

Spectra-trait PLSR example using leaf-level spectra and specific leaf area (SLA) data from more than 40 species grassland species comprising both herbs and graminoids.

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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 specific leaf area (SLA). In this example, the plants were cultivated in an outdoor setting in the botanical garden of the KIT using 40x40 cm pots with an standardized substrate. The data was measured on a weekly basis (the timestamp is included in the dataset).

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 <- "SLA_g_cm"

# What is the source dataset from EcoSIS?
ecosis_id <- "3cf6b27e-d80e-4bc7-b214-c95506e46daa"

# 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] "Output directory: /private/var/folders/xp/h3k9vf3n2jx181ts786_yjrn9c2gjQ/T/RtmpvmlxJe"
```

Grab data from EcoSIS

```
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(),
##   `growth form` = col_character(),
##   species = col_character(),
##   timestamp = col_character()
## )
## i Use `spec()` for the full column specifications.
```

```
## Download complete!
```

```
head(dat_raw)
```

```
## # A tibble: 6 x 2,114
##   `Anthocyanin concen~` `Anthocyanin cont~` `Carotenoid concen~` `Carotenoid conte~`
##           <dbl>           <dbl>           <dbl>           <dbl>
## 1           0.00106           0.997           0.00799           7.49
## 2           0.00357           1.22           0.0221           7.53
## 3           0.00252           1.14           0.0188           8.55
## 4           0.00310           2.26           0.0158          11.5
## 5           0.00412           1.73           0.0216           9.08
## 6           0.00397           1.02           0.0336           8.66
## # ... with 2,110 more variables: Chlorophyll concentration (mg/g) <dbl>,
## #   Chlorophyll content ( g/cm ) <dbl>, LDMC (g/g) <dbl>, LFA (mg/cm ) <dbl>,
## #   LWC (mg/cm ) <dbl>, SLA (g/cm ) <dbl>, growth form <chr>, species <chr>,
## #   timestamp <chr>, 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>, 445 <dbl>, 446 <dbl>,
## #   447 <dbl>, 448 <dbl>, 449 <dbl>, 450 <dbl>, 451 <dbl>, 452 <dbl>,
## #   453 <dbl>, 454 <dbl>, 455 <dbl>, 456 <dbl>, 457 <dbl>, 458 <dbl>,
## #   459 <dbl>, 460 <dbl>, 461 <dbl>, 462 <dbl>, 463 <dbl>, 464 <dbl>,
## #   465 <dbl>, 466 <dbl>, 467 <dbl>, 468 <dbl>, 469 <dbl>, 470 <dbl>,
## #   471 <dbl>, 472 <dbl>, 473 <dbl>, 474 <dbl>, 475 <dbl>, 476 <dbl>,
## #   477 <dbl>, 478 <dbl>, 479 <dbl>, 480 <dbl>, 481 <dbl>, 482 <dbl>,
## #   483 <dbl>, 484 <dbl>, 485 <dbl>, 486 <dbl>, 487 <dbl>, 488 <dbl>,
## #   489 <dbl>, 490 <dbl>, ...
```

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

```
## [1] "Anthocyanin concentration (mg/g)" "Anthocyanin content ( g/cm )"
## [3] "Carotenoid concentration (mg/g)" "Carotenoid content ( g/cm )"
## [5] "Chlorophyll concentration (mg/g)" "Chlorophyll content ( g/cm )"
## [7] "LDMC (g/g)" "LFA (mg/cm )"
## [9] "LWC (mg/cm )" "SLA (g/cm )"
## [11] "growth form" "species"
## [13] "timestamp" "400"
## [15] "401" "402"
## [17] "403" "404"
## [19] "405" "406"
## [21] "407" "408"
## [23] "409" "410"
## [25] "411" "412"
## [27] "413" "414"
## [29] "415" "416"
## [31] "417" "418"
## [33] "419" "420"
## [35] "421" "422"
## [37] "423" "424"
## [39] "425" "426"
```

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 13
##   `Anthocyanin concen~` `Anthocyanin cont~` `Carotenoid concen~` `Carotenoid conte~`
##   <dbl> <dbl> <dbl> <dbl>
## 1 0.00106 0.997 0.00799 7.49
## 2 0.00357 1.22 0.0221 7.53
## 3 0.00252 1.14 0.0188 8.55
## 4 0.00310 2.26 0.0158 11.5
## 5 0.00412 1.73 0.0216 9.08
## 6 0.00397 1.02 0.0336 8.66
## # ... with 9 more variables: Chlorophyll concentration (mg/g) <dbl>,
## # Chlorophyll content ( g/cm ) <dbl>, LDMC (g/g) <dbl>, LFA (mg/cm ) <dbl>,
## # LWC (mg/cm ) <dbl>, SLA (g/cm ) <dbl>, growth form <chr>, species <chr>,
## # timestamp <chr>
sample_info2 <- sample_info %>%
  select(Plant_Species=species,Growth_Form=`growth form`,timestamp,SLA_g_cm=`SLA (g/cm )`)
head(sample_info2)

## # A tibble: 6 x 4
##   Plant_Species Growth_Form timestamp SLA_g_cm
##   <chr> <chr> <chr> <dbl>
## 1 Calamagrostis epigejos graminoid 5/25/2016 12:20 107.
## 2 Anthoxanthum odoratum graminoid 5/27/2016 8:40 293.
## 3 Alopecurus pratensis graminoid 5/27/2016 9:23 220.
## 4 Festuca ovina graminoid 5/27/2016 9:23 137.
## 5 Agrostis capillaris graminoid 5/27/2016 9:42 237.
## 6 Aegopodium podagraria forb 5/25/2016 12:20 388.
plsr_data <- data.frame(sample_info2,Spectra)
rm(sample_info,sample_info2,Spectra)
```

