

# Spectra-trait PLSR example using leaf-level spectra and leaf mass per area (LMA) data from CONUS NEON sites

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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

### Load libraries

```
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
```

## 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_gDW_m2"

# What is the source dataset from EcoSIS?
ecosis_id <- "5617da17-c925-49fb-b395-45a51291bd2d"

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

## Set working directory (scratch space)

```
## [1] "/private/var/folders/xp/h3k9vf3n2jx181ts786_yjrn9c2gjQ/T/Rtmp8AgaLd"
```

## Grab data from EcoSIS

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

URL: <https://ecosis.org/package/fresh-leaf-spectra-to-estimate-lma-over-neon-domains-in-eastern-united-states>

```
## [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(),
```

```
##   Affiliation = col_character(),
```

```
##   `Common Name` = col_character(),
```

```
## Domain = col_character(),
## Functional_type = col_character(),
## `Latin Genus` = col_character(),
## `Latin Species` = col_character(),
## PI = col_character(),
## Project = col_character(),
## Sample_ID = col_character(),
## `USDA Symbol` = col_character()
## )
## i Use `spec()` for the full column specifications.

## Download complete!

head(dat_raw)

## # A tibble: 6 x 2,162
##   Affiliation      `Common Name` Domain Functional_type   LMA `Latin Genus`
##   <chr>           <chr>      <chr>    <chr>          <dbl> <chr>
## 1 University of Wiscon~ black walnut D02    broadleaf      72.9 Juglans
## 2 University of Wiscon~ black walnut D02    broadleaf      72.9 Juglans
## 3 University of Wiscon~ black walnut D02    broadleaf      60.8 Juglans
## 4 University of Wiscon~ black walnut D02    broadleaf      60.8 Juglans
## 5 University of Wiscon~ black walnut D02    broadleaf      85.9 Juglans
## 6 University of Wiscon~ black walnut D02    broadleaf      85.9 Juglans
## # ... with 2,156 more variables: Latin Species <chr>, PI <chr>, Project <chr>,
## #   Sample_ID <chr>, USDA Symbol <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>, 441 <dbl>, 442 <dbl>,
## #   443 <dbl>, 444 <dbl>, ...

names(dat_raw)[1:40]

## [1] "Affiliation"      "Common Name"      "Domain"            "Functional_type"
## [5] "LMA"              "Latin Genus"      "Latin Species"     "PI"
## [9] "Project"          "Sample_ID"        "USDA Symbol"       "350"
## [13] "351"              "352"              "353"               "354"
## [17] "355"              "356"              "357"               "358"
## [21] "359"              "360"              "361"               "362"
## [25] "363"              "364"              "365"               "366"
## [29] "367"              "368"              "369"               "370"
## [33] "371"              "372"              "373"               "374"
## [37] "375"              "376"              "377"               "378"
```

## Create full plsr dataset

```
### Create plsr 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 11
##   Affiliation      `Common Name` Domain Functional_type   LMA `Latin Genus`
##   <chr>           <chr>         <chr>    <chr>         <dbl> <chr>
## 1 University of Wiscon~ black walnut D02    broadleaf      72.9 Juglans
## 2 University of Wiscon~ black walnut D02    broadleaf      72.9 Juglans
## 3 University of Wiscon~ black walnut D02    broadleaf      60.8 Juglans
## 4 University of Wiscon~ black walnut D02    broadleaf      60.8 Juglans
## 5 University of Wiscon~ black walnut D02    broadleaf      85.9 Juglans
## 6 University of Wiscon~ black walnut D02    broadleaf      85.9 Juglans
## # ... with 5 more variables: Latin Species <chr>, PI <chr>, Project <chr>,
## #   Sample_ID <chr>, USDA Symbol <chr>

sample_info2 <- sample_info %>%
  select(Domain,Functional_type,Sample_ID,USDA_Species_Code=`USDA Symbol`,LMA_gDW_m2=LMA)
head(sample_info2)

## # A tibble: 6 x 5
##   Domain Functional_type Sample_ID USDA_Species_Code LMA_gDW_m2
##   <chr>    <chr>         <chr>    <chr>         <dbl>
## 1 D02    broadleaf      P0001    JUNI           72.9
## 2 D02    broadleaf      L0001    JUNI           72.9
## 3 D02    broadleaf      P0002    JUNI           60.8
## 4 D02    broadleaf      L0002    JUNI           60.8
## 5 D02    broadleaf      P0003    JUNI           85.9
## 6 D02    broadleaf      L0003    JUNI           85.9

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

## Create cal/val datasets

```
### Create cal/val datasets
## Make a stratified random sampling in the strata USDA_Species_Code and Domain

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=2356812,
                                              prop=0.8, group_variables=c("USDA_Species_Code","Domain"))
names(split_data)

