# R code for applying phylogenetic comparative methods to phenological datasets

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February 27, 2019

## Contents

## Introduction

Whether closely related species flower at same time is an old question in plant phenology (see Robertson 1895, Kochmer & Handel 1986), but only recently has this issue been explored at species level, thanks to increasingly available molecular data. This question is the focus of studies at local scales (examples in Staggemeier et al. 2010, Chang-Yang et al. 2013, Cortés-Flores et al. 2015), regional scales (Staggemeier et al. 2015) and global scales (Du et al. 2015, Davies et al. 2013); for a literature review please see Table 1 in the article "The circular nature of recurrent life-cycle events: a test comparing tropical and temperate phenology" published in the Journal of Ecology.

Identifying whether some species exhibit conservative phenological patterns that are phylogenetically structured is useful for making predictions in a scenario of global warming effects (Davis et al. 2010, Willis et al. 2008). In this code, four metrics of phylogenetic signal are explored in the context of phenological research:

1. Pagel's Lambda;
2. Blomberg's K-statistic;
3. Mantel coeficient of correlation;
4. R-square from Phylogenetic EigenVector Regression (PVR).

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.

## Input data

At least two datasets are needed to run the analyses. The first is a phenological dataset - for example, the starting dates of flowering for a pool of species in the studied community or mean dates per species based on a herbarium data review. The literature suggests working with at least 30 species per assemblage or community, because the power to detect phylogenetic signal in communities decreases in accordance with the number of species number.

In the phenological dataset (Table 1), the first column represents the species names (eg. t48, t67, t3, t13, ...), and second column shows the dates, as day of the year (DOY), when phenological activity was recorded. The DOY for the case studies given as examples in this code represents the average of the first flowering date (FFD) for each species in the community (i.e. the average is based on the FFD for all individuals for each species). Different kinds of phenological parameters can be analysed, such as first phenological dates or peak dates for any phenophase (flowering, fruiting, leafing).

The date or angle of just one phenological event per species is defined — for instance, first flowering date (FFD) — and it always falls within the year or circle. In the other words, any DOY corresponds to only one date of the year (from Jan 1st to Dec 31st) or one angle in the circle (from 0 degree to 360 degrees). This is the very core of our proposal: the understanding that the year, or circle, repeats itself over time.

Our proposal also allows comparison of signal across regions and climates (resting and non-resting). Our method focuses on how to perform global comparisons across high and low latitudes within hemispheres, and across hemispheres, using data from regions with and without resting seasons. However, to compare species occurring in mid to high latitudes across hemispheres, it is necessary to standardise the zero point of the dataset, prior to analysis, to account for differences between austral and boreal seasons (see Keogan et al. 2018 and Davies et al. 2013). For example, when studying species occurring in mid-North and mid-South latitudes, the zero point of the circular analyses should be standardised

to the date (or angle) of minimum daylight hours (winter solstice).

Table 1: Species first flowering date (FFD)

| Species | FFD |
|---|---|
| t48 | 237 |
| t67 | 205 |
| t3 | 228 |
| t13 | 197 |
| t84 | 110 |
| t99 | 205 |

The second dataset is a nexus file (.nex) containing the time-calibrated molecular phylogenetic hypothesis for the studied species (Figure 1). Here, we present the code to run the analyses for four hypothetical communities, illustrating the four case studies presented in the article.

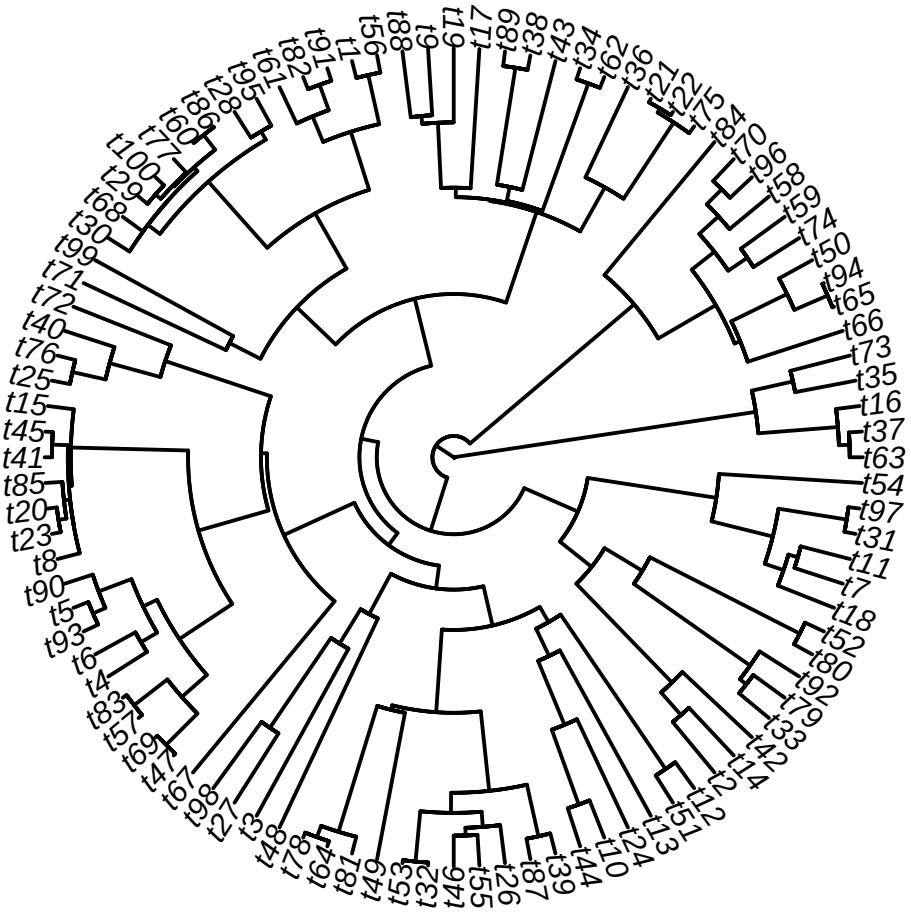


Figure 1: Time-calibrated molecular phylogenetic hypothesis

## Code

### Loading the required packages

```
# Loading the required packages (Please, check that all packages are
# installed before loading; PVR is provided in the Dryad folder because the
# version in CRAN has problems)
packages <- c("phytools", "picante", "phylobase", "adephylo", "circular", "PVR",
    "lubridate", "ecodist")
```

### Loading your data

```
# Phylogenetic hypothesis
phy<-read.nexus("tree_example.nex") #time-calibrated molecular phylogenetic hypothesis
# First flowering dates
FFD<-read.table("pheno_example1.txt")
# Please note that regular years (i.e. 365 days) and leap years (366 days)
# result in different angular transformations when converting from DOY
# (day of the year) to angles, so you must input the year of your study.
# In case you do not have the mean date per species, but you do have the
# mean date per individual, you can use the lubridate R package to convert
# the individual dates into angles and estimate the mean date per species
# using the circular package before to run the analyses
# of PhySignalPheno function.
```

```r
year<-2018 # change here for the year of your study

dates<-FFD
```

### Main function: PhySignalPheno

This function requires four arguments, they are:

1. phy: time-calibrated molecular phylogenetic hypothesis as a nexus file;
2. dates: the file with phenological dates (first dates or peak dates);
3. year: the year of study;
4. name: the name of the community, the results saved in a separate file will use this name. Use letters without spaces or symbols.

This function produce a list containing:

