

# 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

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## 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", "here", "plotrix", "ggplot2", "gridExtra", "spectratrait")
invisible(lapply(list.of.packages, library, character.only = TRUE))

## Warning: package 'pls' was built under R version 4.3.1
##
## Attaching package: 'pls'
## The following object is masked from 'package:stats':
##
##   loadings
## Warning: package 'dplyr' was built under R version 4.3.1
##
## 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/Library/CloudStorage/OneDrive-NASA/Data/Github/spectratrait
## Warning: package 'plotrix' was built under R version 4.3.1
## Warning: package 'ggplot2' was built under R version 4.3.1
##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
```

```
##      combine
```

## Step 2. Setup other functions and options

### ### Setup options

#### *# 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/th/fpt_z3417gn8xgply92pvy6r0000gq/T/RtmpZlgv21"
```

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

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

```
## [1] "Output directory: /Users/sserbin/Library/CloudStorage/OneDrive-NASA/Data/Github/spectratrait/vi"
```

### ### Get source dataset from EcoSIS

```
dat_raw <- spectratrait::get_ecosis_data(ecosis_id = ecosis_id)
```

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

```
## Downloading data...
```

```
## Rows: 256 Columns: 2164
```

```
## -- Column specification -----
```

```
## Delimiter: ","
```

```
## chr      (4): Latin Species, ids, plot code, species code
```

```
## dbl (2160): Cw/EWT (cm3/cm2), Leaf area (mm2), Leaf calcium content per leaf...
```

```
##
```

```
## i Use `spec()` to retrieve the full column specification for this data.
```

```
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
## Download complete!
```

```
head(dat_raw)
```

```
## # A tibble: 6 x 2,164
##   `Cw/EWT (cm3/cm2)` `Latin Species`   `Leaf area (mm2)` `Leaf calcium content~1
##           <dbl> <chr>                <dbl>                <dbl>
## 1           0.00887 Arrhenatherum ela~           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 ela~           671.                0.0286
## 6           0.0153  Crepis capillaris        1401.                0.0470
## # i abbreviated name: 1: `Leaf calcium content per leaf area (mg/mm2)`
## # i 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>, ...
```

