

Color Analysis of Floral Tissues

K. Uckele

2025-01-29

Contents

Introduction	2
Setup	2
Load Required Libraries	2
Set working directory	2
Define Custom Operators	2
Authenticate Google Sheets Access	2
Quality Control	3
Load Spectral Data from Google Sheets	3
Spectral Data Processing	3
Convert Data to rspec Objects	3
Average the Spectra	4
Fix Negative Reflectance Values	6
Determine Smoothing Parameter	6
Smooth the Spectral Data	7
Scale the Spectral Data	7
Plot Processed Spectra	8
Define Common Plotting Parameters	8
Bract Spectra Plot	8
Petal Spectra Plot	9
Labellum Spectra Plot	10
Combine and Save Spectral Plots with Highlighted Parents	11
Spectral Descriptors	12
Define spectral descriptors	12
Calculate Spectral Descriptors	12
Bract	12
Plot Bract Spectral Descriptors Histograms	12
Petal Summary	13
Plot Petal Spectral Descriptors Histograms	13
Labellum Summary	14
Plot Labellum Spectral Descriptors Histograms	14
Data Formatting and Export	15
Reformat Rownames	15
Subset and Rename Columns	15
Convert Rownames to a Column	16
Merge Summary Dataframes	16

Introduction

This analysis explores the color properties of different floral tissues — bract, petal, and labellum — using spectral data sourced from Google Sheets. The analysis includes data loading, quality control, spectral processing, visualization, and the computation of summary descriptors.

Setup

Load Required Libraries

```
## libraries
library(googlesheets4)
library(cowplot)
library(dplyr)

##
## 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

library(tibble)
library(knitr)
library(rmarkdown)
library(pavo)
```

Set working directory

```
# Set the root directory to the project root
knitr::opts_knit$set(root.dir = normalizePath("../"))
```

Define Custom Operators

```
# Define a 'not in' operator
`%notin%` = Negate(`%in%`)
```

Authenticate Google Sheets Access

Authenticate access to Google Sheets using your email. Ensure that the email has the necessary permissions to access the sheets.

```
# Authenticate with Google Sheets
gs4_auth(email = "kuckele@ucsc.edu")
```

Quality Control

Load Spectral Data from Google Sheets

We load the spectral data for bract, petal, and labellum from the specified Google Sheets.

```
# Specify the Google Sheets ID
sheet_id <- "12NWtlqKbLPaXU-rVBTqMQjY_6jH1DulVvNHS_QXAvFI"

# Load data for different floral tissues
bract <- read_sheet(ss = sheet_id, sheet = "Bract")

## v Reading from "Color".
## v Range 'Bract'.

petal <- read_sheet(ss = sheet_id, sheet = "Petal")

## v Reading from "Color".
## v Range 'Petal'.

labellum <- read_sheet(ss = sheet_id, sheet = "Labellum")

## v Reading from "Color".
## v Range 'Labellum'.
```

Spectral Data Processing

Convert Data to rspec Objects

The spectral data is converted into rspec objects using the pavo package for further analysis.

```
# Set seed for reproducibility
set.seed(1612217)

# Convert datasets to rspec objects with wavelength limits
bract_spec <- as.rspec(bract, lim = c(300, 700), whichwl = 1)

## The spectral data contain 555 negative value(s),
## which may produce unexpected results if used in models.
## Consider using procspec() to correct them.

petal_spec <- as.rspec(petal, lim = c(300, 700), whichwl = 1)

## The spectral data contain 272 negative value(s),
## which may produce unexpected results if used in models.
## Consider using procspec() to correct them.

labellum_spec <- as.rspec(labellum, lim = c(300, 700), whichwl = 1)

# change column names
colnames(bract_spec) <- gsub("-", "x", colnames(bract_spec))
colnames(petal_spec) <- gsub("-", "x", colnames(petal_spec))
colnames(labellum_spec) <- gsub("-", "x", colnames(labellum_spec))
```

Note: The conversion may produce warnings about negative values in spectral data, which are addressed in subsequent steps.