1. Phylogenetic signal for all four metrics (statistic and p-value);
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 file that will be saved in your working directory, remember to set the working directory before starting the analyses. This file is a matrix (containing DOY, phenological scores, angles, and phylogenetic vectors selected in PVR analysis) that 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 versus phylogenetic vector).

```r
PhySignalPheno <- function(phy, dates, year=NULL, name=NULL){
  #verify whether the phylogenetic hypothesis is ok
  if(!is.binary.tree(phy)){ stop("phylogenies must be binary")}
  if(!is.ultrametric(phy)){stop("phylogenies must be ultrametric")}
  # to convert dates in angles
  leap_year(year) # true or false to identify leap years
  # for a leap year, the angles will be 360/366=0.9836065573770492, if not
  # 360/365=0.9863013698630137

  # Matching Phylo and Pheno(dates)
     # IMPORTANT STEP to compare taxa present in phylogeny with dates of each
      # species, pruning and sorting the two kinds of data to match one another
      # for subsequent analysis
      # Species names must be written identically in both the phylogeny and
      # the phenological datasets.
  phylo_traits<-match.phylo.data(phy, dates)
  phy <- phylo_traits$phy
  dates<-phylo_traits$data
  angles<-matrix(NA, nrow(dates), ncol(dates))
  for (i in 1:nrow(dates)) {
    angles[i, 1] <- round(
    ifelse(leap_year(year) == "TRUE",
    dates[i, 1] * 0.9863013698630137,
    dates[i, 1] * 0.9836065573770492
```

```
  ),3)
}
rownames(angles)<-row.names(dates)
matriz.Y <- matrix(angles, nrow = length(angles),
                   ncol = length(angles),
                   byrow = FALSE)
rownames(matriz.Y)<-rownames(angles)
colnames(matriz.Y)<-rownames(angles)
step_1<-matriz.Y-t(matriz.Y) #difference between each pair of species
step_2<-abs(step_1) # transforming differences to absolute values
step_3<-ifelse(step_2>180, step_2-360, step_2)
step_4<-abs(step_3) # transforming to absolute values
dist_angular<-as.dist(step_4) # matrix showing the angular distances
# between species
pcoa<-dudi.pco(dist_angular, scannf = FALSE, nf = 2)  # Principal Coordinate
# Analysis to extract the scores that represent the angles on a linear scale
explic.ax1<-pcoa$eig[1]/sum(pcoa$eig)
explic.ax2<-pcoa$eig[2]/sum(pcoa$eig)
scores_PCoA<-round(pcoa$li, 3)
rownames(scores_PCoA)<-rownames(angles)
# Matching Phylo and Pheno(scores)
phylo_traits<-match.phylo.data(phy, scores_PCoA)
phy <- phylo_traits$phy
scores <- phylo_traits$data
```

```
colnames(scores)<-colnames(scores_PCoA)


##### Phylogenetic signal calculations #####


### Phylogenetic EigenVector Regression ###
pvr.scores <- PVRdecomp(phy, scale=TRUE)
PVR.r.scores <- PVR(pvr.scores,phy, scores[,1],
                    method = "moran", scaled=TRUE)
PVR.r2.scores <- round(PVR.r.scores@PVR$R2, digits=3)
PVR_model.scores<-lm(scores[,1] ~ PVR.r.scores@Selection$Vectors)
PVR.r.scores@Selection$Id
p.value.PVR.scores<-
  round(pf(summary(PVR_model.scores)$fstatistic[1],
                            summary(PVR_model.scores)$fstatistic[2],
                             summary(PVR_model.scores)$fstatistic[3],
                             lower.tail = F),4)
RESU <- matrix(NA, nrow=nrow(scores), 3+(ncol(PVR.r.scores@Selection$Id)))
RESU <- cbind(dates, scores, angles, PVR.r.scores@Selection$Vectors)
write.table(RESU, paste("pheno_phylo_variables_", name, ".txt", sep = ""))
# This table contains:
    # DOY,
    # Phenological Scores,
    # Angles,
    # Phylogenetic vectors selected in PVR analysis.
```

```
### Mantel ###
  dist.p <- as.dist(cophenetic(phy))
dist.y <- dist_angular
mantel.r.angle <-
round(vegan::mantel(dist.y, dist.p, permutation = 1000)$statistic,
digits = 3)
mantel.r.signif.angle <-
round(vegan::mantel(dist.y,
                    dist.p,
                    permutation = 1000)$signif,
      digits = 3)
set.seed(5)
correl_mantel_flor<-mgram(dist.p,dist.y, nperm = 999)

### Blomberg's K ###
scores_1 <- scores[, 1]
names(scores_1) <- phy$tip.label
K_circularax1<-phylosig(phy, scores_1, method="K", test=TRUE, nsim=1000)
K_circularax1.K <-round(K_circularax1$K, digits=3)
K_circularax1.p<-round(K_circularax1$P, digits=3)

### Pagel's Lambda ###
lambda <- phylosig(phy, scores_1, method="lambda", test=TRUE, nsim=1000)
```

```
  lambda.val <- round(lambda$lambda, digits = 3)
  lambda.p <- round(lambda$P, digits = 3)


  return(list(
    Phylogenetic_signal =
      c(
    pvr.scores=PVR.r2.scores,
    p.PVR.scores=p.value.PVR.scores,
    mantel.Correl=mantel.r.angle,
    mantel.sig=mantel.r.signif.angle,
    K=K_circularax1.K , K.p=K_circularax1.p,
    lambda = lambda.val, lambda.p = lambda.p),
    Angular_PCOA_axis = pcoa,
    selected.vectors.PVR = PVR.r.scores@Selection$Id,
    Mantel = list(Distances = cbind(dist.y = dist.y,
                                    dist.p = dist.p),
                  Correlogram = correl_mantel_flor),
    Angles_and_Dates = list(angles = angles, dates = dates)))
}
```

## Examples (including graphics)

### Resting system with FFDs phylogenetically structured

```
FFD <- read.table("pheno_example1.txt")
head(FFD)

##         FFD
## t48 236.751
## t67 204.725
## t3  228.168
## t13 197.096
## t84 109.652
## t99 205.033

resu_example1 <-
PhySignalPheno(phy, FFD, year = 2018, name = c("example_1"))
resu_example1$Phylogenetic_signal

##         pvr.scores p.PVR.scores.value      mantel.Correl
##              0.703              0.000              0.369
##         mantel.sig                  K              K.p
##              0.001              1.105              0.001
##             lambda           lambda.p
##              0.982              0.000
```

```r
dates<-resu_example1$Angles_and_Dates$dates
pheno_angles <- circular(
  resu_example1$Angles_and_Dates$angles,
  type = "angles",
  units = "degrees",
  rotation = "clock",
  modulo = "2pi"
  )

on <- par(mfrow = c(1, 2))
hist(
  resu_example1$Angles_and_Dates$dates[, 1],
  main = "Flowering dates (DOY)",
  cex.main = 0.8,
  xlim = c((min(dates) - 30), max(dates) + 30),
  border = "plum4",
  col = "plum",
  xlab = "DOY: day of the year",
  cex = 1
)

plot(
  pheno_angles,
  stack = TRUE,
```

```
  rotation = "clock",
  zero = pi / 2,
  cex = 1,
  axes = F,
  ticks = F,
  shrink = 1.2,
  col = "black"
)

rose.diag(
  pheno_angles,
  unit = "degrees",
  bins = 12,
  axes = TRUE,
  ticks = TRUE,
  tcl = 0.05,
  tcl.text = -0.16,
  border = "plum4",
  col = "plum",
  tol = 0.2,
  radii.scale = "linear",
  rotation = "clock",
  zero = pi / 2,
  prop = 2.0,
```

```
  lty = 1,
  lwd = 2.5,
  cex = 0.8,
  add = TRUE
)


axis.circular(
  at = circular(seq(pi / 12, 2 * pi, pi / 6)),
  labels = c(
    "Mar",
    "Feb",
    "Jan",
    "Dec",
    "Nov",
    "Oct",
    "Sep",
    "Aug",
    "Jul",
    "Jun",
    "May",
    "Apr"),
  cex = 0.8,
  tcl.text = 0.20
)
```

```
title("Flowering dates (angles)", cex.main = 0.8)
par(on)
```

```
corDegrade_linear <- colorRampPalette(
  c(
    "midnightblue",
    "navyblue",
    "dodgerblue3",
    "lightskyblue",
    "chartreuse4",
    "yellowgreen",
    "yellow",
    "orange",
    "tomato1",
    "red3",
    "red4",
    "maroon1"
  ))

plot1 <- phylo4d(phy,
                 cbind(dates = resu_example1$Angles_and_Dates$dates,
                       axis = resu_example1$Angular_PCOA_axis$li))
table.phylo4d(
  plot1,
```