```
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~1`
##   <dbl> <chr>                                <dbl>                <dbl>
## 1      0.00887 Arrhenatherum ela~          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 ela~          671.                0.0286
## 6      0.0153  Crepis capillaris         1401.               0.0470
## # i abbreviated name: 1: `Leaf calcium content per leaf area (mg/mm2)`
## # i 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>, ...

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

pls_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
## 1 Arrhenatherum elatius      Arrela DC1 0.003420518 34.20518 0.070667
## 2 Bromus sterilis      Broste DC1 0.002816940 28.16940 0.105300
## 5 Arrhenatherum elatius      Arrela DC2 0.003611619 36.11619 0.076300
## 6 Crepis capillaris      Creves DC2 0.002828699 28.28699 0.062717
## 11 Carex arenaria      Carare DC3 0.010579908 105.79908 0.115885
## 16 Elytrigia juncea      Elyjun DC4 0.012400353 124.00353 0.116320
##      Wave_501 Wave_502
## 1 0.07160 0.072533
## 2 0.10710 0.109030
## 5 0.07670 0.077300
## 6 0.06365 0.064850
## 11 0.11705 0.118450
## 16 0.11745 0.118850
```

```
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=""))

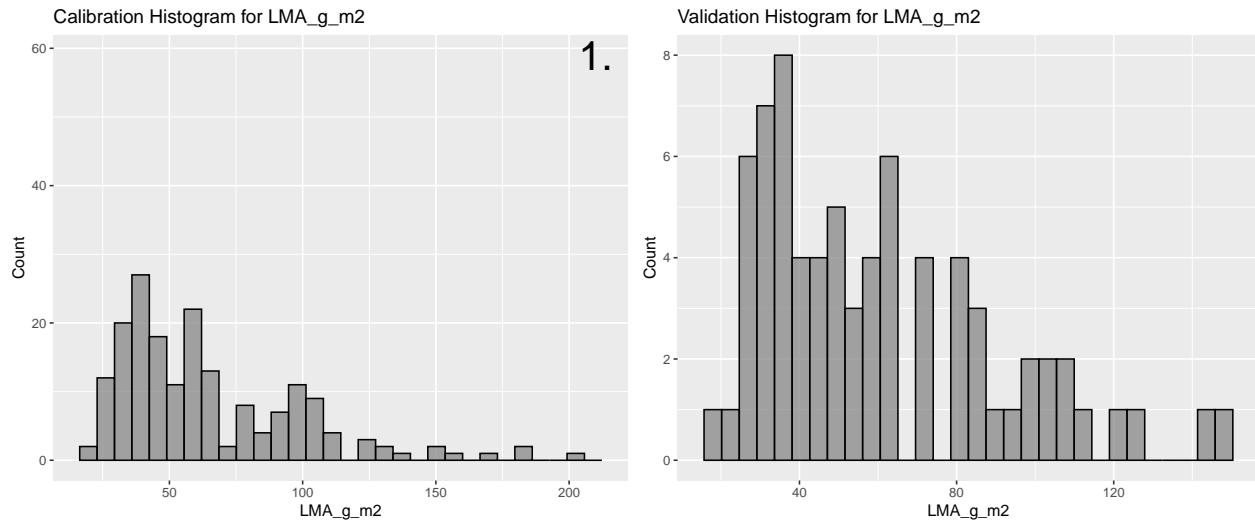
## [1] "Val observations: 73"

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)

## Warning: `qplot()` was deprecated in ggplot2 3.4.0.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

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/m<sup>2</sup>) 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
## 1 Arrhenatherum elatius      Arrela DC1 0.003420518 34.20518
## 2 Bromus sterilis           Broste DC1 0.002816940 28.16940
## 5 Arrhenatherum elatius      Arrela DC2 0.003611619 36.11619
## 6 Crepis capillaris         Creves DC2 0.002828699 28.28699
## 11 Carex arenaria           Carare DC3 0.010579908 105.79908
## 16 Elytrigia juncea         Elyjun DC4 0.012400353 124.00353

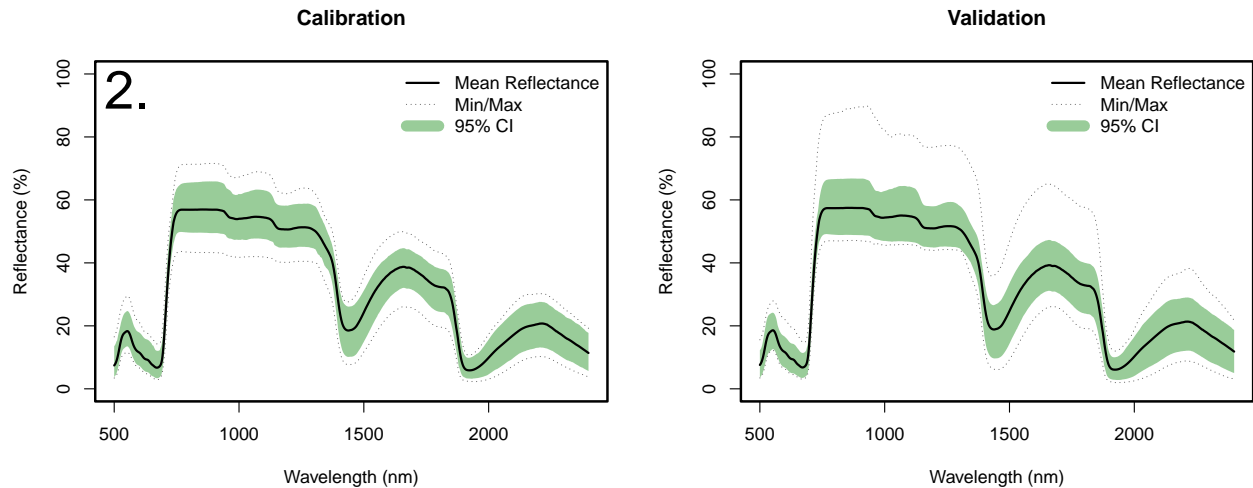
```

