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*Goal*

Meta-analysis using long-term phenology data testing for global changes in species synchrony across functional groups.

*Contributors:*

Deirdre Loughnan

Lizzie Wolkovich

Heather Kharouba

Simon Joly

Geoffrey Legault

Micheal Betancourt

*General Files*

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| **Files** | **Where** | **What** |
| README.txt | [Github](https://github.com/DeirdreLoughnan/Synchrony) | Outline of repo and experimental aims |
| Synchrony\_hypotheses.tex | [Github](https://github.com/DeirdreLoughnan/Synchrony)/notes/ | Outline of hypotheses |
| Synchrony\_data/ | [Github](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data)/Input/ | Folder of individual synchrony data files that are sourced in the main model code |

*Data and Code*

**Github**

<https://github.com/DeirdreLoughnan/Synchrony>

<https://github.com/DeirdreLoughnan/Synchrony_data>

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| **Files** | **Where** | **What** |
| Rcode | [Github:](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | R code for running models and cleaning data |
| Input | [Github:](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input) | Data files called in running model |
| Cohen | [Github: Input/Cohen](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data/Cohen) | Datafile from Cohen et al. 2018 |
| Heather | [Github: Input/Heather](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data/Heather) | Datafile from Kharouba et al. 2018 |
| Newdata | [Github: Input/Newdata](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data/Newdata) | Datafiles for new scraped data/Dryad |
| RISData | [Github: Input/RISData](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data/RISData) | RIS moth and aphid data |
| Thackeray | [Github:Input/Thackeray](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data/Thackeray) | A subset of the data from Thackeray et al. 2016 |
| cleaningcode | [Github:Input/cleaningcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input/Synchrony_data/cleaningcode) | Code to clean newscraped/Dryad data |
| Stan | [Github: Stan](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Stan) | Stan code |
| notes | [Github: Synchrony](https://github.com/DeirdreLoughnan/Synchrony/tree/master/notes) | Thoughts and outlines |
| combiningallphenodata.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Merging all the phenology data from 3 meta-analyses and new studies |
| getting\_worldclim\_data.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code to get worldclim data |
| generate\_data\_whinge.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Generating test data with a hinge |
| generate\_data.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Generating test data |
| ggtree\_plotting.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code to make phylogeny fig |
| Latitudinal\_model.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/blob/master/Rcode) | Latitudinal analyses |
| manuscriptValues.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | File generating referenced values in manuscript |
| modeling\_plotting.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Plotting code for ms |
| null\_model\_plotting.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Null model code and plots |
| phylogeny\_final.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Main model code |
| phylogeny\_groups.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Main model for 4 common groups |
| poc\_genquanblock.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Testing whether different code for generated quantities blocks do differ |
| simdata\_twospint.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code for testing for trends in multi sp interactions |
| simdata\_twoSpint\_terraqu.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code for testing for trends in multi sp interactions grouped by terrestrial or aquatic species |
| singlesp\_analysis\_generatedata.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code for running stan model on generated data |
| singlesp\_analysis\_realdata.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code for running stan model on real data |
| table\_synch\_source.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Generating table of data sources for manuscript |
| singlesp\_analysis\_realdata\_covmat.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code for running stan model on real data and testing the covariance matrix |
| worldClimSlopesContinents.R | [Github: Synchrony/Rcode](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Rcode) | Code for running climate models for 12 and 3 month climate data for each continent |
| dat\_fin\_Dec2021\_w\_neg\_mod.csv | [Github: Synchrony/Input](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input) | A csv file of all the synchrony data to date merged together |
| synchronyTree.tre | [Github: Synchrony/Input](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input) | Phylogeny of all species |
| taxonlvl\_spname.csv | [Github: Synchrony/Input](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input) | Taxonomic information for each species |
| twelve\_month\_mean\_clim\_indivlatlong.csv | [Github: Synchrony/Input](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input) | Climate data for each site, 12 month mean values |
| same3\_month\_mean\_clim\_indivlatlong.csv | [Github: Synchrony/Input](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Input) | Climate data for each site, 3 month mean values |
| singlesp\_randslopes\_wcov.stan | [Github: Synchrony/Stan](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Stan) | Stan code with covariance matrix, random slopes, random intercepts |
| singlesp\_randslopes.stan | [Github: Synchrony/Stan](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Stan) | Stan code with random only |
| singlesp\_randslopesint.stan | [Github: Synchrony/Stan](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Stan) | Stan code with random slopes, random intercepts |
| slopeTempSimplest.stan | [Github: Synchrony/Stan](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Stan) | Stan code for estimating temperature slopes for 12 and 3 month climate means |
| phylogeny\_synchrony\_cholesky\_mainMdl.stan | [Github: Synchrony/Stan](https://github.com/DeirdreLoughnan/Synchrony/tree/master/Stan) | Stan final model: phylogeny |
| Modelpres\_Aug42020.tex | [Github: Synchrony/notes](https://github.com/DeirdreLoughnan/Synchrony/tree/master/notes) | Making slides to present at bayes class |
| Synch\_model\_breakdown\_Nov2018 | [Github: Synchrony/notes](https://github.com/DeirdreLoughnan/Synchrony/tree/master/notes) | Scan of model outline from Lizzie |
| Thoughts\_on\_analysis.rtf | [Github: Synchrony/notes](https://github.com/DeirdreLoughnan/Synchrony/tree/master/notes) | Random notes and thoughts |



Notes on publishing data: We aim to publish as much data as possible, but require the permission of Thackeray, Cohen and Kharouba. At a minimum, we will publish the scraped data from the 16 Cohen papers DL scraped and the new interaction data DL scraped.