

Spectra-trait PLSR example using leaf-level spectra and leaf mass per area (LMA) data from 36 species growing in *Rosa rugosa* invaded coastal grassland communities in Belgium

Shawn P. Serbin, Julien Lamour, & Jeremiah Anderson

Overview

This is an R Markdown Notebook to illustrate how to retrieve a dataset from the EcoSIS spectral database, choose the “optimal” number of pls components, and fit a pls model for leaf-mass area (LMA)

Getting Started

Step 1. Load libraries needed to run example script

```
list.of.packages <- c("pls", "dplyr", "reshape2", "here", "plotrix", "ggplot2", "gridExtra",
                      "spectratrait")
invisible(lapply(list.of.packages, library, character.only = TRUE))

##
## Attaching package: 'pls'
## The following object is masked from 'package:stats':
##
##   loadings
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
## here() starts at /Users/sserbin/Data/GitHub/spectratrait
##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##   combine
```

Step 2. Setup other functions and options

```
### Setup other functions and options
# not in
`%notin%` <- Negate(`%in%`)

# Script options
pls::pls.options(plsralg = "oscorespls")
pls::pls.options("plsralg")

## $plsralg
## [1] "oscorespls"

# Default par options
opar <- par(no.readonly = T)

# What is the target variable?
inVar <- "LMA_g_m2"

# What is the source dataset from EcoSIS?
ecosis_id <- "9db4c5a2-7eac-4e1e-8859-009233648e89"

# Specify output directory, output_dir
# Options:
# tempdir - use a OS-specified temporary directory
# user defined PATH - e.g. "~/scratch/PLSR"
output_dir <- "tempdir"
```

Step 3. Set working directory (scratch space)

```
## [1] "/private/var/folders/xp/h3k9vf3n2jx181ts786_yjrn9c2gjQ/T/Rtmp0iM2dc"
```

Step 4. Pull example dataset from EcoSIS (ecosis.org)

```
print(paste0("Output directory: ",getwd())) # check wd

## [1] "Output directory: /Users/sserbin/Data/GitHub/spectratrait/vignettes"

### Get source dataset from EcoSIS
dat_raw <- spectratrait::get_ecosis_data(ecosis_id = ecosis_id)

## [1] "**** Downloading Ecosis data ****"

## Downloading data...

##
## -- Column specification -----
## cols(
##   .default = col_double(),
##   `Latin Species` = col_character(),
##   ids = col_character(),
##   `plot code` = col_character(),
##   `species code` = col_character()
## )
```

```
## i Use `spec()` for the full column specifications.
```

```
## Download complete!
```

```
head(dat_raw)
```

```
## # A tibble: 6 x 2,164
##   `Cw/EWT (cm3/cm2` `Latin Species`   `Leaf area (mm2` `Leaf calcium content pe~
##           <dbl> <chr>                <dbl>                <dbl>
## 1         0.00887 Arrhenatherum el~         696.                0.0291
## 2         0.00824 Bromus sterilis         447.                0.0230
## 3         0.0280  Jacobaea vulgaris        2418.                0.0950
## 4         0.0106  Rubus caesius         5719.                0.0700
## 5         0.00851 Arrhenatherum el~         671.                0.0286
## 6         0.0153  Crepis capillaris        1401.                0.0470
## # ... with 2,160 more variables:
## #   Leaf magnesium content per leaf area (mg/mm2) <dbl>,
## #   Leaf mass per area (g/cm2) <dbl>,
## #   Leaf nitrogen content per leaf area (mg/mm2) <dbl>,
## #   Leaf phosphorus content per leaf area (mg/mm2) <dbl>,
## #   Leaf potassium content per leaf area (mg/mm2) <dbl>,
## #   Plant height vegetative (cm) <dbl>, ids <chr>, plot code <chr>,
## #   species code <chr>, 350 <dbl>, 351 <dbl>, 352 <dbl>, 353 <dbl>, 354 <dbl>,
## #   355 <dbl>, 356 <dbl>, 357 <dbl>, 358 <dbl>, 359 <dbl>, 360 <dbl>,
## #   361 <dbl>, 362 <dbl>, 363 <dbl>, 364 <dbl>, 365 <dbl>, 366 <dbl>,
## #   367 <dbl>, 368 <dbl>, 369 <dbl>, 370 <dbl>, 371 <dbl>, 372 <dbl>,
## #   373 <dbl>, 374 <dbl>, 375 <dbl>, 376 <dbl>, 377 <dbl>, 378 <dbl>,
## #   379 <dbl>, 380 <dbl>, 381 <dbl>, 382 <dbl>, 383 <dbl>, 384 <dbl>,
## #   385 <dbl>, 386 <dbl>, 387 <dbl>, 388 <dbl>, 389 <dbl>, 390 <dbl>,
## #   391 <dbl>, 392 <dbl>, 393 <dbl>, 394 <dbl>, 395 <dbl>, 396 <dbl>,
## #   397 <dbl>, 398 <dbl>, 399 <dbl>, 400 <dbl>, 401 <dbl>, 402 <dbl>,
## #   403 <dbl>, 404 <dbl>, 405 <dbl>, 406 <dbl>, 407 <dbl>, 408 <dbl>,
## #   409 <dbl>, 410 <dbl>, 411 <dbl>, 412 <dbl>, 413 <dbl>, 414 <dbl>,
## #   415 <dbl>, 416 <dbl>, 417 <dbl>, 418 <dbl>, 419 <dbl>, 420 <dbl>,
## #   421 <dbl>, 422 <dbl>, 423 <dbl>, 424 <dbl>, 425 <dbl>, 426 <dbl>,
## #   427 <dbl>, 428 <dbl>, 429 <dbl>, 430 <dbl>, 431 <dbl>, 432 <dbl>,
## #   433 <dbl>, 434 <dbl>, 435 <dbl>, 436 <dbl>, 437 <dbl>, 438 <dbl>,
## #   439 <dbl>, 440 <dbl>, ...
```

```
names(dat_raw)[1:40]
```

```
## [1] "Cw/EWT (cm3/cm2)"
## [2] "Latin Species"
## [3] "Leaf area (mm2)"
## [4] "Leaf calcium content per leaf area (mg/mm2)"
## [5] "Leaf magnesium content per leaf area (mg/mm2)"
## [6] "Leaf mass per area (g/cm2)"
## [7] "Leaf nitrogen content per leaf area (mg/mm2)"
## [8] "Leaf phosphorus content per leaf area (mg/mm2)"
## [9] "Leaf potassium content per leaf area (mg/mm2)"
## [10] "Plant height vegetative (cm)"
## [11] "ids"
## [12] "plot code"
## [13] "species code"
## [14] "350"
## [15] "351"
```

```
## [16] "352"
## [17] "353"
## [18] "354"
## [19] "355"
## [20] "356"
## [21] "357"
## [22] "358"
## [23] "359"
## [24] "360"
## [25] "361"
## [26] "362"
## [27] "363"
## [28] "364"
## [29] "365"
## [30] "366"
## [31] "367"
## [32] "368"
## [33] "369"
## [34] "370"
## [35] "371"
## [36] "372"
## [37] "373"
## [38] "374"
## [39] "375"
## [40] "376"
```

