

CaféLab

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```
# Librerias
if (!require(PerformanceAnalytics)) install.packages("PerformanceAnalytics")

## Loading required package: PerformanceAnalytics
## Loading required package: xts
## Loading required package: zoo
##
## Attaching package: 'zoo'
## The following objects are masked from 'package:base':
##
##   as.Date, as.Date.numeric
##
## Attaching package: 'PerformanceAnalytics'
## The following object is masked from 'package:graphics':
##
##   legend
if (!require(ggplot2)) install.packages("gggplot2")

## Loading required package: ggplot2
library(PerformanceAnalytics)
library(readr)
library(ggplot2)
library(cowplot)
library(dplyr)

##
## ##### Warning from 'xts' package #####
## #
## # The dplyr lag() function breaks how base R's lag() function is supposed to #
## # work, which breaks lag(my_xts). Calls to lag(my_xts) that you type or #
## # source() into this session won't work correctly. #
## #
## # Use stats::lag() to make sure you're not using dplyr::lag(), or you can add #
## # conflictRules('dplyr', exclude = 'lag') to your .Rprofile to stop #
## # dplyr from breaking base R's lag() function. #
## #
## # Code in packages is not affected. It's protected by R's namespace mechanism #
## # Set `options(xts.warn_dplyr_breaks_lag = FALSE)` to suppress this warning. #
## #
```

```
## #####
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:xts':
##
##     first, last
##
## The following objects are masked from 'package:stats':
##
##     filter, lag
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
##Lectura de datos
ACh <- read_csv("AChMN.csv")

## Rows: 421 Columns: 5
## -- Column specification -----
## Delimiter: ","
## dbl (5): nm, 75, 15, 18, 225
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
AMi <- read_csv("AMi.csv")

## Rows: 421 Columns: 5
## -- Column specification -----
## Delimiter: ","
## dbl (5): nm, 75, 15, 18, 225
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
AGo <- read_csv("AGo.csv")

## Rows: 421 Columns: 5
## -- Column specification -----
## Delimiter: ","
## dbl (5): nm, 75, 15, 18, 225
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
AOx <- read_csv("AOx.csv")

## Rows: 421 Columns: 5
## -- Column specification -----
## Delimiter: ","
## dbl (5): nm, 75, 15, 18, 225
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```

Ailly <- read_csv("Ailly.csv")

## Rows: 421 Columns: 2
## -- Column specification -----
## Delimiter: ","
## dbl (2): nm, 15
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
#Agregamos las columnas 75,18 y 225 a Ailly para evitar errores y que tenga las mismas columnas que los
Ailly$'75' <- 0
Ailly$'18' <- 0
Ailly$'225' <- 0

Ailly <- Ailly[, c('nm', "75", "15", "18", "225")]

ACh[ACh == 0] <- NA
AGo[AGo == 0] <- NA
AMi[AMi ==0] <- NA
AOx[AOx ==0] <- NA
Ailly[Ailly ==0] <- NA

```

Relizaremos una grafica que contenga a todas las muestras de café con los rangos donde se deberian de ver las 2 BANDAS.

Primero encontremos los rangos de las bandas utilizando los datos de Chiapas (ACh)

```

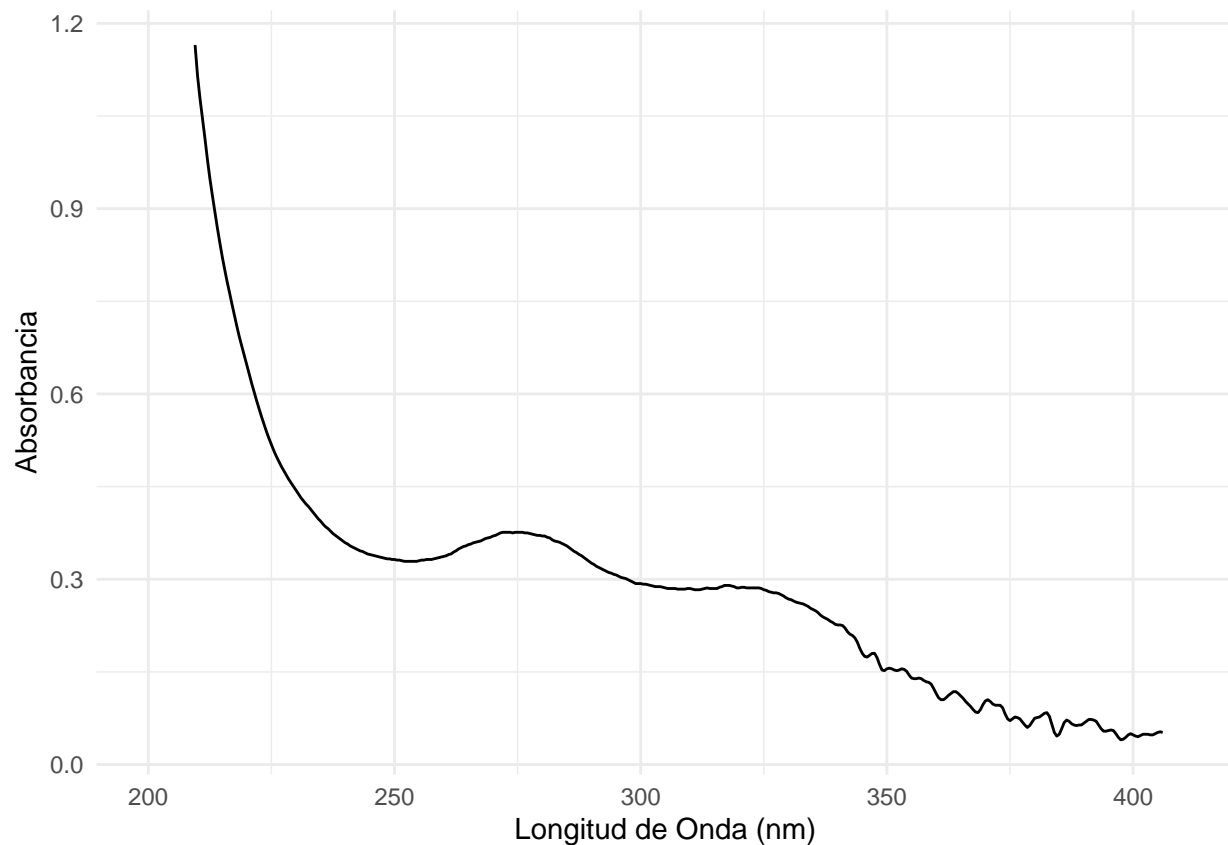
gg1 <- ggplot(data=ACh, aes(x=nm,y=`75`)) +
  geom_line() +
  labs(
    x = "Longitud de Onda (nm)",
    y = "Absorbancia",
  ) +
  theme_minimal() # Aplica un tema limpio
gg1

```