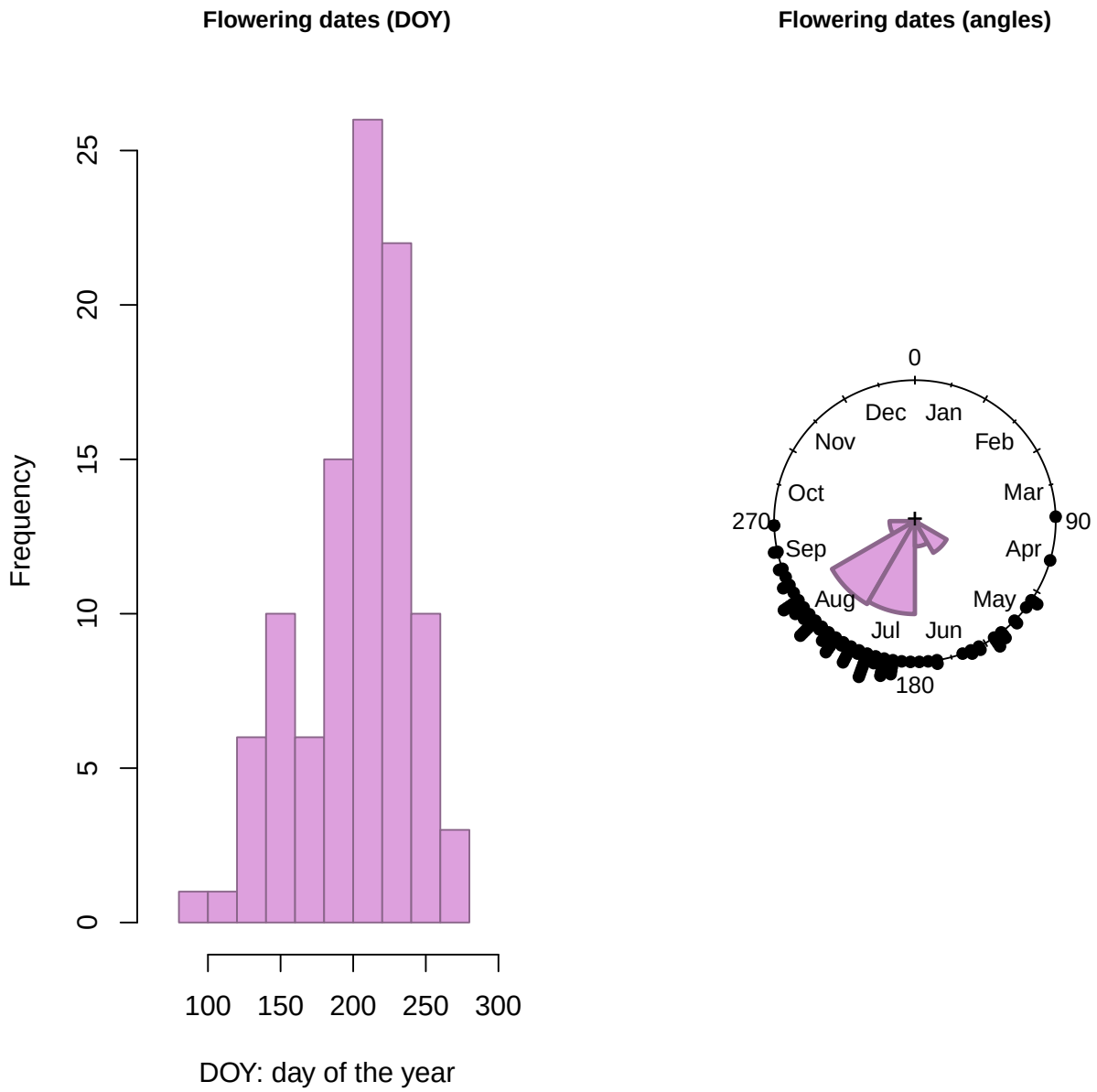


Figure 2: Distribution of FFDs (first flowering dates)

```
  ratio.tree = 0.968,
  var.label = c("Dates", "Scores of the first PCoA axis"),
  cex.symbol = 1,
  grid = FALSE,
  pch = 15,
  box = F,
  center = F,
  scale = F,
  symbol = "colors",
  col = corDegrade_linear(365),
  cex.label = 0.5,
  cex = 1,
  legend = TRUE,
  show.tip.label = FALSE
)
title("Phenological variables mapped over the tree", cex.main = 0.8)
```

```
on <- par(
  mfrow = c(1, 2), oma = c(2, 2, 2, 1), mar = c(4, 4, 2, 1))


plot(
  resu_example1$Mantel$Distances[, 1] ~ resu_example1$Mantel$Distances[, 2],
  xlab = "Phylogenetic distances",
  ylab = "Phenological distances",
```

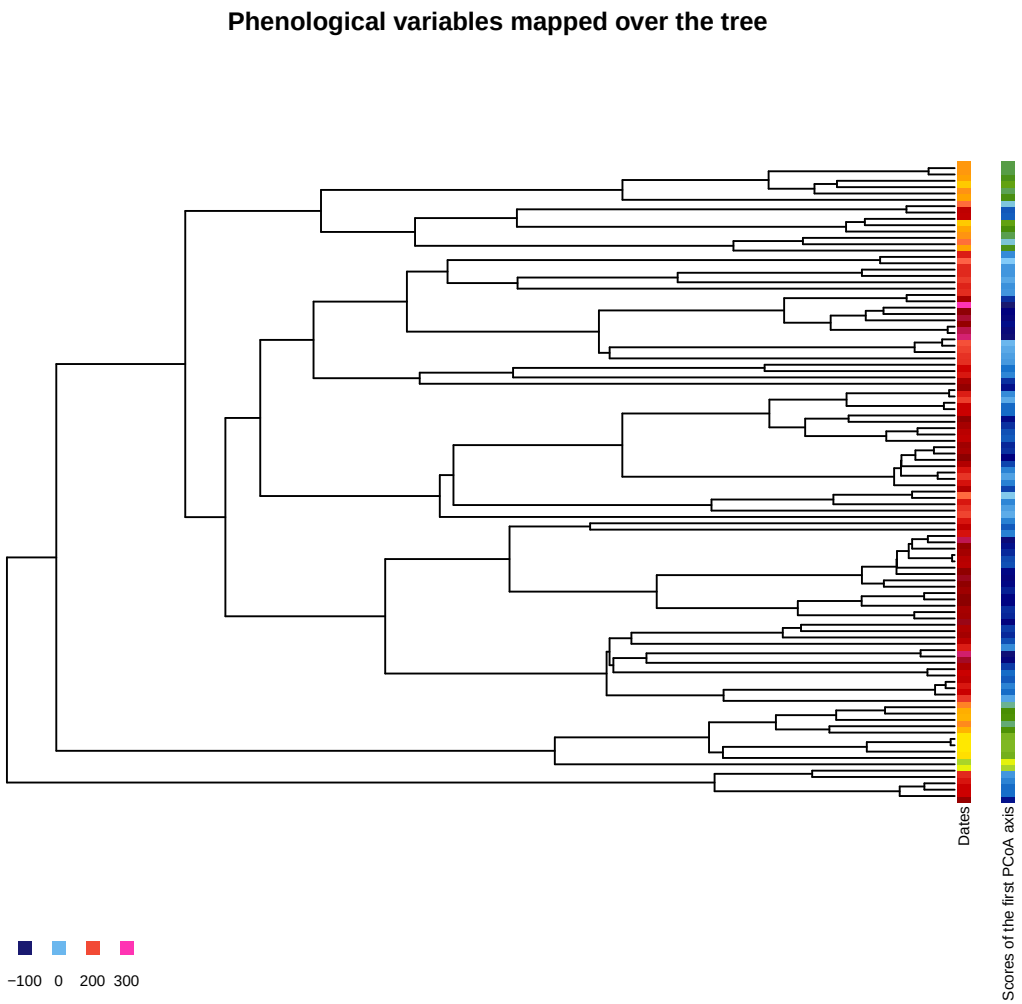


Figure 3: Phylogenetic structure of flowering dates and scores of the PCoA axes

```
  bty = "l",
  pch = 19,
  cex = 0.5)
title(main = "Relationship between distances",
      cex.main = 0.8)


plot.mgram(
  resu_example1$Mantel$Correlogram,
  xlab = "Midpoint of the distance class",
  bty = "l",
  ylab = "Mantel r")
title(main = "Mantel correlogram", cex.main = 0.8)


par(on)
```

