

There are 4 files contained within this supplement.

1) Family morphology analysis

There are two files within this directory containing the family-specific summaries required for visualizing the difference between the morphological metric (NND scores and hull size) for the empirical and random distributions, as well as perform the path analyses.

- a. hull.res.full.csv
- b. nnd.res.full.csv

2) Genetic analyses

There are six files in this directory containing all the species-specific information on sequence diversity (π) with corresponding information on allopatry states, mass (g), and range size (polygon size).

- a. Co1.taxonomy.csv
- b. Cytb.taxonomy.csv
- c. Mc1r.taxonomy.csv
- d. mt.taxonomy.csv
- e. nd2.taxonomy.csv
- f. rag1.taxonomy.csv

3) Global maps

There are nine files in this directory containing the mean scores for the corresponding genetic and morphological variables across the 61,483 sampling locations. To plot the scores the individual variables should be combined with the coords.RDS object which contains the coordinates of the sampling locations.

- a. coords.RDS
- b. global.co1.scores.RDS
- c. global.cytb.scores.RDS
- d. global.mc1r.scores.RDS
- e. global.mt.scores.RDS
- f. global.rag1.scores.RDS
- g. global.nd2.scores.RDS
- h. global.hull.size.RDS
- i. global.nnd.scores.RDS

4) GeneticCoverageSummary.xls

This Excel file has two sheets:

- 1) **NumberSequencesPerSpecies:** This sheet has species (rows) and genes (columns) with the number of sequences used to calculate π in each case using the raw data downloaded from GenBank (the averages of the columns of this sheet correspond to the mean sequences per species reported in Table 1).
- 2) **NumberBPperSpecies:** This sheet has species (rows) and genes (columns) with the number of base pairs available for each species to calculate π in each case. These values are taken from the family-specific alignments for each gene. There are fewer species in this alignment than the previous sheet as this calculation is performed after vetting of taxonomy and removal of extinct species, such as the Hawai'i 'ō'ō (*Moho nobilis*, an extinct member of the order Passeriformes) as these taxa no longer have spatial data. A species will automatically be 0 when represented by a single sequence.