```

## Warning: Removed 27 rows containing missing values or values outside the scale range
## (`geom_line()`).

```



Veamos que se pueden apreciar dos bandas significativas.

- Banda1 : 275 aprox
- Banda2 : 325 aprox

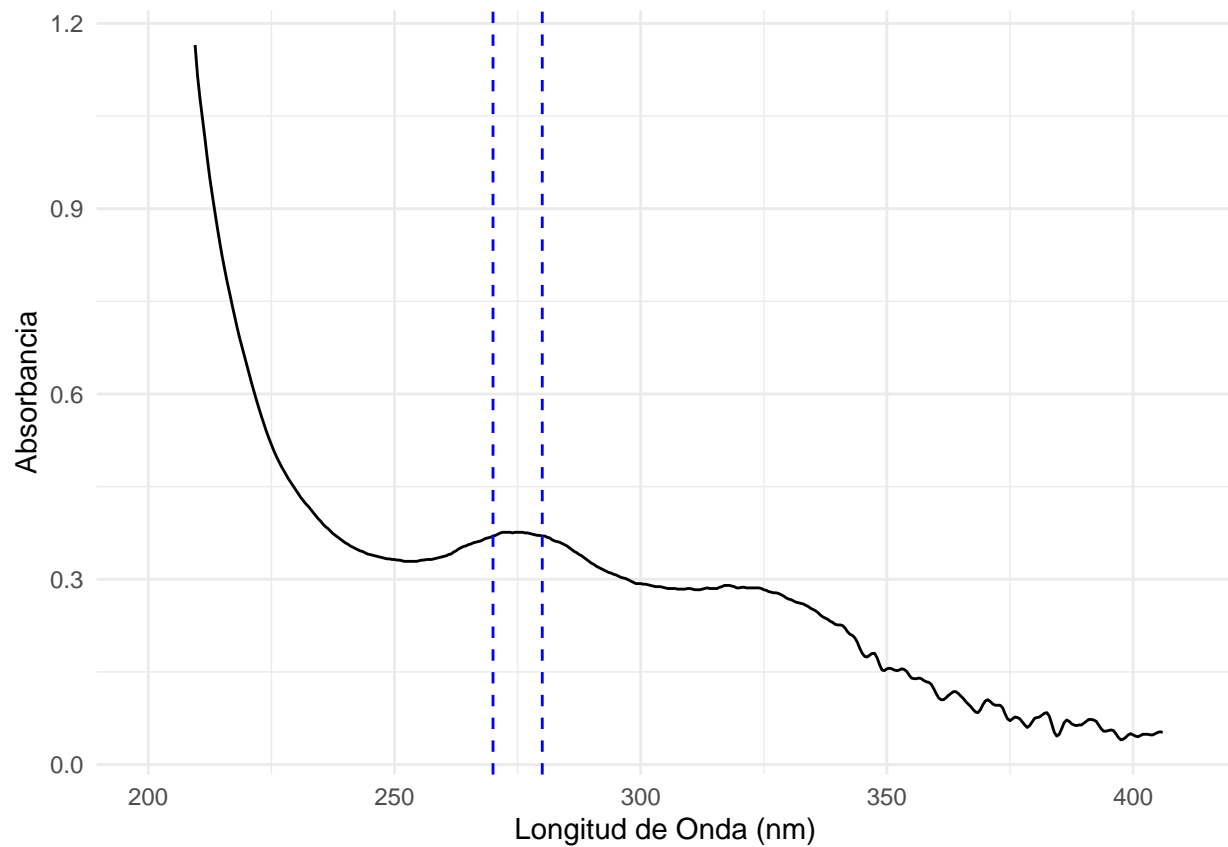
Daremos un intervalo de confianza del 95%, esto es:

Rangos:

- Banda1 : (270,280) – en azul
- Banda2 : (320,330) – en rojo

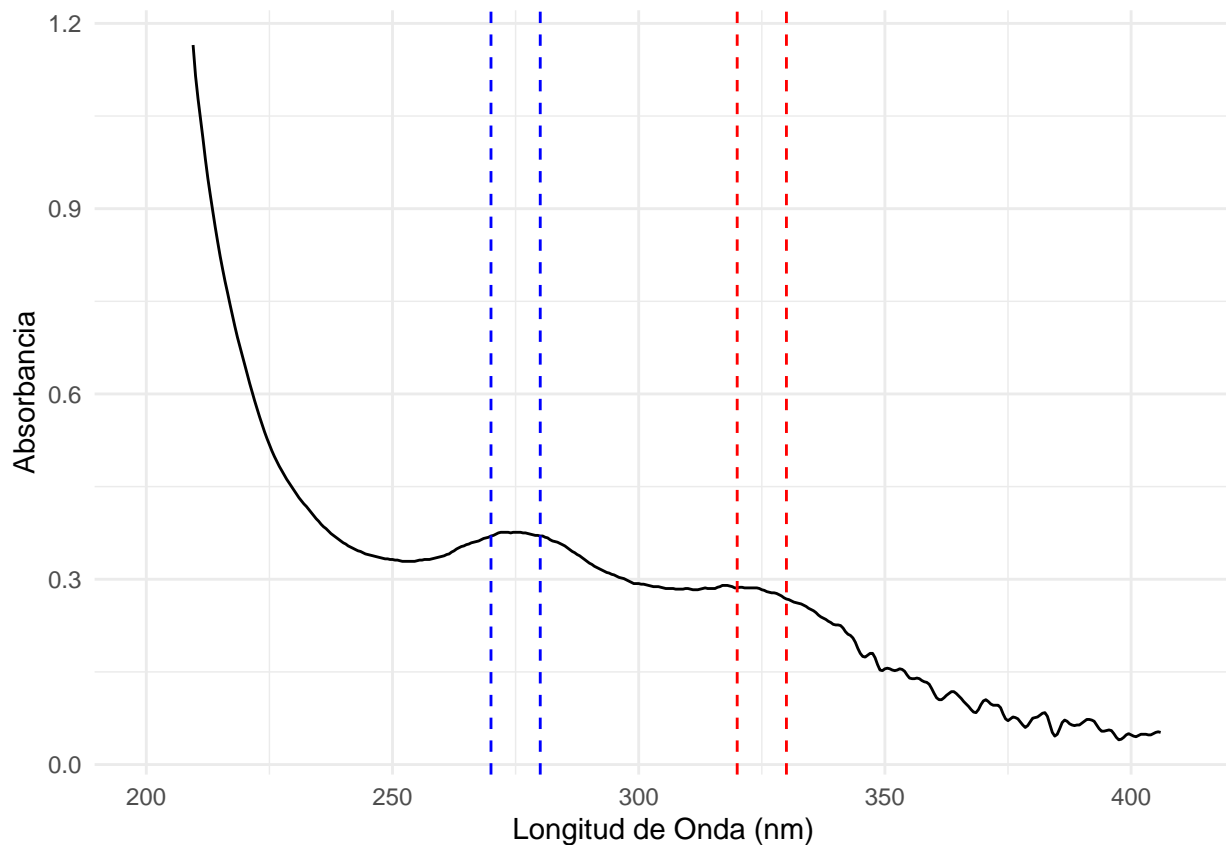
```
#----- BANDA 1-----
gg1_rango_B1 <- gg1 +
  geom_vline(xintercept = 270,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280,color = "blue", linetype = "dashed")
gg1_rango_B1
```