Step 5. Create full pls dataset

```
### Create pls dataset
Start.wave <- 500
End.wave <- 2400
wv <- seq(Start.wave,End.wave,1)
Spectra <- as.matrix(dat_raw[,names(dat_raw) %in% wv])
colnames(Spectra) <- c(paste0("Wave_",wv))
sample_info <- dat_raw[,names(dat_raw) %notin% seq(350,2500,1)]
head(sample_info)

## # A tibble: 6 x 13
##   `Cw/EWT (cm3/cm2~` `Latin Species`   `Leaf area (mm2~` `Leaf calcium content pe~
##           <dbl> <chr>                   <dbl>                <dbl>
## 1         0.00887 Arrhenatherum el~         696.                0.0291
## 2         0.00824 Bromus sterilis         447.                0.0230
## 3         0.0280  Jacobaea vulgaris       2418.                0.0950
## 4         0.0106  Rubus caesius         5719.                0.0700
## 5         0.00851 Arrhenatherum el~         671.                0.0286
## 6         0.0153  Crepis capillaris       1401.                0.0470
## # ... with 9 more variables:
## #   Leaf magnesium content per leaf area (mg/mm2) <dbl>,
## #   Leaf mass per area (g/cm2) <dbl>,
## #   Leaf nitrogen content per leaf area (mg/mm2) <dbl>,
## #   Leaf phosphorus content per leaf area (mg/mm2) <dbl>,
## #   Leaf potassium content per leaf area (mg/mm2) <dbl>,
## #   Plant height vegetative (cm) <dbl>, ids <chr>, plot code <chr>,
```

```
## # species code <chr>
sample_info2 <- sample_info %>%
  select(Plant_Species=`Latin Species`,Species_Code=`species code`,Plot=`plot code`,
         LMA_g_cm2=`Leaf mass per area (g/cm2)`)
sample_info2 <- sample_info2 %>%
  mutate(LMA_g_m2=LMA_g_cm2*10000)
head(sample_info2)

## # A tibble: 6 x 5
##   Plant_Species      Species_Code Plot  LMA_g_cm2 LMA_g_m2
##   <chr>             <chr>      <chr>    <dbl>    <dbl>
## 1 Arrhenatherum elatius Arrela      DC1     0.00342    34.2
## 2 Bromus sterilis      Broste      DC1     0.00282    28.2
## 3 Jacobaea vulgaris     Jacvul      DC1     0.00417    41.7
## 4 Rubus caesius         Rubcae      DC1     0.00566    56.6
## 5 Arrhenatherum elatius Arrela      DC2     0.00361    36.1
## 6 Crepis capillaris     Creves      DC2     0.00283    28.3

plsr_data <- data.frame(sample_info2,Spectra)
rm(sample_info,sample_info2,Spectra)
```

Step 6. Example data cleaning.

```
#### Example data cleaning. End user needs to do what's appropriate for their
#### data. This may be an iterative process.
# Keep only complete rows of inVar and spec data before fitting
plsr_data <- plsr_data[complete.cases(plsr_data[,names(plsr_data) %in%
                                         c(inVar,paste0("Wave_",wv))]),]
```

Step 7. Create cal/val datasets

```
method <- "dplyr" #base/dplyr
# base R - a bit slow
# dplyr - much faster
split_data <- spectratrait::create_data_split(dataset=plsr_data, approach=method,
                                              split_seed=7529075, prop=0.8,
                                              group_variables="Species_Code")
names(split_data)

## [1] "cal_data" "val_data"

cal.plsr.data <- split_data$cal_data
head(cal.plsr.data)[1:8]
```

```
##      Plant_Species Species_Code Plot  LMA_g_cm2 LMA_g_m2 Wave_500 Wave_501
## 1 Ammophila arenaria    Ammare  MC2  0.01679492 167.9492 0.135785 0.13685
## 2 Ammophila arenaria    Ammare  WC3  0.01844376 184.4376 0.151750 0.15275
## 3 Ammophila arenaria    Ammare  MC4  0.02030190 203.0190 0.156830 0.15790
## 4 Ammophila arenaria    Ammare  ZC2  0.01591894 159.1894 0.144450 0.14525
## 5 Ammophila arenaria    Ammare  ZC1  0.01483469 148.3469 0.147665 0.14910
## 6 Ammophila arenaria    Ammare  ZC3  0.01802409 180.2409 0.130885 0.13175
##      Wave_502
```

```
## 1 0.138150
## 2 0.154150
## 3 0.159065
## 4 0.146220
## 5 0.150330
## 6 0.132750
```

```
val.plsr.data <- split_data$val_data
head(val.plsr.data)[1:8]
```

```
##      Plant_Species Species_Code Plot   LMA_g_cm2 LMA_g_m2   Wave_500
## 184  Jacobaea vulgaris   Jacvul  WC2 0.003551614  35.51614 0.06736887
## 185  Potentilla reptans   Potrep  WC2 0.005586320  55.86320 0.07125000
## 186    Rubus caesius     Rubcae  WC2 0.005803902  58.03902 0.05993560
## 187    Urtica dioica     Urtdio  WC2 0.005215705  52.15705 0.06508300
## 188  Ammophila arenaria   Ammare  WC3 0.018443757 184.43757 0.15175000
## 189  Jacobaea vulgaris   Jacvul  WC3 0.004980002  49.80002 0.06805547
##      Wave_501   Wave_502
## 184 0.06870667 0.07014220
## 185 0.07235000 0.07368350
## 186 0.06162000 0.06352233
## 187 0.06625000 0.06758350
## 188 0.15275000 0.15415000
## 189 0.06938000 0.07093553
```

```
rm(split_data)
```

```
# Datasets:
```

```
print(paste("Cal observations: ",dim(cal.plsr.data)[1],sep=""))
```

```
## [1] "Cal observations: 183"
```

```
print(paste("Val observations: ",dim(val.plsr.data)[1],sep=""))
```

```
## [1] "Val observations: 73"
```

```
text_loc <- c(max(hist(cal.plsr.data[,paste0(inVar)], plot=FALSE)$counts),
              max(hist(cal.plsr.data[,paste0(inVar)], plot=FALSE)$mids))
cal_hist_plot <- qplot(cal.plsr.data[,paste0(inVar)],geom="histogram",
                      main = paste0("Calibration Histogram for ",inVar),
                      xlab = paste0(inVar),ylab = "Count",fill=I("grey50"),col=I("black"),
                      alpha=I(.7)) +
  annotate("text", x=text_loc[2], y=text_loc[1], label= "1.",size=10)
val_hist_plot <- qplot(val.plsr.data[,paste0(inVar)],geom="histogram",
                      main = paste0("Validation Histogram for ",inVar),
                      xlab = paste0(inVar),ylab = "Count",fill=I("grey50"),col=I("black"),
                      alpha=I(.7))
histograms <- grid.arrange(cal_hist_plot, val_hist_plot, ncol=2)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

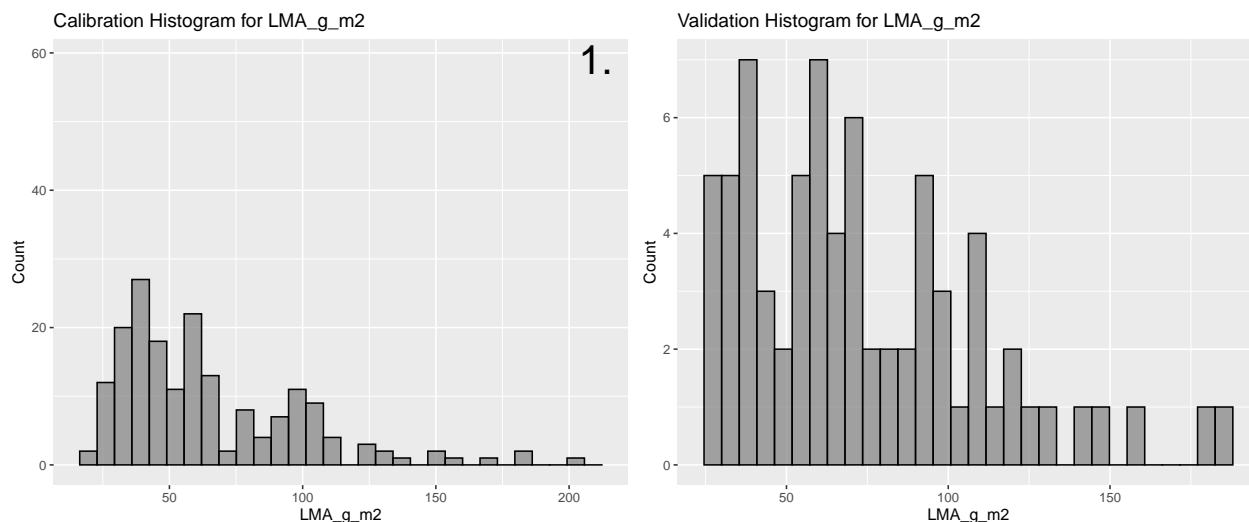


Figure S1. The resulting leaf mass area (LMA, g/m2) distribution (histogram) for the calibration (i.e. model training) and validation datasets. The data was split using the spectratrait::create_data_split() function using "Species_Code" as the group_variable and using a data split proportion per group of 80% to calibration and 20% to validation