## 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, targetVariable=inVar,
                                                  method=method,
                                                  maxComps=maxComps, seg=seg,
                                                  random_seed=random_seed)

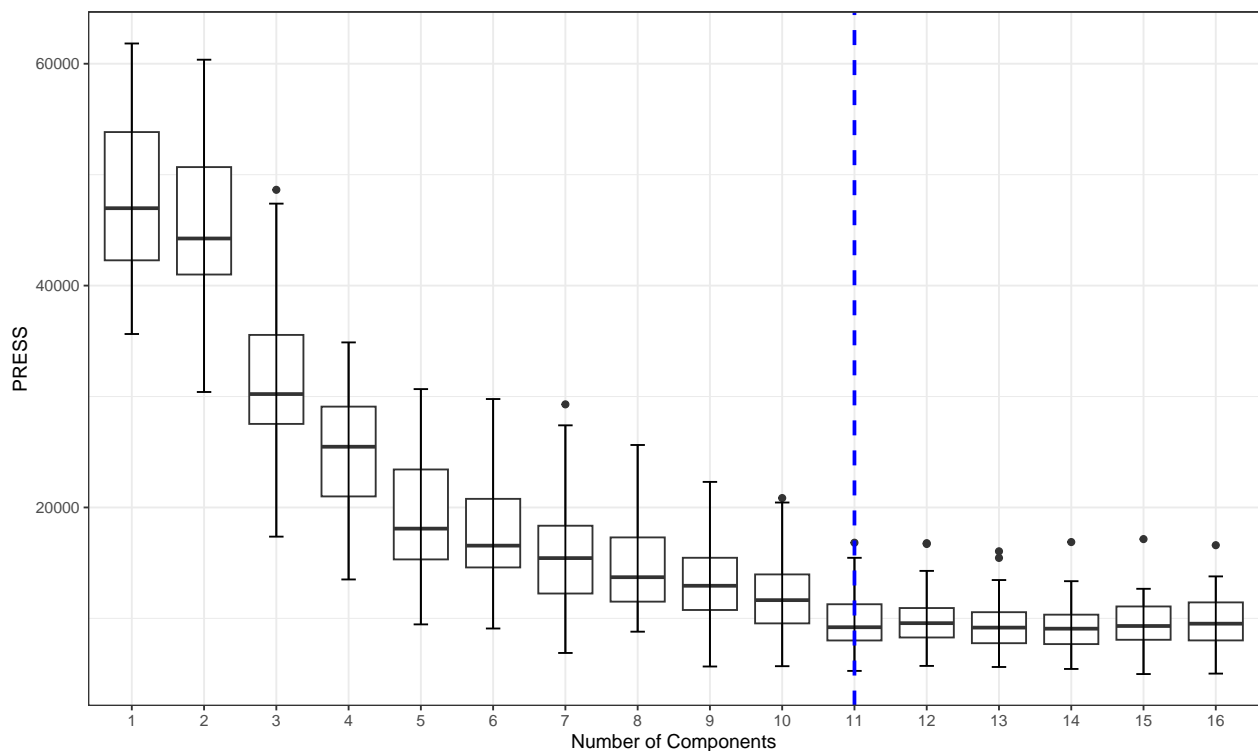
  print(paste0("*** Optimal number of components: ", nComps))
} else {
```



```
nComps <- spectratrait::find_optimal_components(dataset=cal.plsr.data, targetVariable=inVar,
method=method,
maxComps=maxComps, iterations=iterations,
seg=seg, prop=prop,
random_seed=random_seed)
}
```

```
## [1] "*** Identifying optimal number of PLSR components ***"
## [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="LOO",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)