```
## Warning: Removed 27 rows containing missing values or values outside the scale range
## (`geom_line()`).
```



```
#----- BANDA 2-----
gg1_rango_B2 <- gg1_rango_B1 +
  geom_vline(xintercept = 320,color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330,color = "red", linetype = "dashed")
gg1_rango_B2
```

```
## Warning: Removed 27 rows containing missing values or values outside the scale range
## (`geom_line()`).
```



Ahora juntamos las 4 gráficas faltantes para ver sus comportamientos dentro de los intervalos.

NO vamos a incluir al café Illy, esto debido a que se realizó con 15g.

```
AMi$grupo <- "AMi"
AGo$grupo <- "AGo"
ACh$grupo <- "ACh"
AOx$grupo <- "AOx"
AIlly$grupo <- "AIlly"

df_todo <- rbind(ACh,AGo,AIlly,AMi, AOx)
```

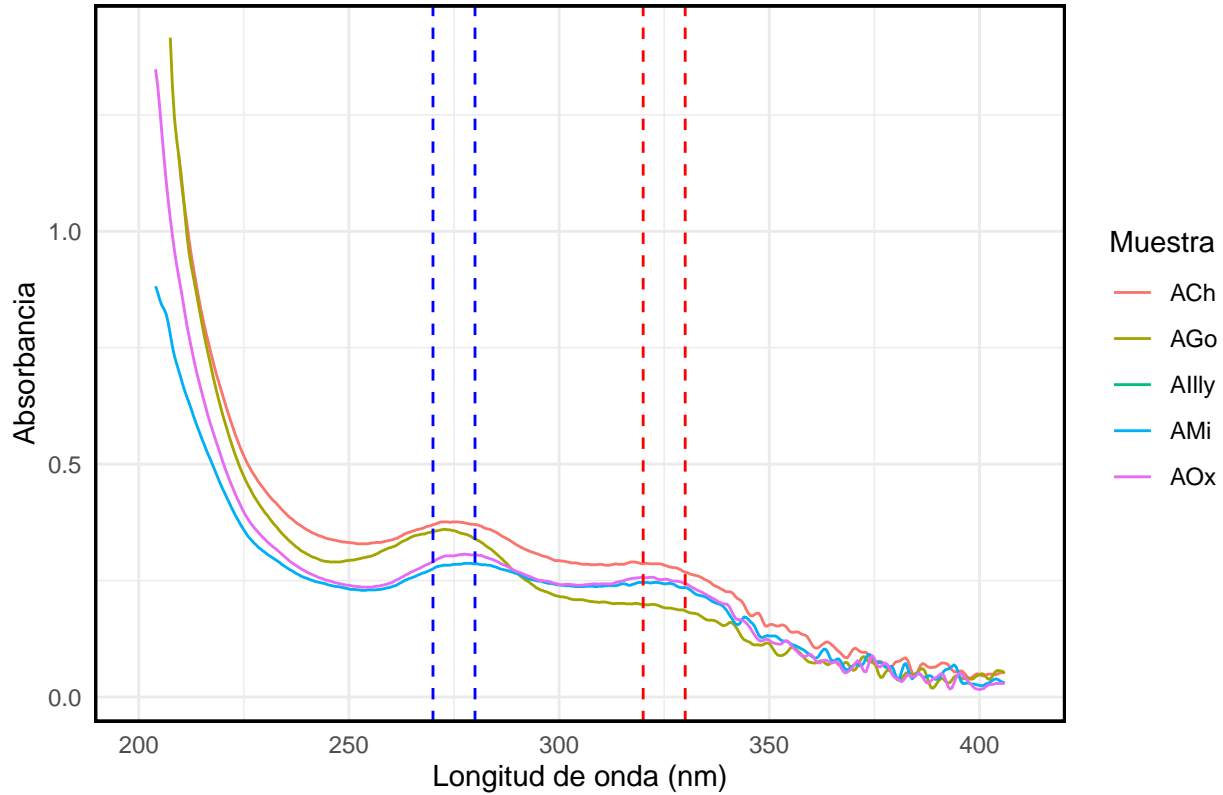
Gráficas de los 3 diferentes diluciones

```
gg1_todo <- ggplot(df_todo, aes(x = nm, y = `75`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (7.5 g)",
       x = "Longitud de onda (nm)",
       y = "Absorbancia",
       color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320,color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330,color = "red", linetype = "dashed") +
  theme_minimal() +
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
```

