This supplemental folder includes the files necessary to replicate the analyses in Congreve et al. “An Early Burst in brachiopod evolution corresponding with significant climatic shifts during the Great Ordovician Biodiversification Event”. There are two R-files of importance:

1. Supplemental\_Code.r
2. Strophomenoid\_Analyses\_Source\_Code.r

The first file is the “main” program, which calls upon a series of functions defined in the 2nd file in order to evaluate different rate models. There is also a folder, “data”, which includes the data files that Supplemental\_Code.r uses, including:

1. Strophomenoidea\_Congreve\_et\_al\_2019\_Genus.nex (the original character matrix)
2. strophomenid\_ord\_tree.txt (the model cladogram)
3. Possible\_FAs\_Used.csv (possible first appearance dates for the analyzed taxa based on 100 random replications)
4. P\_First\_Appearances\_Averaged.csv (the prior probabilities of those first appearance dates)
5. Ordovician\_Fuzzy\_Ranges.csv (upper and lower bounds of both the first and last appearances of analyzed taxa)
6. Gap\_Probabilities\_BDS.csv (the probabilities of particular gaps given origination, extinction and sampling rates from different intervals of time)

Note that these files can be replaced with different files for different taxa or with routines (included in Strophomenoid\_Analyses\_Source\_Code.r).

I have divided the program into five sections. The first, “Get Phylogeny & Character Data” simply loads the relevant datafiles, including the character data and the model cladogram. The second, “Use Parsimony to 'Seed' Analysis” uses the model cladogram and character data to establish minimum numbers of changes for each character & minimum derivations for each state. These are used in the third part, “Get Rate Distribution for Tip-Dating Approach”, where a series of models (uniform, exponential, lognormal and gamma) are evaluated in order to determine the best distribution of rate variation for those characters. The fourth section, “Get FA Priors”, gets the prior probability that a taxon’s “true” first appearance is (say) 450 Ma when the oldest possible age for that FA is 451 Ma and the youngest possible is 449.5 Ma. Here, results are simply read in: again, routines for calculating these distributions are provided in the source code file. The final part, “Prepare Search Loop!”, evaluates a series of rate hypotheses over a range of divergence times and different first appearance times for each sampled taxon. This generates a series of csv and RData files that are the main results of this analysis.