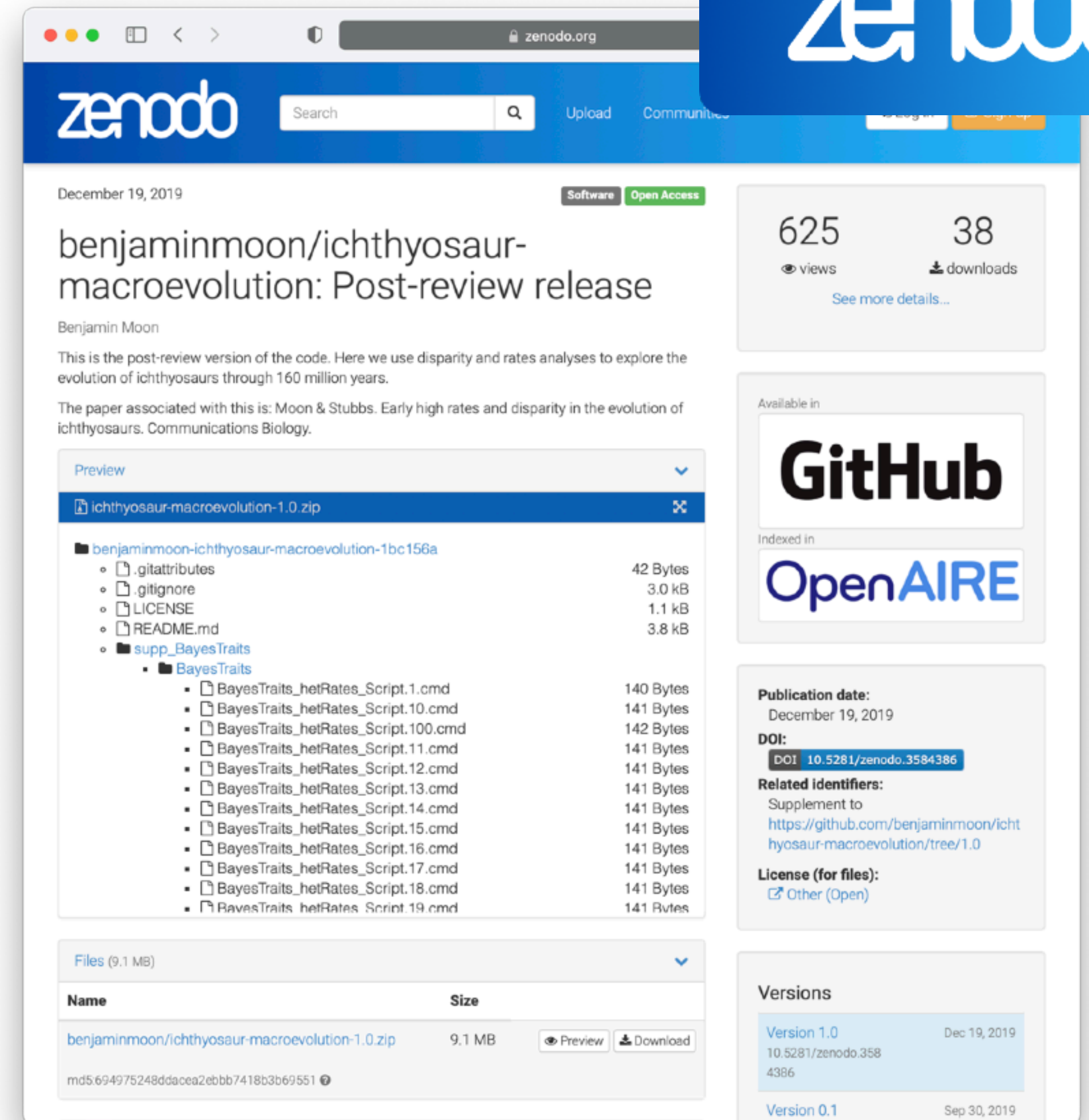


Replication

Open science

- Git and GitHub for development
 - shortcut: bcmoon.uk/agj6fg8h
- **Zenodo for release archiving**
 - DOI: [10.5281/zenodo.3584386](https://doi.org/10.5281/zenodo.3584386)
- Available for and used by reviewers



The screenshot shows the Zenodo website interface for a repository. At the top right, there is a blue Zenodo logo. The main header includes the Zenodo logo, a search bar, and links for 'Upload' and 'Communities'. The repository page is for 'benjaminmoon/ichthyosaur-macroevo: Post-review release', dated December 19, 2019, and marked as 'Software' and 'Open Access'. It shows 625 views and 38 downloads. The description states it is the post-review version of the code for exploring ichthyosaur evolution. The 'Preview' section shows a file tree for 'benjaminmoon-ichthyosaur-macroevo-1bc156a', including .gitattributes, .gitignore, LICENSE, README.md, and a subdirectory 'supp_BayesTraits' containing 19 .cmd files. The 'Files' section at the bottom shows a single file 'benjaminmoon/ichthyosaur-macroevo-1.0.zip' (9.1 MB) with preview and download buttons. On the right sidebar, it indicates the repository is available in GitHub and indexed in OpenAIRE. It also lists the publication date, DOI (10.5281/zenodo.3584386), related identifiers, and license information.

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 >
45102:R [-] 20:1
open-sci-5 ~/G/i/supp_code nvim .39 5.15 ? 2021-03-24 Wed 16:24:54
24/03, 4:24 pm ~/O/C/t/revision
```