```
gg1_todo
```

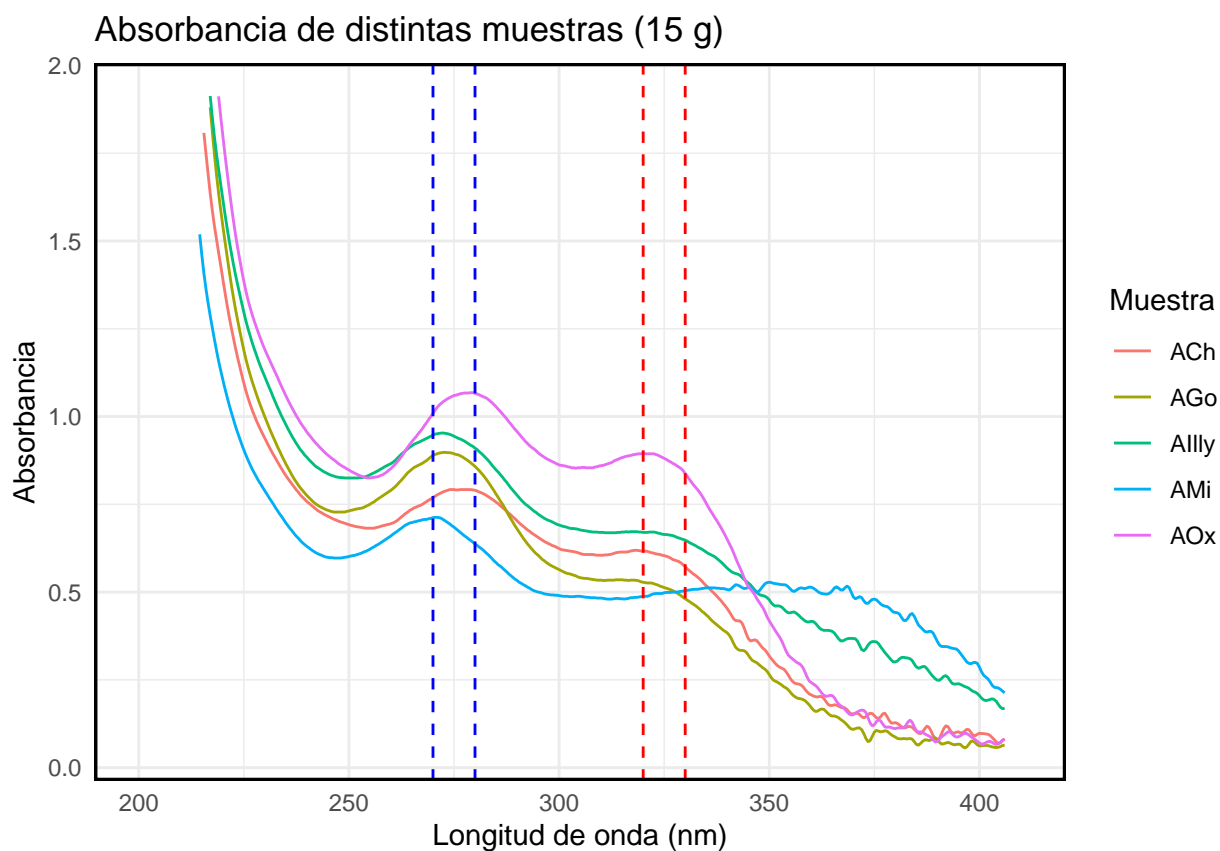
```
## Warning: Removed 503 rows containing missing values or values outside the scale range  
## (`geom_line()`).
```

Absorbancia de distintas muestras (7.5 g)



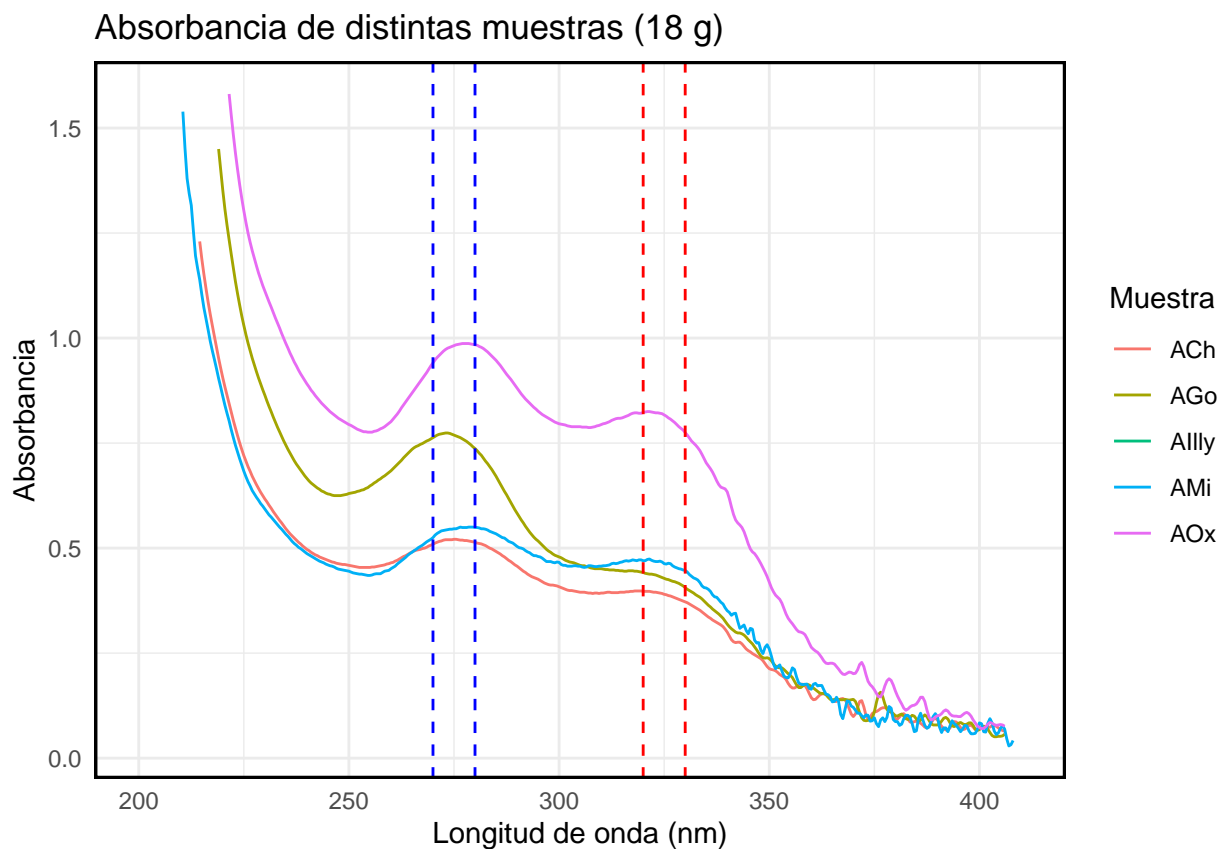
```
gg1_todo <- ggplot(df_todo, aes(x = nm, y = `15`, color = grupo)) +  
  geom_line() +  
  labs(title = "Absorbancia de distintas muestras (15 g)",  
        x = "Longitud de onda (nm)",  
        y = "Absorbancia",  
        color = "Muestra") + # Nombre de la leyenda  
  geom_vline(xintercept = 270, color = "blue", linetype = "dashed") +  
  geom_vline(xintercept = 280, color = "blue", linetype = "dashed") +  
  geom_vline(xintercept = 320, color = "red", linetype = "dashed") +  
  geom_vline(xintercept = 330, color = "red", linetype = "dashed") +  
  theme_minimal() +  
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))  
gg1_todo
```