## [1] "cal_data" "val_data"
```

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

```
##   Domain Functional_type Sample_ID USDA_Species_Code LMA_gDW_m2   Wave_500
## 1    D08      broadleaf    L2644             ACBA      44.18 0.04170800
## 2    D08      broadleaf    L2646             ACBA      41.71 0.05067800
## 3    D08      broadleaf    L2645             ACBA      40.66 0.04701700
## 4    D08      broadleaf    P2639             ACBA      44.18 0.04125300
## 5    D03      broadleaf    P0614             ACFL      52.91 0.03895800
## 6    D03      broadleaf    L0609             ACFL      81.67 0.04186169
##      Wave_501   Wave_502
## 1 0.04208700 0.04283700
## 2 0.05087600 0.05153500
## 3 0.04718200 0.04766500
## 4 0.04150300 0.04247100
## 5 0.03915100 0.03956200
## 6 0.04217802 0.04258768
```

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

```
##      Domain Functional_type Sample_ID USDA_Species_Code LMA_gDW_m2 Wave_500
## 4923    D08      broadleaf    P2462             <NA>      21.10 0.044964
## 4924    D08      broadleaf    L2462             SANI      100.72 0.068921
## 4925    D08      broadleaf    P2463             <NA>      29.59 0.036254
## 4926    D08      broadleaf    L2463             SANI      96.48 0.051810
## 4927    D08      broadleaf    P2464             <NA>      31.08 0.056587
## 4928    D08      broadleaf    L2464             SANI      61.40 0.037310
##      Wave_501 Wave_502
## 4923 0.045854 0.046911
## 4924 0.069633 0.070254
## 4925 0.036999 0.037671
## 4926 0.052113 0.052896
## 4927 0.057006 0.057734
## 4928 0.037223 0.037671
```

```
rm(split_data)
```

```
# Datasets:
```

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

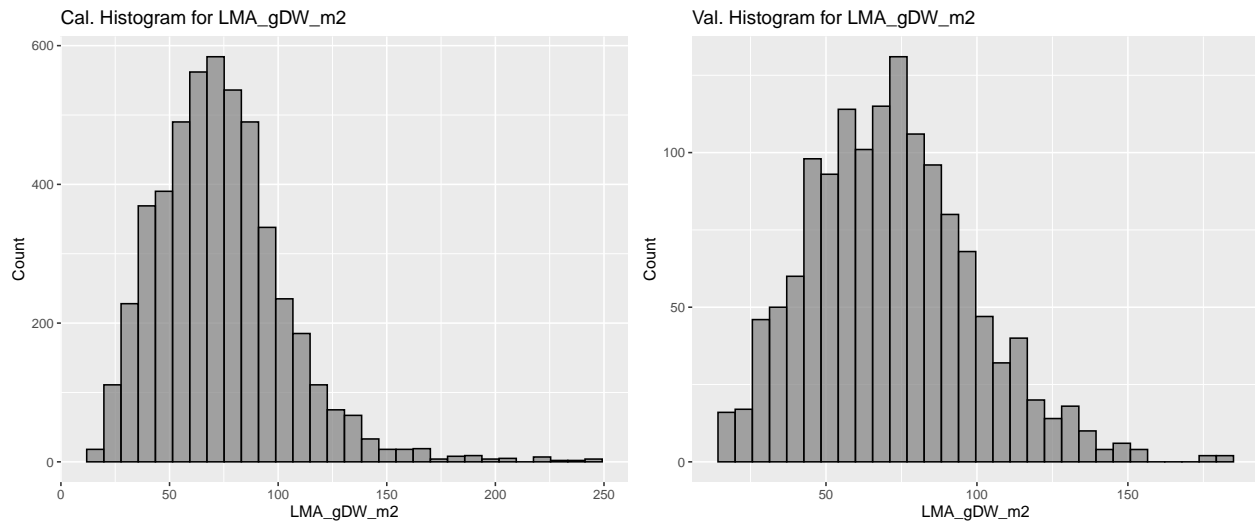
```
## [1] "Cal observations: 4922"
```

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

```
## [1] "Val observations: 1390"
```

```
cal_hist_plot <- qplot(cal.plsr.data[,paste0(inVar)],geom="histogram",
  main = paste0("Cal. Histogram for ",inVar),
  xlab = paste0(inVar),ylab = "Count",fill=I("grey50"),
  col=I("black"),alpha=I(.7))
val_hist_plot <- qplot(val.plsr.data[,paste0(inVar)],geom="histogram",
  main = paste0("Val. 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`.
```