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,wv)]),]
# Remove suspect high values
plsr_data <- plsr_data[ plsr_data[,inVar] <= 500, ]
```

Create cal/val datasets

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

method <- "base" #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="Plant_Species")

## Calamagrostis epigejos    Cal: 80%
## Anthoxanthum odoratum    Cal: 80%
## Alopecurus pratensis    Cal: 80%
## Festuca ovina    Cal: 78.9473684210526%
## Agrostis capillaris    Cal: 82.3529411764706%
## Aegopodium podagraria    Cal: 80%
## Arrhenatherum elatius    Cal: 82.3529411764706%
## Arctium lappa    Cal: 83.3333333333333%
## Urtica dioica    Cal: 78.9473684210526%
## Cirsium arvense    Cal: 80%
## Geranium pratense    Cal: 81.25%
## Geum urbanum    Cal: 80%
## Digitalis purpurea    Cal: 81.25%
## Stellaria media    Cal: 77.7777777777778%
## Trisetum flavescens    Cal: 80%
## Trifolium pratense    Cal: 80.9523809523809%
## Geranium robertianum    Cal: 78.5714285714286%
## Plantago major    Cal: 85.7142857142857%
## Nardus stricta    Cal: 78.9473684210526%
## Lamium purpureum    Cal: 77.7777777777778%
## Clinopodium vulgare    Cal: 78.5714285714286%
## Poa annua    Cal: 75%
## Campanula rotundifolia    Cal: 78.5714285714286%
## Taraxacum spec.    Cal: 80%
## Digitaria sanguinalis    Cal: 85.7142857142857%
## Holcus lanatus    Cal: 82.3529411764706%
## Lapsana communis    Cal: 75%
## Apera spica-venti    Cal: 80%
## Alopecurus geniculatus    Cal: 75%
```

```
## Bromus hordeaceus    Cal: 80%
## Phalaris arundinaceae Cal: 81.25%
## Thlaspi arvense Not enough observations
## Origanum vulgare    Cal: 77.7777777777778%
## Pulicaria dysenterica Cal: 79.1666666666667%
## Deschampsia cespitosa Cal: 80%
## Cirsium acaule      Cal: 80%
## Brachypodium sylvaticum Cal: 80%
## Centaureum erythraea Cal: 77.7777777777778%
## Luzula multiflora    Cal: 78.5714285714286%
## Filipendula ulmaria  Cal: 78.5714285714286%
## Anthyllis vulneraria Cal: 75%
## Medicago lupulina   Cal: 75%
## Succisa pratensis    Cal: 83.3333333333333%
## Scirpus sylvaticus   Cal: 77.7777777777778%
## Molinia caerulea     Cal: 83.3333333333333%
```

```
names(split_data)
```

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

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

```
##           Plant_Species Growth_Form      timestamp SLA_g_cm  Wave_500
## 1 Calamagrostis epigejos   graminoid 5/25/2016 12:20 106.6500 0.09180559
## 2 Anthoxanthum odoratum   graminoid 5/27/2016 8:40 293.3565 0.09022668
## 3 Alopecurus pratensis    graminoid 5/27/2016 9:23 220.2703 0.07998340
## 4 Festuca ovina           graminoid 5/27/2016 9:23 137.1220 0.05205080
## 5 Agrostis capillaris     graminoid 5/27/2016 9:42 237.4237 0.06695127
## 6 Aegopodium podagraria    forb     5/25/2016 12:20 388.2384 0.04091566
##      Wave_501 Wave_502 Wave_503
## 1 0.09293251 0.09417092 0.09552863
## 2 0.09125158 0.09237300 0.09359694
## 3 0.08109460 0.08231389 0.08365015
## 4 0.05256869 0.05314560 0.05378355
## 5 0.06766205 0.06845248 0.06932220
## 6 0.04169865 0.04257613 0.04355737
```

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

```
##           Plant_Species Growth_Form      timestamp SLA_g_cm  Wave_500
## 9 Urtica dioica           forb     5/25/2016 12:37 284.6788 0.04716736
## 15 Stellaria media        forb     5/25/2016 13:21 418.4284 0.05694278
## 23 Alopecurus pratensis    graminoid 6/1/2016 11:32 218.2117 0.08135086
## 44 Alopecurus pratensis    graminoid 6/8/2016 8:37 216.7568 0.10062342
## 46 Agrostis capillaris     graminoid 6/8/2016 9:05 231.5292 0.08099724
## 47 Aegopodium podagraria    forb     6/7/2016 9:05 311.4018 0.03778815
```

```
##      Wave_501   Wave_502   Wave_503
## 9  0.04781633 0.04854276 0.04935320
## 15 0.05811729 0.05940497 0.06080936
## 23 0.08249180 0.08373915 0.08509719
## 44 0.10190706 0.10330054 0.10480538
## 46 0.08178586 0.08265099 0.08360108
## 47 0.03845043 0.03919155 0.04001581
```

```
rm(split_data)
```

```
# Datasets:
```

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

```
## [1] "Cal observations: 490"
```