```
## Warning: Removed 206 rows containing missing values or values outside the scale range  
## (`geom_line()`).
```



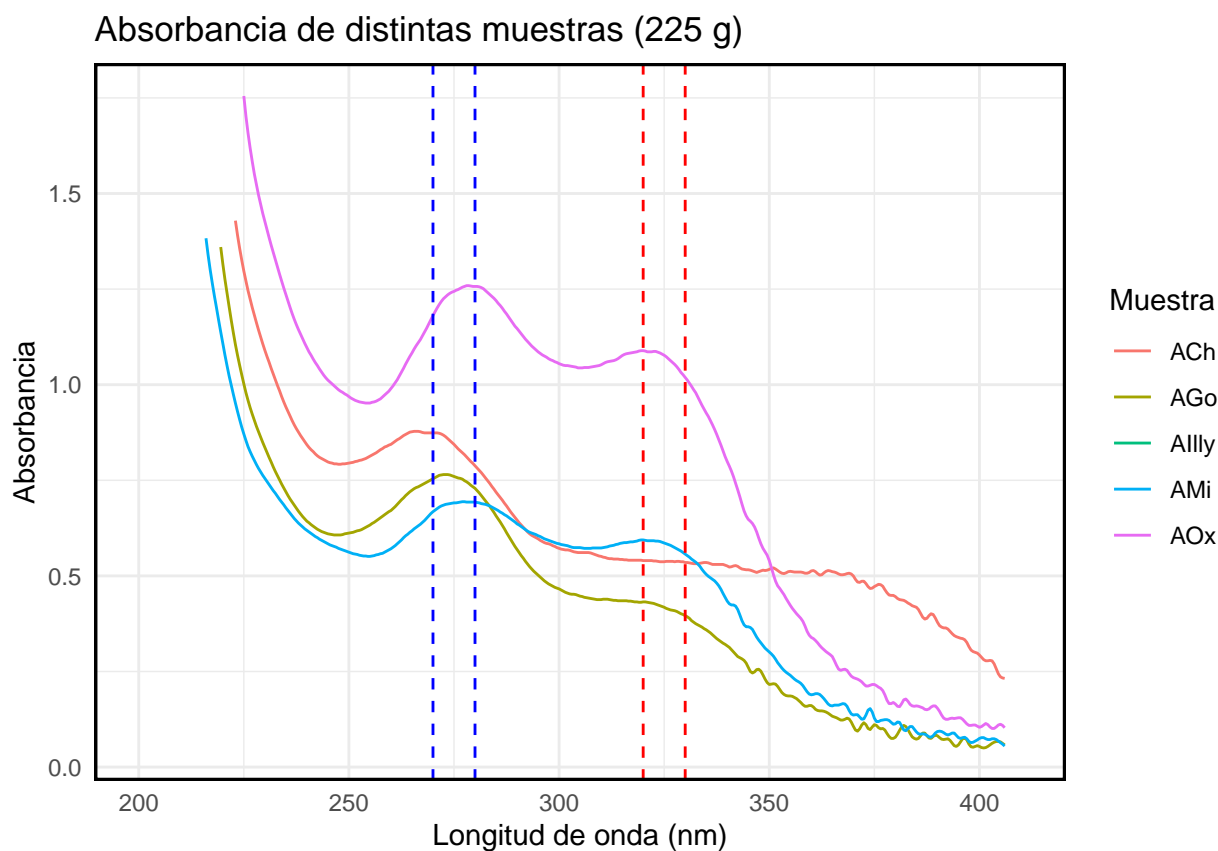
```
gg1_todo <- ggplot(df_todo, aes(x = nm, y = `18`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (18 g)",
        x = "Longitud de onda (nm)",
        y = "Absorbancia",
        color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270, color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280, color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320, color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330, color = "red", linetype = "dashed") +
  theme_minimal() +
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
gg1_todo
```

```
## Warning: Removed 580 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

```
gg1_todo <- ggplot(df_todo, aes(x = nm, y = `225`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (225 g)",
    x = "Longitud de onda (nm)",
    y = "Absorbancia",
    color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320,color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330,color = "red", linetype = "dashed") +
  theme_minimal() +
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
gg1_todo
```

```
## Warning: Removed 620 rows containing missing values or values outside the scale range
## (`geom_line()`).
```



ZOOM ## Acotemos los datos de [270,330]

```
AGo_filtrado <- AGo %>%
  filter(nm >= 270, nm <= 330)

ACh_filtrado <- ACh %>%
  filter(nm >= 270, nm <= 330)

AIly_filtrado <- AIly %>%
  filter(nm >= 270, nm <= 330)

AMi_filtrado <- AMi %>%
  filter(nm >= 270, nm <= 330)

AOx_filtrado <- AOx %>%
  filter(nm >= 270, nm <= 330)
```

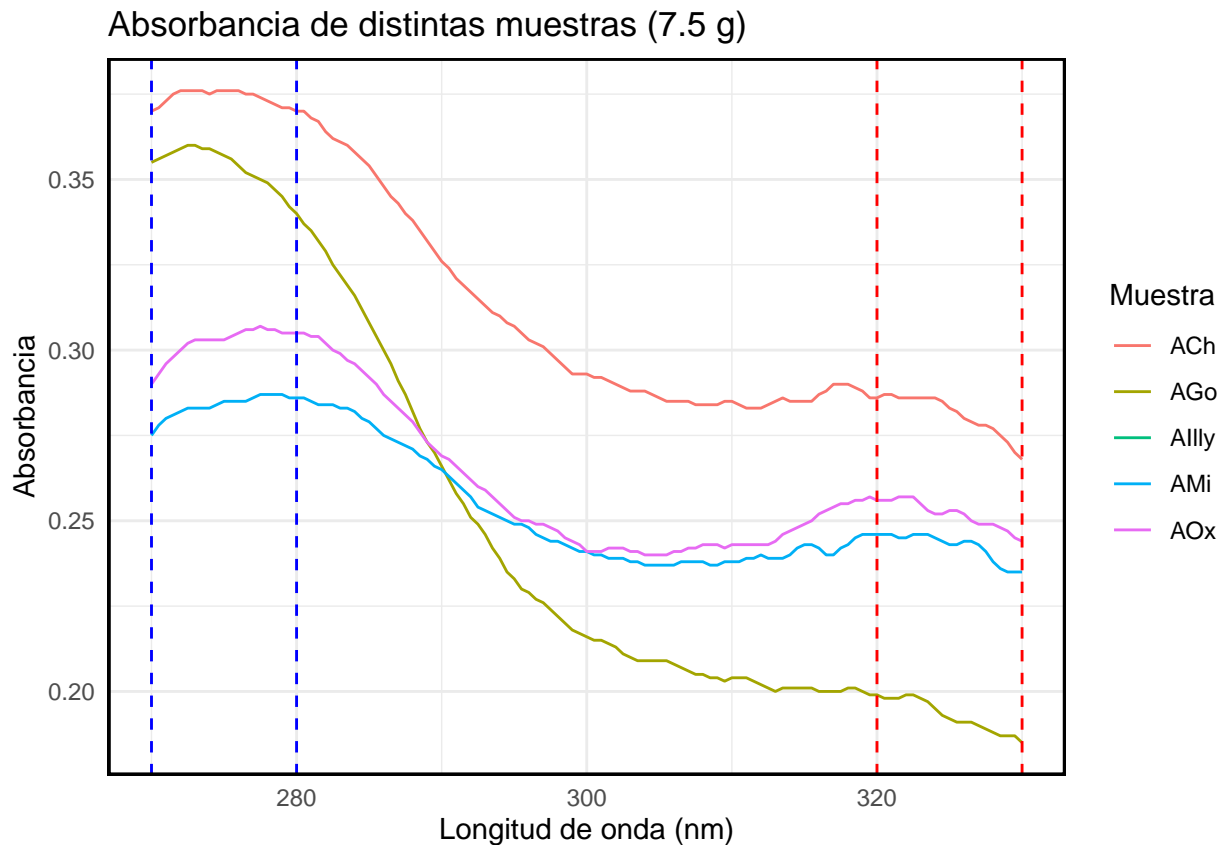
Creemos un data frame con todos los datos filtrados

```
AMi_filtrado$grupo <- "AMi"
AGo_filtrado$grupo <- "AGo"
ACh_filtrado$grupo <- "ACh"
AOx_filtrado$grupo <- "AOx"
AIly_filtrado$grupo <- "AIly"

df_todo_filtrado <- rbind(ACh_filtrado, AGo_filtrado, AIly_filtrado, AMi_filtrado, AOx_filtrado)
```