```
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)
```

## 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]

##   Domain Functional_type Sample_ID USDA_Species_Code LMA_gDW_m2
## 1   D08      broadleaf   L2644          ACBA      44.18
## 2   D08      broadleaf   L2646          ACBA      41.71
## 3   D08      broadleaf   L2645          ACBA      40.66
## 4   D08      broadleaf   P2639          ACBA      44.18
## 5   D03      broadleaf   P0614          ACFL      52.91
## 6   D03      broadleaf   L0609          ACFL      81.67

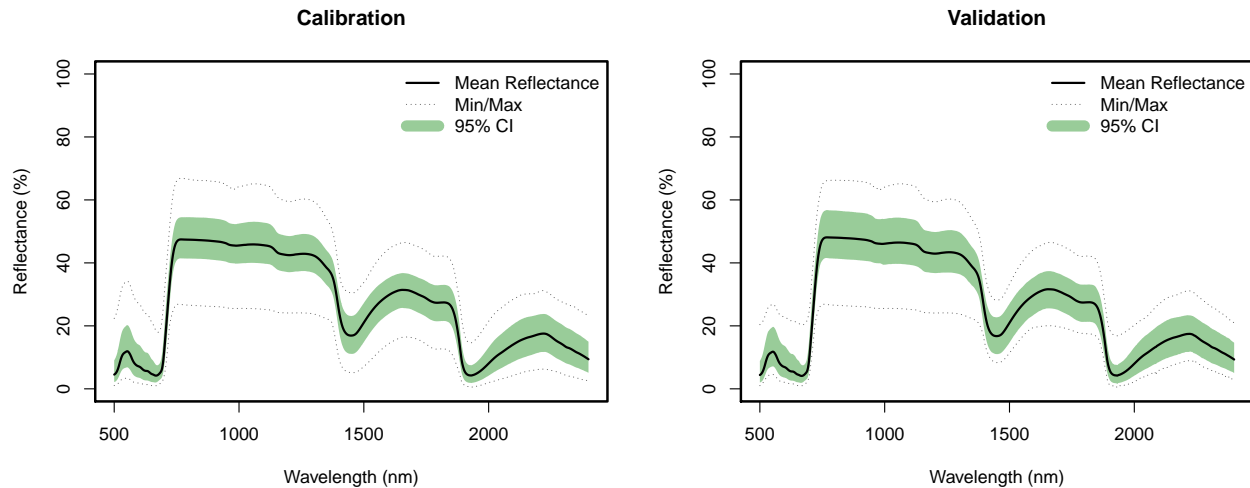
val_spec <- as.matrix(val.plsr.data[, which(names(val.plsr.data) %in% paste0("Wave_",wv))])
val.plsr.data <- data.frame(val.plsr.data[, which(names(val.plsr.data) %notin% paste0("Wave_",wv))],
                           Spectra=I(val_spec))
head(val.plsr.data)[1:5]
```

```
##   Domain Functional_type Sample_ID USDA_Species_Code LMA_gDW_m2
## 4923   D08      broadleaf   P2462          <NA>      21.10
## 4924   D08      broadleaf   L2462          SANI      100.72
## 4925   D08      broadleaf   P2463          <NA>      29.59
```

```
## 4926    D08    broadleaf    L2463    SANI    96.48
## 4927    D08    broadleaf    P2464    <NA>    31.08
## 4928    D08    broadleaf    L2464    SANI    61.40
```

plot cal and val spectra

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



```
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))
```

Use Jackknife permutation to determine 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 <- "firstPlateau" #pls, firstPlateau, firstMin
random_seed <- 2356812
seg <- 250
maxComps <- 20
iterations <- 40
```

```

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)
}

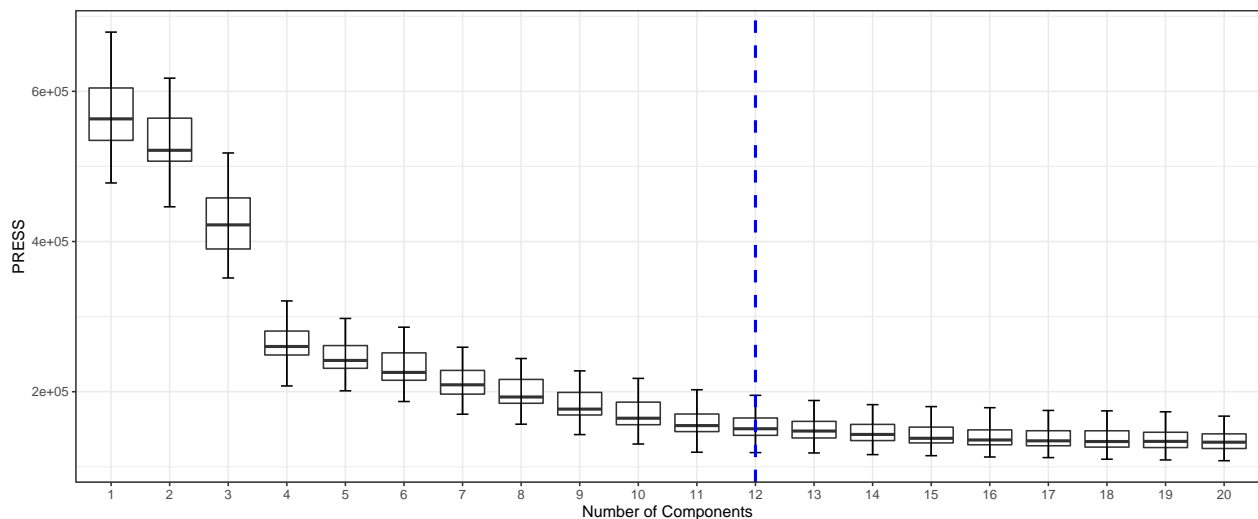
```

```

## [1] "*** Running permutation test. Please hang tight, this can take awhile ***"
## [1] "Options:"
## [1] "Max Components: 20 Iterations: 40 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: 12"

```