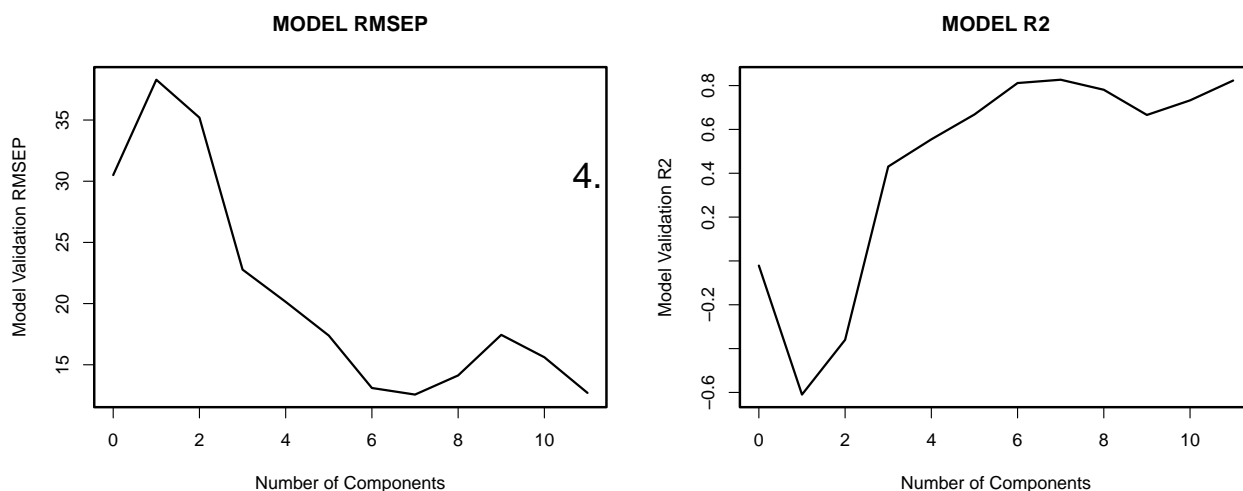
## (Intercept)      1 comps      2 comps      3 comps      4 comps      5 comps
##      30.50       38.30       35.20       22.78       20.14       17.39
##      6 comps      7 comps      8 comps      9 comps     10 comps     11 comps
##      13.10       12.56       14.13       17.45       15.61       12.70

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
##     -0.02137     -0.60981     -0.36001     0.43050     0.55467     0.66818
##      6 comps      7 comps      8 comps      9 comps     10 comps     11 comps
##      0.81156      0.82673      0.78088      0.66593      0.73244      0.82292

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,intercept=F)[[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
## 1 Arrhenatherum elatius    Arrela DC1 0.003420518 34.20518      36.09345
## 2 Bromus sterilis         Broste DC1 0.002816940 28.16940      42.52977
```

```
## 5 Arrhenatherum elatius Arrela DC2 0.003611619 36.11619 21.87053
## 6 Crepis capillaris Creves DC2 0.002828699 28.28699 20.66219
## 11 Carex arenaria Carare DC3 0.010579908 105.79908 99.79501
## 16 Elytrigia juncea Elyjun DC4 0.012400353 124.00353 105.16400
## PLSR_Residuals
## 1 1.888268
## 2 14.360370
## 5 -14.245663
## 6 -7.624796
## 11 -6.004066
## 16 -18.839527
```

```
val.R2 <- round(pls::R2(plsr.out,newdata=val.plsr.data,intercept=F)[[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)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: The `size` argument of `element_rect()` is deprecated as of ggplot2 3.4.0.
## i Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
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))