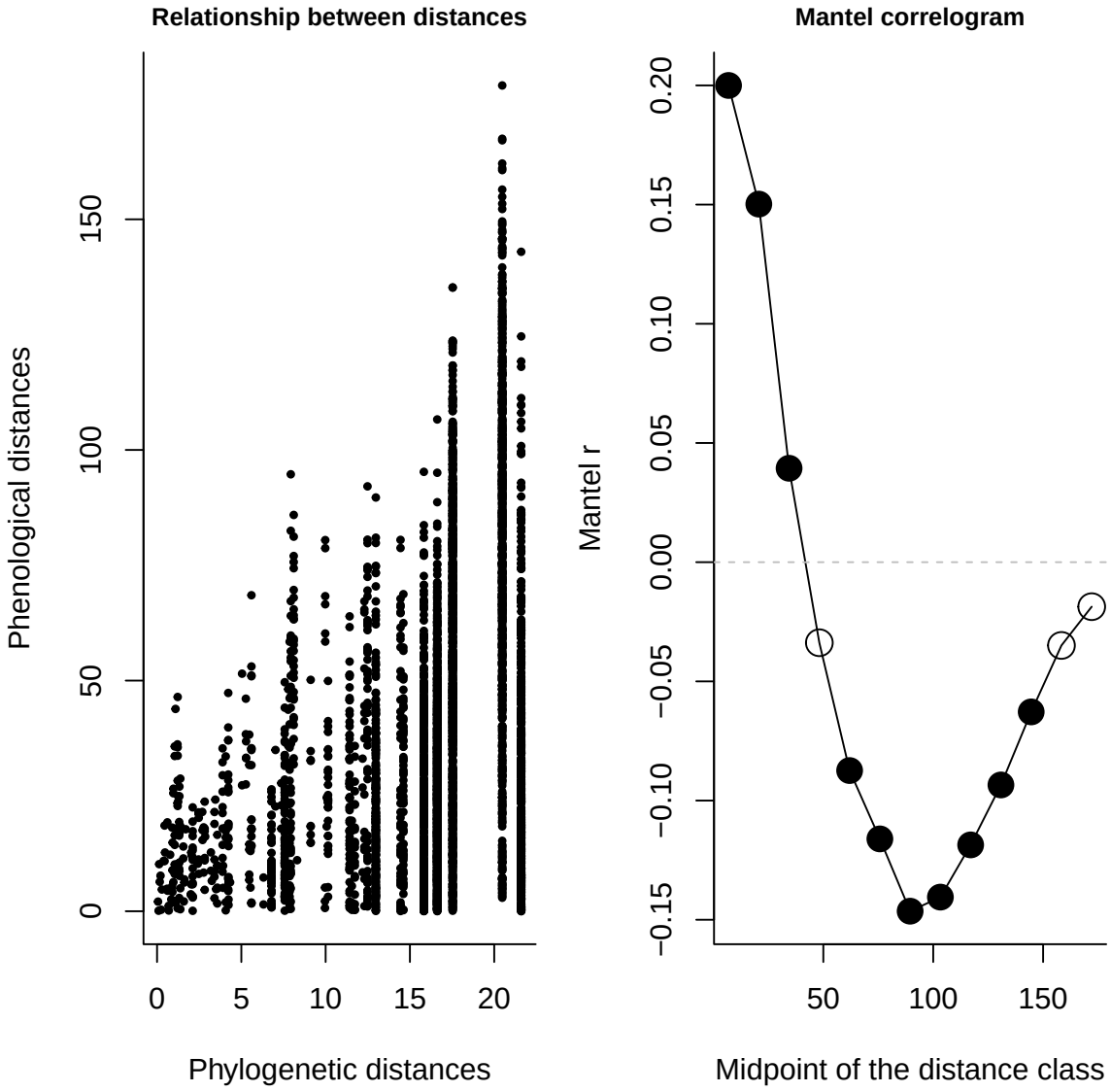


Figure 4: Correlation between phylogenetic and phenological distances

### Non-resting system with FFDs phylogenetically structured

```
FFD <- read.table("pheno_example2.txt")
head(FFD)

##         FFD
## t48 224.858
## t67 216.917
## t3  212.464
## t13 142.974
## t84 225.373
## t99 222.713

resu_example2 <-
PhySignalPheno(phy, FFD, year = 2018, name = c("example_2"))
resu_example2$Phylogenetic_signal

##         pvr.scores p.PVR.scores.value      mantel.Correl
##             0.0110             0.3068            -0.0080
##         mantel.sig                  K               K.p
##             0.5690             0.0570            0.6250
##             lambda           lambda.p
##             0.0000             1.0000
```

```r
dates<-resu_example2$Angles_and_Dates$dates

pheno_angles <- circular(
  resu_example2$Angles_and_Dates$angles,
  type = "angles",
  units = "degrees",
  rotation = "clock",
  modulo = "2pi")


on <- par(mfrow = c(1, 2))
hist(
  resu_example2$Angles_and_Dates$dates[, 1],
  main = "Flowering dates (DOY)",
  cex.main = 0.8,
  xlim = c((min(dates) - 30), max(dates) + 30),
  border = "plum4",
  col = "plum",
  xlab = "DOY: day of the year",
  cex = 1)



plot(
  pheno_angles,
  stack = TRUE,
  rotation = "clock",
```

```
  zero = pi / 2,
  cex = 1,
  axes = F,
  ticks = F,
  shrink = 1.2,
  col = "black")

rose.diag(
  pheno_angles,
  unit = "degrees",
  bins = 12,
  axes = TRUE,
  ticks = TRUE,
  tcl = 0.05,
  tcl.text = -0.16,
  border = "plum4",
  col = "plum",
  tol = 0.2,
  radii.scale = "linear",
  rotation = "clock",
  zero = pi / 2,
  prop = 2.0,
  lty = 1,
  lwd = 2.5,
```

```
  cex = 0.8,
  add = TRUE)


axis.circular(
  at = circular(seq(pi / 12, 2 * pi, pi / 6)),
  labels = c(
    "Mar",
    "Feb",
    "Jan",
    "Dec",
    "Nov",
    "Oct",
    "Sep",
    "Aug",
    "Jul",
    "Jun",
    "May",
    "Apr"),
  cex = 0.8,
  tcl.text = 0.20)
title("Flowering dates (angles)", cex.main = 0.8)
par(on)
```

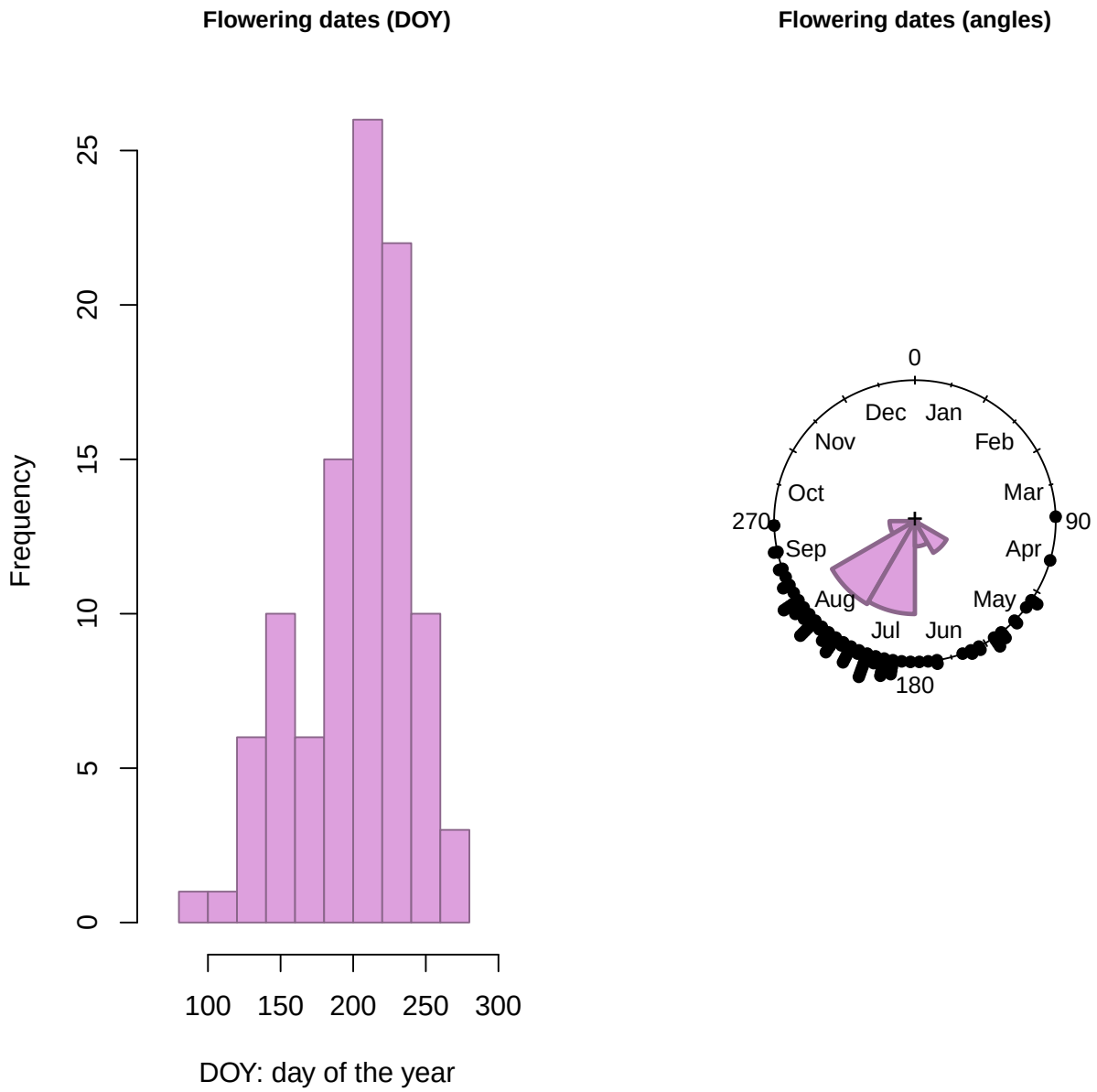


Figure 5: Distribution of FFDs (first flowering dates)

```
corDegrade_linear <- colorRampPalette(
  c(
    "midnightblue",
    "navyblue",
    "dodgerblue3",
    "lightskyblue",
    "chartreuse4",
    "yellowgreen",
    "yellow",
    "orange",
    "tomato1",
    "red3",
    "red4",
    "maroon1"))


plot1 <- phylo4d(phy,
                 cbind(dates = resu_example2$Angles_and_Dates$dates,
                       axis = resu_example2$Angular_PCOA_axis$li))
table.phylo4d(
  plot1,
  ratio.tree = 0.968,
  var.label = c("Dates", "Scores of the first PCoA axis",
                "Scores of the second PCoA axis"),
  cex.symbol = 1,
```

```
  grid = FALSE,
  pch = 15,
  box = F,
  center = F,
  scale = F,
  symbol = "colors",
  col = corDegrade_linear(365),
  cex.label = 0.5,
  cex = 1,
  legend = TRUE,
  show.tip.label = FALSE)
title("Phenological variables mapped over the tree", cex.main = 0.8)
```

```
on <- par(
  mfrow = c(1, 2), oma = c(2, 2, 2, 1),  mar = c(4, 4, 2, 1))


plot(
  resu_example2$Mantel$Distances[, 1] ~ resu_example2$Mantel$Distances[, 2],
  xlab = "Phylogenetic distances",
  ylab = "Phenological distances",
  bty = "l",
  pch = 19,
  cex = 0.5)
title(main = "Relationship between distances"
```