```

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

```

```

## quartz_off_screen
##           3

```

```

dev.off();

```

```

## pdf
##    2

```

## Fit final model

```

### Fit final model
segs <- 100
plsr.out <- plsr(as.formula(paste(inVar,"~","Spectra")),scale=FALSE,ncomp=nComps,

```



```

validation="CV",
segments=segs, segment.type="interleaved",trace=FALSE,
data=cal.plsr.data)
fit <- plsr.out$fitted.values[,1,nComps]
pls.options(parallel = NULL)

# External validation fit stats
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
##      27.155      17.610      16.595      15.483      13.235      12.374
##      6 comps      7 comps      8 comps      9 comps     10 comps     11 comps
##      11.499      10.722      10.269      9.647       9.197       9.319
##     12 comps
##      9.515

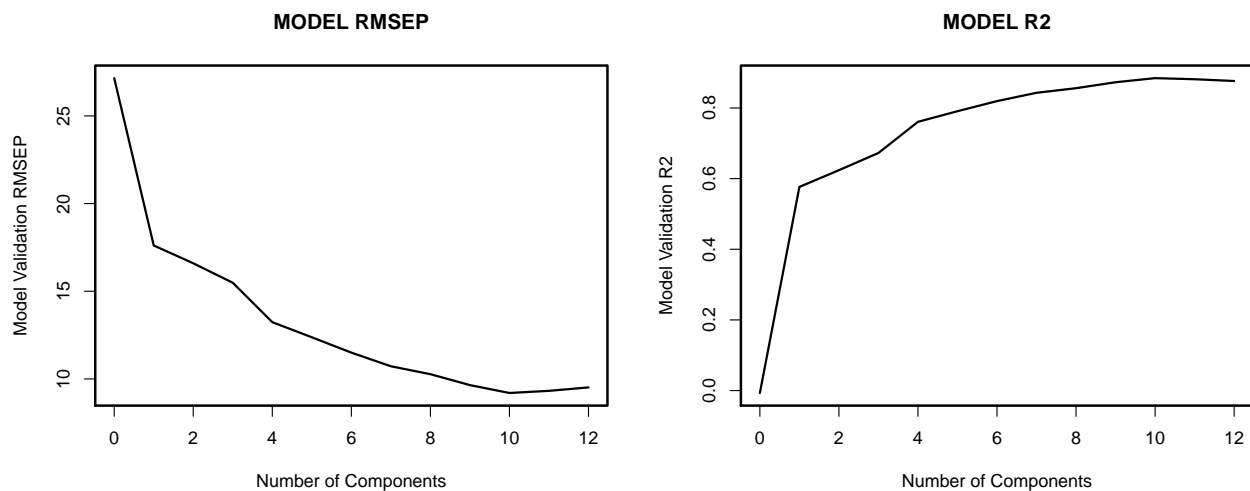
plot(pls::RMSEP(plsr.out,estimate=c("test"),newdata = val.plsr.data),
     main="MODEL RMSEP",
     xlab="Number of Components",ylab="Model Validation RMSEP",lty=1,col="black",
     cex=1.5,lwd=2)
box(lwd=2.2)

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

## (Intercept)      1 comps      2 comps      3 comps      4 comps      5 comps
##     -0.006901     0.576543     0.623949     0.672643     0.760799     0.790906
##      6 comps      7 comps      8 comps      9 comps     10 comps     11 comps
##      0.819456     0.843031     0.856001     0.872913     0.884511     0.881406
##     12 comps
##      0.876368

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)

```



```
par(opar)
```

## 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)
```

##	Domain	Functional_type	Sample_ID	USDA_Species_Code	LMA_gDW_m2	PLSR_Predicted
## 1	D08	broadleaf	L2644	ACBA	44.18	53.00773
## 2	D08	broadleaf	L2646	ACBA	41.71	44.02712
## 3	D08	broadleaf	L2645	ACBA	40.66	46.76972
## 4	D08	broadleaf	P2639	ACBA	44.18	49.62804
## 5	D03	broadleaf	P0614	ACFL	52.91	64.78900
## 6	D03	broadleaf	L0609	ACFL	81.67	96.85291

```
## PLSR_CV_Predicted PLSR_CV_Residuals
## 1 53.03952 8.859523
## 2 44.03282 2.322823
## 3 46.90528 6.245280
## 4 49.80084 5.620843
## 5 64.98964 12.079641
## 6 96.86039 15.190390
```

```
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)
```

##	Domain	Functional_type	Sample_ID	USDA_Species_Code	LMA_gDW_m2
## 4923	D08	broadleaf	P2462	<NA>	21.10
## 4924	D08	broadleaf	L2462	SANI	100.72
## 4925	D08	broadleaf	P2463	<NA>	29.59
## 4926	D08	broadleaf	L2463	SANI	96.48
## 4927	D08	broadleaf	P2464	<NA>	31.08
## 4928	D08	broadleaf	L2464	SANI	61.40

```
## PLSR_Predicted PLSR_Residuals
## 4923 21.14155 0.04155041
## 4924 89.65467 -11.06533484
## 4925 27.94765 -1.64234512
## 4926 92.46121 -4.01879017
## 4927 40.73367 9.65367301
## 4928 65.94687 4.54686556
```

```
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))

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",