```
ggsave(filename = file.path(outdir,paste0(inVar,"_Cal_Val_Histograms.png")),
        plot = histograms, device="png", width = 30, height = 12, units = "cm",
        dpi = 300)
# output cal/val data
write.csv(cal.plsr.data,file=file.path(outdir,paste0(inVar,'_Cal_PLSR_Dataset.csv')),
          row.names=FALSE)
write.csv(val.plsr.data,file=file.path(outdir,paste0(inVar,'_Val_PLSR_Dataset.csv')),
          row.names=FALSE)
```

Step 8. Create calibration and validation PLSR datasets

```
### Format PLSR data for model fitting
cal_spec <- as.matrix(cal.plsr.data[, which(names(cal.plsr.data) %in%
                                             paste0("Wave_",wv))])
cal.plsr.data <- data.frame(cal.plsr.data[, which(names(cal.plsr.data) %notin%
                                                  paste0("Wave_",wv))],
                           Spectra=I(cal_spec))
head(cal.plsr.data)[1:5]
```

```
##      Plant_Species Species_Code Plot  LMA_g_cm2 LMA_g_m2
## 1 Ammophila arenaria      Ammare MC2 0.01679492 167.9492
## 2 Ammophila arenaria      Ammare WC3 0.01844376 184.4376
## 3 Ammophila arenaria      Ammare MC4 0.02030190 203.0190
## 4 Ammophila arenaria      Ammare ZC2 0.01591894 159.1894
## 5 Ammophila arenaria      Ammare ZC1 0.01483469 148.3469
## 6 Ammophila arenaria      Ammare ZC3 0.01802409 180.2409
```

```
val_spec <- as.matrix(val.plsr.data[, which(names(val.plsr.data) %in%
                                             paste0("Wave_",wv))])
val.plsr.data <- data.frame(val.plsr.data[, which(names(val.plsr.data) %notin%
                                                  paste0("Wave_",wv))],
```

```

Spectra=I(val_spec))
head(val.plsr.data)[1:5]

##      Plant_Species Species_Code Plot   LMA_g_cm2  LMA_g_m2
## 184  Jacobaea vulgaris      Jacvul  WC2 0.003551614 35.51614
## 185  Potentilla reptans     Potrep  WC2 0.005586320 55.86320
## 186    Rubus caesius       Rubcae  WC2 0.005803902 58.03902
## 187    Urtica dioica       Urtdio  WC2 0.005215705 52.15705
## 188  Ammophila arenaria     Ammare  WC3 0.018443757 184.43757
## 189  Jacobaea vulgaris      Jacvul  WC3 0.004980002 49.80002

```

Step 9. Calibration and Validation spectra plot

```

par(mfrow=c(1,2)) # B, L, T, R
spectratrait::f.plot.spec(Z=cal.plsr.data$Spectra,wv=wv,
                          plot_label="Calibration")
text(550,95,labels = "2.",cex=3)
spectratrait::f.plot.spec(Z=val.plsr.data$Spectra,wv=wv,
                          plot_label="Validation")

```

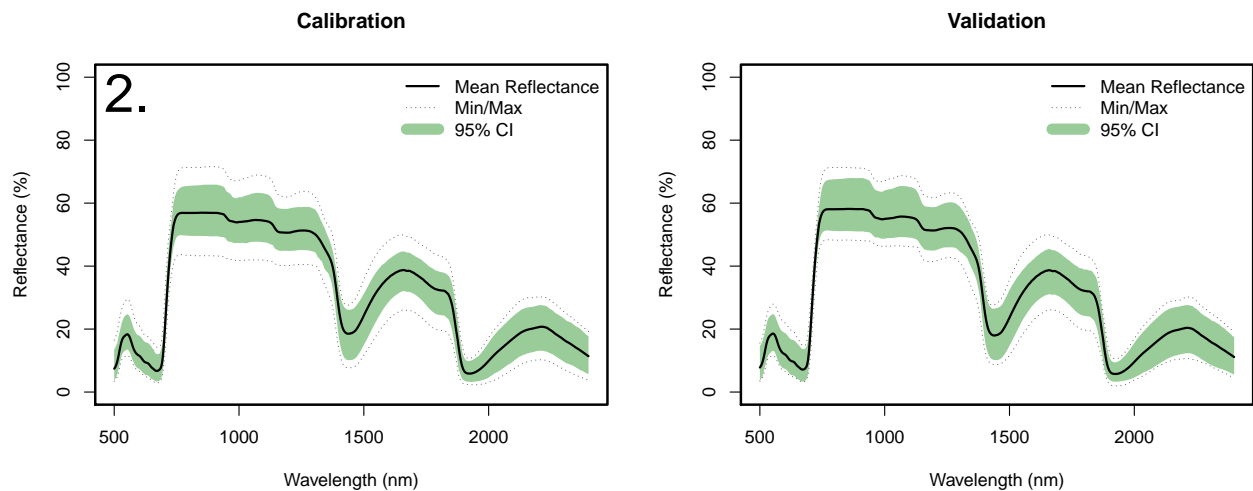


Figure S2. The resulting calibration and validation spectral reflectance distribution by wavelength. The spectra split was done at the same time as LMA, as described in Supplemental Figure S1.

```

dev.copy(png,file.path(outdir,paste0(inVar,'_Cal_Val_Spectra.png')),
         height=2500,width=4900, res=340)

```

```

## quartz_off_screen
##      3

```

```
dev.off();
```

```

## pdf
##    2
par(mfrow=c(1,1))

```


Step 10. Use permutation to determine the optimal number of components

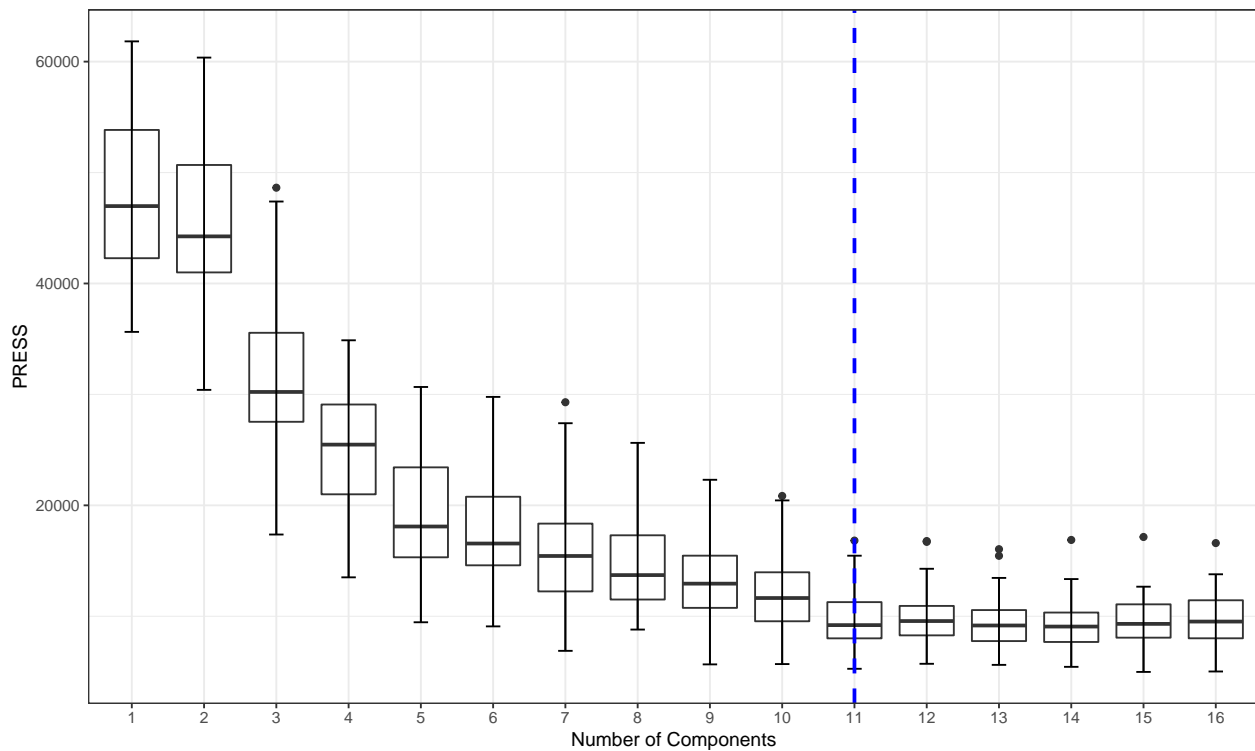
```
### Use permutation to determine the optimal number of components
if(grepl("Windows", sessionInfo()$running)){
  pls.options(parallel = NULL)
} else {
  pls.options(parallel = parallel::detectCores()-1)
}