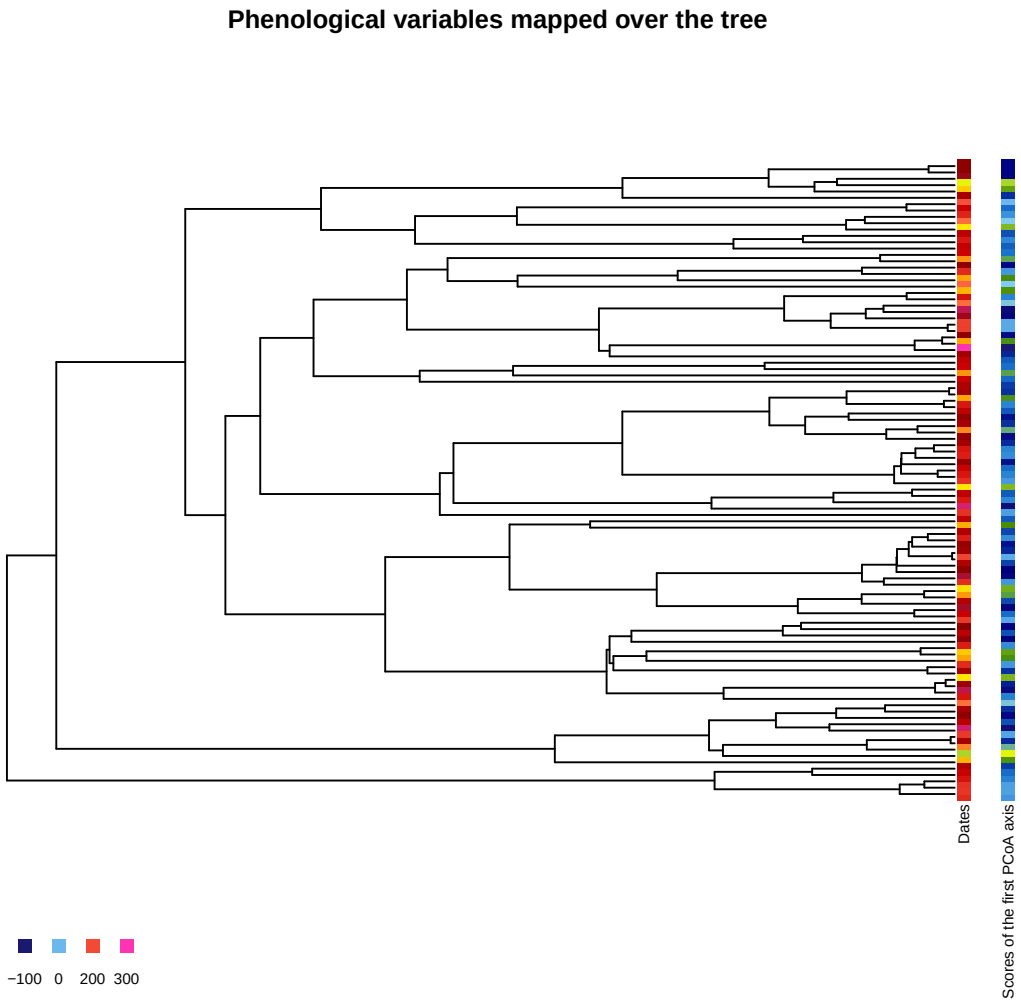


Figure 6: Phylogenetic structure of flowering dates and scores of the PCoA axes

```
      , cex.main = 0.8)


plot.mgram(
  resu_example2$Mantel$Correlogram,
  xlab = "Midpoint of the distance class",
  bty = "l",
  ylab = "Mantel r")
title(main = "Mantel correlogram", cex.main = 0.8)


par(on)
```

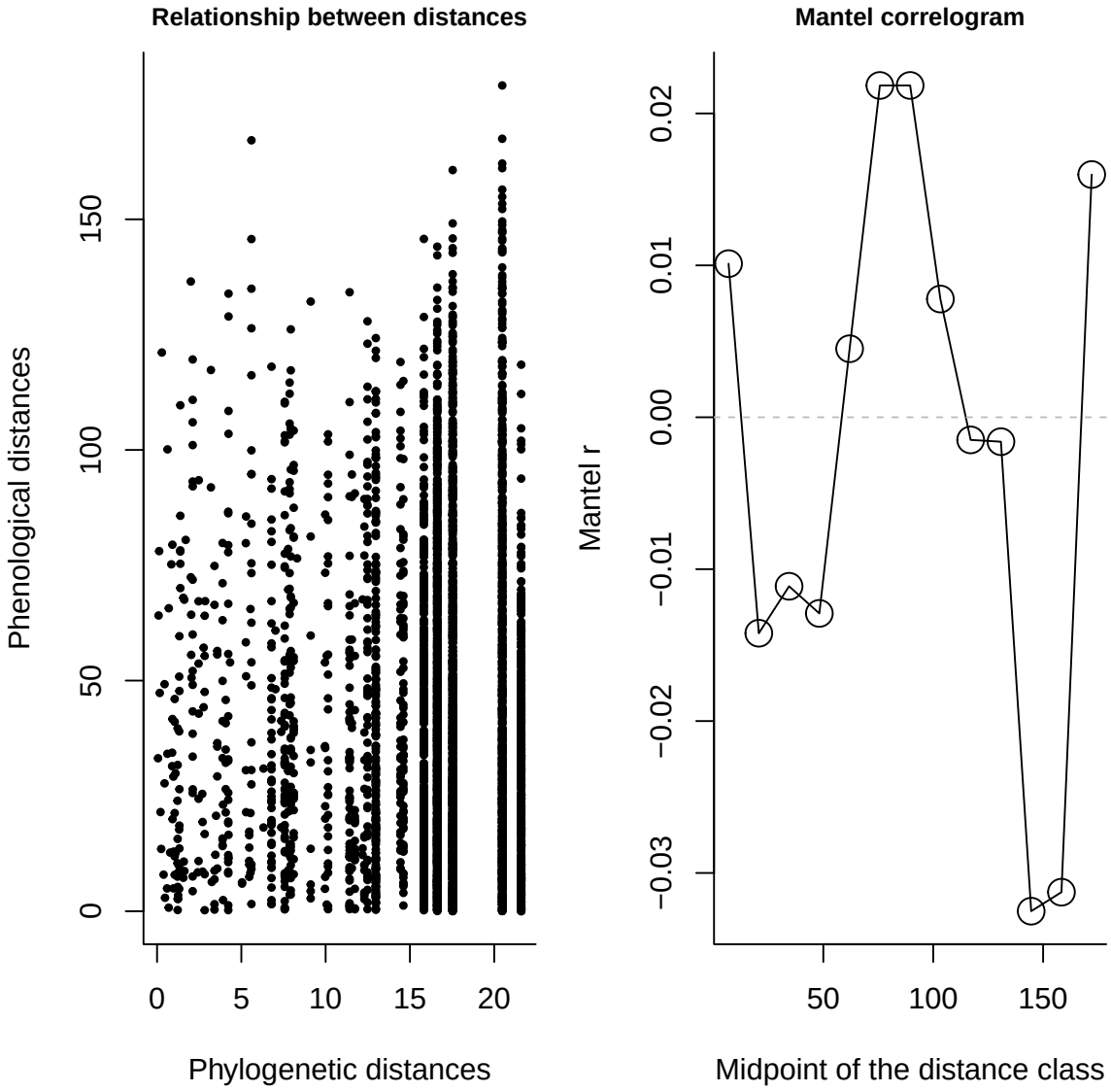


Figure 7: Correlation between phylogenetic and phenological distances

### Resting system with FFDs without phylogenetic signal

```
FFD <- read.table("pheno_example3.txt")
head(FFD)

##         FFD
## t48  67.502
## t67   3.449
## t3   50.335
## t13 353.193
## t84 178.304
## t99   4.065

resu_example3 <-
PhySignalPheno(phy, FFD, year = 2018, name = c("example_3"))
resu_example3$Phylogenetic_signal

##         pvr.scores p.PVR.scores.value      mantel.Correl
##              0.671              0.000              0.342
##         mantel.sig                  K                K.p
##              0.001              0.813              0.001
##             lambda           lambda.p
##              0.972              0.000
```

```r
dates<-resu_example3$Angles_and_Dates$dates

pheno_angles <- circular(
  resu_example3$Angles_and_Dates$angles,
  type = "angles",
  units = "degrees",
  rotation = "clock",
  modulo = "2pi")


on <- par(mfrow = c(1, 2))
hist(
  resu_example3$Angles_and_Dates$dates[, 1],
  main = "Flowering dates (DOY)",
  cex.main = 0.8,
  xlim = c((min(dates) - 30), max(dates) + 30),
  border = "plum4",
  col = "plum",
  xlab = "DOY: day of the year",
  cex = 1)



plot(
  pheno_angles,
  stack = TRUE,
  rotation = "clock",
```

```
  zero = pi / 2,
  cex = 1,
  axes = F,
  ticks = F,
  shrink = 1.2,
  col = "black")

rose.diag(
  pheno_angles,
  unit = "degrees",
  bins = 12,
  axes = TRUE,
  ticks = TRUE,
  tcl = 0.05,
  tcl.text = -0.16,
  border = "plum4",
  col = "plum",
  tol = 0.2,
  radii.scale = "linear",
  rotation = "clock",
  zero = pi / 2,
  prop = 2.0,
  lty = 1,
  lwd = 2.5,
```

```
  cex = 0.8,
  add = TRUE)


axis.circular(
  at = circular(seq(pi / 12, 2 * pi, pi / 6)),
  labels = c(
    "Mar",
    "Feb",
    "Jan",
    "Dec",
    "Nov",
    "Oct",
    "Sep",
    "Aug",
    "Jul",
    "Jun",
    "May",
    "Apr"),
  cex = 0.8,
  tcl.text = 0.20)
title("Flowering dates (angles)", cex.main = 0.8)
par(on)
```