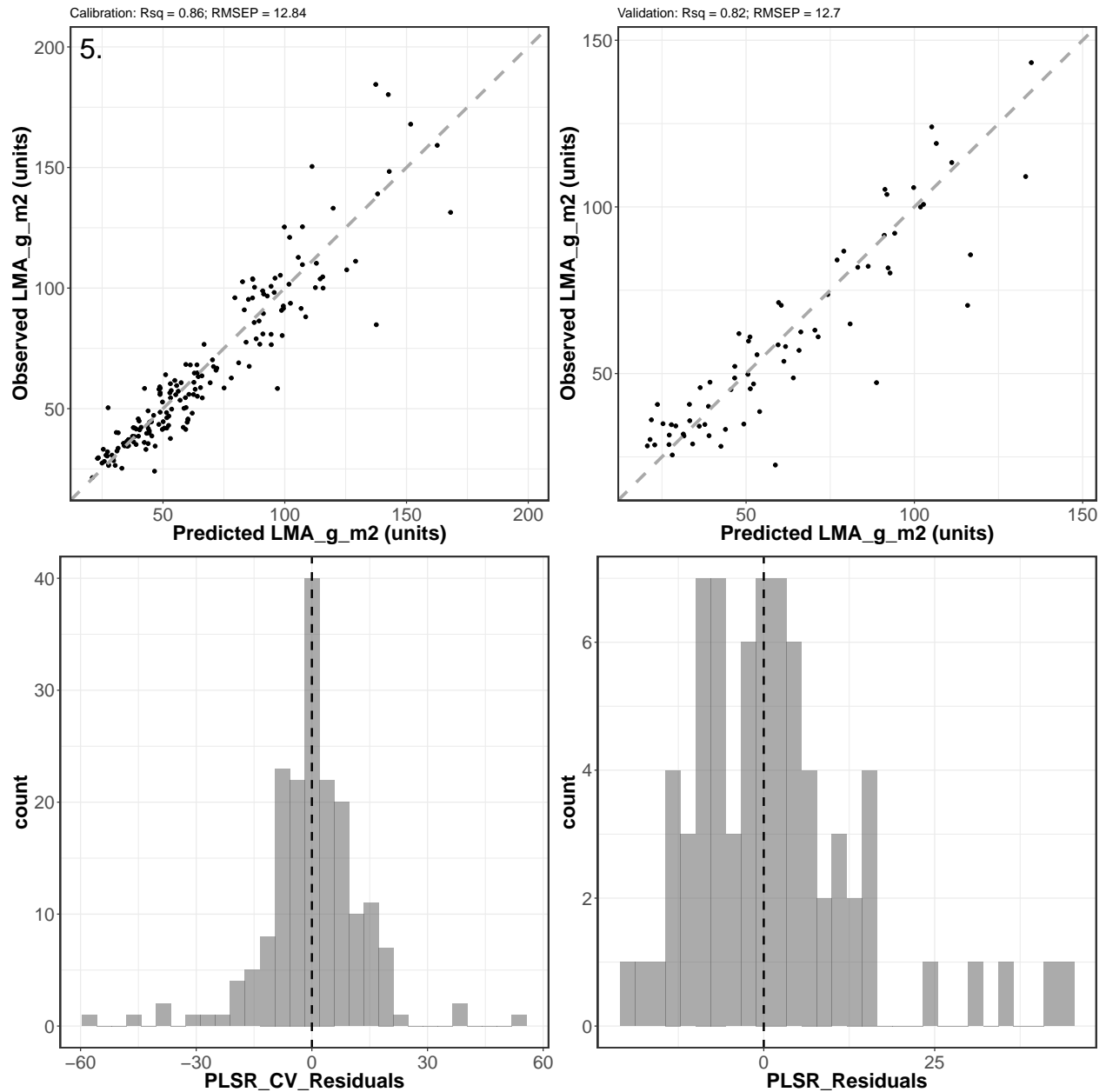
# plot cal/val side-by-side
scatterplots <- grid.arrange(cal_scatter_plot, val_scatter_plot, cal_resid_histogram,
val_resid_histogram, nrow=2, ncol=2)

## Warning: Removed 6 rows containing missing values or values outside the scale range
## (`geom_point()`).

## Warning: Removed 3 rows containing missing values or values outside the scale range
## (`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