method <- "firstMin" #pls, firstPlateau, firstMin
random_seed <- 7529075
seg <- 80
maxComps <- 16
iterations <- 50
prop <- 0.70
if (method=="pls") {
  nComps <- spectratrait::find_optimal_components(dataset=cal.plsr.data, method=method,
                                                  maxComps=maxComps, seg=seg,
                                                  random_seed=random_seed)

  print(paste0("*** Optimal number of components: ", nComps))
} else {
  nComps <- spectratrait::find_optimal_components(dataset=cal.plsr.data, method=method,
                                                  maxComps=maxComps, iterations=iterations,
                                                  seg=seg, prop=prop,
                                                  random_seed=random_seed)
}

## [1] "*** Running permutation test. Please hang tight, this can take awhile ***"
## [1] "Options:"
## [1] "Max Components: 16 Iterations: 50 Data Proportion (percent): 70"
## [1] "*** Providing PRESS and coefficient array output ***"

## No id variables; using all as measure variables
## [1] "*** Optimal number of components based on t.test: 11"
```



*# Figure S3. Selection of the optimal number of components based on the
minimization of the PRESS statistic. In this example we show "firstMin"
option that selects the number of components corresponding to the first
statistical minimum PRESS value (vertical broken blue line).*

```
dev.copy(png,file.path(outdir,paste0(paste0("Figure_3_",inVar,
                                           "_PLSR_Component_Selection.png"))),
         height=2800, width=3400, res=340)
```

```
## quartz_off_screen
##                      3
dev.off();
```

```
## pdf
##    2
```

Step 11. Fit final model

```
### Fit final model - using leave-one-out cross validation
plsr.out <- plsr(as.formula(paste(inVar,"~","Spectra")),scale=FALSE,ncomp=nComps,
                validation="L00",trace=FALSE,data=cal.plsr.data)
fit <- plsr.out$fitted.values[,1,nComps]
pls.options(parallel = NULL)

# External validation fit stats
text_loc <- c(max(RMSEP(plsr.out, newdata = val.plsr.data)$comps),
              RMSEP(plsr.out, newdata = val.plsr.data)$val[1])
par(mfrow=c(1,2)) # B, L, T, R
pls::RMSEP(plsr.out, newdata = val.plsr.data)
```

```
## (Intercept)      1 comps      2 comps      3 comps      4 comps      5 comps
##      37.79      32.71      30.36      23.51      21.58      18.46
##      6 comps      7 comps      8 comps      9 comps     10 comps     11 comps
##      15.89      15.44      15.52      15.19      15.14      13.68
```

```
plot(pls::RMSEP(plsr.out,estimate=c("test"),newdata = val.plsr.data), main="MODEL RMSEP",
     xlab="Number of Components",ylab="Model Validation RMSEP",lty=1,col="black",cex=1.5,lwd=2)
text(text_loc[1],text_loc[2],labels = "4.", cex=2)
box(lwd=2.2)
```

```
pls::R2(plsr.out, newdata = val.plsr.data)
```

```
## (Intercept)      1 comps      2 comps      3 comps      4 comps      5 comps
##     -0.06195      0.20461      0.31467      0.58911      0.65365      0.74649
##      6 comps      7 comps      8 comps      9 comps     10 comps     11 comps
##      0.81222      0.82276      0.82084      0.82841      0.82945      0.86090
```

```
plot(pls::R2(plsr.out,estimate=c("test"),newdata = val.plsr.data), main="MODEL R2",
     xlab="Number of Components",ylab="Model Validation R2",lty=1,col="black",cex=1.5,lwd=2)
box(lwd=2.2)
```

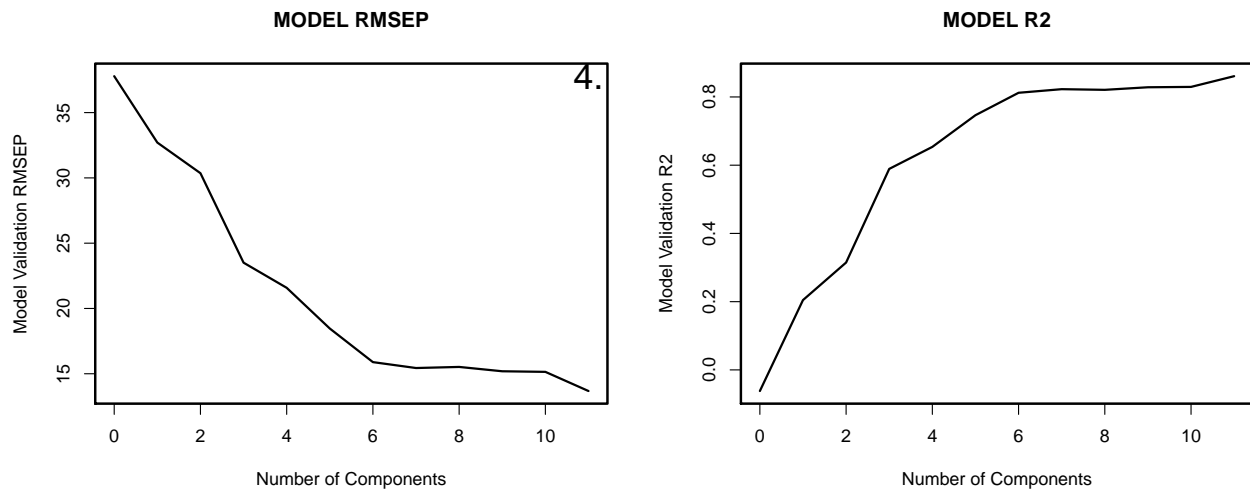


Figure S4. A plot of the validation root mean square error of prediction (RMSEP, left) and coefficient of determination (right) for the 0 to optimal number of components

```
dev.copy(png,file.path(outdir,paste0(paste0(inVar,"_Validation_RMSEP_R2_by_Component.png"))),
         height=2800, width=4800, res=340)
```

```
## quartz_off_screen
##      3
```

```
dev.off();
```

```
## pdf
##      2
```

```
par(opar)
```

Step 12. PLSR fit observed vs. predicted plot data

```
#calibration
cal.plsr.output <- data.frame(cal.plsr.data[, which(names(cal.plsr.data) %notin%
                                                    "Spectra")],
                              PLSR_Predicted=fit,
                              PLSR_CV_Predicted=as.vector(plsr.out$validation$pred[, ,
                                                                                               nComps]))

cal.plsr.output <- cal.plsr.output %>%
  mutate(PLSR_CV_Residuals = PLSR_CV_Predicted-get(inVar))
head(cal.plsr.output)
```