```

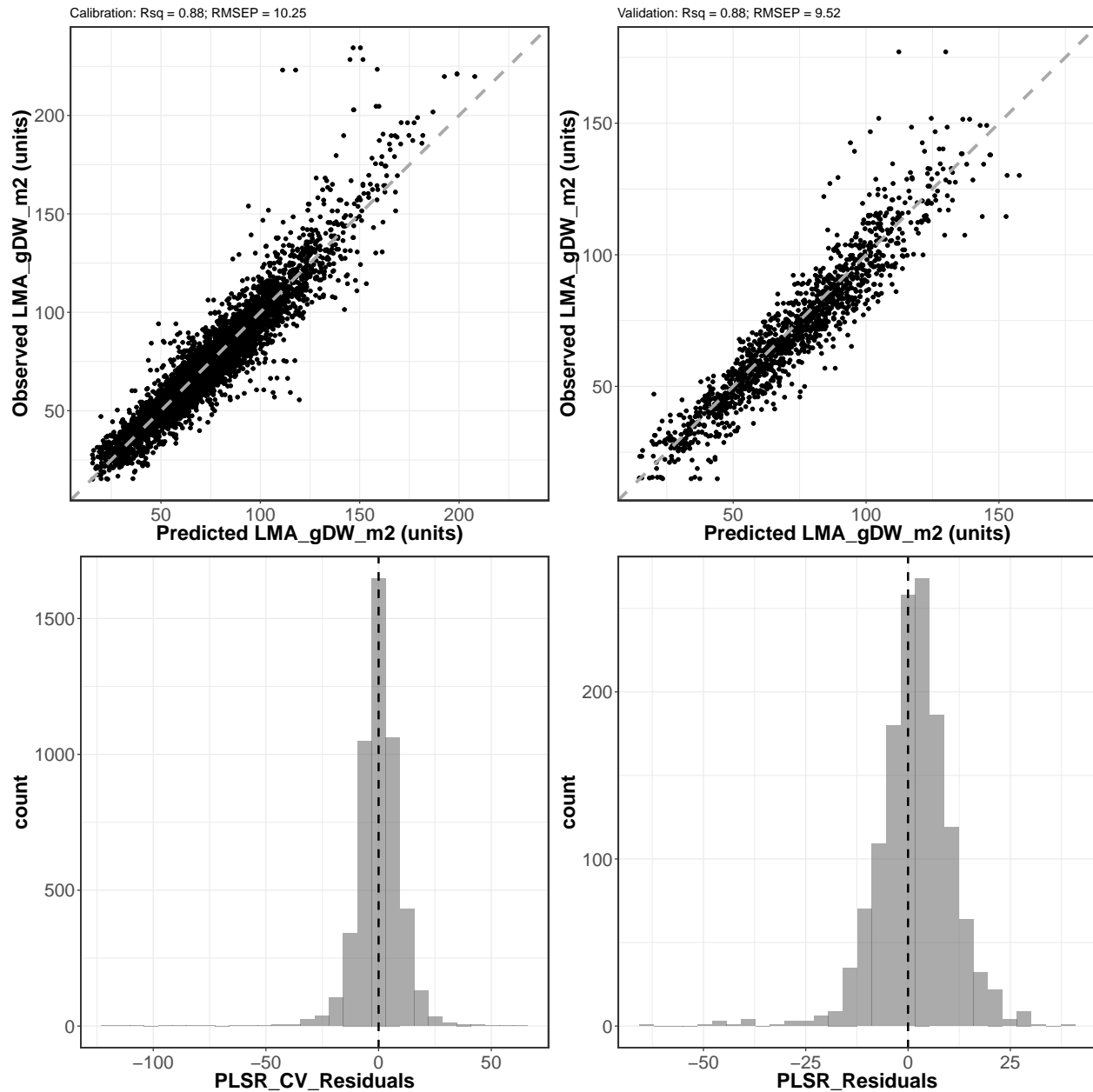
```

    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 21 rows containing missing values (geom_point).
## Warning: Removed 5 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`.

```



```
ggsave(filename = file.path(outdir,paste0(inVar,"_Cal_Val_scatterplots.png")),
        plot = scatterplots, device="png", width = 32, height = 30, units = "cm",
        dpi = 300)
```