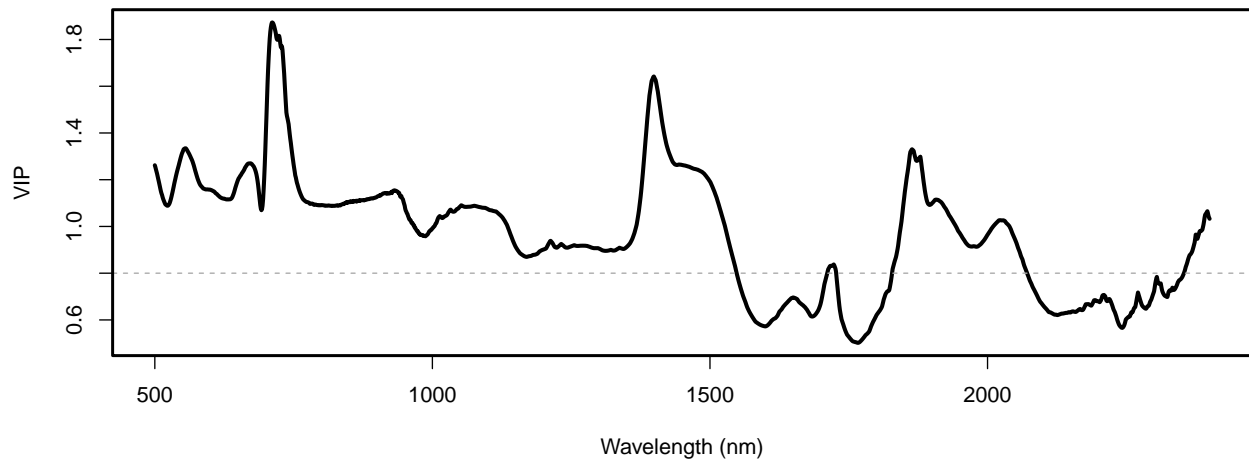
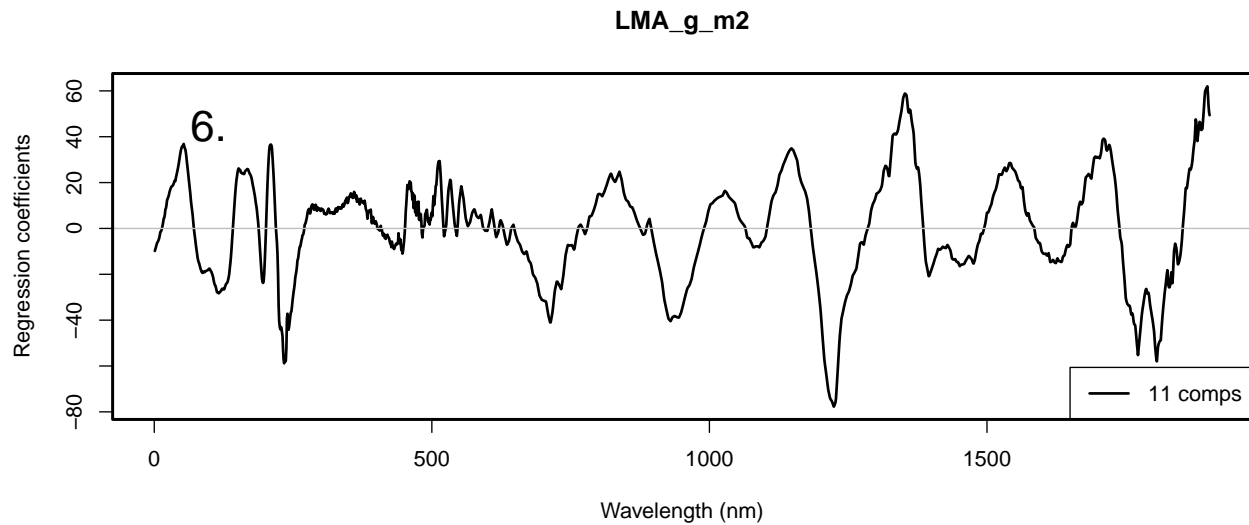
```
vips <- spectratrait::VIP(plsr.out)[nComps,]

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)

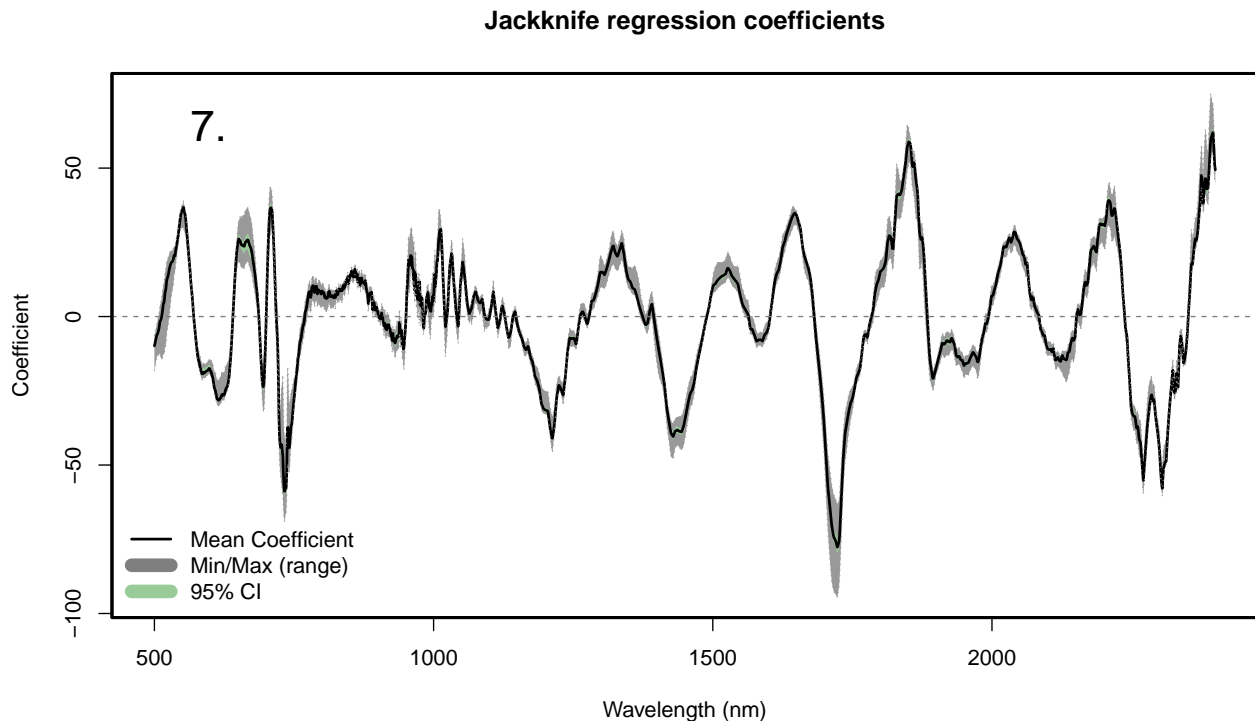
##           Plant_Species Species_Code Plot   LMA_g_cm2 LMA_g_m2 PLSR_Predicted
## 1  Arrhenatherum elatius      Arrela DC1 0.003420518  34.20518      36.09345
## 2    Bromus sterilis      Broste DC1 0.002816940  28.16940      42.52977
## 5  Arrhenatherum elatius      Arrela DC2 0.003611619  36.11619      21.87053
## 6    Crepis capillaris      Creves DC2 0.002828699  28.28699      20.66219
## 11   Carex arenaria      Carare DC3 0.010579908 105.79908      99.79501
## 16   Elytrigia juncea      Elyjun DC4 0.012400353 124.00353     105.16400
##      PLSR_Residuals      LCI      UCI      LPI      UPI
## 1      1.888268  35.22975  36.83681 11.182998  61.00390
## 2     14.360370  41.61622  43.52851 17.617164  67.44238
## 5    -14.245663  20.07042  23.96996 -3.085793  46.82685
## 6     -7.624796  20.27384  21.15353 -4.234964  45.55935
## 11    -6.004066  98.52166 100.58017 74.888636 124.70139
## 16   -18.839527 104.18470 105.69273 80.260059 130.06795

### 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, intercept=F)$val[nComps],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))
```