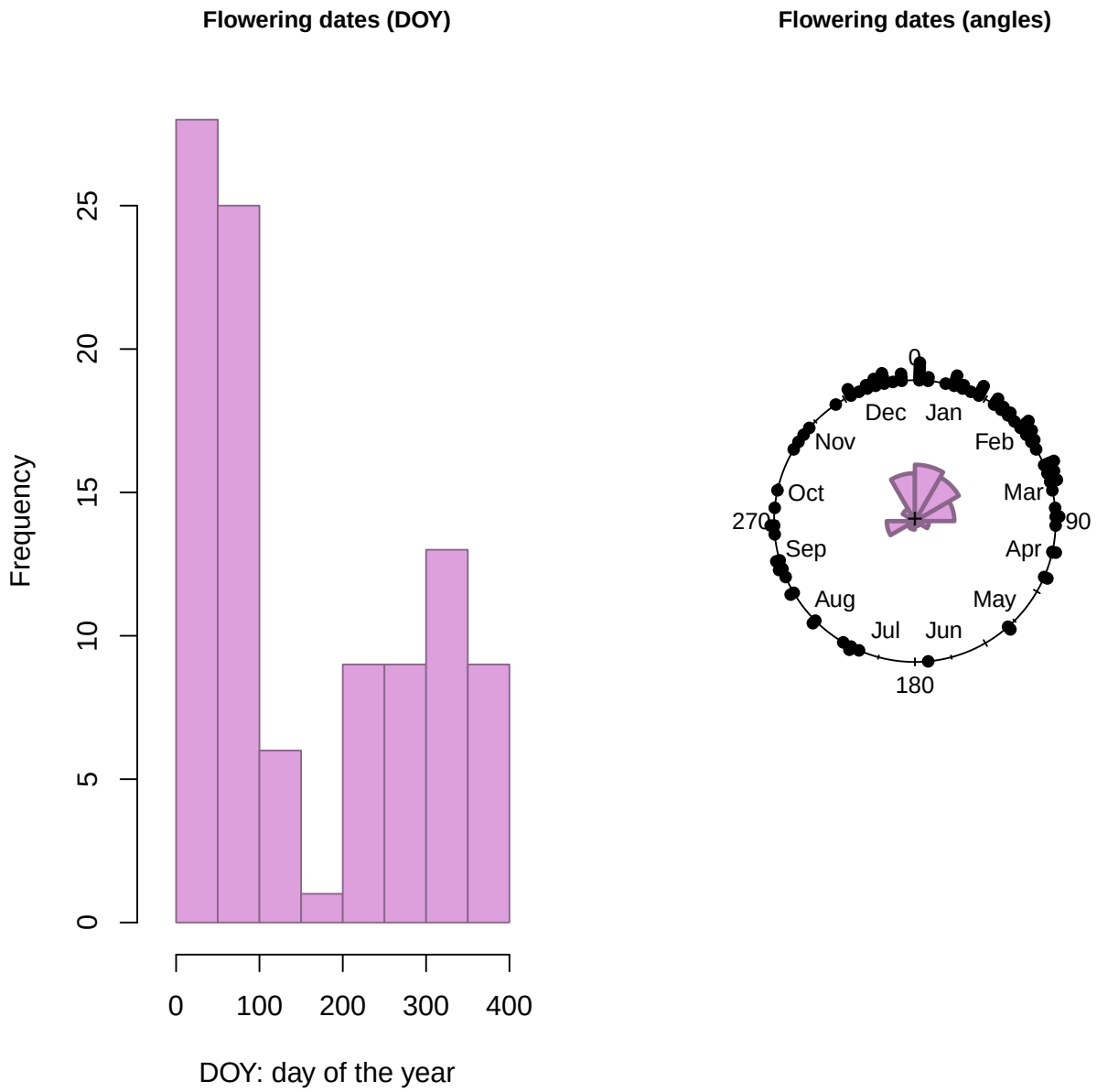


Figure 8: Distribution of FFDs (first flowering dates)

```
corDegrade_linear <- colorRampPalette(
  c(
    "midnightblue",
    "navyblue",
    "dodgerblue3",
    "lightskyblue",
    "chartreuse4",
    "yellowgreen",
    "yellow",
    "orange",
    "tomato1",
    "red3",
    "red4",
    "maroon1"))


plot1 <- phylo4d(phy,
                 cbind(dates = resu_example3$Angles_and_Dates$dates,
                       axis = resu_example3$Angular_PCOA_axis$li))


table.phylo4d(
  plot1,
  ratio.tree = 0.968,
  var.label = c("Dates", "Scores of the first PCoA axis",
                "Scores of the second PCoA axis"),
```

```
  cex.symbol = 1,
  grid = FALSE,
  pch = 15,
  box = F,
  center = F,
  scale = F,
  symbol = "colors",
  col = corDegrade_linear(365),
  cex.label = 0.5,
  cex = 1,
  legend = TRUE,
  show.tip.label = FALSE)
 title("Phenological variables mapped over the tree", cex.main = 0.8)
```

```
on <- par(
  mfrow = c(1, 2),  oma = c(2, 2, 2, 1),  mar = c(4, 4, 2, 1))


plot(
  resu_example3$Mantel$Distances[, 1] ~
    resu_example3$Mantel$Distances[, 2],
  xlab = "Phylogenetic distances",
  ylab = "Phenological distances",
  bty = "l",
  pch = 19,
```

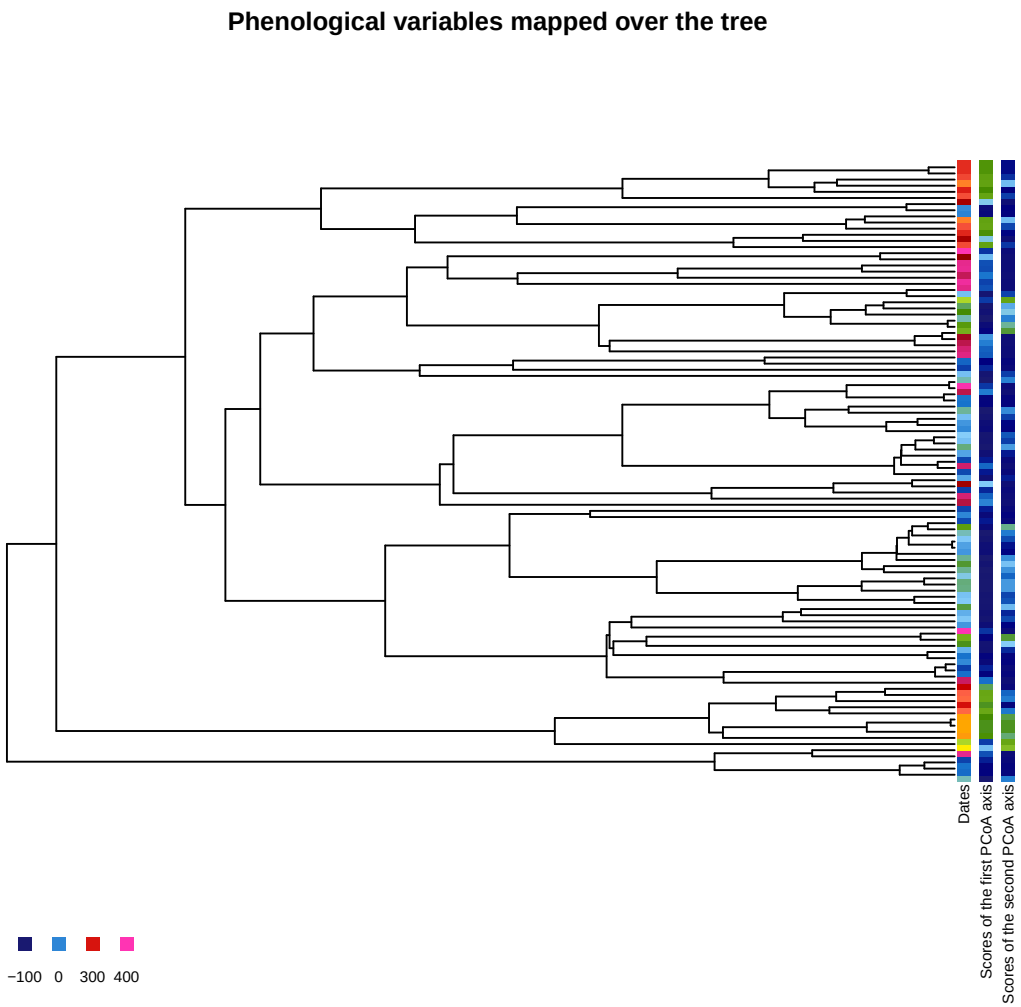


Figure 9: Phylogenetic structure of flowering dates and scores of the PCoA axes

```
  cex = 0.5)
title(main = "Relationship between distances", cex.main = 0.8)


plot.mgram(
  resu_example3$Mantel$Correlogram,
  xlab = "Midpoint of the distance class",
  bty = "l",
  ylab = "Mantel r")
title(main = "Mantel correlogram", cex.main = 0.8)


par(on)
```