## Generate Coefficient and VIP plots

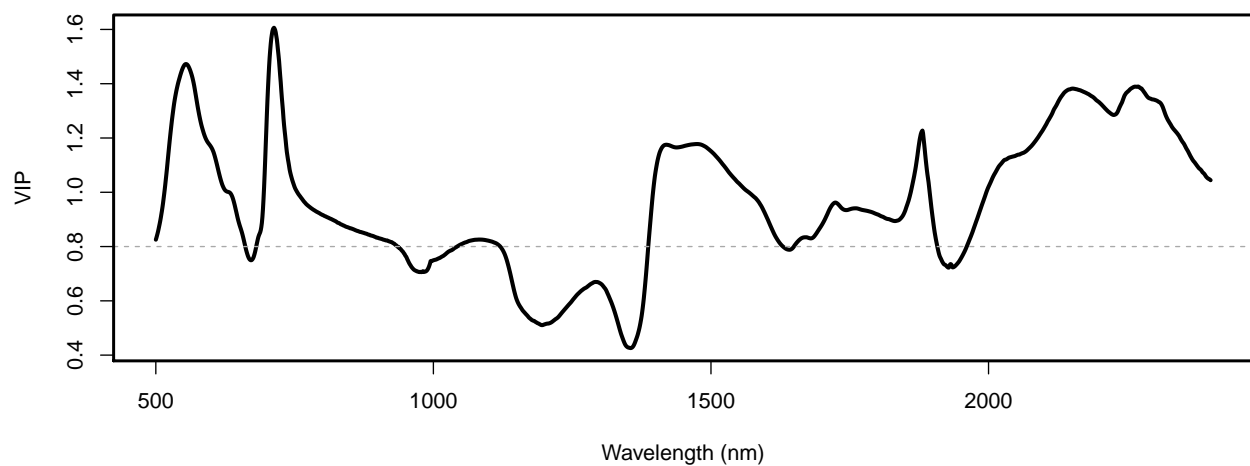
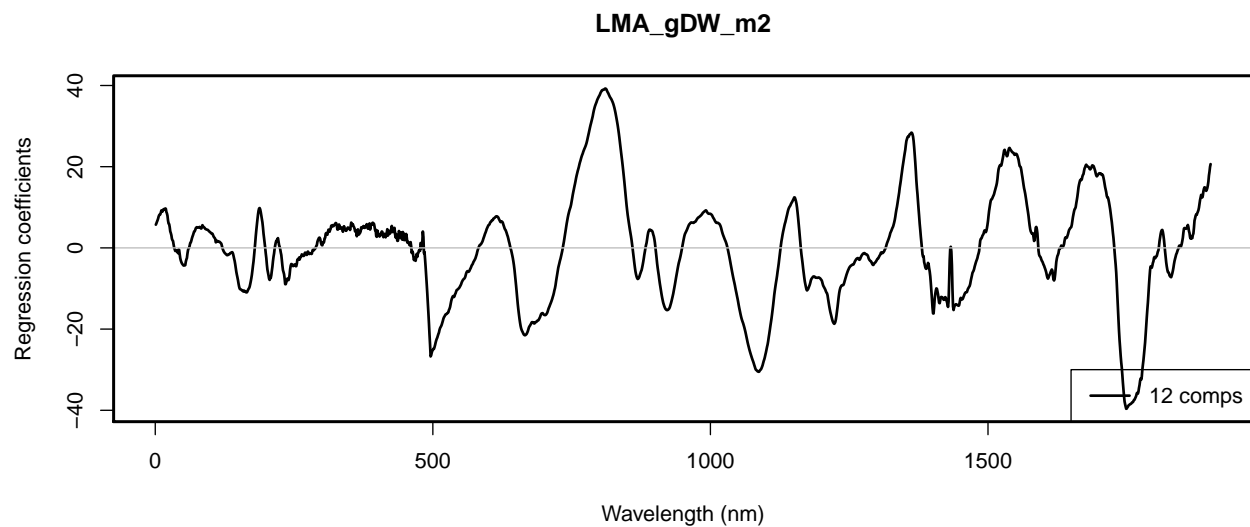
```
vips <- spectratrait::VIP(plsr.out)[nComps,]

par(mfrow=c(2,1))
plot(plsr.out, plottype = "coef",xlab="Wavelength (nm)",
      ylab="Regression coefficients",legendpos = "bottomright",
      ncomp=nComps,lwd=2)
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)

```



```

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
par(opar)