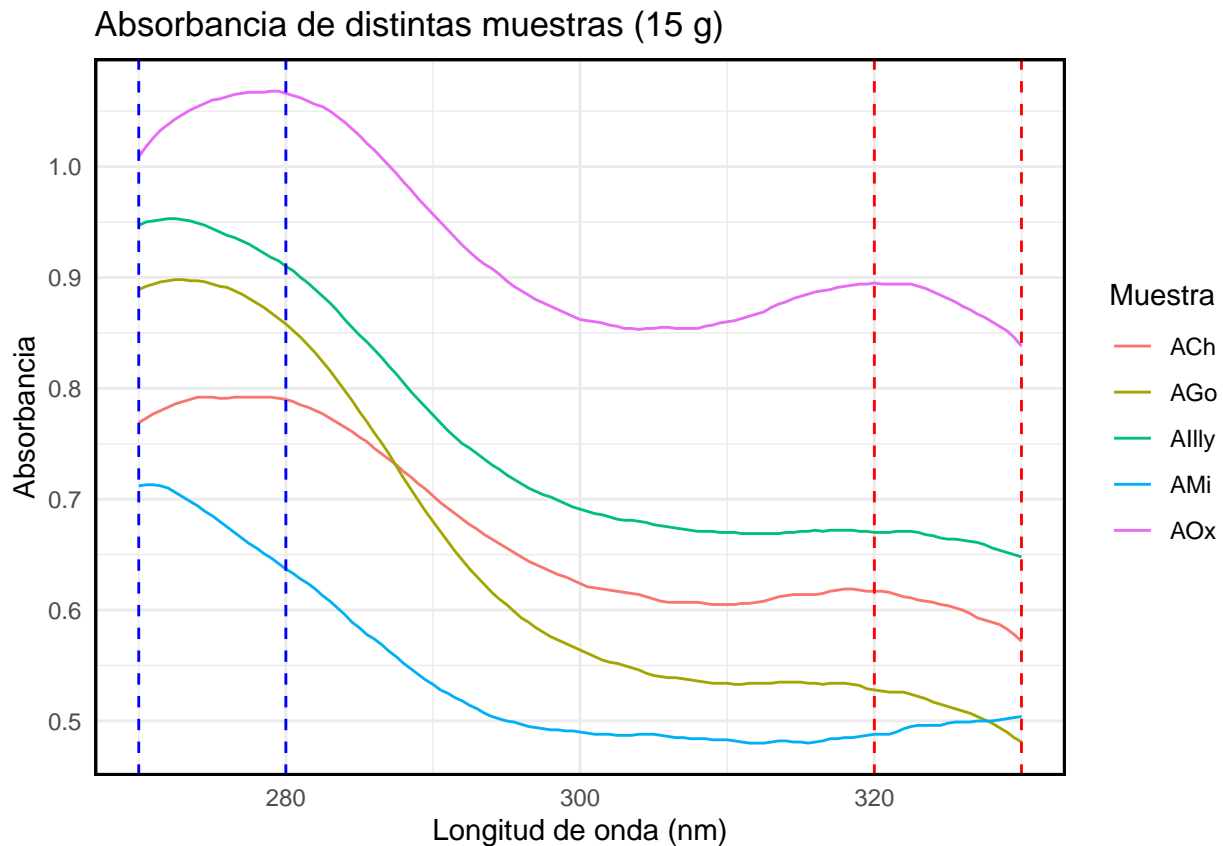
```
gg1_todo_filtrado_75 <- ggplot(df_todo_filtrado, aes(x = nm, y = `75`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (7.5 g)",
        x = "Longitud de onda (nm)",
        y = "Absorbancia",
        color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320,color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330,color = "red", linetype = "dashed") +
  theme_minimal() +
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
gg1_todo_filtrado_75
```

```
## Warning: Removed 121 rows containing missing values or values outside the scale range
## (`geom_line()`).
```