```
##      Plant_Species Species_Code Plot  LMA_g_cm2 LMA_g_m2 PLSR_Predicted
## 1 Ammophila arenaria      Ammare MC2 0.01679492 167.9492      154.1892
## 2 Ammophila arenaria      Ammare WC3 0.01844376 184.4376      147.0878
## 3 Ammophila arenaria      Ammare MC4 0.02030190 203.0190      153.8674
## 4 Ammophila arenaria      Ammare ZC2 0.01591894 159.1894      161.6047
## 5 Ammophila arenaria      Ammare ZC1 0.01483469 148.3469      144.9268
## 6 Ammophila arenaria      Ammare ZC3 0.01802409 180.2409      148.2100
##      PLSR_CV_Predicted PLSR_CV_Residuals
## 1          151.7161      -16.233027
## 2          137.3863      -47.051273
## 3          144.2584      -58.760574
## 4          162.6250       3.435614
## 5          142.9101      -5.436767
## 6          142.5160      -37.724928
```

```
cal.R2 <- round(pls::R2(plsr.out)[[1]][nComps],2)
cal.RMSEP <- round(sqrt(mean(cal.plsr.output$PLSR_CV_Residuals^2)),2)

val.plsr.output <- data.frame(val.plsr.data[, which(names(val.plsr.data) %notin%
                                                    "Spectra")],
                              PLSR_Predicted=as.vector(predict(plsr.out,
                                                                newdata = val.plsr.data,
                                                                ncomp=nComps,
                                                                type="response")[,1]))

val.plsr.output <- val.plsr.output %>%
  mutate(PLSR_Residuals = PLSR_Predicted-get(inVar))
head(val.plsr.output)
```

```
##      Plant_Species Species_Code Plot  LMA_g_cm2 LMA_g_m2 PLSR_Predicted
## 184 Jacobaea vulgaris      Jacvul WC2 0.003551614 35.51614      43.51586
## 185 Potentilla reptans      Potrep WC2 0.005586320 55.86320      61.41726
## 186 Rubus caesius          Rubcae WC2 0.005803902 58.03902      45.55789
## 187 Urtica dioica          Urtdio WC2 0.005215705 52.15705      46.65139
## 188 Ammophila arenaria      Ammare WC3 0.018443757 184.43757      147.08781
## 189 Jacobaea vulgaris      Jacvul WC3 0.004980002 49.80002      53.09532
##      PLSR_Residuals
## 184          7.999719
## 185          5.554059
## 186         -12.481126
## 187         -5.505664
## 188        -37.349758
## 189          3.295298
```

```

val.R2 <- round(pls::R2(plsr.out,newdata=val.plsr.data)[[1]][nComps],2)
val.RMSEP <- round(sqrt(mean(val.plsr.output$PLSR_Residuals^2)),2)

rng_quant <- quantile(cal.plsr.output[,inVar], probs = c(0.001, 0.999))
cal_scatter_plot <- ggplot(cal.plsr.output, aes(x=PLSR_CV_Predicted, y=get(inVar))) +
  theme_bw() + geom_point() + geom_abline(intercept = 0, slope = 1, color="dark grey",
                                          linetype="dashed", size=1.5) +

  xlim(rng_quant[1], rng_quant[2]) +
  ylim(rng_quant[1], rng_quant[2]) +
  labs(x=paste0("Predicted ", paste(inVar), " (units)"),
       y=paste0("Observed ", paste(inVar), " (units)"),
       title=paste0("Calibration: ", paste0("Rsqr = ", cal.R2), "; ",
                paste0("RMSEP = ", cal.RMSEP))) +
  theme(axis.text=element_text(size=18), legend.position="none",
        axis.title=element_text(size=20, face="bold"),
        axis.text.x = element_text(angle = 0,vjust = 0.5),
        panel.border = element_rect(linetype = "solid", fill = NA, size=1.5)) +
  annotate("text", x=rng_quant[1], y=rng_quant[2], label= "5.",size=10)

cal_resid_histogram <- ggplot(cal.plsr.output, aes(x=PLSR_CV_Residuals)) +
  geom_histogram(alpha=.5, position="identity") +
  geom_vline(xintercept = 0, color="black",
            linetype="dashed", size=1) + theme_bw() +
  theme(axis.text=element_text(size=18), legend.position="none",
        axis.title=element_text(size=20, face="bold"),
        axis.text.x = element_text(angle = 0,vjust = 0.5),
        panel.border = element_rect(linetype = "solid", fill = NA, size=1.5))

rng_quant <- quantile(val.plsr.output[,inVar], probs = c(0.001, 0.999))
val_scatter_plot <- ggplot(val.plsr.output, aes(x=PLSR_Predicted, y=get(inVar))) +
  theme_bw() + geom_point() + geom_abline(intercept = 0, slope = 1, color="dark grey",
                                          linetype="dashed", size=1.5) +

  xlim(rng_quant[1], rng_quant[2]) +
  ylim(rng_quant[1], rng_quant[2]) +
  labs(x=paste0("Predicted ", paste(inVar), " (units)"),
       y=paste0("Observed ", paste(inVar), " (units)"),
       title=paste0("Validation: ", paste0("Rsqr = ", val.R2), "; ",
                paste0("RMSEP = ", val.RMSEP))) +
  theme(axis.text=element_text(size=18), legend.position="none",
        axis.title=element_text(size=20, face="bold"),
        axis.text.x = element_text(angle = 0,vjust = 0.5),
        panel.border = element_rect(linetype = "solid", fill = NA, size=1.5))

val_resid_histogram <- ggplot(val.plsr.output, aes(x=PLSR_Residuals)) +
  geom_histogram(alpha=.5, position="identity") +
  geom_vline(xintercept = 0, color="black",
            linetype="dashed", size=1) + theme_bw() +
  theme(axis.text=element_text(size=18), legend.position="none",
        axis.title=element_text(size=20, face="bold"),
        axis.text.x = element_text(angle = 0,vjust = 0.5),
        panel.border = element_rect(linetype = "solid", fill = NA, size=1.5))

# plot cal/val side-by-side

```

```
scatterplots <- grid.arrange(cal_scatter_plot, val_scatter_plot, cal_resid_histogram,
                             val_resid_histogram, nrow=2, ncol=2)
```

```
## Warning: Removed 6 rows containing missing values (geom_point).
```

```
## Warning: Removed 6 rows containing missing values (geom_point).
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