```

## Jackknife validation

```

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

seg <- 100
jk.plsr.out <- pls::plsr(as.formula(paste(inVar,"~","Spectra")), scale=FALSE,
                        center=TRUE, ncomp=nComps,
                        validation="CV", segments = seg,
                        segment.type="interleaved", 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],,,]

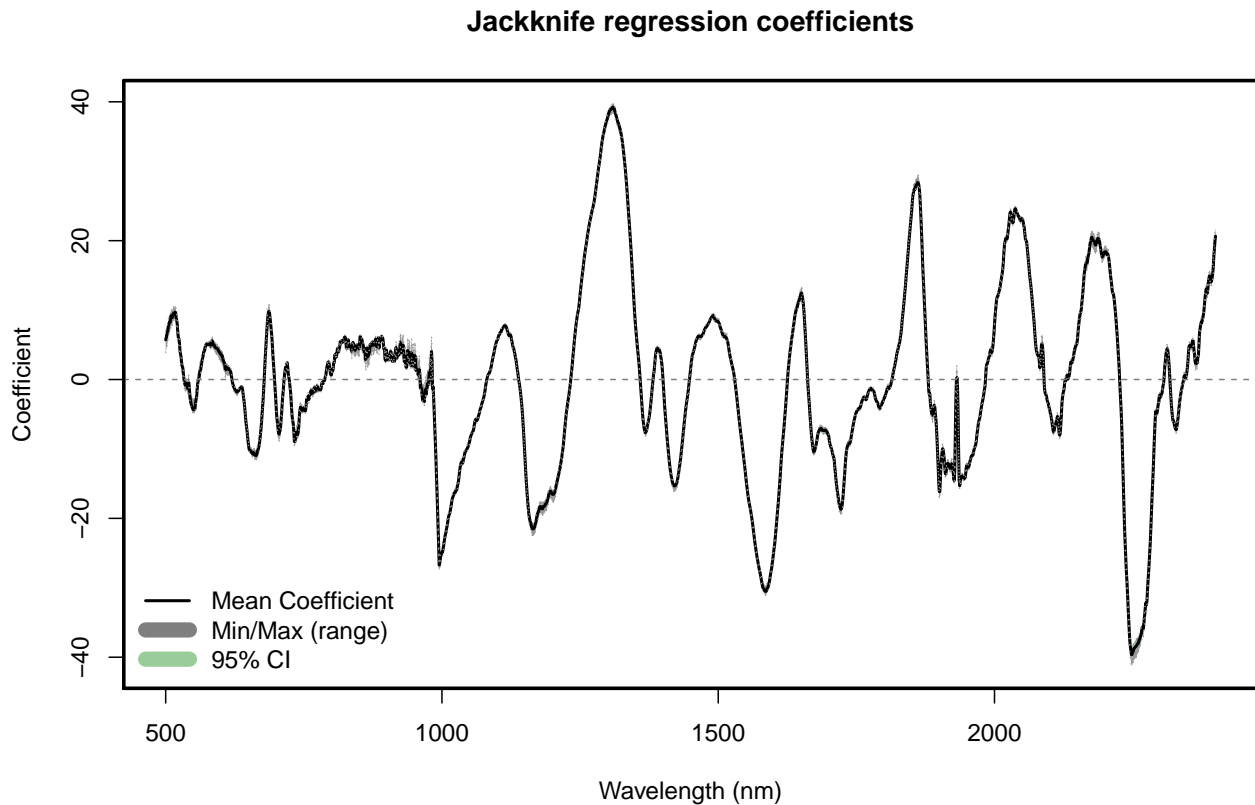
interval <- c(0.025,0.975)
Jackknife_Pred <- val.plsr.data$Spectra %*% Jackknife_coef +
  matrix(rep(Jackknife_intercept, length(val.plsr.data[,inVar])), byrow=TRUE,
          ncol=length(Jackknife_intercept))
Interval_Conf <- apply(X = Jackknife_Pred,MARGIN = 1,
                      FUN = quantile,probs=c(interval[1],interval[2]))
sd_mean <- apply(X = Jackknife_Pred,MARGIN = 1,FUN =sd)
sd_res <- sd(val.plsr.output$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)

```

##	Domain	Functional_type	Sample_ID	USDA_Species_Code	LMA_gDW_m2	
## 4923	D08	broadleaf	P2462	<NA>	21.10	
## 4924	D08	broadleaf	L2462	SANI	100.72	
## 4925	D08	broadleaf	P2463	<NA>	29.59	
## 4926	D08	broadleaf	L2463	SANI	96.48	
## 4927	D08	broadleaf	P2464	<NA>	31.08	
## 4928	D08	broadleaf	L2464	SANI	61.40	
##	PLSR_Predicted	PLSR_Residuals	LCI	UCI	LPI	UPI
## 4923	21.14155	0.04155041	20.94847	21.30604	2.789108	39.49399
## 4924	89.65467	-11.06533484	89.45021	89.97246	71.301221	108.00811
## 4925	27.94765	-1.64234512	27.73172	28.16789	9.594597	46.30071
## 4926	92.46121	-4.01879017	92.26489	92.73225	74.107998	110.81442
## 4927	40.73367	9.65367301	40.50065	40.92588	22.380204	59.08714
## 4928	65.94687	4.54686556	65.77618	66.17712	47.594178	84.29955

