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#### *Goal*

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

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#### *General Files*

Files	Where	What
Loughnan <i>et al.</i> (2024)	Loughnan, D, S. Joly, G. Legault, H. M. Kharbouba, M. Betancourt, E. M. Wolkovich. 2024. Phenology varies with phylogeny but not by trophic level with climate change. <i>Nature Ecology &amp; Evolution</i> . <b>8</b> : 1889-1896. <a href="https://www.nature.com/articles/s41559-024-02499-1">https://www.nature.com/articles/s41559-024-02499-1</a>	Publication
Archived data	<a href="https://knb.ecoinformatics.org/view/doi%3A10.5063%2FF12J69B2">https://knb.ecoinformatics.org/view/doi%3A10.5063%2FF12J69B2</a>	Data and code
README.txt	<a href="#">Github</a>	Outline of repo and experimental aims
Synchrony_hypotheses.tex	<a href="#">Github</a> /notes/	Outline of hypotheses
Synchrony_data/	<a href="#">Github</a> /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](https://github.com/DeirdreLoughnan/Synchrony_data)

Files	Where	What
Rcode	<a href="#">Github:</a>	R code for running models and cleaning data
Input	<a href="#">Github:</a>	Data files called in running model
Cohen	<a href="#">Github: Input/Cohen</a>	Datafile from Cohen et al. 2018
Heather	<a href="#">Github: Input/Heather</a>	Datafile from Kharouba et al. 2018
Newdata	<a href="#">Github: Input/Newdata</a>	Datafiles for new scraped data/Dryad
RISData	<a href="#">Github: Input/RISData</a>	RIS moth and aphid data
Thackeray	<a href="#">Github: Input/Thackeray</a>	A subset of the data from Thackeray et al. 2016
cleaningcode	<a href="#">Github: Input/cleaningcode</a>	Code to clean newscraped/ Dryad data
Stan	<a href="#">Github: Stan</a>	Stan code
notes	<a href="#">Github: Synchrony</a>	Thoughts and outlines
combiningallphenodata.R	<a href="#">Github: Synchrony/Rcode</a>	Merging all the phenology data from 3 meta-analyses and new studies
getting_worldclim_data.R	<a href="#">Github: Synchrony/Rcode</a>	Code to get worldclim data
generate_data_whinge.R	<a href="#">Github: Synchrony/Rcode</a>	Generating test data with a hinge
generate_data.R	<a href="#">Github: Synchrony/Rcode</a>	Generating test data
ggtree_plotting.R	<a href="#">Github: Synchrony/Rcode</a>	Code to make phylogeny fig
Latitudinal_model.R	<a href="#">Github: Synchrony/Rcode</a>	Latitudinal analyses
manuscriptValues.R	<a href="#">Github: Synchrony/Rcode</a>	File generating referenced values in manuscript
modeling_plotting.R	<a href="#">Github: Synchrony/Rcode</a>	Plotting code for ms
null_model_plotting.R	<a href="#">Github: Synchrony/Rcode</a>	Null model code and plots
phylogeny_final.R	<a href="#">Github: Synchrony/Rcode</a>	Main model code
phylogeny_groups.R	<a href="#">Github: Synchrony/Rcode</a>	Main model for 4 common groups

poc_genquanblock.R	<a href="#">Github: Synchrony/Rcode</a>	Testing whether different code for generated quantities blocks do differ
simdata_twospint.R	<a href="#">Github: Synchrony/Rcode</a>	Code for testing for trends in multi sp interactions
simdata_twoSpint_terraqu.R	<a href="#">Github: Synchrony/Rcode</a>	Code for testing for trends in multi sp interactions grouped by terrestrial or aquatic species
singlesp_analysis_generatedata.R	<a href="#">Github: Synchrony/Rcode</a>	Code for running stan model on generated data
singlesp_analysis_realdata.R	<a href="#">Github: Synchrony/Rcode</a>	Code for running stan model on real data
table_synch_source.R	<a href="#">Github: Synchrony/Rcode</a>	Generating table of data sources for manuscript
singlesp_analysis_realdata_covmat.R	<a href="#">Github: Synchrony/Rcode</a>	Code for running stan model on real data and testing the covariance matrix
worldClimSlopesContinents.R	<a href="#">Github: Synchrony/Rcode</a>	Code for running climate models for 12 and 3 month climate data for each continent
dat_fin_Dec2021_w_neg_mod.csv	<a href="#">Github: Synchrony/Input</a>	A csv file of all the synchrony data to date merged together
synchronyTree.tre	<a href="#">Github: Synchrony/Input</a>	Phylogeny of all species
taxonlvl_spname.csv	<a href="#">Github: Synchrony/Input</a>	Taxonomic information for each species
twelve_month_mean_clim_indivlatlong.csv	<a href="#">Github: Synchrony/Input</a>	Climate data for each site, 12 month mean values
same3_month_mean_clim_indivlatlong.csv	<a href="#">Github: Synchrony/Input</a>	Climate data for each site, 3 month mean values

singlesp_randslopes_wcov.stan	<a href="#">Github: Synchrony/Stan</a>	Stan code with covariance matrix, random slopes, random intercepts
singlesp_randslopes.stan	<a href="#">Github: Synchrony/Stan</a>	Stan code with random only
singlesp_randslopesint.stan	<a href="#">Github: Synchrony/Stan</a>	Stan code with random slopes, random intercepts
slopeTempSimplest.stan	<a href="#">Github: Synchrony/Stan</a>	Stan code for estimating temperature slopes for 12 and 3 month climate means
phylogeny_synchrony_cholesky_mainMdl.stan	<a href="#">Github: Synchrony/Stan</a>	Stan final model: phylogeny
Modelpres_Aug42020.tex	<a href="#">Github: Synchrony/notes</a>	Making slides to present at bayes class
Synch_model_breakdown_No v2018	<a href="#">Github: Synchrony/notes</a>	Scan of model outline from Lizzie
Thoughts_on_analysis.rtf	<a href="#">Github: Synchrony/notes</a>	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.