**Description of files two datasets used in Mellor et al.**

**Files**

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| --- | --- |
| **File name** | **Description** |
| *consensus\_parrot\_tree* | Consensus parrot phylogenetic tree used for between wild biology predictor checks, and those between predictors and the 10 pet parrot population characteristics |
| *Figure 2 - FDB v food handling graph - Mellor et al* | R script for making Figure 2 in Mellor et al. (feather damaging behaviour v food handling) |
| *Figure 3 - body SB v brain volume graph - Mellor et al* | R script for making Figure 3 in Mellor et al. (whole body stereotypic behaviour v brain volume) |
| *Fig 4 - oral SB v brain volume - Mellor et al* | R script for making Figure 4 in Mellor et al. (oral stereotypic behaviour v brain volume) |
| *Figure S1 - parrot phylogenetic tree used for analyses - Mellor et al* | R script for making Figure S1 in Mellor et al. (phylogenetic tree used in analyses, terminal branches coloured according to availability of outcome data for a given species) |
| *influ\_phylm2\_Paterno\_et\_al* | Custom written function for detecting influential species (from Gustavo Paterno). Please cite him accordingly – see file for details |
| *parrot\_comp\_data* | Comparative dataset |
| *parrot\_comp\_data\_tree* | Dataset used to make Figure S1 (phylogenetic tree) |
| *parrot\_trees* | 1,000 parrot phylogenetic trees used as a tree block for the final hypothesis-testing models (and used to build the consensus tree) |
| *plot\_influ\_phylm2\_Paterno\_et\_al* | Custom written function for plotting parameters generated from influ\_phylm2 (from Gustavo Paterno). Please cite him accordingly – see file for details |
| *script for between-predictor checks - Mellor et al* | R script for analyses making between wild biology predictor checks |
| *script for building a consensus parrot tree - Mellor et al* | R script for making the parrot consensus tree (based on Liam Revell’s phytools blog; see here: <http://blog.phytools.org/2016/03/method-to-compute-consensus-edge.html>) |
| *script for captive pop characteristics-predictor checks - Mellor et al* | R script for analyses making wild biology predictor-pet parrot population characteristic checks |
| *script for final hypothesis-testing models over a tree block - Mellor et al* | R script for final hypothesis-testing models over a tree block (loop based on example code from Miquel Vall-Llosera) |
| *script to detect influential species - Table S7 - Mellor et al* | R script for detecting influential species in significant/trend final hypothesis-testing models |
| *summary\_influ\_phylm2\_Paterno\_et\_al* | Custom written function for summarising parameters generated from influ\_phylm2 (from Gustavo Paterno). Please cite him accordingly – see file for details |
| *usage\_influ\_phylm2\_Paterno\_et\_al* | Example from Gustavo Paterno on how to use the customised functions mentioned above. Please cite him accordingly – see file for details |

**Variables in main comparative dataset (parrot\_comp\_data.csv)**

|  |  |
| --- | --- |
| **Variable name** | **Details** |
| **Species\_name** | Species scientific name |
| **English** | Species common name |
| *Outcome variables* |  |
| **FDB** | Prevalence of feather-damaging behaviour |
| **OSB** | Prevalence of oral stereotypic behaviour |
| **BSB** | Prevalence of whole body stereotypic behaviour |
| **Hatch\_rate** | Captive hatch rates (chicks hatched/breeding pair/year) |
| *Wild biology predictor variables* |  |
| **Max\_feed\_size** | Maximum feeding group size |
| **Communal\_roost** | Presence/absence of communal roosting when sleeping (yes v no) |
| **Communal\_roost\_code** | As above, but coded 1 = yes, 0 = no |
| **Food\_search** | Percentage diet requiring extensive food search |
|  |  |
| **Food\_handling** | Percentage diet requiring extensive food handling |
| **Habitat\_breadth** | Count of main habitat types in the native range |
|  |  |
| **Diet\_breadth** | Count of main food types in the native range |
| **Innovation** | Total number of feeding innovations reported in the literature (relating to specific geographic regions) |
| **Inn\_region** | Whether/not a species’ native range includes one of the geographic regions mentioned above (1 = yes, 0 = no) |
| **Brain\_vol** | Species’ average endocranial volume (ml) |
| **IUCN\_code** | Status in the International Union for Conservation of Nature Red List of Threatened Species (ranked 1-5): Least Concern, Near Threatened, Vulnerable, Endangered, Critically Endangered |
| **Hatch\_n\_breed\_pairs** | Number of breeding pairs contributing to calculation of captive hatch rates |
| **Nat\_fecund** | Natural fecundity (product of the median eggs/clutch and clutches/year) |
| **Body\_mass** | Species’ average body mass (g) |
| **Research\_effort** | Research effort (number of published papers) |
| *Pet parrot population characteristics* |  |
| **Prop\_adult** | Proportion of a species’ population which is adult (v pubescent) |
| **Prop\_known** | Proportion of a species’ population which is of known sex (v unknown) |
| **Prop\_female** | Proportion of a species’ population which is female (v male) |
| **Human\_reared** | Proportion of a species’ population which has been entirely human-reared (v some parental rearing) |
| **Stand\_cage** | Proportion of a species’ population housed in a standard-sized cage (v larger) |
| **Prop\_isolated** | Proportion of a species’ population housed in conspecific social isolation (v some social contact) |
| **Short\_feed** | Proportion of a species’ population with short captive feeding times (v long [>2hrs]) |
| **Cap\_diet\_div** | Count of main food types in diet |
| **Early\_EE** | Early (rearing) enrichment diversity |
| **Current\_EE** | Current enrichment diversity |
|  |  |

**Variables from dataset used to make Figure S1 (phylogenetic tree; parrot\_comp\_data\_tree.csv)**

|  |  |
| --- | --- |
| **Variable name** | **Details** |
| **Species\_name** | Species scientific name |
| **Species\_lab** | Tip label used on the tree (species name without the underscore) |
| **FDB** | Prevalence of feather-damaging behaviour |
| **OSB** | Prevalence of oral stereotypic behaviour |
| **BSB** | Prevalence of whole body stereotypic behaviour |
| **Hatch\_rate** | Captive hatch rates (chicks hatched/breeding pair/year) |
| **Outcome\_data** | Does the species have both types of outcome variable data (‘Both’; coloured orange on the tree), stereotypic behaviour data only (‘Behaviour’; green on the tree), or hatch rate data only (‘Reproduction’; blue on the tree) |