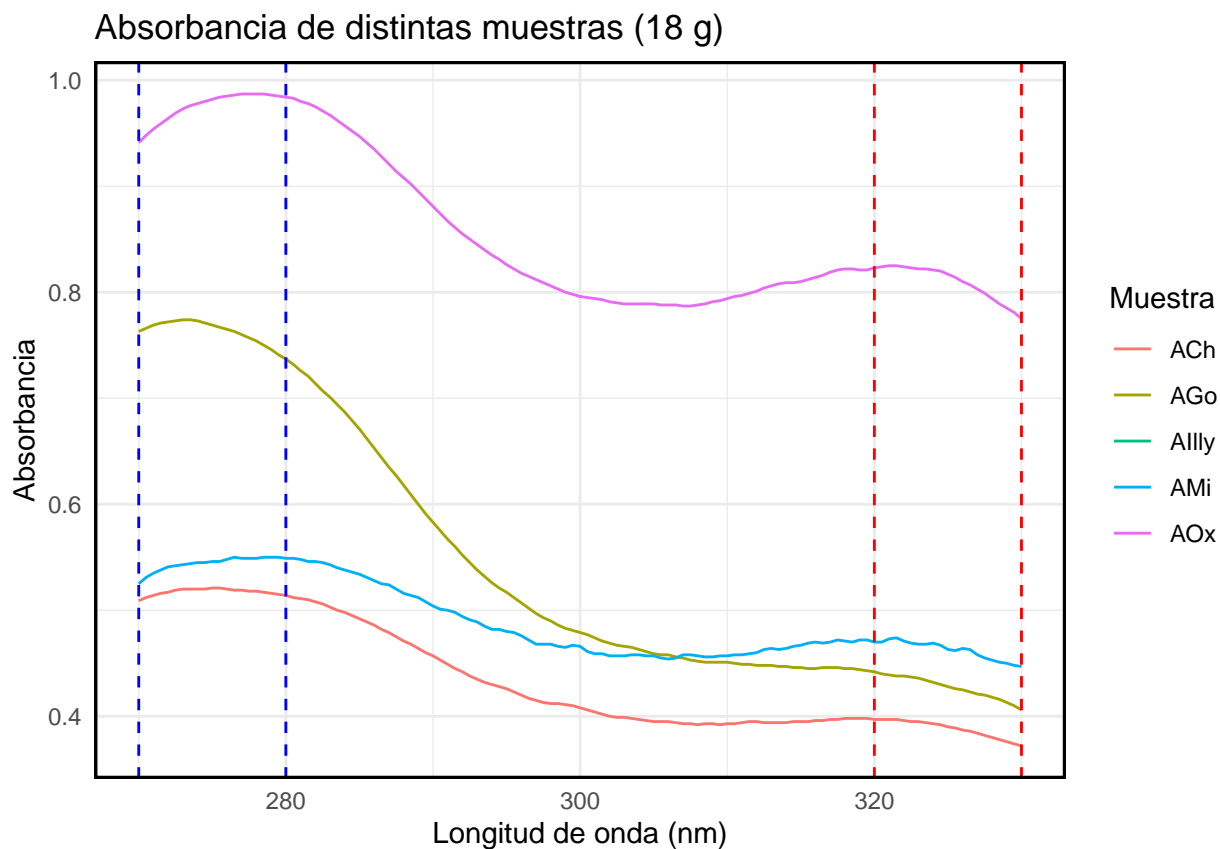
```
#-----
gg1_todo_filtrado_15 <- ggplot(df_todo_filtrado, aes(x = nm, y = `15`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (15 g)",
        x = "Longitud de onda (nm)",
        y = "Absorbancia",
        color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320,color = "red", linetype = "dashed") +
```

```
geom_vline(xintercept = 330,color = "red", linetype = "dashed") +
theme_minimal() +
theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
gg1_todo_filtrado_15
```



```
#-----
gg1_todo_filtrado_18 <- ggplot(df_todo_filtrado, aes(x = nm, y = `18`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (18 g)",
        x = "Longitud de onda (nm)",
        y = "Absorbancia",
        color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280,color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320,color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330,color = "red", linetype = "dashed") +
  theme_minimal() +
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
gg1_todo_filtrado_18
```

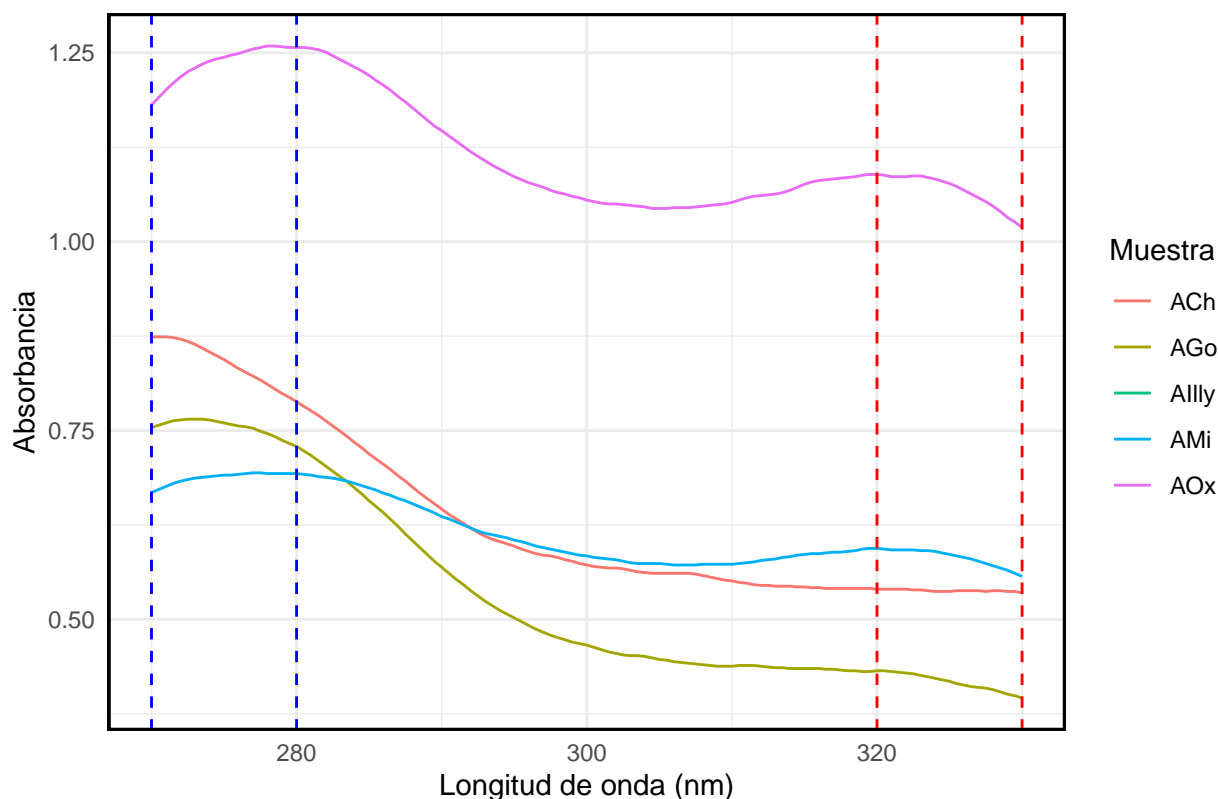
```
## Warning: Removed 121 rows containing missing values or values outside the scale range
## (`geom_line()`).
```



```
#-----
gg1_todo_filtrado_225 <- ggplot(df_todo_filtrado, aes(x = nm, y = `225`, color = grupo)) +
  geom_line() +
  labs(title = "Absorbancia de distintas muestras (225 g)",
        x = "Longitud de onda (nm)",
        y = "Absorbancia",
        color = "Muestra") + # Nombre de la leyenda
  geom_vline(xintercept = 270, color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 280, color = "blue", linetype = "dashed") +
  geom_vline(xintercept = 320, color = "red", linetype = "dashed") +
  geom_vline(xintercept = 330, color = "red", linetype = "dashed") +
  theme_minimal() +
  theme(panel.border = element_rect(color = "black", fill = NA, linewidth = 1))
gg1_todo_filtrado_225
```

```
## Warning: Removed 121 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

Absorbancia de distintas muestras (225 g)



```
df_todo_filtrado[df_todo_filtrado == NA] <- 0
```

```
df_max_grupo_75 <- df_todo_filtrado %>%
  group_by(grupo) %>%
  filter(`75` == max(`75`, na.rm = TRUE))
```

