

Source code to replicate the analysis and figures presented in the article:

A synthesis of animal-mediated seed dispersal of palms reveals distinct biogeographic differences in species interactions *The Journal of Biogeography*. 2018.(in revision)

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1) Structure of this repository

```
/JBI_Palms_REPO
|-- /AppendixTables
|   |-- MetadataAppendix1.pdf
|   |-- MetadataAppendix2.pdf
|   |-- Appendix1-DataSources.xls # References to datasources for palm-frugivore interactions included
|   |-- Appendix2-IndividualPalmSC.xls # Table of Sampling completeness per palm species.
|-- /DATA
|   |-- PalmFrugDatasetOCT2018.csv # Palm-frugivore Interactions dataset
|   |-- datasetMetatada.pdf # Metadata of PalmFrugDatasetOCT2018.csv
|   |-- world.checklist.csv # Check list of palm occurrences by TDWG level 3 botanical countries
|   |-- BotanicalCountries # Shapefile of TDWG level 3 botanical countries
|       |-- TDWG_level3_Coordinates.dbf
|       |-- TDWG_level3_Coordinates.prj
|       |-- TDWG_level3_Coordinates.sbn
|       |-- TDWG_level3_Coordinates.sbx
|       |-- TDWG_level3_Coordinates.shp
|       |-- TDWG_level3_Coordinates.shp.xml
|       |-- TDWG_level3_Coordinates.shx
|-- /figs # Raw figures created from scripts
|   |-- ChordDiagramAfr.eps
|   |-- ChordDiagramNeo.eps
|   |-- InteractionsVsStudies.eps
|   |-- SamplingCompletenessA.eps
|   |-- SamplingCompletenessB.eps
|   |-- TraitMatching.eps
|-- /Scripts_R # Scripts to replicate the contents of the article
|   |-- Beckett2016LPA_wb_plus.R # Beckett's Modularity function
|   |-- CustomFunctions.R # Custom functions written for this article
|   |-- ReplicateAnalysis.R # Script to replicate analysis
|   |-- ReplicateFigures.R # Script to produce the figures in /figs
|   |-- shiny.R # Shiny app to dynamically visualize sampling accumulation curves per species
|-- JBI_Palms_REPO.Rproj # R container folder
|-- README.md
```

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|-- README.html  
|-- README.pdf
```

2) Instructions

- 1) Open the R container folder
- 2) Run ReplicateAnalysis.R and ReplicateFigures.R scripts (**other scripts are sourced within**)

NOTE: Modularity replicates are TIME CONSUMING, currently those are commented in ReplicateAnalysis.R
// If you want to re-run them and see the output uncomment those first.