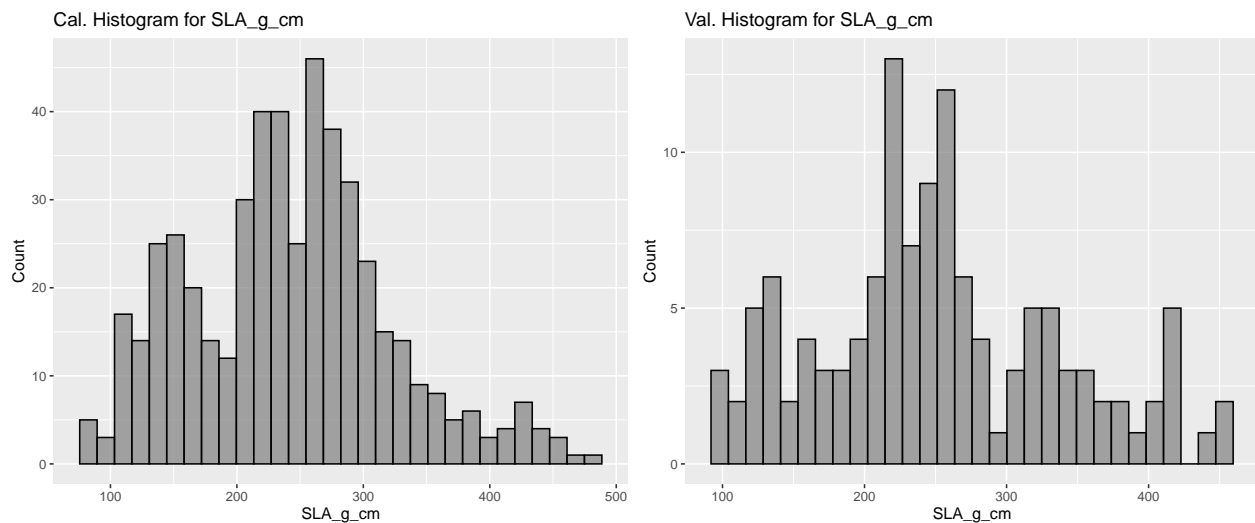
```
print(paste("Val observations: ",dim(val.plsr.data)[1],sep=""))
```

```
## [1] "Val observations: 124"
```

```
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]
```

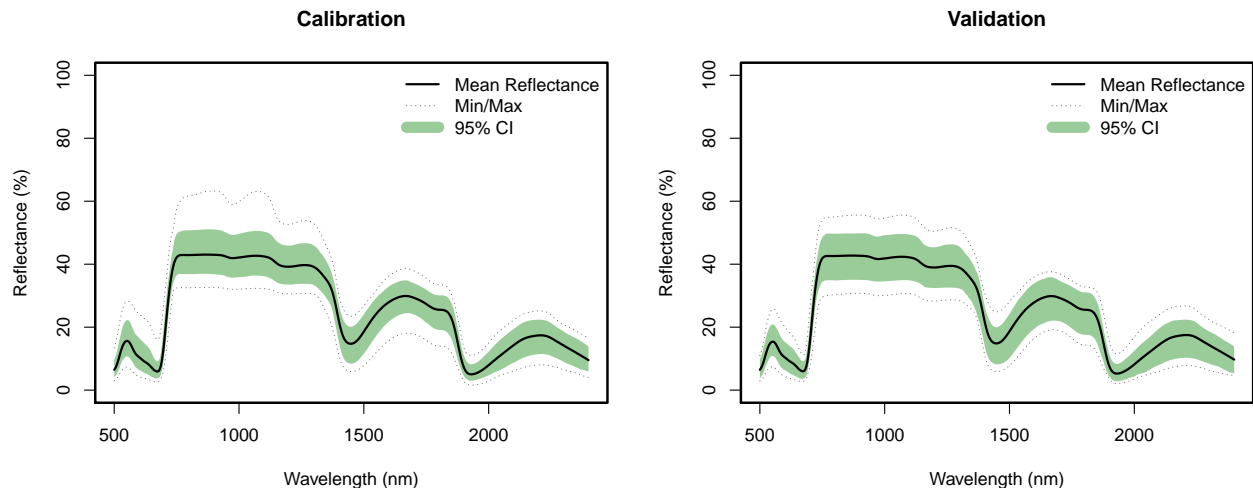
```
##           Plant_Species Growth_Form      timestamp SLA_g_cm CalVal
## 1 Calamagrostis epigejos   graminoid 5/25/2016 12:20 106.6500   Cal
## 2 Anthoxanthum odoratum   graminoid 5/27/2016 8:40 293.3565   Cal
## 3 Alopecurus pratensis    graminoid 5/27/2016 9:23 220.2703   Cal
## 4 Festuca ovina           graminoid 5/27/2016 9:23 137.1220   Cal
## 5 Agrostis capillaris     graminoid 5/27/2016 9:42 237.4237   Cal
## 6 Aegopodium podagraria   forb     5/25/2016 12:20 388.2384   Cal
```

```
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 Growth_Form      timestamp SLA_g_cm CalVal
## 9           Urtica dioica      forb 5/25/2016 12:37 284.6788   Val
## 15          Stellaria media      forb 5/25/2016 13:21 418.4284   Val
## 23 Alopecurus pratensis    graminoid 6/1/2016 11:32 218.2117   Val
## 44 Alopecurus pratensis    graminoid 6/8/2016 8:37 216.7568   Val
## 46 Agrostis capillaris     graminoid 6/8/2016 9:05 231.5292   Val
## 47 Aegopodium podagraria   forb     6/7/2016 9:05 311.4018   Val
```

