**Data: Morphological adaptations linked to flight efficiency and aerial lifestyle determine natal dispersal distance in birds**

**Overview**

These data and code replicate the analyses presented in Weeks *et al.* (2022). Morphological adaptations linked to flight efficiency and aerial lifestyle determine natal dispersal distance in birds. *Functional Ecology*.

**Data**

*Data File 1: Hackett\_Full\_MRC\_tree*

This file contains a 50% maximum rule consensus phylogeny for all birds in the Newick format. It is a consensus of 1,000 phylogenies from a posterior distribution of a global phylogeny of the birds of the world (Jetz *et al.* 2021), and was generated following the methods of Rubollini *et al.* (2015).

*Data File 2: Weeks\_etal\_2022\_data.csv*

This file contains 9 columns of data (listed below, followed by a description of the data in each column). Each row contains a single independent estimate of natal dispersal distance for a species (i.e. if multiple studies estimated dispersal distance for a single species, that species appears in multiple rows).

Species = the names of the species each row of data are associated with

coll\_meth = whether the natal dispersal distance data were collected using banding data or

radiotag data

Aerial.lifestyle = the score for the species on the Aerial Lifestyle Index presented in Weeks *et al.*

(2022)

dir\_est\_mean\_F = the mean estimate of natal dispersal distance for females\*

dir\_est\_mean\_M = the mean estimate of natal dispersal distance for males\*

diet\_1 = each species was assigned to one of three dietary categories based on their trophic niche

(C = carnivore, H = herbivore, and O = omnivore)

migrant = each species was classified as “migratory” or “non-migratory”, following Sheard *et al.*

(2020)

Hab\_1 = the primary habitat type of each species (O = open, low density vegetation habitat, S = semi-open, mid-density vegetation habitat, and C = closed, high density vegetation habitat), following Pigot & Tobias (2015)

HWI = mean hand-wing index for each species, from Sheard *et al.* (2020)

\*When the values for female and male distances are identical, different estimates based on sex were not available in the original data source

**Running the Analyses**

In order to re-create the analyses presented in Weeks et al. (2022), open the R script, “Data\_Analyses\_3-26-22.R” in R Open Software. This script requires the R packages: ape v5.0, geiger 2.0.7, and nlme 3.1-140, available from CRAN (<https://cran.r-project.org/>) and a version of R that supports these packages (e.g., R v3.6 – 4.2.0). The data files should be placed in a local directory, and this directory should be set as the working directory for the R session. After this, the script can be run without any modification to replicate all data preparation and modeling from the Weeks et al. (2022) paper. Information on the purpose of each segment of code is provided within the .R file itself.

**Contact**

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**References**

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