Average the Spectra

Aggregate the spectral data by sample names, averaging replicates.

```
# Extract sample names by removing trailing numbers in parentheses
bract_samples <- gsub("\\([0-9]+\\)$", "", names(bract_spec))[-1]
petal_samples <- gsub("\\([0-9]+\\)$", "", names(petal_spec))[-1]
labellum_samples <- gsub("\\([0-9]+\\)$", "", names(labellum_spec))[-1]

# Verify sample counts
table(bract_samples)
```

```
## bract_samples
##      125      126      39  39x10 39x109 39x110 39x115 39x116 39x117  39x12 39x122
##        2        3        1        2        1        2        2        1        3        2        2
## 39x123 39x125 39x126  39x13 39x130 39x136  39x14  39x15  39x16  39x17  39x2
##        2        2        2        1        3        2        3        2        4        2        2
## 39x21  39x23  39x25  39x27  39x34  39x39  39x4  39x40  39x41  39x44  39x46
##        2        2        2        2        2        2        2        2        2        2        2
## 39x49  39x50  39x51  39x55  39x56  39x57  39x6  39x60  39x65  39x67  39x68
##        2        2        2        2        2        2        2        2        2        2        1
## 39x75  39x77  39x78  39x79  39x8  39x81  39x82  39x86  39x87  39x89  39x92
##        2        2        2        2        1        2        3        1        1        2        2
## 39x93  39x95  39x96  39x98  62x10 62x103 62x105 62x109 62x116 62x119 62x122
##        2        2        2        2        1        2        2        1        1        2        1
## 62x125 62x128 62x129  62x13 62x130 62x131 62x134 62x135 62x136 62x137 62x138
##        1        1        2        2        1        2        1        2        2        1        1
## 62x139 62x14 62x140 62x143 62x144 62x147 62x151 62x152 62x153 62x154 62x157
##        1        1        2        1        2        1        1        3        2        2        2
## 62x158 62x16 62x162 62x167 62x168 62x169  62x17 62x172 62x173 62x175 62x18
##        2        2        2        2        1        1        2        2        2        2        1
## 62x182 62x185 62x188 62x189  62x19 62x190 62x197 62x200 62x206  62x21 62x214
##        1        2        1        1        2        2        2        2        2        2        1
## 62x218 62x219  62x22 62x220 62x225 62x233 62x234 62x240 62x251 62x252 62x258
##        2        2        2        1        2        1        1        2        2        1        1
## 62x261 62x264 62x265 62x267 62x268 62x276 62x282 62x293 62x296 62x300 62x302
##        2        2        1        2        2        1        1        2        1        1        1
## 62x303 62x304 62x305 62x306 62x307 62x308 62x309 62x310 62x313 62x315 62x322
##        2        1        1        1        2        1        2        1        1        1        1
## 62x324 62x327 62x332 62x337 62x338 62x351 62x355 62x359 62x363 62x370  62x5
##        1        1        2        1        2        1        2        2        2        1        1
## 62x57  62x58  62x59  62x60  62x63  62x65  62x66  62x69  62x73  62x74  62x75
##        2        2        2        1        1        1        1        2        2        1        1
## 62x77  62x83  62x87  62x91  62x92  62x94  62x96  BRAC
##        1        2        1        2        2        1        1        2
```

```
table(petal_samples)
```

```
## petal_samples
##      125      126      39  39x10 39x109 39x110 39x115 39x116 39x117  39x12 39x122
##        2        2        1        2        1        2        2        1        3        2        2
## 39x123 39x125 39x126  39x13 39x130 39x136  39x14  39x15  39x16  39x17  39x2
##        2        2        2        1        3        2        3        2        4        2        2
## 39x21  39x23  39x25  39x27  39x34  39x39  39x4  39x40  39x41  39x44  39x46
##        2        2        2        2        2        2        2        2        2        2        2
## 39x49  39x50  39x51  39x55  39x56  39x57  39x6  39x60  39x65  39x67  39x68
```

```
##      2      2      2      2      2      2      2      2      2      2      1
## 39x75 39x77 39x78 39x79 39x8 39x81 39x82 39x86 39x87 39x89 39x92
##      2      2      2      2      1      2      3      1      1      2      2
## 39x93 39x95 39x96 39x98 62x10 62x103 62x105 62x109 62x116 62x119 62x122
##      2      2      2      2      1      2      2      1      1      2      1
## 62x125 62x128 62x129 62x13 62x130 62x131 62x134 62x135 62x136 62x137 62x138
##      1      1      2      2      1      2      1      2      2      1      1
## 62x139 62x14 62x140 62x143 62x144 62x147 62x151 62x152 62x153 62x154 62x157
##      1      1      2      1      2      1      1      3      2      2      2
## 62x158 62x16 62x162 62x167 62x168 62x169 62x17 62x172 62x173 62x175 62x18
##      2      2      2      2      1      1      2      2      2      2      1
## 62x182 62x185 62x188 62x189 62x19 62x190 62x197 62x200 62x206 62x21 62x214
##      1      2      1      1      2      2      2      2      2      2      1
## 62x218 62x219 62x22 62x220 62x225 62x233 62x234 62x240 62x251 62x252 62x258
##      2      2      2      1      2      1      1      2      2      1      1
## 62x261 62x262 62x264 62x265 62x268 62x276 62x282 62x293 62x296 62x300 62x302
##      2      2      2      1      2      1      1      2      1      1      1
## 62x303 62x304 62x305 62x306 62x307 62x308 62x309 62x310 62x313 62x315 62x322
##      2      1      1      1      2      1      2      1      1      1      1
## 62x324 62x327 62x332 62x337 62x338 62x351 62x355 62x359 62x363 62x370 62x5
##      1      1      2      1      2      1      2      2      2      1      1
## 62x57 62x58 62x59 62x60 62x63 62x65 62x66 62x69 62x73 62x74 62x75
##      2      2      2      1      1      1      1      2      2      1      1
## 62x77 62x83 62x87 62x91 62x92 62x94 62x96 BRAC
##      1      2      1      2      2      1      1      2
```

```
table(labellum_samples)
```

```
## labellum_samples
##      125      126      39 39x10 39x109 39x110 39x115 39x116 39x117 39x12 39x122
##      2      2      1      2      1      2      2      1      3      2      2
## 39x123 39x125 39x126 39x13 39x130 39x136 39x14 39x15 39x16 39x17 39x2
##      2      2      2      1      3      2      3      2      4      2      2
## 39x21 39x23 39x25 39x27 39x34 39x39 39x4 39x40 39x41 39x44 39x46
##      2      2      2      2      2      2      2      2      2      2      2
## 39x49 39x50 39x51 39x55 39x56 39x57 39x6 39x60 39x65 39x67 39x68
##      2      2      2      2      2      2      2      2      2      2      1
## 39x75 39x77 39x78 39x79 39x8 39x81 39x82 39x86 39x87 39x89 39x92
##      2      2      2      2      1      2      3      1      1      2      2
## 39x93 39x95 39x96 39x98 62x10 62x103 62x105 62x109 62x116 62x119 62x122
##      2      2      2      2      1      2      2      1      1      2      1
## 62x125 62x128 62x129 62x13 62x130 62x131 62x134 62x135 62x136 62x137 62x138
##      1      1      2      2      1      2      1      2      2      1      1
## 62x139 62x14 62x140 62x143 62x144 62x147 62x151 62x152 62x153 62x154 62x157
##      1      1      2      1      2      1      1      3      2      2      2
## 62x158 62x16 62x162 62x167 62x168 62x169 62x17 62x172 62x173 62x175 62x18
##      2      2      2      2      1      1      2      2      2      2      1
## 62x182 62x185 62x188 62x189 62x19 62x190 62x197 62x200 62x206 62x21 62x214
##      1      2      1      1      2      2      2      2      2      2      1
## 62x218 62x219 62x22 62x220 62x225 62x233 62x234 62x240 62x251 62x252 62x258
##      2      2      2      1      2      1      1      2      2      1      1
## 62x261 62x262 62x264 62x265 62x268 62x276 62x282 62x293 62x296 62x300 62x302
##      2      2      2      1      2      1      1      2      1      1      1
## 62x303 62x304 62x305 62x306 62x307 62x308 62x309 62x310 62x313 62x315 62x322
##      2      1      1      1      2      1      2      1      1      1      1
```

```
## 62x324 62x327 62x332 62x337 62x338 62x351 62x355 62x359 62x363 62x370 62x5
##      1      1      2      2      2      1      2      2      2      1      1
## 62x57 62x58 62x59 62x60 62x63 62x65 62x66 62x69 62x73 62x74 62x75
##      2      2      2      1      1      1      1      2      2      1      1
## 62x77 62x83 62x87 62x91 62x92 62x94 62x96 BRAC
##      1      2      1      2      2      1      1      2
```

```
# Aggregate spectra by sample names using mean
bract_spec_avg <- aggspec(bract_spec, by = bract_samples, FUN = mean)
petal_spec_avg <- aggspec(petal_spec, by = petal_samples, FUN = mean)
labellum_spec_avg <- aggspec(labellum_spec, by = labellum_samples, FUN = mean)
```