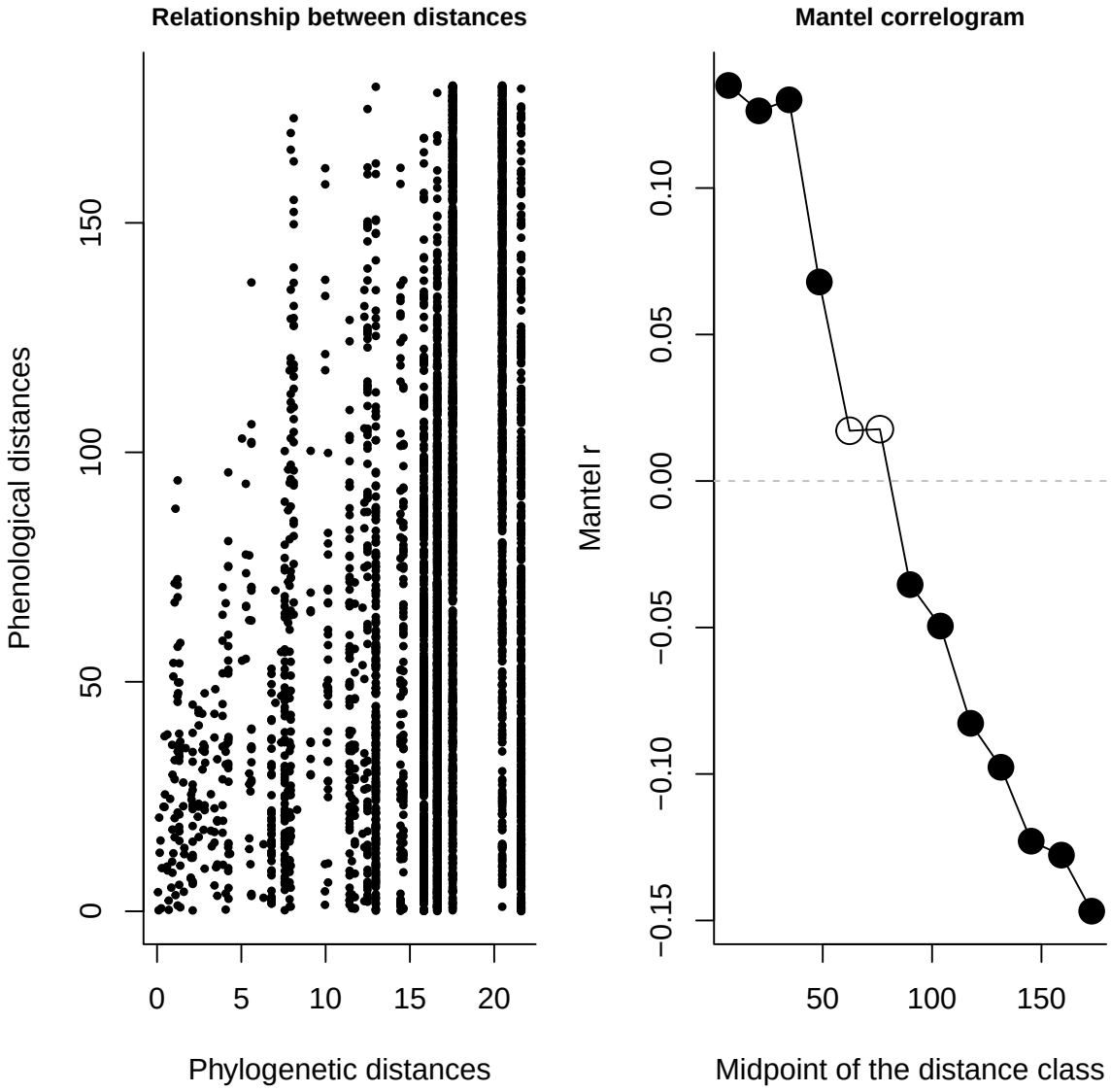


Figure 10: Correlation between phylogenetic and phenological distances

### Non-resting system with FFDs without phylogenetic signal

```
FFD <- read.table("pheno_example4.txt")
head(FFD)

##         FFD
## t48  43.715
## t67  27.835
## t3   18.927
## t13 244.948
## t84  44.747
## t99  39.426

resu_example4 <-
PhySignalPheno(phy, FFD, year = 2018, name = c("example_4"))
resu_example4$Phylogenetic_signal

##         pvr.scores p.PVR.scores.value      mantel.Correl
##              0.012              0.270             -0.023
##         mantel.sig                  K               K.p
##              0.761              0.044              0.845
##             lambda           lambda.p
##              0.000              1.000
```

```r
dates<-resu_example4$Angles_and_Dates$dates
pheno_angles <- circular(
  resu_example4$Angles_and_Dates$angles,
  type = "angles",
  units = "degrees",
  rotation = "clock",
  modulo = "2pi")

on <- par(mfrow = c(1, 2))
hist(
  resu_example4$Angles_and_Dates$dates[, 1],
  main = "Flowering dates (DOY)",
  cex.main = 0.8,
  xlim = c((min(dates) - 30), max(dates) + 30),
  border = "plum4",
  col = "plum",
  xlab = "DOY: day of the year",
  cex = 1)

plot(
  pheno_angles,
  stack = TRUE,
  rotation = "clock",
  zero = pi / 2,
```

```
  cex = 1,
  axes = F,
  ticks = F,
  shrink = 1.2,
  col = "black")


rose.diag(
  pheno_angles,
  unit = "degrees",
  bins = 12,
  axes = TRUE,
  ticks = TRUE,
  tcl = 0.05,
  tcl.text = -0.16,
  border = "plum4",
  col = "plum",
  tol = 0.2,
  radii.scale = "linear",
  rotation = "clock",
  zero = pi / 2,
  prop = 2.0,
  lty = 1,
  lwd = 2.5,
  cex = 0.8,
```

```
  add = TRUE)


axis.circular(
  at = circular(seq(pi / 12, 2 * pi, pi / 6)),
  labels = c(
    "Mar",
    "Feb",
    "Jan",
    "Dec",
    "Nov",
    "Oct",
    "Sep",
    "Aug",
    "Jul",
    "Jun",
    "May",
    "Apr"),
  cex = 0.8,
  tcl.text = 0.20)
title("Flowering dates (angles)", cex.main = 0.8)
par(on)
```