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

```

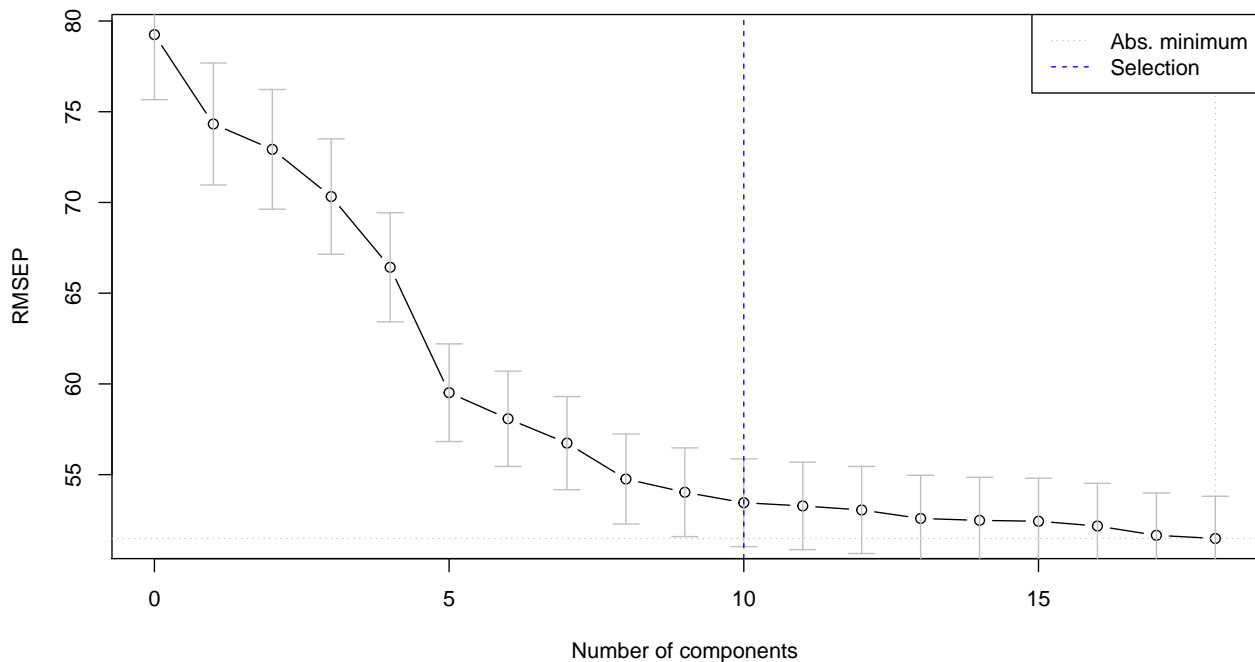
### Use permutation to determine the optimal number of components
if(grepl("Windows", sessionInfo())$running){
  pls.options(parallel = NULL)
} else {
  pls.options(parallel = parallel::detectCores()-1)
}

method <- "pls" #pls, firstPlateau, firstMin
random_seed <- 2356812
seg <- 100
maxComps <- 18
iterations <- 50
prop <- 0.70
if (method=="pls") {
  # pls package approach - faster but estimates more components....
  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 PLS permutation test ***"

```



```
## [1] "*** Optimal number of components: 10"
```

```
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

```
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)
```

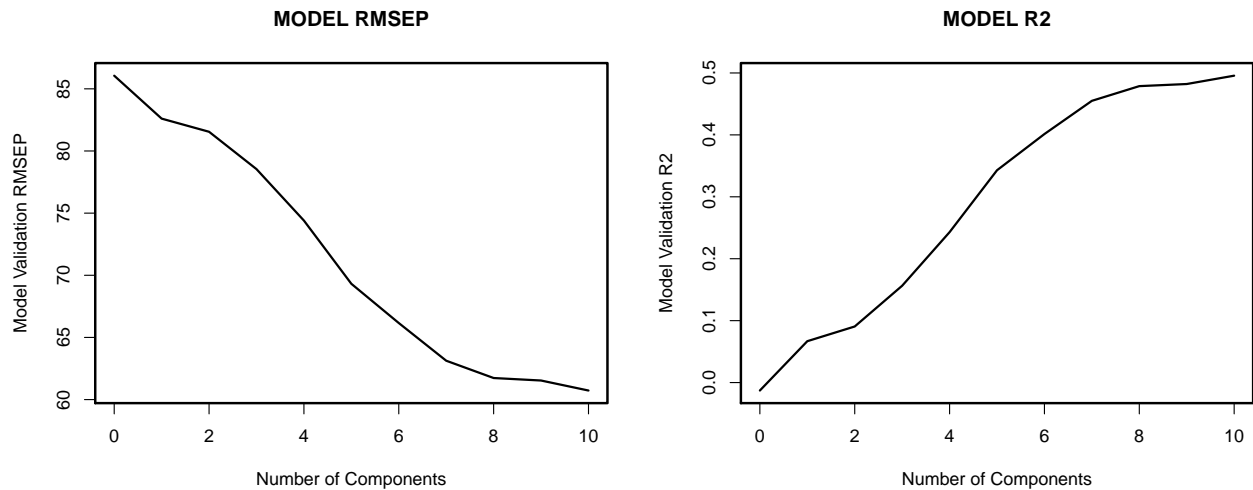
	1 comps	2 comps	3 comps	4 comps	5 comps
## (Intercept)	86.06	82.60	81.55	78.54	74.40
##	66.16	63.13	61.74	61.53	60.73

