

This document details all of the material provided as part of this Dryad repository and how the data are organized. Major bullet points correspond to folders within the directory, with individual files and sub-directories listed also. The R markdown file used to generate these documents is provided in the supplement to the main manuscript.

➤ Scripts

Three R scripts used to generate the principal results of the paper

- *geo.div.rates.R* – Paint geographic states to nodes and branches (Figure 2A)
- *overlap.any.range.R* – Record whether a species is allopatric given the ranges of its family members (Figure 2B)
- *pigot.div.comparison.R* – Compare the diversification histories between the first and second half of a phylogeny (following Pigot et al., 2010).
- *phylo.sister.ages.R* – Calculate ages of nodes that subtend two extant species

➤ Method 1 results – Paint geography states (Figure 2A)

The files for each clade are lists where each element is a family-specific result. Each family-specific result is, itself, a list with three entries: node states, branch states, and phylogeny.

For each clade there are four files: the main results, the results when a threshold value was used when defining allopatry, and the corresponding STRAPP results.

- *geo.results.bird.RDS*
- *geo.results.bird.threshold.RSD*
- *birdSTRAPP2a.RDS*
- *birdSTRAPP2a_threshold.RDS*
- *geo.results.mammal.RDS*
- *geo.results.mammal.threshold.RDS*
- *mammalSTRAPP2a.RDS*
- *mammalSTRAPP2a_threshold.RDS*
- *geo.results.amphibian.RDS*
- *geo.results.amphibian.threshold.RDS*
- *amphibianSTRAPP2a.RDS*
- *amphibianSTRAPP2a_threshold.RDS*

➤ Method 2 results – Mapping geographic states of terminal taxa (Figure 2B)

The terminal branch states using the second approach from the paper are provided as a list with an entry for each family. 0 corresponds to sympatry, 1 to allopatry.

For each clade there are three files: the main results, the results when a threshold value was used when defining allopatry, and the STRAPP results.

- *bird_terminal_branch_states_2b.RDS*
- *bird_terminal_branch_states_2b_threshold.RDS*
- *birdSTRAPP2b.RDS*
- *birdSTRAPP2b_threshold.RDS*
- *mammal_terminal_branch_states_2b.RDS*
- *mammal_terminal_branch_states_2b_threshold.RDS*
- *mammalSTRAPP2b.RDS*
- *mammalSTRAPP2b_threshold.RDS*
- *amphibian_terminal_branch_states_2b.RDS*
- *amphibian_terminal_branch_states_2b_threshold.RDS*
- *amphibianSTRAPP2b.RDS*
- *amphibianSTRAPP2b_threshold.RDS*

➤ Method 3 results – Max overlap (Figure 2C)

The three .csv files correspond to the maximum and mean number of overlapping ranges for each family within the three major clades.

- *bird.overlaps.csv*
- *mammal.overlaps.csv*
- *amphib.overlaps.csv*

➤ BAMM rate phylogenies

These data are provided as a single tree file for birds, and as .RDS objects for mammals and amphibians where the BAMM data were individually subset to the taxonomic coverage of the families within those clades

- *bird_speciation_rate_phy.tre*
- *mammal.family.rate.phy.RDS*
- *amphibian.family.rate.phy.RDS*

➤ Synonymy

The synonymy data used for the analysis of birds.

➤ Phylogenetic data

The phylogenetic hypotheses used as part of this work

- *AmphibianTreeFinal*: The amphibian data after re-running TACT
- *Jetz.TACT.MCC.newick*: The bird data after re-running TACT
- *UphamMCC*: A maximum clade credibility tree from the posterior of Upham et al.