

Description for files to be available on Dryad containing the analyses executed for the article "The circular nature of recurrent life-cycle events: a test comparing tropical and temperate phenology". The function proposed here tests phylogenetic signal in plant phenology considering the circularity of temporal data. Any query or suggestion please write to v.staggemeier@gmail.com.

Files:

1. [PhylogSignal_CircData.pdf](#) - PDF containing a short theoretical background and explanations about the input datasets and all results created with the function "PhySignalPheno". Some suggestions to create graphics are available here.
2. [tree_example.nex](#) – a nexus file containing the phylogenetic relationships simulated for 100 species.
3. Simulated phenological datasets illustrating the four case studies:
[pheno_example1.txt](#) (Resting system with FFDs phylogenetically structured),
[pheno_example2.txt](#) (Non-resting system with FFDs phylogenetically structured),
[pheno_example3.txt](#) (Resting system with FFDs without phylogenetic signal),
[pheno_example4.txt](#) (Non-resting system with FFDs without phylogenetic signal).
4. [PhySignalPheno.R](#): R code for the function PhySignalPheno. This function produces a list containing:
 1. Phylogenetic signal for all four metrics;
 2. PCoA results;
 3. P-value for selected vectors in PVR analysis;
 4. Mantel results;
 5. Angles (degrees) and dates in days of the year (DOY);

The function also produces a matrix that will be saved in your working directory. Data saved in this matrix (DOY, phenological scores, angles, and phylogenetic vectors selected in PVR analysis) can be used for additional analyses, for example to examine the residuals from PVR, or to build graphics to examine the patterns in your dataset (e.g. FFD x phylogenetic vector).

Please note that all analyses were conducted in R version 3.3.2, RStudio Version 1.1.447, and PVR package Version: 0.2.1 (this package is provided below because the present version in CRAN has problems).