```
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
##    -0.01288      0.06681      0.09056      0.15636      0.24295      0.34288
##      6 comps      7 comps      8 comps      9 comps     10 comps
##      0.40138      0.45499      0.47875      0.48216      0.49563
```

```
plot(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)
```



```
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)
```

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 Growth_Form      timestamp SLA_g_cm CalVal
## 1 Calamagrostis epigejos  graminoid 5/25/2016 12:20 106.6500   Cal
## 2 Anthoxanthum odoratum  graminoid 5/27/2016 8:40 293.3565   Cal
## 3 Alopecurus pratensis  graminoid 5/27/2016 9:23 220.2703   Cal
## 4 Festuca ovina         graminoid 5/27/2016 9:23 137.1220   Cal
```

```
## 5   Agrostis capillaris   graminoid  5/27/2016 9:42 237.4237   Cal
## 6   Aegopodium podagraria   forb 5/25/2016 12:20 388.2384   Cal
##   PLSR_Predicted PLSR_CV_Predicted PLSR_CV_Residuals
## 1      231.9307      234.1193      127.469378
## 2      237.6749      236.7755      -56.581079
## 3      262.8365      263.8336      43.563272
## 4      126.5863      128.8382      -8.283722
## 5      251.2489      251.3030      13.879308
## 6      277.2292      274.2644     -113.974044

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 Growth_Form      timestamp SLA_g_cm CalVal