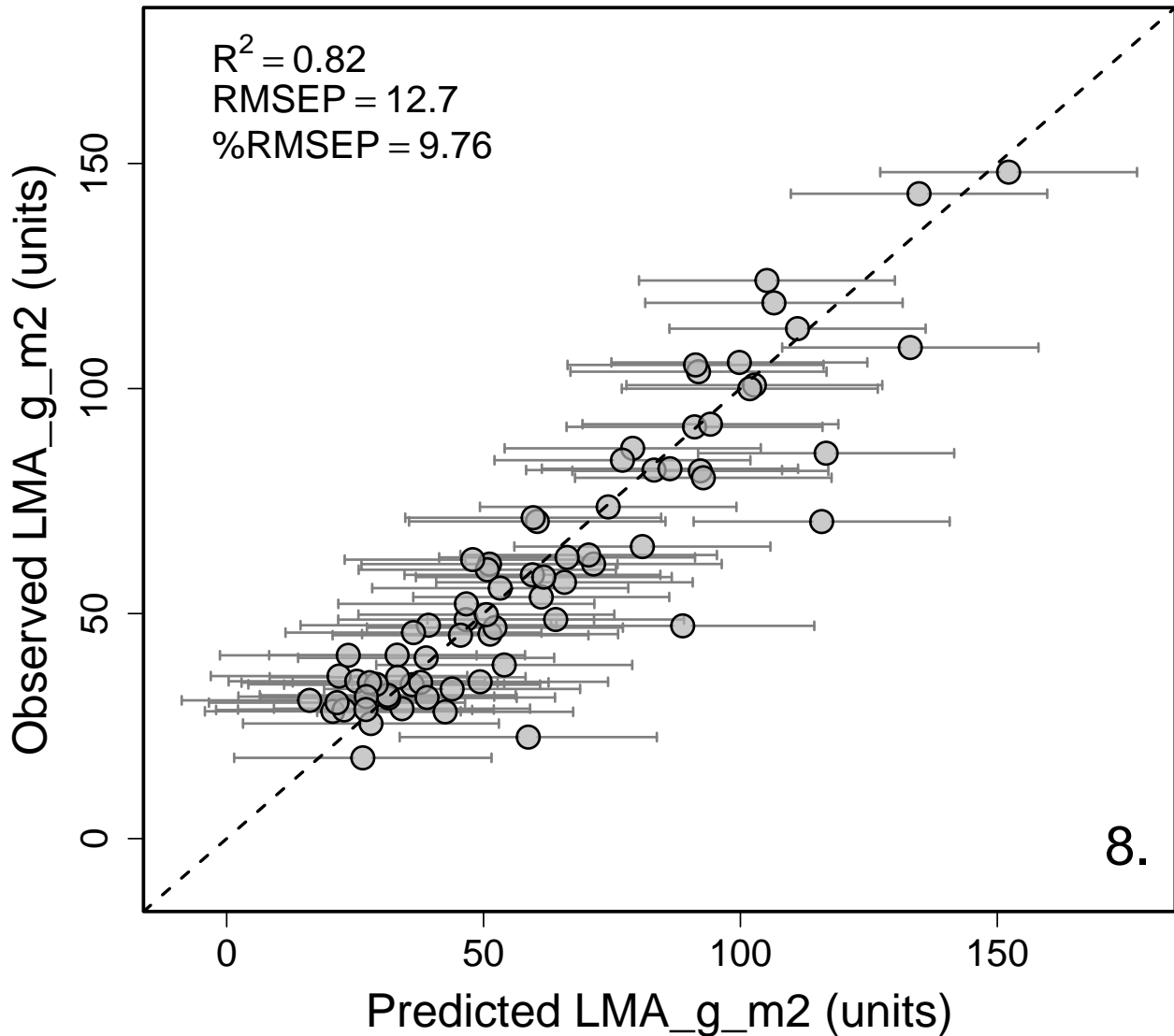
```
par(mfrow=c(1,1), mar=c(4.2,5.3,1,0.4), oma=c(0, 0.1, 0, 0.2))
```

```
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/th/fpt_z3417gn8xgply92pvy6r0000gq/T//RtmpZlgv21"
```

```
# 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"
```