Fix Negative Reflectance Values

Negative reflectance values are corrected by adding the minimum reflectance.

```
# Fix negative values by adding the minimum reflectance
bract_spec_avg <- procspec(bract_spec_avg, fixneg = "admin")
```

```
## processing options applied:
## Negative value correction: added min to all reflectance
petal_spec_avg <- procspec(petal_spec_avg, fixneg = "admin")
```

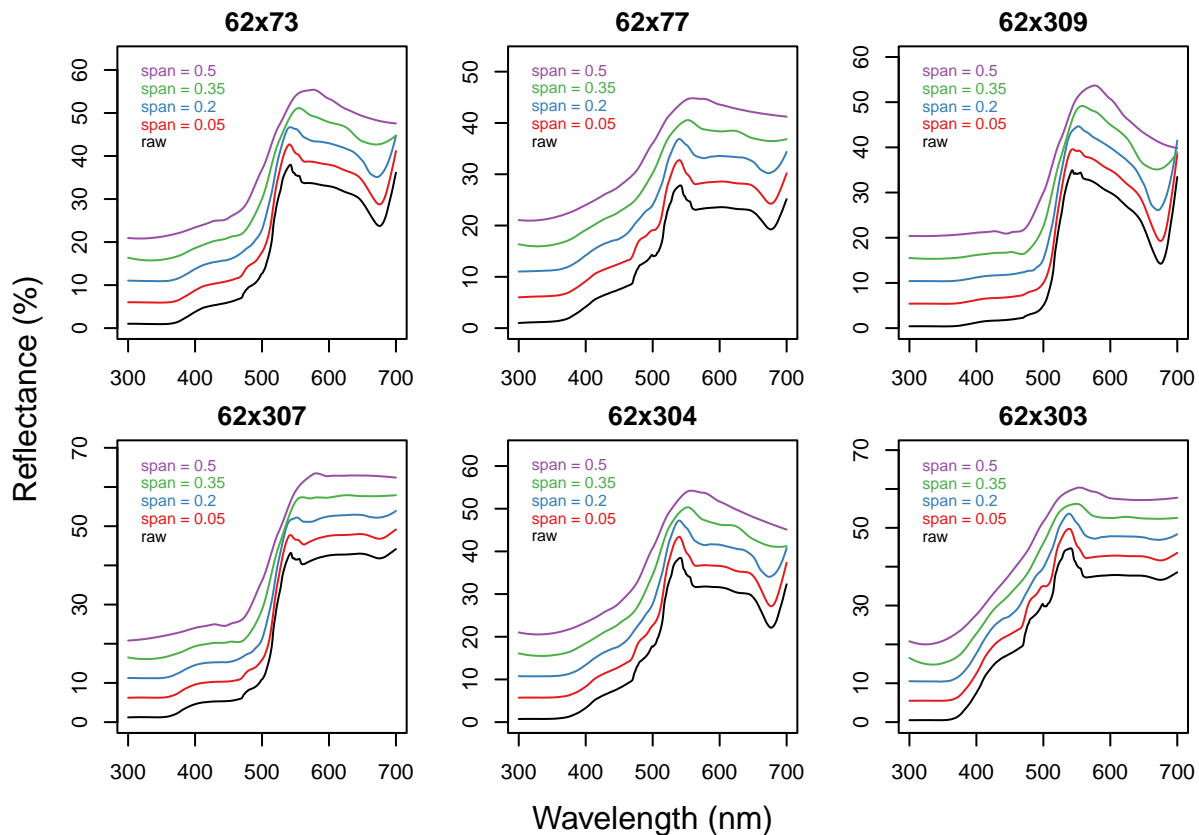
```
## processing options applied:
## Negative value correction: added min to all reflectance
labellum_spec_avg <- procspec(labellum_spec_avg, fixneg = "admin")
```

```
## processing options applied:
## Negative value correction: added min to all reflectance
```