## 9      Urtica dioica      forb 5/25/2016 12:37 284.6788   Val
## 15     Stellaria media      forb 5/25/2016 13:21 418.4284   Val
## 23   Alopecurus pratensis   graminoid 6/1/2016 11:32 218.2117   Val
## 44   Alopecurus pratensis   graminoid 6/8/2016 8:37 216.7568   Val
## 46   Agrostis capillaris   graminoid 6/8/2016 9:05 231.5292   Val
## 47   Aegopodium podagraria   forb 6/7/2016 9:05 311.4018   Val
##   PLSR_Predicted PLSR_Residuals
## 9      240.6023     -44.076512
## 15     248.6923    -169.736117
## 23     211.4638     -6.747881
## 44     275.4544     58.697587
## 46     290.4019     58.872672
## 47     274.2311    -37.170622
```

```
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("Rsq = ", 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("Rsq = ", val.R2), "; ", paste0("RMSEP = ",
                                                                                   val.RMSEP))) +

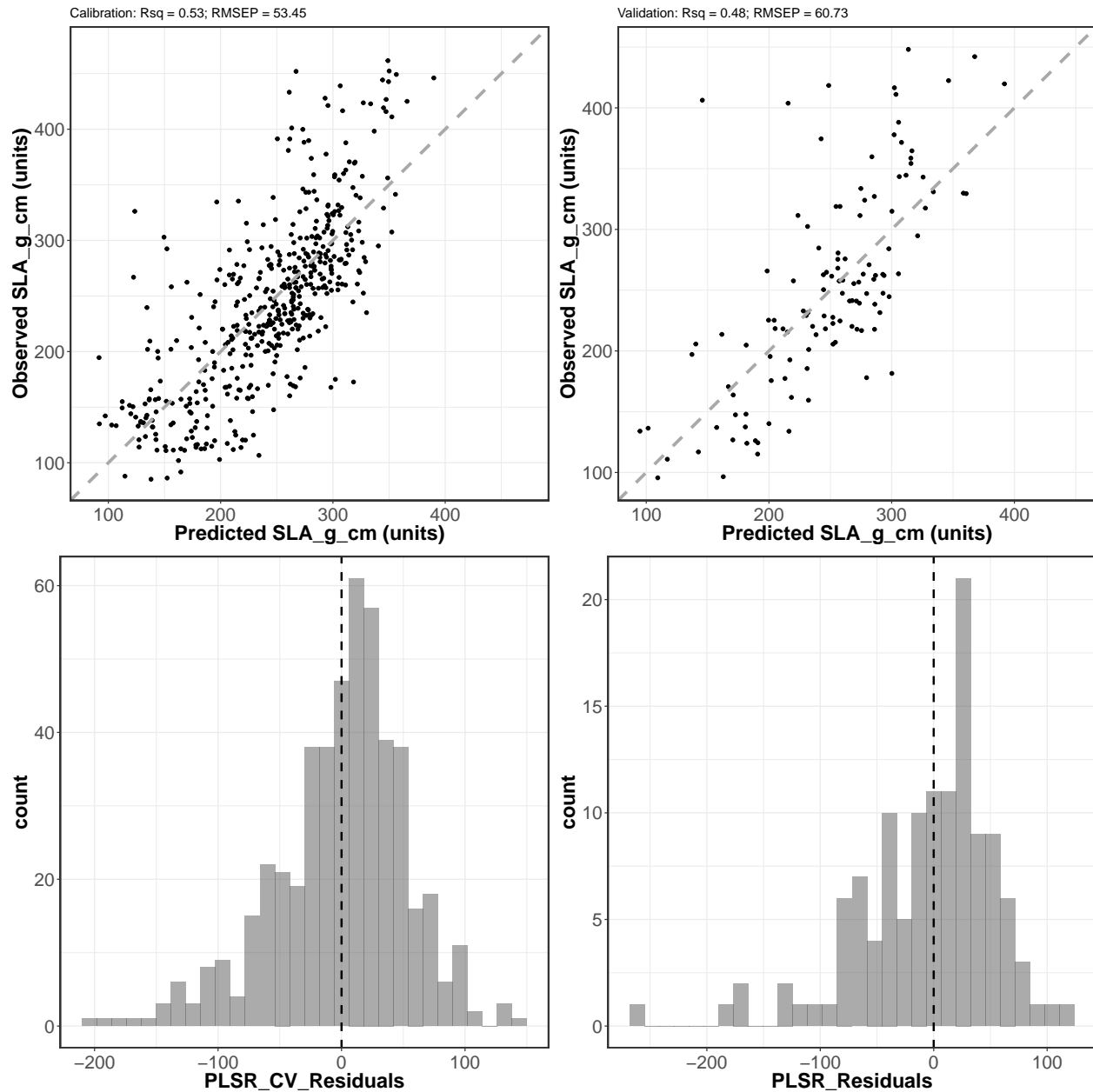
  theme(axis.text=element_text(size=18), legend.position="none",
        axis.title=element_text(size=20, face="bold"),
        axis.text.x = element_text(angle = 0,vjust = 0.5),
        panel.border = element_rect(linetype = "solid", fill = NA, size=1.5))

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 7 rows containing missing values (geom_point).
## Warning: Removed 3 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

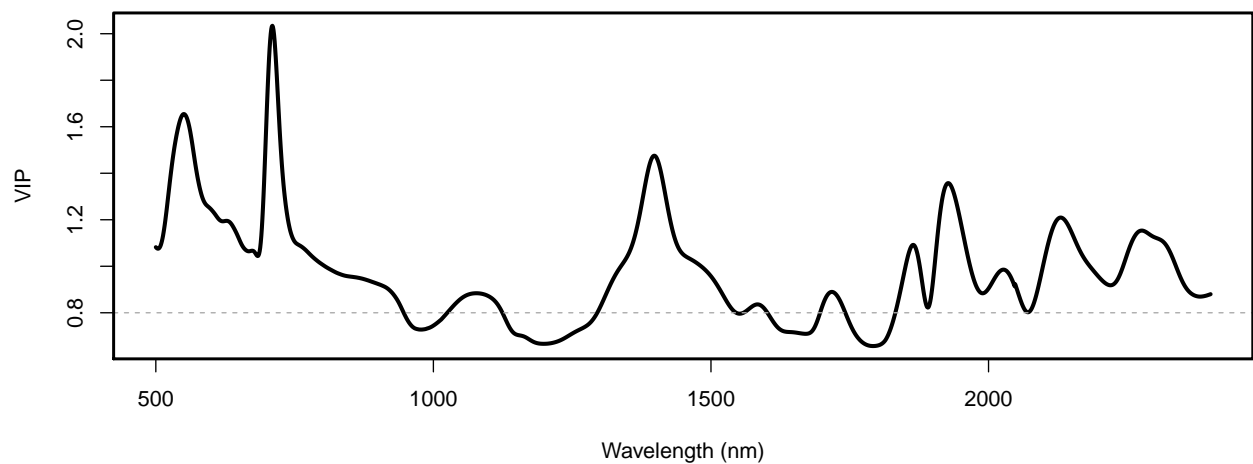
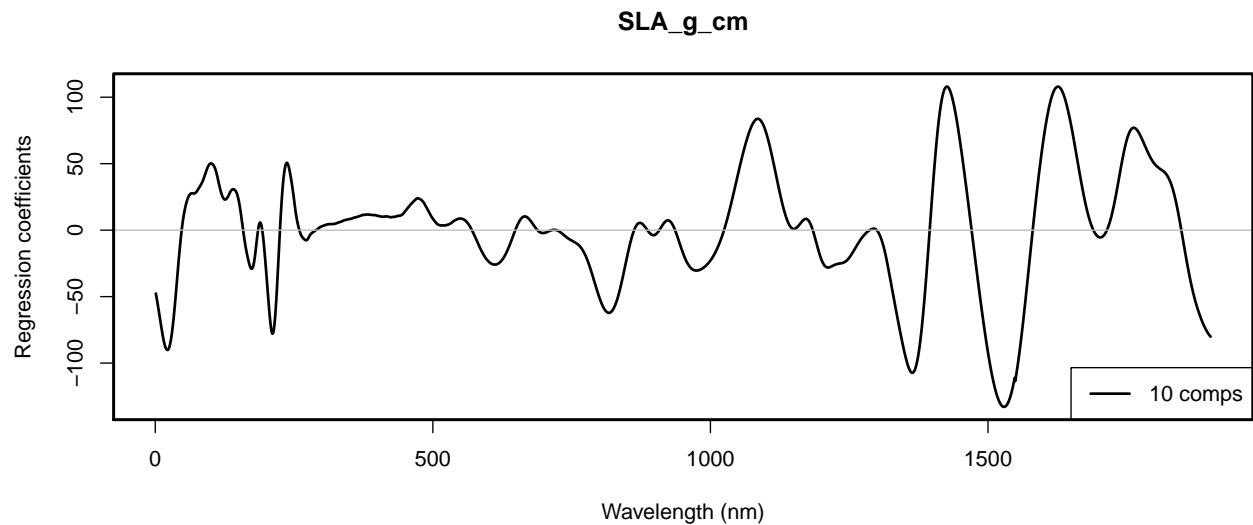
```
vips <- spectratrait::VIP(plsr.out)[nComps,]