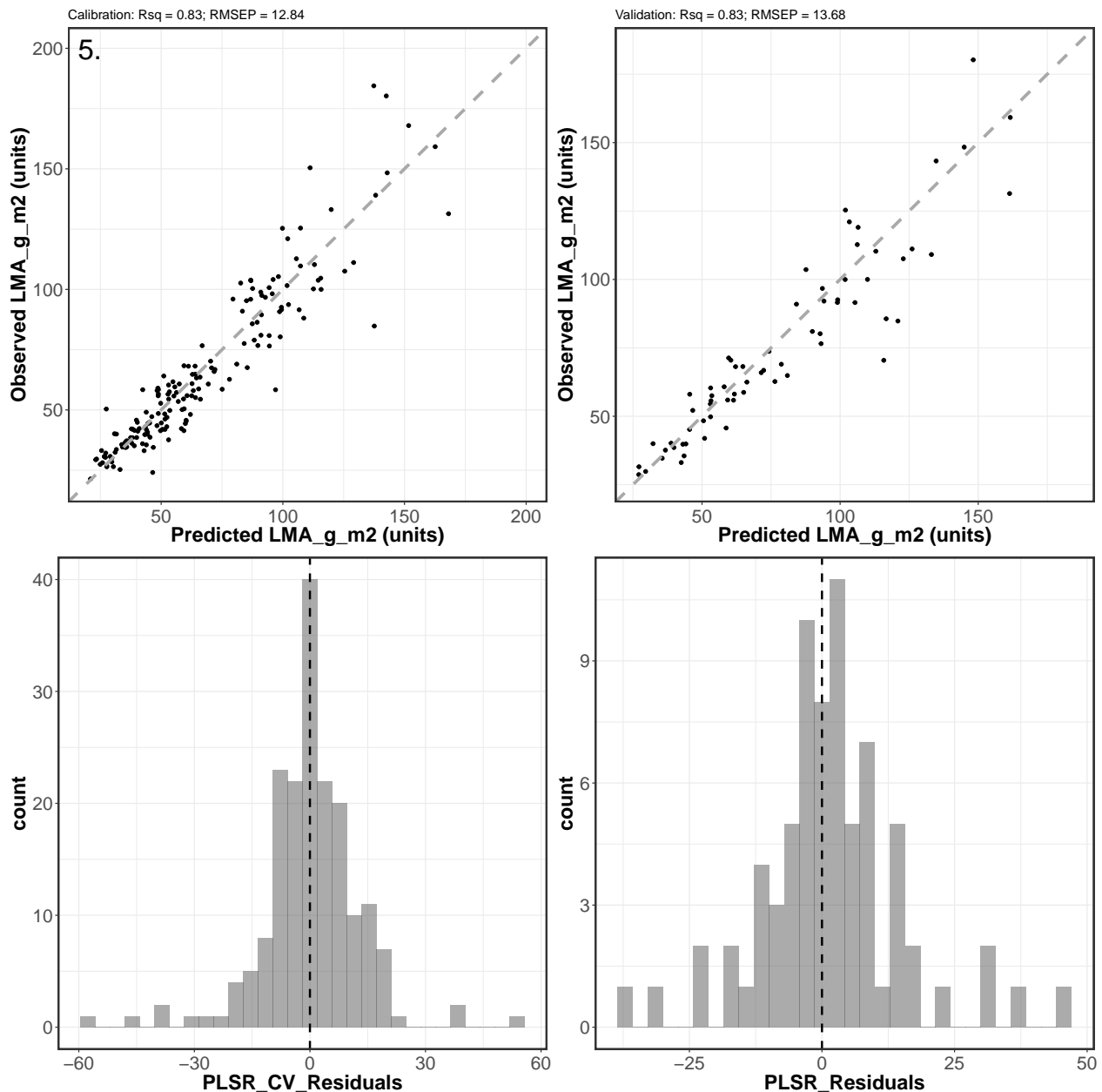
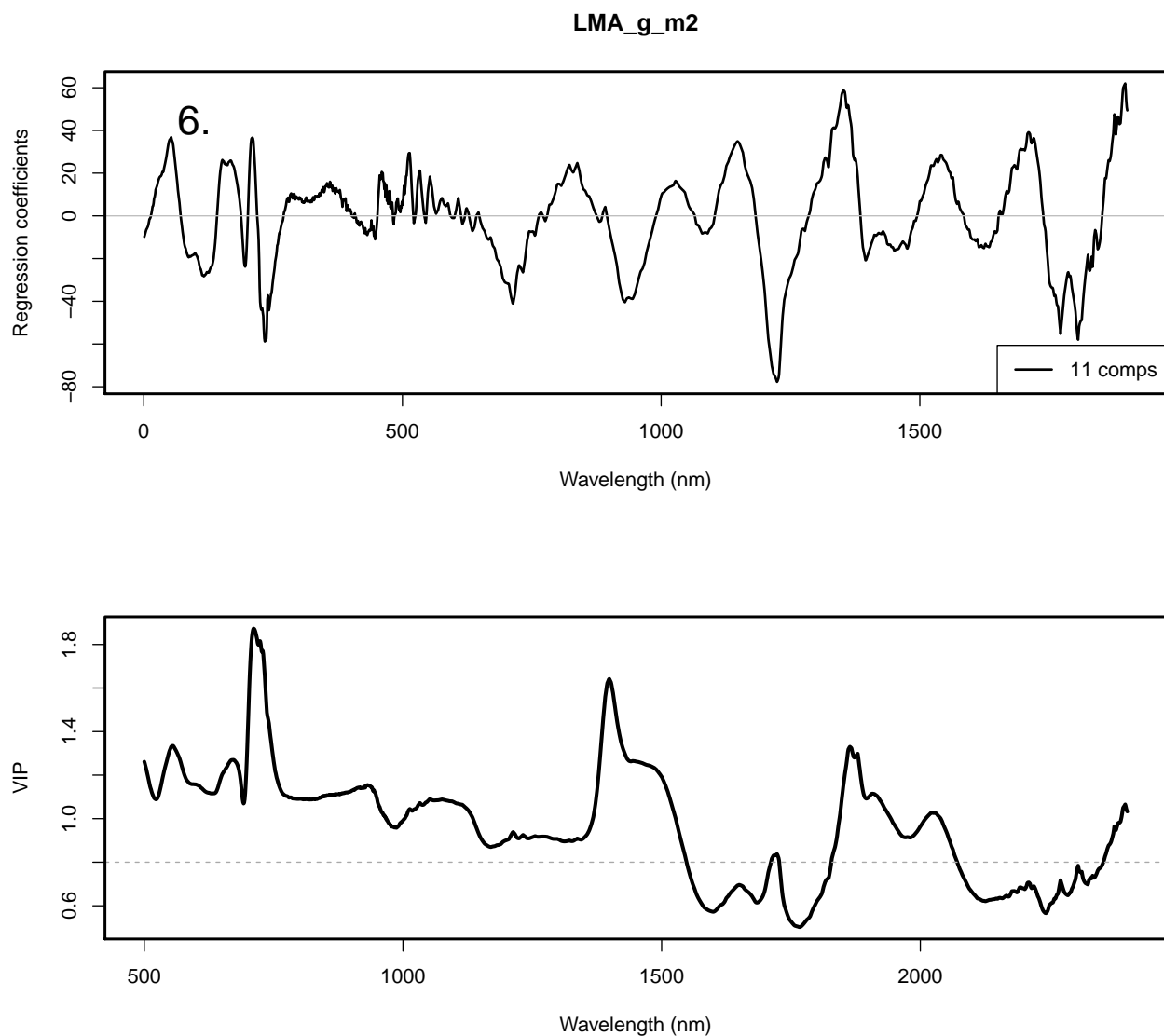


Figure S5. The calibration model and independent validation scatter plot results for
the example LMA PLSR model (top row). Also shown are the calibration model and
validation PLSR residuals, where the calibration results are based on the internal
model cross-validation and the validation residuals are the predicted minus observed
values of LMA.

Step 13. Generate Coefficient and VIP plots

```
vips <- spectratrait::VIP(plsr.out)[nComps,]

par(mfrow=c(2,1))
plot(plsr.out, plottype = "coef",xlab="Wavelength (nm)",
     ylab="Regression coefficients",legendpos = "bottomright",
     ncomp=nComps,lwd=2)
legend("topleft",legend = "6.", cex=2, bty="n")
box(lwd=2.2)
plot(seq(Start.wave,End.wave,1),vips,xlab="Wavelength (nm)",ylab="VIP",cex=0.01)
lines(seq(Start.wave,End.wave,1),vips,lwd=3)
abline(h=0.8,lty=2,col="dark grey")
box(lwd=2.2)
```



*# Figure S6. The calibration model PLSR regression coefficient (top) and variable
importance of projection (bottom) plots*

```
dev.copy(png,file.path(outdir,paste0(inVar,'_Coefficient_VIP_plot.png')),
```

```
height=3100, width=4100, res=340)
```

```
## quartz_off_screen
## 3
```

```
dev.off();
```

```
## pdf
## 2
```