Determine Smoothing Parameter

Use `plotsmooth` to visualize and decide on an appropriate smoothing span.

```
# Plot to determine suitable smoothing span
plotsmooth(bract_spec_avg[,1:7],
           minsmooth = 0.05,
           maxsmooth = 0.5,
           curves = 4,
           ask = FALSE)
```



Choose a span (e.g., 0.2) based on the plot to balance smoothness and data fidelity.

Smooth the Spectral Data

Apply smoothing to the spectral data using the chosen span.

```
# Apply smoothing with span = 0.2
bract_spec_sm <- procspec(bract_spec_avg, opt = "smooth", span = 0.2)
```

```
## processing options applied:
## smoothing spectra with a span of 0.2
```

```
petal_spec_sm <- procspec(petal_spec_avg, opt = "smooth", span = 0.2)
```

```
## processing options applied:
## smoothing spectra with a span of 0.2
```

```
labellum_spec_sm <- procspec(labellum_spec_avg, opt = "smooth", span = 0.2)
```

```
## processing options applied:
## smoothing spectra with a span of 0.2
```

Scale the Spectral Data

Scale the spectral data to different reference points for comparative analysis.

```
# Scale spectra to both minimum and maximum reflectance
bract_spec_scalemminmax <- procspec(bract_spec_sm, opt = c("min", "max"))
```

```
## processing options applied:
## Scaling spectra to a minimum value of zero
```

```
## Scaling spectra to a maximum value of 1
petal_spec_scaleminmax <- procspec(petal_spec_sm, opt = c("min", "max"))

## processing options applied:
## Scaling spectra to a minimum value of zero
## Scaling spectra to a maximum value of 1
labellum_spec_scaleminmax <- procspec(labellum_spec_sm, opt = c("min", "max"))

## processing options applied:
## Scaling spectra to a minimum value of zero
## Scaling spectra to a maximum value of 1
```

Plot Processed Spectra

Visualize the processed spectral data for each floral tissue, highlighting specific samples.

Define Common Plotting Parameters

```
# Define a color palette for highlighting specific samples
highlight_colors <- c(rep("lightgrey", 170), "gold1", "gold1", "darkgreen")
```