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 <- 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],,,]

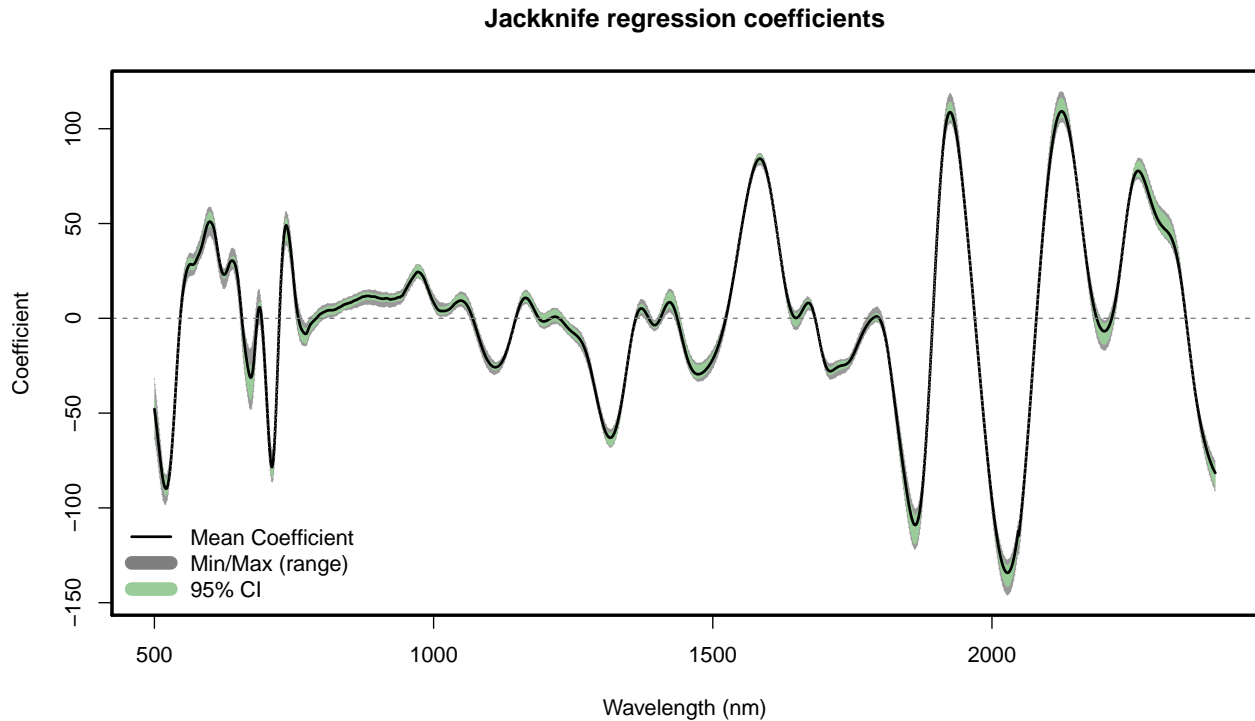
interval <- c(0.025,0.975)
Jackknife_Pred <- val.plsr.data$Spectra %*% Jackknife_coef +
  matrix(rep(Jackknife_intercept, length(val.plsr.data[,inVar])), byrow=TRUE,
          ncol=length(Jackknife_intercept))
Interval_Conf <- apply(X = Jackknife_Pred, MARGIN = 1, FUN = quantile,
                      probs=c(interval[1], interval[2]))
sd_mean <- apply(X = Jackknife_Pred, MARGIN = 1, FUN = sd)
sd_res <- sd(val.plsr.output$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	Growth_Form	timestamp	SLA_g_cm	CalVal	
## 9	Urtica dioica	forb	5/25/2016 12:37	284.6788	Val	
## 15	Stellaria media	forb	5/25/2016 13:21	418.4284	Val	
## 23	Alopecurus pratensis	graminoid	6/1/2016 11:32	218.2117	Val	
## 44	Alopecurus pratensis	graminoid	6/8/2016 8:37	216.7568	Val	
## 46	Agrostis capillaris	graminoid	6/8/2016 9:05	231.5292	Val	
## 47	Aegopodium podagraria	forb	6/7/2016 9:05	311.4018	Val	
##	PLSR_Predicted	PLSR_Residuals	LCI	UCI	LPI	UPI
## 9	240.6023	-44.076512	237.5315	250.4949	121.3665	359.8380
## 15	248.6923	-169.736117	246.6740	250.9811	129.6378	367.7468
## 23	211.4638	-6.747881	207.9159	212.8904	92.4012	330.5265
## 44	275.4544	58.697587	272.8887	276.9933	156.4053	394.5035
## 46	290.4019	58.872672	288.2699	291.6463	171.3562	409.4475
## 47	274.2311	-37.170622	272.4991	276.1200	155.1831	393.2792