Step 14. Permutation analysis to derive uncertainty estimates

```
if(grepl("Windows", sessionInfo()$running)){
  pls.options(parallel=NULL)
} else {
  pls.options(parallel = parallel::detectCores()-1)
}

jk.plsr.out <- pls::plsr(as.formula(paste(inVar,"~","Spectra")), scale=FALSE,
                        center=TRUE, ncomp=nComps, validation="LOO", trace=FALSE,
                        jackknife=TRUE,
                        data=cal.plsr.data)
pls.options(parallel = NULL)

Jackknife_coef <- spectratrait::f.coef.valid(plsr.out = jk.plsr.out,
                                             data_plsr = cal.plsr.data,
                                             ncomp = nComps, inVar=inVar)

Jackknife_intercept <- Jackknife_coef[1,,]
Jackknife_coef <- Jackknife_coef[2:dim(Jackknife_coef)[1],,,]

interval <- c(0.025,0.975)
Jackknife_Pred <- val.plsr.data$Spectra %*% Jackknife_coef +
  matrix(rep(Jackknife_intercept, length(val.plsr.data[,inVar])), byrow=TRUE,
         ncol=length(Jackknife_intercept))
Interval_Conf <- apply(X = Jackknife_Pred, MARGIN = 1, FUN = quantile,
                      probs=c(interval[1], interval[2]))
sd_mean <- apply(X = Jackknife_Pred, MARGIN = 1, FUN = sd)
sd_res <- sd(val.plsr.output$PLSR_Residuals)
sd_tot <- sqrt(sd_mean^2+sd_res^2)
val.plsr.output$LCI <- Interval_Conf[1,]
val.plsr.output$UCI <- Interval_Conf[2,]
val.plsr.output$LPI <- val.plsr.output$PLSR_Predicted-1.96*sd_tot
val.plsr.output$UPI <- val.plsr.output$PLSR_Predicted+1.96*sd_tot
head(val.plsr.output)
```

	Plant_Species	Species_Code	Plot	LMA_g_cm2	LMA_g_m2	PLSR_Predicted
## 184	Jacobaea vulgaris	Jacvul	WC2	0.003551614	35.51614	43.51586
## 185	Potentilla reptans	Potrep	WC2	0.005586320	55.86320	61.41726
## 186	Rubus caesius	Rubcae	WC2	0.005803902	58.03902	45.55789
## 187	Urtica dioica	Urt dio	WC2	0.005215705	52.15705	46.65139
## 188	Ammophila arenaria	Ammare	WC3	0.018443757	184.43757	147.08781
## 189	Jacobaea vulgaris	Jacvul	WC3	0.004980002	49.80002	53.09532
##	PLSR_Residuals	LCI	UCI	LPI	UPI	
## 184	7.999719	42.58086	44.15724	16.70642	70.32530	


```
## 185      5.554059  60.10507  62.52674  34.59536  88.23916
## 186     -12.481126  44.66849  48.22967  18.70489  72.41090
## 187     -5.505664  45.70375  47.84938  19.82512  73.47765
## 188    -37.349758 145.09309 148.61694 120.18052 173.99510
## 189      3.295298  52.40880  53.97806  26.28498  79.90565
```

```
### Permutation coefficient plot
spectratrait::f.plot.coef(Z = t(Jackknife_coef), wv = wv,
                          plot_label="Jackknife regression coefficients",position = 'bottomleft')
abline(h=0,lty=2,col="grey50")
legend("topleft",legend = "7.", cex=2, bty="n")
box(lwd=2.2)
```

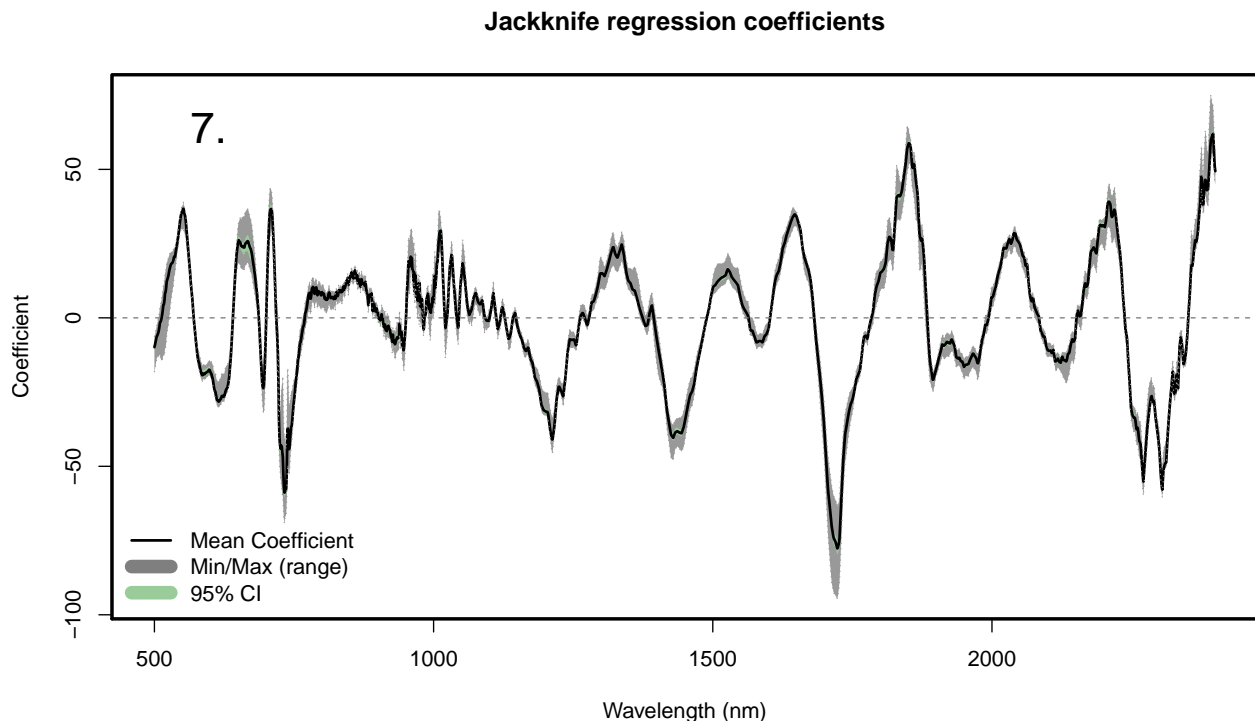


Figure S7. The calibration model jackknife PLSR regression coefficients

```
dev.copy(png,file.path(outdir,paste0(inVar,'_Jackknife_Regression_Coefficients.png')),
         height=2100, width=3800, res=340)
```

```
## quartz_off_screen
##      3
```

```
dev.off();
```

```
## pdf
##    2
```