Bract Spectra Plot

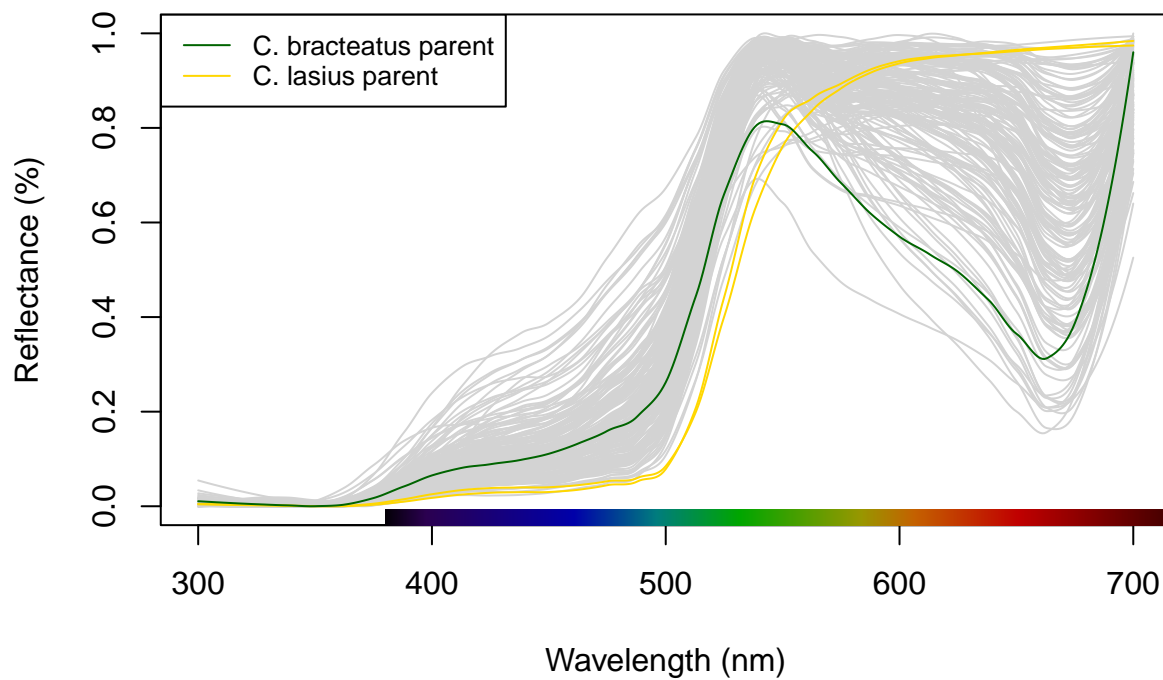
```
# Order samples to highlight specific ones
order_spec_bract <- c(
  which(names(bract_spec_scaleminmax) == "125"),
  which(names(bract_spec_scaleminmax) == "126"),
  which(names(bract_spec_scaleminmax) == "BRAC")
)

# Reorder columns to place highlighted samples at the end
columns_bract <- 1:ncol(bract_spec_scaleminmax)
order_spec_bract <- c(columns_bract[columns_bract %notin% order_spec_bract], order_spec_bract)

# Plot the spectra
plot(bract_spec_scaleminmax[order_spec_bract], type = "o",
     col = highlight_colors, main = "Bract Spectra",
     xlab = "Wavelength (nm)", ylab = "Reflectance (%)")

# Add a legend
legend("topleft", legend = c("C. bracteatus parent", "C. lasius parent"),
     col = c("darkgreen", "gold1"), lty = 1, cex = 0.8)
```


Bract Spectra



Petal Spectra Plot

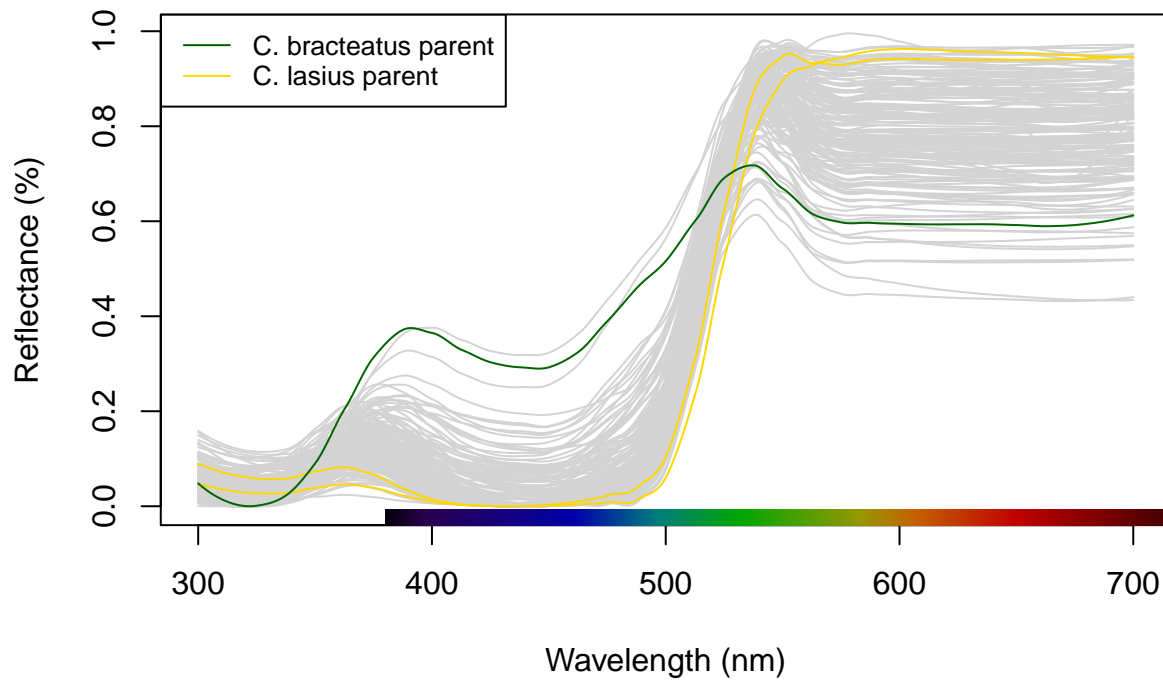
```
# Order samples to highlight specific ones
order_spec_petal <- c(
  which(names(petal_spec_scaleminmax) == "125"),
  which(names(petal_spec_scaleminmax) == "126"),
  which(names(petal_spec_scaleminmax) == "BRAC")
)

# Reorder columns to place highlighted samples at the end
columns_petal <- 1:ncol(petal_spec_scaleminmax)
order_spec_petal <- c(columns_petal[columns_petal %notin% order_spec_petal], order_spec_petal)

# Plot the spectra
plot(petal_spec_scaleminmax[order_spec_petal], type = "o",
     col = highlight_colors, main = "Petal Spectra",
     xlab = "Wavelength (nm)", ylab = "Reflectance (%)")

# Add a legend
legend("topleft", legend = c("C. bracteatus parent", "C. lasius parent"),
     col = c("darkgreen", "gold1"), lty = 1, cex = 0.8)
```

