/matrix.nex") %>%
                  Claddis::MorphDistMatrixFast()
   6 # get taxon ages
    7 taxon_ages <- read.table("./data/ichthyosaur_occurrences.tsv",</pre>
                               header
                                       = TRUE,
                               row.names = 1,
                                         = "\t")
  11
  12 # get bins
  ▶13 bins <- list(# bins corresponding to epochs
                  epochs = read.table("./data/epoch_bins.tsv",
  15
                                       header = TRUE,
  16
                                                 = "\t"),
  17
                  # 10 Ma bins aligned to the base of the Jurassic (201.3 Ma)
  18
                  tenMa_bJ = data.frame(max_age = seq(251.3, 100, -10),
  19
  20
                                         min_age = seq(241.3, 90, -10),
                                         row.names = paste0("bin", seq(1, 16)))
  21
  22
  23 # bin taxa and remove outgroup taxon _Hupehsuchus_nanchangensis_
  24 outgroup <- "Hupehsuchus_nanchangensis"
  25 bin_data <- lapply(bins, function(scheme) {</pre>
  26 data <- list()
      for (bin in seq_along(rownames(scheme))) {
NORMAL '> master 1A-disparity_analyses.R
                                                    utf-8 A @r 5% 31:1
20 >
76083:R [-]
                                                                         20:1
                                   .89 4.96 ?
                                                    2021-03-24 Wed 16:27:37
open-sci-5 ~/G/i/supp_code nvim
                    □ ~/O/C/t/revision
© 24/03, 4:27 pm
```

Reach

Open science

- Open Access publication
 - Communications Biology
 - DOI: 10.1038/s42003-020-0779-6
- Open review
- Press release
 - Twitter
 - Popular in Japan





How clades diversify early in their history is integral to understanding the origins of biodiversity and ecosystem recovery following mass extinctions. Moreover, diversification can represent evolutionary opportunities and pressures following ecosystem changes. Ichthyosaurs, Mesozoic marine reptiles, appeared after the end-Permian mass extinction and provide opportunities to assess clade diversification in a changed world. Using recent cladistic data, skull length data, and the most complete phylogenetic trees to date for the group, we present a combined disparity, morphospace, and evolutionary rates analysis that reveals the tempo and mode of ichthyosaur morphological evolution through 160 million years. Ichthyosaur evolution shows an archetypal early burst trend, driven by ecological opportunity in Triassic seas, and an evolutionary bottleneck leading to a long-term reduction in evolutionary rates and disparity. This is represented consistently across all analytical methods by a Triassic peak in ichthyosaur disparity and evolutionary rates, and