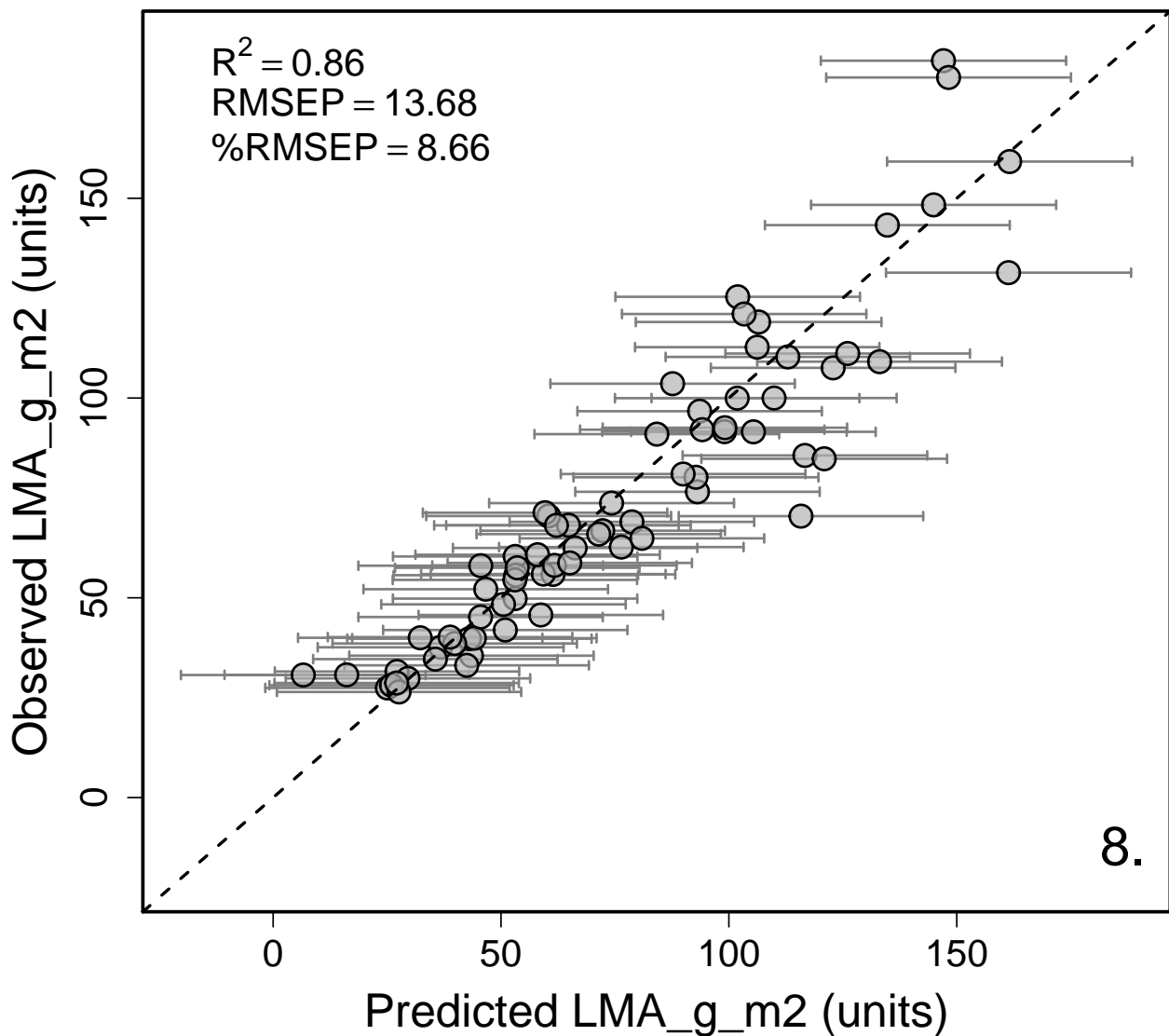
```
### Permutation validation plot
rmsep_percrmsep <- spectratrait::percent_rmse(plsr_dataset = val.plsr.output,
                                              inVar = inVar,
                                              residuals = val.plsr.output$PLSR_Residuals,
                                              range="full")

RMSEP <- rmsep_percrmsep$rmse
perc_RMSEP <- rmsep_percrmsep$perc_rmse
```

```

r2 <- round(pls::R2(plsr.out, newdata = val.plsr.data)$val[nComps+1],2)
expr <- vector("expression", 3)
expr[[1]] <- bquote(R^2==.(r2))
expr[[2]] <- bquote(RMSEP==.(round(RMSEP,2)))
expr[[3]] <- bquote("%RMSEP"==.(round(perc_RMSEP,2)))
rng_vals <- c(min(val.plsr.output$LPI), max(val.plsr.output$UPI))
par(mfrow=c(1,1), mar=c(4.2,5.3,1,0.4), oma=c(0, 0.1, 0, 0.2))
plotrix::plotCI(val.plsr.output$PLSR_Predicted, val.plsr.output[,inVar],
  li=val.plsr.output$LPI, ui=val.plsr.output$UPI, gap=0.009, sfrac=0.004,
  lwd=1.6, xlim=c(rng_vals[1], rng_vals[2]), ylim=c(rng_vals[1], rng_vals[2]),
  err="x", pch=21, col="black", pt.bg=scales::alpha("grey70",0.7), scol="grey50",
  cex=2, xlab=paste0("Predicted ", paste(inVar, " (units)"),
  ylab=paste0("Observed ", paste(inVar, " (units)"),
  cex.axis=1.5, cex.lab=1.8)
abline(0,1,lty=2,lw=2)
legend("topleft", legend=expr, bty="n", cex=1.5)
legend("bottomright", legend="8.", bty="n", cex=2.2)
box(lwd=2.2)

```



```
# Figure S8. Independent validation results for the LMA PLSR model with associated
# jackknife uncertainty estimate 95% prediction intervals for each estimate LMA
# value. The %RMSEP is the model prediction performance standardized to the
# percentage of the response range, in this case the range of LMA values
```

```
dev.copy(png,file.path(outdir,paste0(inVar,"_PLSR_Validation_Scatterplot.png")),
         height=2800, width=3200, res=340)
```

```
## quartz_off_screen
##           3
```

```
dev.off();
```

```
## pdf
##    2
```

Step 15. Output permutation coefficients for later use

```
out.jk.coefs <- data.frame(Iteration=seq(1,length(Jackknife_intercept),1),
                          Intercept=Jackknife_intercept,t(Jackknife_coef))
head(out.jk.coefs)[1:6]
```

```
##      Iteration Intercept  Wave_500  Wave_501  Wave_502  Wave_503
## Seg 1         1  18.33909  -7.580446  -6.724083  -5.886226  -4.984744
## Seg 2         2  21.22164  -8.574931  -7.084795  -6.255716  -5.384000
## Seg 3         3  19.63843 -18.104491 -17.260522 -16.154983 -14.960119
## Seg 4         4  15.90905 -10.715594  -9.874766  -8.926979  -8.007834
## Seg 5         5  17.51805  -8.952143  -8.305344  -7.136167  -6.221407
## Seg 6         6  12.18563  -7.702160  -7.128890  -6.532276  -5.840220
```

```
write.csv(out.jk.coefs,file=file.path(outdir,
                                     paste0(inVar,
                                             '_Jackknife_PLSR_Coefficients.csv')),
          row.names=FALSE)
```

Step 16. Output remaining core PLSR outputs

```
print(paste("Output directory: ", outdir))
```

```
## [1] "Output directory: /var/folders/xp/h3k9vf3n2jx181ts786_yjrn9c2gjq/T//Rtmp0iM2dc"
```

```
# Observed versus predicted
```

```
write.csv(cal.plsr.output,file=file.path(outdir,
                                         paste0(inVar,'_Observed_PLSR_CV_Pred_',
                                                  nComps,'comp.csv')),
          row.names=FALSE)
```

```
# Validation data
```

```
write.csv(val.plsr.output,file=file.path(outdir,
                                         paste0(inVar,'_Validation_PLSR_Pred_',
                                                  nComps,'comp.csv')),
          row.names=FALSE)
```

```

# Model coefficients
coefs <- coef(plsr.out,ncomp=nComps,intercept=TRUE)
write.csv(coefs,file=file.path(outdir,
                               paste0(inVar,'_PLSR_Coefficients_',
                                       nComps,'comp.csv')),
          row.names=TRUE)

# PLSR VIP
write.csv(vips,file=file.path(outdir,
                              paste0(inVar,'_PLSR_VIPs_',
                                      nComps,'comp.csv')))

```

Step 17. Confirm files were written to temp space

```

print("**** PLSR output files: ")

## [1] "**** PLSR output files: "
print(list.files(outdir)[grep(pattern = inVar, list.files(outdir))])

## [1] "Figure_3_LMA_g_m2_PLSR_Component_Selection.png"
## [2] "LMA_g_m2_Cal_PLSR_Dataset.csv"
## [3] "LMA_g_m2_Cal_Val_Histograms.png"
## [4] "LMA_g_m2_Cal_Val_Scatterplots.png"
## [5] "LMA_g_m2_Cal_Val_Spectra.png"
## [6] "LMA_g_m2_Coefficient_VIP_plot.png"
## [7] "LMA_g_m2_Jackknife_PLSR_Coefficients.csv"
## [8] "LMA_g_m2_Jackknife_Regression_Coefficients.png"
## [9] "LMA_g_m2_Observed_PLSR_CV_Pred_11comp.csv"
## [10] "LMA_g_m2_PLSR_Coefficients_11comp.csv"
## [11] "LMA_g_m2_PLSR_Validation_Scatterplot.png"
## [12] "LMA_g_m2_PLSR_VIPs_11comp.csv"
## [13] "LMA_g_m2_Val_PLSR_Dataset.csv"
## [14] "LMA_g_m2_Validation_PLSR_Pred_11comp.csv"
## [15] "LMA_g_m2_Validation_RMSEP_R2_by_Component.png"

```