Petal Spectra



Labellum Spectra Plot

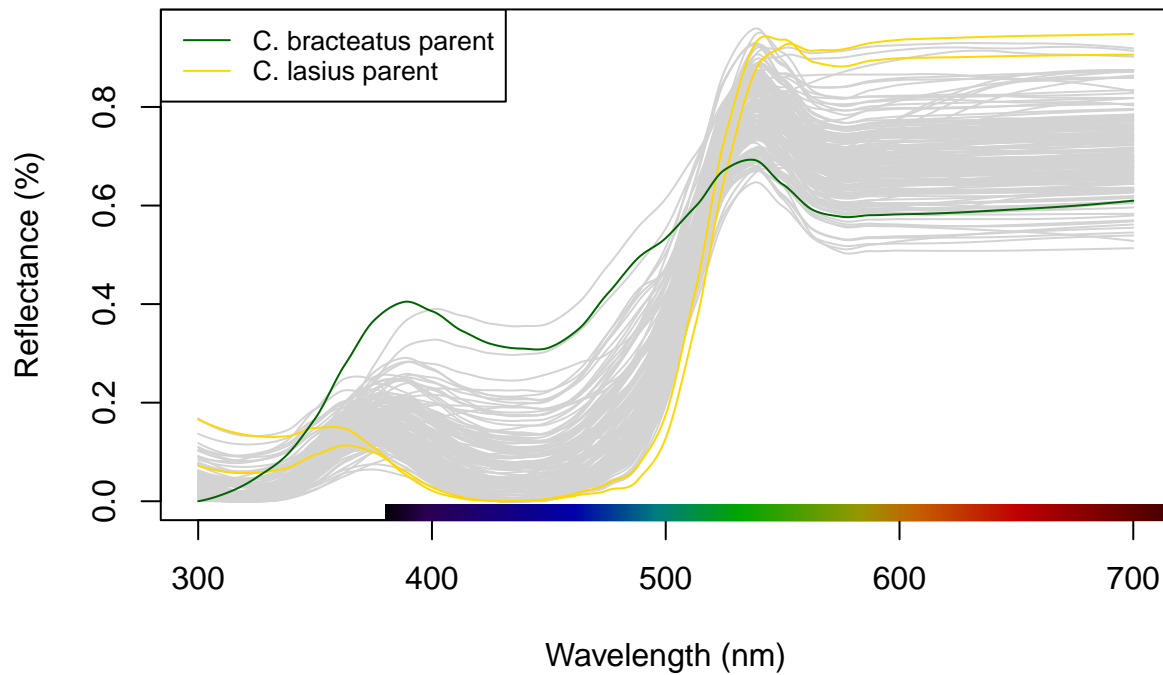
```
# Order samples to highlight specific ones
order_spec_labellum <- c(
  which(names(labellum_spec_scaleminmax) == "125"),
  which(names(labellum_spec_scaleminmax) == "126"),
  which(names(labellum_spec_scaleminmax) == "BRAC")
)

# Reorder columns to place highlighted samples at the end
columns_labellum <- 1:ncol(labellum_spec_scaleminmax)
order_spec_labellum <- c(columns_labellum[columns_labellum %notin% order_spec_labellum], order_spec_labellum)

# Plot the spectra
plot(labellum_spec_scaleminmax[order_spec_labellum], type = "o",
     col = highlight_colors, main = "Labellum Spectra",
     xlab = "Wavelength (nm)", ylab = "Reflectance (%)")

# Add a legend
legend("topleft", legend = c("C. bracteatus parent", "C. lasius parent"),
     col = c("darkgreen", "gold1"), lty = 1, cex = 0.8)
```

Labellum Spectra



Combine and Save Spectral Plots with Highlighted Parents

```
# Save combined spectra plots with highlighted parental samples
pdf("./results/figures/Combined_Spectra_Bract_Petal_Labellum_Cbracteatus_Clasius_hybrids.pdf", width = 10)
par(mfrow = c(1, 3))
# Increase left margin to provide more space for y-axis labels
par(mar = c(5, 5, 4, 2) + 0.1) # c(bottom, left, top, right)
plot(bract_spec_scaleminmax[order_spec_bract], type = "o", col = highlight_colors,
     main = "Bract spectra", xlab = "Wavelength (nm)", ylab = "Reflectance (%)",
     cex.main = 3, cex.lab = 2.5, cex.axis = 2, lwd = 2)
legend("topleft", legend = c("C. bracteatus parent", "C. lasius parent"),
     col = c("darkgreen", "gold1"), lty = 1, cex = 2.5, bty = "n")
plot(petal_spec_scaleminmax[order_spec_petal], type = "o", col = highlight_colors,
     main = "Petal spectra", xlab = "Wavelength (nm)", ylab = "Reflectance (%)",
     cex.main = 3, cex.lab = 2.5, cex.axis = 2, lwd = 2)
legend("topleft", legend = c("C. bracteatus parent", "C. lasius parent"),
     col = c("darkgreen", "gold1"), lty = 1, cex = 2.5, bty = "n")
plot(labellum_spec_scaleminmax[order_spec_labellum], type = "o", col = highlight_colors,
     main = "Labellum spectra", xlab = "Wavelength (nm)", ylab = "Reflectance (%)",
     cex.main = 3, cex.lab = 2.5, cex.axis = 2, lwd = 2)
legend("topleft", legend = c("C. bracteatus parent", "C. lasius parent"),
     col = c("darkgreen", "gold1"), lty = 1, cex = 2.5, bty = "n")
dev.off()
```