```
## Warning: There was 1 warning in `filter()`.
## i In argument: ``75` == max(`75`, na.rm = TRUE)`.
```

```
## i In group 3: `grupo = "AIlly"`.
```

```
## Caused by warning in `max()`:
```

```
## ! no non-missing arguments to max; returning -Inf
```

```
df_max_grupo_15 <- df_todo_filtrado %>%
  group_by(grupo) %>%
  filter(`15` == max(`15`, na.rm = TRUE))
```

```
df_max_grupo_18 <- df_todo_filtrado %>%
  group_by(grupo) %>%
  filter(`18` == max(`18`, na.rm = TRUE))
```

```
## Warning: There was 1 warning in `filter()`.
## i In argument: ``18` == max(`18`, na.rm = TRUE)`.
```

```
## i In group 3: `grupo = "AIlly"`.
```

```
## Caused by warning in `max()`:
```

```
## ! no non-missing arguments to max; returning -Inf
```

```
df_max_grupo_225 <- df_todo_filtrado %>%
  group_by(grupo) %>%
  filter(`225` == max(`225`, na.rm = TRUE))
```

```
## Warning: There was 1 warning in `filter()`.
## i In argument: ``225` == max(`225`, na.rm = TRUE)`.
## i In group 3: `grupo = "Ailly"`.
## Caused by warning in `max()`:
## ! no non-missing arguments to max; returning -Inf
```

```
df_max_grupo_75
```

```
## # A tibble: 15 x 6
## # Groups:   grupo [4]
##   nm   `75`   `15`   `18`   `225` grupo
##   <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
## 1 272  0.376 0.783 0.517 0.871 ACh
## 2 272. 0.376 0.786 0.519 0.868 ACh
## 3 273  0.376 0.788 0.52  0.864 ACh
## 4 274. 0.376 0.79  0.52  0.859 ACh
## 5 274. 0.376 0.792 0.52  0.849 ACh
## 6 275  0.376 0.792 0.521 0.844 ACh
## 7 276. 0.376 0.791 0.521 0.838 ACh
## 8 276  0.376 0.791 0.52  0.832 ACh
## 9 272. 0.36  0.898 0.773 0.765 AGo
## 10 273  0.36  0.898 0.774 0.765 AGo
## 11 278. 0.287 0.66  0.549 0.694 AMi
## 12 278  0.287 0.656 0.549 0.693 AMi
## 13 278. 0.287 0.651 0.55  0.693 AMi
## 14 279  0.287 0.647 0.55  0.693 AMi
## 15 278. 0.307 1.07  0.987 1.26 A0x
```

```
df_max_grupo_15
```

```
## # A tibble: 17 x 6
## # Groups:   grupo [5]
##   nm   `75`   `15`   `18`   `225` grupo
##   <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
## 1 274  0.375 0.792 0.52  0.854 ACh
## 2 274. 0.376 0.792 0.52  0.849 ACh
## 3 275  0.376 0.792 0.521 0.844 ACh
## 4 276. 0.375 0.792 0.519 0.827 ACh
## 5 277  0.375 0.792 0.519 0.822 ACh
## 6 278. 0.374 0.792 0.518 0.817 ACh
## 7 278  0.373 0.792 0.518 0.811 ACh
## 8 278. 0.372 0.792 0.517 0.805 ACh
## 9 279  0.371 0.792 0.516 0.799 ACh
## 10 272. 0.36  0.898 0.773 0.765 AGo
## 11 273  0.36  0.898 0.774 0.765 AGo
## 12 272  NA    0.953 NA    NA    Ailly
## 13 272. NA    0.953 NA    NA    Ailly
## 14 270. 0.278 0.713 0.531 0.672 AMi
## 15 271  0.28  0.713 0.535 0.676 AMi
## 16 279  0.305 1.07  0.986 1.26 A0x
## 17 280. 0.305 1.07  0.985 1.26 A0x
```

```
df_max_grupo_18
```

```
## # A tibble: 12 x 6
## # Groups:   grupo [4]
```

```
##      nm `75` `15` `18` `225` grupo
##      <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
## 1 275 0.376 0.792 0.521 0.844 ACh
## 2 276. 0.376 0.791 0.521 0.838 ACh
## 3 273 0.36 0.898 0.774 0.765 AGo
## 4 274. 0.359 0.897 0.774 0.765 AGo
## 5 276. 0.285 0.67 0.55 0.693 AMi
## 6 278. 0.287 0.651 0.55 0.693 AMi
## 7 279 0.287 0.647 0.55 0.693 AMi
## 8 280. 0.286 0.642 0.55 0.693 AMi
## 9 277 0.306 1.07 0.987 1.25 AOx
## 10 278. 0.307 1.07 0.987 1.26 AOx
## 11 278 0.306 1.07 0.987 1.26 AOx
## 12 278. 0.306 1.07 0.987 1.26 AOx
```

```
df_max_grupo_225
```

```
## # A tibble: 10 x 6
## # Groups:   grupo [4]
##      nm `75` `15` `18` `225` grupo
##      <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
## 1 270 0.37 0.769 0.509 0.874 ACh
## 2 270. 0.371 0.773 0.512 0.874 ACh
## 3 271 0.373 0.777 0.514 0.874 ACh
## 4 272. 0.36 0.898 0.773 0.765 AGo
## 5 273 0.36 0.898 0.774 0.765 AGo
## 6 274. 0.359 0.897 0.774 0.765 AGo
## 7 277 0.286 0.665 0.549 0.694 AMi
## 8 278. 0.287 0.66 0.549 0.694 AMi
## 9 278 0.306 1.07 0.987 1.26 AOx
## 10 278. 0.306 1.07 0.987 1.26 AOx
```

Máximos de bandas

(veamos que algunos máximos se repiten).

Para (7.5g)

- Allly -
- ACh - (272.0,272.5,273,273.5,274,275,275.5,276)nm / 0.376
- AGo - (272.5,273)nm / 0.360
- AMi - (277.5,278,278.5,279)nm / 0.287
- AOx - (277.5)nm / 0.307

Para (15g)

- Allly - (272.0,272.5)nm / 0.953
- ACh - (274.0,274.5,275.0,276.5,277,277.5,278.0,278.5,279.0)nm / 0.792
- AGo - (273.0)nm / 0.898
- AMi - (270.5,271.0)nm / 0.713
- AOx - (279.0,279.5)nm / 1.068

Para (18g)

- Allly -
- ACh - (275.0,275.5)nm / 0.521
- AGo - (273.0,273.5)nm / 0.774
- AMi - (276.5,278.5,279.0,279.5,)nm / 0.550
- AOx - (277.0,277.5,278.0,278.5)nm / 0.987