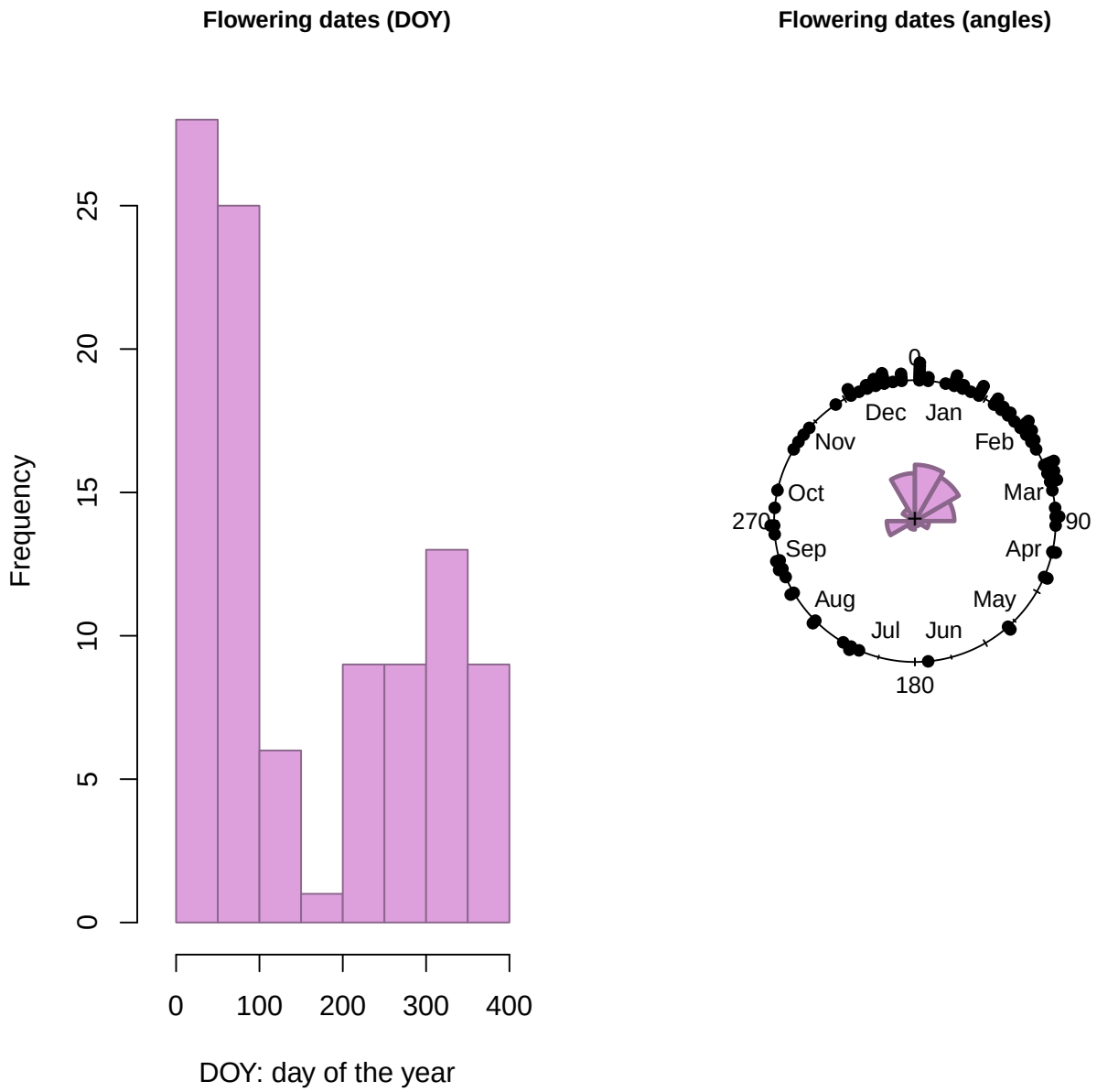


Figure 11: Distribution of FFDs (first flowering dates)

```
corDegrade_linear <- colorRampPalette(
  c(
    "midnightblue",
    "navyblue",
    "dodgerblue3",
    "lightskyblue",
    "chartreuse4",
    "yellowgreen",
    "yellow",
    "orange",
    "tomato1",
    "red3",
    "red4",
    "maroon1"))


plot1 <- phylo4d(phy,
                 cbind(dates = dates, axis = resu_example4$Angular_PCOA_axis$li))


table.phylo4d(
  plot1,
  ratio.tree = 0.968,
  var.label = c("Dates", "Scores of the first PCoA axis",
                "Scores of the second PCoA axis"),
  cex.symbol = 1,
```

```
  grid = FALSE,
  pch = 15,
  box = F,
  center = F,
  scale = F,
  symbol = "colors",
  col = corDegrade_linear(365),
  cex.label = 0.5,
  cex = 1,
  legend = TRUE,
  show.tip.label = FALSE)
title("Phenological variables mapped over the tree", cex.main = 0.8)
```

```
on <- par(
  mfrow = c(1, 2),  oma = c(2, 2, 2, 1),  mar = c(4, 4, 2, 1))


plot(
  resu_example4$Mantel$Distances[, 1] ~
    resu_example4$Mantel$Distances[, 2],
  xlab = "Phylogenetic distances",
  ylab = "Phenological distances",
  bty = "l",
  pch = 19,
  cex = 0.5)
```

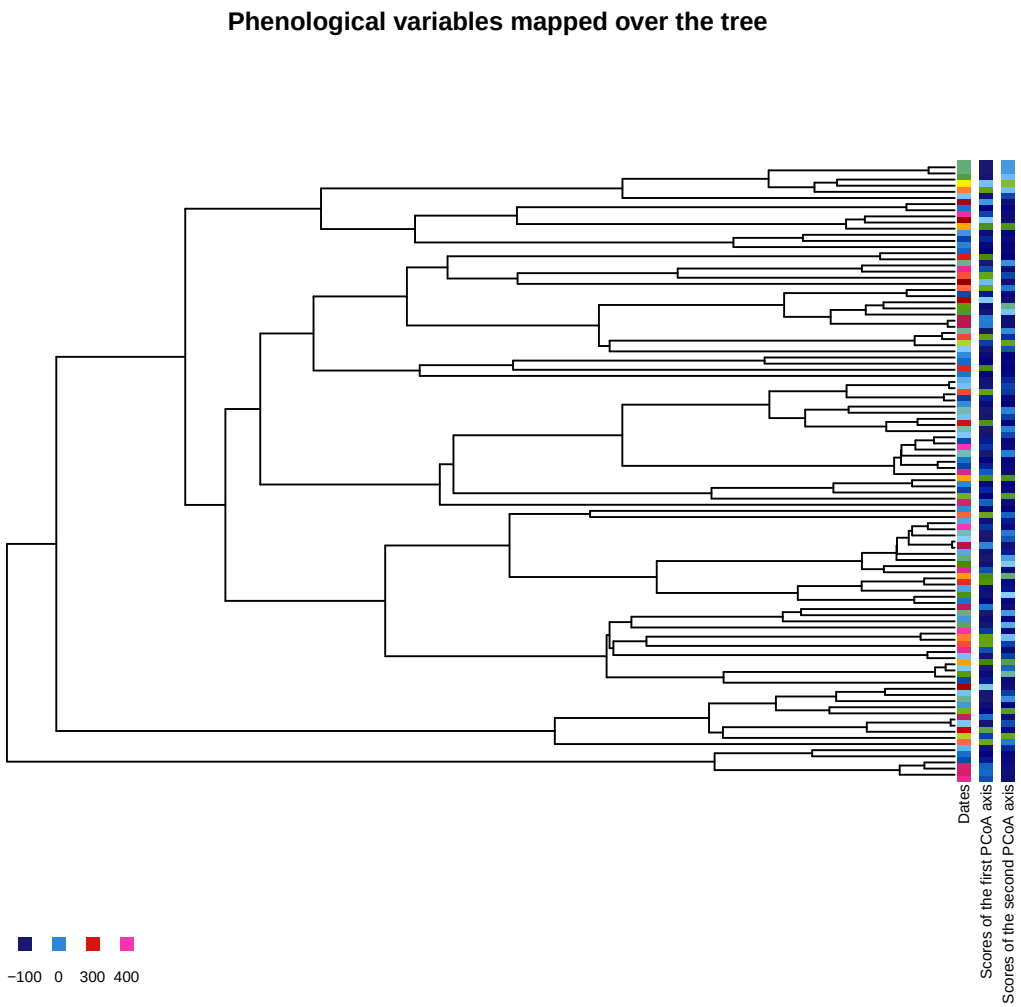


Figure 12: Phylogenetic structure of flowering dates and scores of the PCoA axes

```r
title(main = "Relationship between distances", cex.main = 0.8)


plot.mgram(
  resu_example4$Mantel$Correlogram,
  xlab = "Midpoint of the distance class",
  bty = "l",
  ylab = "Mantel r")
title(main = "Mantel correlogram", cex.main = 0.8)


par(on)
```

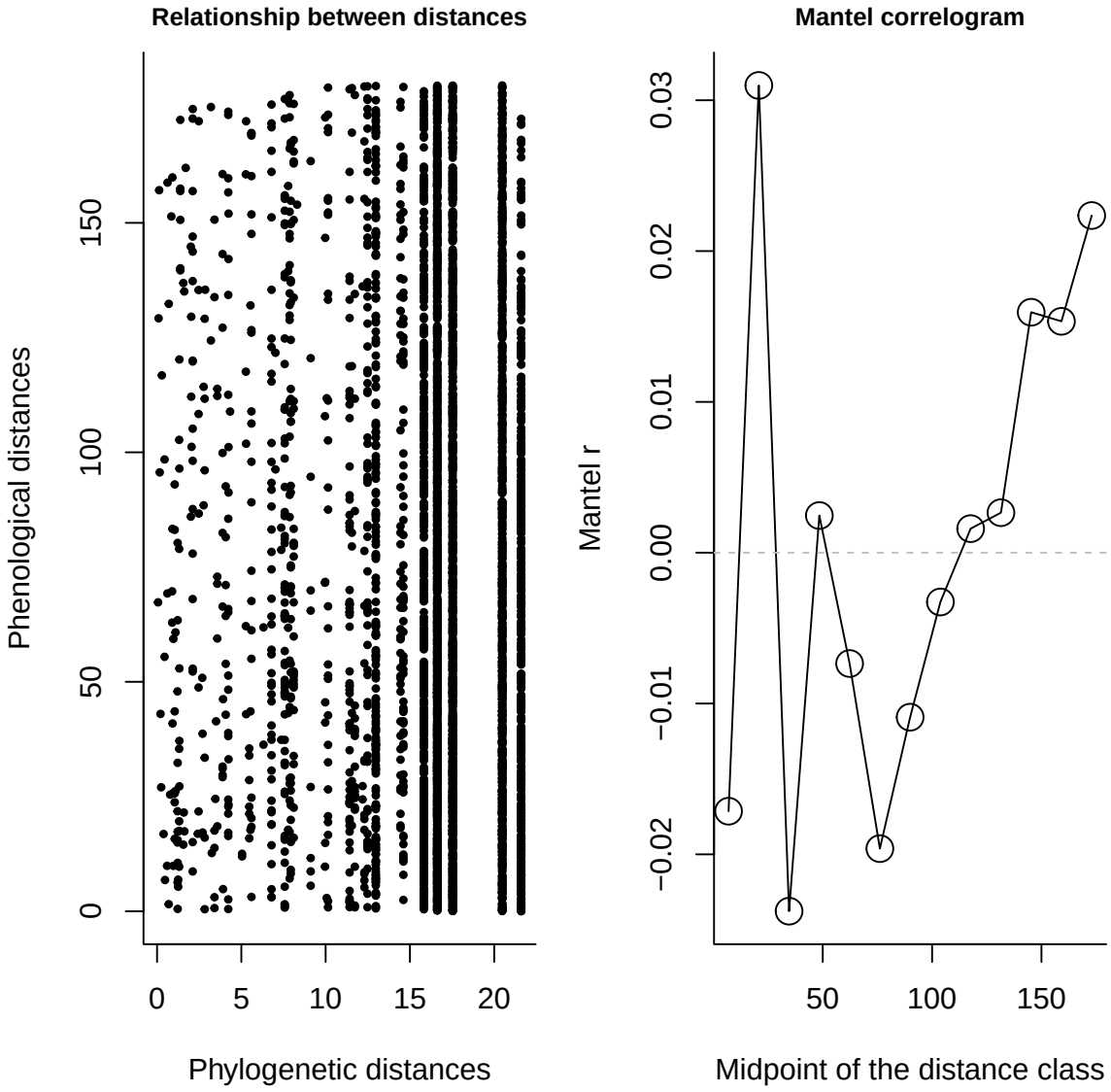


Figure 13: Correlation between phylogenetic and phenological distances

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