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

Spectral Descriptors

We compute various spectral descriptors to quantify the color properties of the floral tissues.

Define spectral descriptors

B1: Total brightness B2: Mean brightness B3: Intensity (Rmax) S1U to S1R: Relative contributions of UV, Violet, Blue, Green, Yellow, and Red spectral ranges to total brightness S2: Spectral saturation (Rmax/Rmin) S3: Chroma S4: Spectral purity S5: Chroma S6: Contrast (Rmax - Rmin) S7: Spectral saturation S8: Chroma ((Rmax - Rmin)/B2) S9: Carotenoid chroma ((R700 - R450)/R700) S10: Peak chroma H1 to H5: Hue metrics (e.g., peak wavelength) Note: Some metrics may be sensitive to spectral noise.

Calculate Spectral Descriptors

Bract

```
# Calculate spectral descriptors for bract
summary_bract <- summary(bract_spec_scaleminmax)

# Remove S2 due to infinite values
summary_bract <- summary_bract %>% select(-S2)

# Extract metrics for parents
bract125 <- round(summary_bract["125", ], 3)
bract126 <- round(summary_bract["126", ], 3)
bractBRAC <- round(summary_bract["BRAC", ], 3)
```

Plot Bract Spectral Descriptors Histograms

```
pdf("../results/figures/bract_descriptors_histograms.pdf", width = 14, height = 10)

# Set up plotting area: 4 rows x 6 columns for histograms
par(mfrow = c(4, 6),          # 4 rows, 6 columns
    mar = c(5, 5, 4, 2) + 0.1, # Margins for each plot: bottom, left, top, right
    oma = c(0, 0, 0, 5))      # Outer margins: bottom, left, top, right

# Loop through each metric and plot histogram with parental lines
for (i in 1:ncol(summary_bract)) {
  hist(summary_bract[, i],
        xlab = colnames(summary_bract)[i],
        main = colnames(summary_bract)[i],
        col = "lightgrey",
        border = "white")

  # Add vertical lines for parental samples
  abline(v = bract125[i], col = 'gold1', lwd = 3)      # C. lasius parent
  abline(v = bract126[i], col = 'gold1', lwd = 3)      # C. lasius parent
  abline(v = bractBRAC[i], col = 'darkgreen', lwd = 3) # C. bracteatus parent
}

# Allow drawing in the outer margin
par(xpd = TRUE)

plot.new()
```

```

# Add a shared legend in the outer right margin
legend("topright",
      inset = c(0, 0), # Adjusts the position of the legend
      legend = c("C. lasius parent", "C. bracteatus parent"),
      col = c("gold1", "darkgreen"),
      lty = 1,          # Line type: solid
      lwd = 3,          # Line width
      cex = 1.5,        # Text size
      bty = "n")        # No box around the legend

# Close the PDF device to save the file
dev.off()

```

```

## pdf
## 2

```

Petal Summary

```

# Calculate summary statistics for petal
summary_petal <- summary(petal_spec_scaleminmax)

# Remove S2 due to infinite values
summary_petal <- summary_petal %>% select(-S2)

# Extract metrics for specific samples
petal125 <- round(summary_petal["125", ], 3)
petal126 <- round(summary_petal["126", ], 3)
petalBRAC <- round(summary_petal["BRAC", ], 3)

```

Plot Petal Spectral Descriptors Histograms

```

pdf("./results/figures/petal_descriptors_histograms.pdf", width = 14, height = 10)

# Set up plotting area: 4 rows x 6 columns for histograms
par(mfrow = c(4, 6),          # 4 rows, 6 columns
    mar = c(5, 5, 4, 2) + 0.1, # Margins for each plot: bottom, left, top, right
    oma = c(0, 0, 0, 5))      # Outer margins: bottom, left, top, right

# Loop through each metric and plot histogram with parental lines
for (i in 1:ncol(summary_petal)) {
  hist(summary_petal[, i],
        xlab = colnames(summary_petal)[i],
        main = colnames(summary_petal)[i],
        col = "lightgrey",
        border = "white")

  # Add vertical lines for parental samples
  abline(v = petal125[i], col = 'gold1', lwd = 3) # C. lasius parent
  abline(v = petal126[i], col = 'gold1', lwd = 3) # C. lasius parent
  abline(v = petalBRAC[i], col = 'darkgreen', lwd = 3) # C. bracteatus parent
}

# Allow drawing in the outer margin