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
```

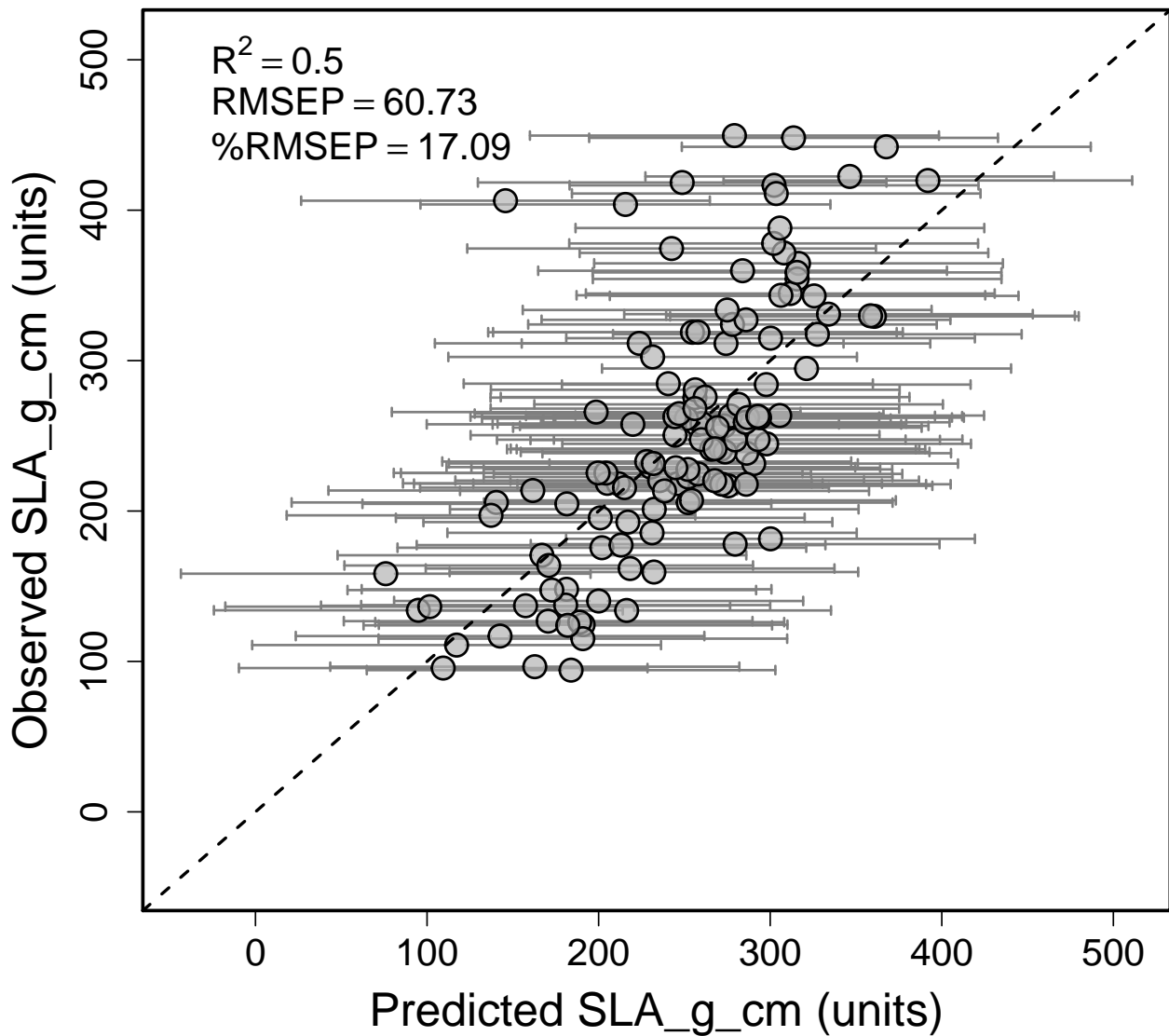
Jackknife validation plot

```
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  246.6837 -49.80782 -52.32289 -54.88084 -57.63716  
## Seg 2         2  254.8287 -52.24947 -54.31513 -56.41444 -58.71748  
## Seg 3         3  246.2546 -54.91885 -57.12727 -59.35903 -61.78247  
## Seg 4         4  249.9940 -49.37912 -51.77580 -54.22486 -56.87922  
## Seg 5         5  257.4183 -45.54171 -47.92949 -50.36257 -53.01337  
## Seg 6         6  247.2549 -40.72975 -42.81360 -44.93902 -47.28299
```

```
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] "SLA_g_cm_Cal_PLSR_Dataset.csv"
## [2] "SLA_g_cm_Cal_Val_Histograms.png"
## [3] "SLA_g_cm_Cal_Val_Scatterplots.png"
## [4] "SLA_g_cm_Cal_Val_Spectra.png"
## [5] "SLA_g_cm_Coefficient_VIP_plot.png"
## [6] "SLA_g_cm_Jackknife_PLSR_Coefficients.csv"
## [7] "SLA_g_cm_Jackknife_Regression_Coefficients.png"
## [8] "SLA_g_cm_Observed_PLSR_CV_Pred_10comp.csv"
## [9] "SLA_g_cm_PLSR_Coefficients_10comp.csv"
## [10] "SLA_g_cm_PLSR_Component_Selection.png"
## [11] "SLA_g_cm_PLSR_Validation_Scatterplot.png"
## [12] "SLA_g_cm_PLSR_VIPs_10comp.csv"
## [13] "SLA_g_cm_Val_PLSR_Dataset.csv"
## [14] "SLA_g_cm_Validation_PLSR_Pred_10comp.csv"
## [15] "SLA_g_cm_Validation_RMSEP_R2_by_Component.png"
```