### Jackknife 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")  
box(lwd=2.2)
```



```
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
```

### Jackknife validation plot

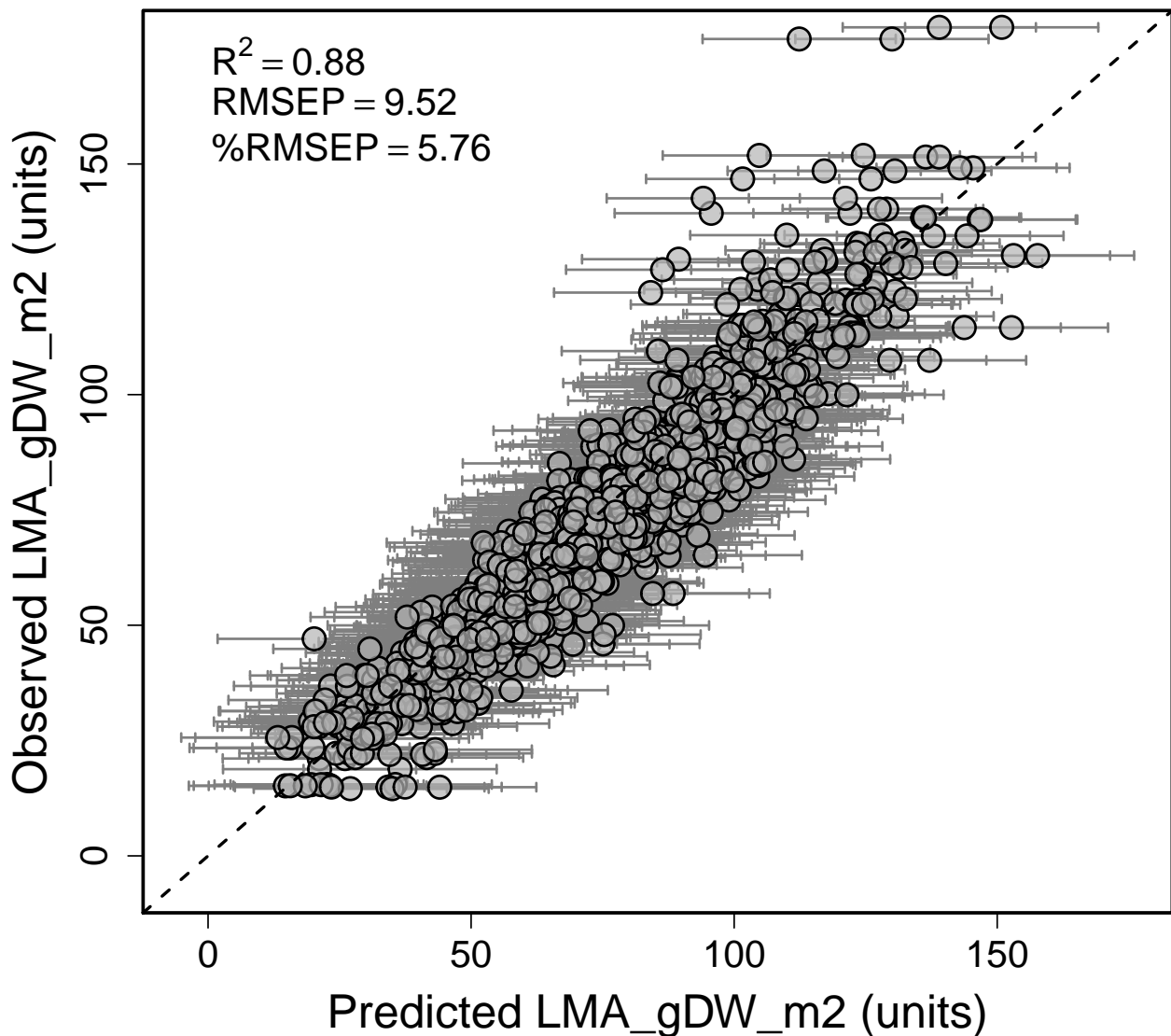
```
rmsep_percrmsep <- spectratrait::percent_rmse(plsr_dataset = val.plsr.output,  
  inVar = inVar,  
  residuals = val.plsr.output$PLSR_Residuals,  
  range="full")  
  
RMSEP <- rmsep_percrmsep$rmse  
perc_RMSEP <- rmsep_percrmsep$perc_rmse  
r2 <- round(pls::R2(plsr.out, newdata = val.plsr.data)$val[nComps+1], 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)
box(lwd=2.2)

```



```

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
```

## Output jackknife results

```
out.jk.coefs <- data.frame(Iteration=seq(1,seg,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  69.44171  5.796399  6.112194  6.482897  6.814518
## Seg 2         2  69.36719  6.316698  6.662910  7.031691  7.382632
## Seg 3         3  68.73866  6.729135  7.031912  7.372056  7.650510
## Seg 4         4  69.09350  5.899933  6.199538  6.614751  6.975426
## Seg 5         5  69.12959  5.355288  5.701339  6.043622  6.383870
## Seg 6         6  68.67202  5.615024  5.968986  6.358249  6.654510
```

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

## Create core PLSR outputs

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

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

```
# 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')))
```

**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] "LMA_gDW_m2_Cal_PLSR_Dataset.csv"
## [2] "LMA_gDW_m2_Cal_Val_Histograms.png"
## [3] "LMA_gDW_m2_Cal_Val_scatterplots.png"
## [4] "LMA_gDW_m2_Cal_Val_Spectra.png"
## [5] "LMA_gDW_m2_Coefficient_VIP_plot.png"
## [6] "LMA_gDW_m2_Jackknife_PLSR_Coefficients.csv"
## [7] "LMA_gDW_m2_Jackknife_Regression_Coefficients.png"
## [8] "LMA_gDW_m2_Observed_PLSR_CV_Pred_12comp.csv"
## [9] "LMA_gDW_m2_PLSR_Coefficients_12comp.csv"
## [10] "LMA_gDW_m2_PLSR_Component_Selection.png"
## [11] "LMA_gDW_m2_PLSR_Validation_Scatterplot.png"
## [12] "LMA_gDW_m2_PLSR_VIPs_12comp.csv"
## [13] "LMA_gDW_m2_Val_PLSR_Dataset.csv"
## [14] "LMA_gDW_m2_Validation_PLSR_Pred_12comp.csv"
```