```

```

par(xpd = TRUE)

plot.new()

# Add a shared legend in the outer right margin
legend("topright",
      inset = c(0, 0), # Adjusts the position of the legend
      legend = c("C. lasius parent", "C. bracteatus parent"),
      col = c("gold1", "darkgreen"),
      lty = 1,          # Line type: solid
      lwd = 3,          # Line width
      cex = 1.5,        # Text size
      bty = "n")        # No box around the legend

# Close the PDF device to save the file
dev.off()

## pdf
## 2

```

Labellum Summary

```

# Calculate summary statistics for labellum
summary_labellum <- summary(labellum_spec_scaleminmax)

# Remove S2 due to infinite values
summary_labellum <- summary_labellum %>% select(-S2)

# Extract metrics for specific samples
labellum125 <- round(summary_labellum["125", ], 3)
labellum126 <- round(summary_labellum["126", ], 3)
labellumBRAC <- round(summary_labellum["BRAC", ], 3)

```

Plot Labellum Spectral Descriptors Histograms

```

pdf("./results/figures/labellum_descriptors_histograms.pdf", width = 14, height = 10)

# Set up plotting area: 4 rows x 6 columns for histograms
par(mfrow = c(4, 6),          # 4 rows, 6 columns
    mar = c(5, 5, 4, 2) + 0.1, # Margins for each plot: bottom, left, top, right
    oma = c(0, 0, 0, 5))      # Outer margins: bottom, left, top, right

# Loop through each metric and plot histogram with parental lines
for (i in 1:ncol(summary_labellum)) {
  hist(summary_labellum[, i],
        xlab = colnames(summary_labellum)[i],
        main = colnames(summary_labellum)[i],
        col = "lightgrey",
        border = "white")

  # Add vertical lines for parental samples
  abline(v = labellum125[i], col = 'gold1', lwd = 3) # C. lasius parent
  abline(v = labellum126[i], col = 'gold1', lwd = 3) # C. lasius parent
}

```

```

    abline(v = labellumBRAC[i], col = 'darkgreen', lwd = 3) # C. bracteatus parent
  }

# Allow drawing in the outer margin
par(xpd = TRUE)

plot.new()

# Add a shared legend in the outer right margin
legend("topright",
      inset = c(0, 0), # Adjusts the position of the legend
      legend = c("C. lasius parent", "C. bracteatus parent"),
      col = c("gold1", "darkgreen"),
      lty = 1,          # Line type: solid
      lwd = 3,          # Line width
      cex = 1.5,        # Text size
      bty = "n")        # No box around the legend

# Close the PDF device to save the file
dev.off()

## pdf
## 2

```

Data Formatting and Export

Reformat Rownames

Replace 'x' with '_' in row names for consistency.

```

# Replace 'x' with '_' in row names
rownames(summary_bract) <- gsub("x", "_", rownames(summary_bract))
rownames(summary_petal) <- gsub("x", "_", rownames(summary_petal))
rownames(summary_labellum) <- gsub("x", "_", rownames(summary_labellum))

```

Subset and Rename Columns

Select relevant metrics and rename columns to indicate their corresponding floral tissue.

```

# Subset relevant columns based on analysis needs
summary_bract <- summary_bract[, c("S1U", "S1V", "S1B", "S1G", "S1R", "S5", "S9", "H4")]
summary_petal <- summary_petal[, c("B3", "S1U", "S1V", "S1B", "S1Y", "S1R", "S5", "S9", "H4")]
summary_labellum <- summary_labellum[, c("B3", "S1B", "S1Y", "S1R", "S5", "S6", "S9", "H3", "H4")]

# Rename columns to include tissue type
colnames(summary_bract) <- c("S1U_bract", "S1V_bract", "S1B_bract", "S1G_bract",
                             "S1R_bract", "S5_bract", "S9_bract", "H4_bract")
colnames(summary_petal) <- c("B3_petal", "S1U_petal", "S1V_petal", "S1B_petal",
                             "S1Y_petal", "S1R_petal", "S5_petal", "S9_bract", "H4_petal")
colnames(summary_labellum) <- c("B3_labellum", "S1B_labellum", "S1Y_labellum",
                                "S1R_labellum", "S5_labellum", "S6_labellum",
                                "S9_bract", "H3_labellum", "H4_labellum")

```

Convert Rownames to a Column

Add the row names as a new column id to facilitate merging.

```
# Convert row names to a column named 'id'
summary_bract <- summary_bract %>% rownames_to_column(var = "id")
summary_petal <- summary_petal %>% rownames_to_column(var = "id")
summary_labellum <- summary_labellum %>% rownames_to_column(var = "id")
```

Merge Summary Dataframes

Combine the summary dataframes for bract, petal, and labellum into a single dataframe.

```
# Merge bract and petal summaries by 'id'
joined_df <- summary_bract %>%
  full_join(summary_petal, by = "id") %>%
  full_join(summary_labellum, by = "id")
```

Export Summary Descriptors to CSV

Save the combined summary descriptors to a CSV file for further analysis or reporting.

```
# Write the combined summary dataframe to a CSV file
write.csv(joined_df, "./results/processed_data/spectral_shape_descriptors.csv",
          quote = FALSE, row.names = FALSE)
```