Compute Biomass

source(here::here("load\_pkgs.R"))

df\_tree <- read\_csv(here::here("data/tree\_data\_full.csv"), col\_types = cols())  
  
# OJO Corección datos P028 // P024 // P024

¿Qué especies tenemos en nuestros plots?

df\_tree %>% group\_by(sp) %>% count() %>% knitr::kable()

## group\_by: one grouping variable (sp)

## count: now 8 rows and 2 columns, one group variable remaining (sp)

|  |  |
| --- | --- |
| sp | n |
| Adec | 1 |
| Aopa | 6 |
| Cmon | 36 |
| Pdul | 9 |
| Pter | 9 |
| Qilex | 3 |
| Qpyr | 3260 |
| Saria | 18 |

¿Cómo de puro o mixed es cada plot?

aux <- df\_tree %>% group\_by(code, sp) %>%   
 count() %>%   
 spread(key = sp, value = n) %>%   
 as.data.frame()

## group\_by: 2 grouping variables (code, sp)

## count: now 144 rows and 3 columns, 2 group variables remaining (code, sp)

## spread: reorganized (sp, n) into (Adec, Aopa, Cmon, Pdul, Pter, …) [was 144x3, now 117x9]

df <- aux %>%   
 # replace(is.na(.), 0) %>%   
 mutate(n\_total = rowSums(dplyr::select(., -code), na.rm = TRUE),  
 per\_pure = round((Qpyr / n\_total)\*100, 2))

## mutate: new variable 'n\_total' with 55 unique values and 0% NA

## new variable 'per\_pure' with 18 unique values and 0% NA

df %>% filter(per\_pure < 100) %>% knitr::kable()

## filter: removed 100 rows (85%), 17 rows remaining

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| code | Adec | Aopa | Cmon | Pdul | Pter | Qilex | Qpyr | Saria | n\_total | per\_pure |
| A01 | NA | NA | 1 | NA | NA | NA | 8 | NA | 9 | 88.89 |
| A05 | NA | NA | 3 | NA | NA | NA | 4 | NA | 7 | 57.14 |
| A07 | NA | NA | 4 | NA | NA | NA | 9 | NA | 13 | 69.23 |
| A08 | NA | NA | 3 | 1 | 4 | NA | 6 | NA | 14 | 42.86 |
| A09 | NA | NA | 2 | 7 | 1 | NA | 5 | NA | 15 | 33.33 |
| A10 | NA | NA | NA | 1 | 4 | NA | 5 | NA | 10 | 50.00 |
| A16 | NA | NA | 1 | NA | NA | NA | 13 | NA | 14 | 92.86 |
| A20 | NA | NA | 2 | NA | NA | NA | 19 | NA | 21 | 90.48 |
| CAM2 | NA | 2 | NA | NA | NA | NA | 18 | 5 | 25 | 72.00 |
| CAM3 | NA | NA | 2 | NA | NA | NA | 15 | NA | 17 | 88.24 |
| CAM4 | NA | 1 | 3 | NA | NA | NA | 7 | 4 | 15 | 46.67 |
| CAN\_RES\_38 | NA | NA | NA | NA | NA | 3 | 28 | NA | 31 | 90.32 |
| DIL3 | NA | NA | 3 | NA | NA | NA | 15 | NA | 18 | 83.33 |
| DIL4 | NA | NA | 1 | NA | NA | NA | 14 | NA | 15 | 93.33 |
| DIL5 | NA | NA | 5 | NA | NA | NA | 9 | NA | 14 | 64.29 |
| DUR2 | 1 | NA | 6 | NA | NA | NA | 34 | NA | 41 | 82.93 |
| DUR3 | NA | 3 | NA | NA | NA | NA | 22 | 9 | 34 | 64.71 |

Añadir datos de la parcela y filtrar por selected

dicc\_plots <- read\_csv(here::here("raw\_data/dicc\_plots.csv"), col\_types = cols())  
  
plot\_s <- dicc\_plots %>%   
 inner\_join(df, by = c("original\_code" = "code")) %>%   
 filter(selected == "TRUE")

## inner\_join: added 10 columns (Adec, Aopa, Cmon, Pdul, Pter, …)

## > rows only in x ( 0)

## > rows only in y ( 0)

## > matched rows 117

## > =====

## > rows total 117

## filter: removed 12 rows (10%), 105 rows remaining

Filtrar datos de los plots seleccionados, y ver que species tenemos

df\_tree\_sel <- df\_tree %>%   
 filter(code %in% plot\_s$original\_code)

## filter: removed 183 rows (5%), 3,159 rows remaining

df\_tree\_sel %>% group\_by(sp) %>% count()

## group\_by: one grouping variable (sp)

## count: now 8 rows and 2 columns, one group variable remaining (sp)

## # A tibble: 8 x 2  
## # Groups: sp [8]  
## sp n  
## <chr> <int>  
## 1 Adec 1  
## 2 Aopa 6  
## 3 Cmon 36  
## 4 Pdul 8  
## 5 Pter 5  
## 6 Qilex 3  
## 7 Qpyr 3082  
## 8 Saria 18

## Componentes de la biomasa

* Stem with bark (commercial volume, up to a top diameter of 7 cm)
* Thick branches (diameter greater than 7 cm)
* Medium branches (diameter between 2 and 7 cm)
* Thin branches (diameter smaller than 2 cm)
* Leaves

Seguimos la misma nomenclatura que Ruiz-Peinado, Montero, and Del Rio (2012)

* : Biomass weight of the stem fraction (kg)
* : Biomass weight of the thick branches fraction (diameter larger than 7 cm) (kg)
* : Biomass weight of medium branches fraction (diameter between 2 and 7 cm) (kg)
* : Biomass weight of thin branches fraction (diameter smaller than 2 cm) with leaves (kg)
* : Biomass weight of the belowground fraction (kg)

## *Quercus pyrenaica*

Fuente: Ruiz-Peinado, Montero, and Del Rio (2012)

* Stem + Thick branches
* Medium branches
* Thin branches
* Roots

# Proposal function  
biomassQpyr <- function(d, h, ...){  
   
 ws <- 0.0261\* d^2 \* h  
 wb7 <- NA   
 wb27 <- (-0.0260 \* d^2) + (0.536 \* h) + (0.00538 \* d^2 \* h)  
 wb2 <- (0.898\*d) - (0.445\*h)  
 wr <- 0.143 \* d^2  
   
 out <- data.frame(ws, wb7, wb27, wb2, wr)  
 return(out)  
}

## Computo de Biomasa para Qp

df\_qpyr <- df\_tree\_sel %>%   
 filter(sp == "Qpyr") %>%   
 filter(dbh > 7) %>%   
 bind\_cols(map2\_dfr(.$dbh, .$h, biomassQpyr))

## filter: removed 77 rows (2%), 3,082 rows remaining

## filter: removed 976 rows (32%), 2,106 rows remaining

# tengo varios valores negativos en wb27   
df\_qpyr %<>% mutate(wb27 = ifelse(wb27 < 0, 0, wb27))

## mutate: changed 3 values (<1%) of 'wb27' (0 new NA)

# Biomasa por plot   
w\_qpyr <- df\_qpyr %>%   
 group\_by(code) %>%   
 summarise\_at(vars(starts\_with("w")), sum)

## group\_by: one grouping variable (code)

## summarise\_at: now 105 rows and 6 columns, ungrouped

??? Que hacemos con los mas pezqueñines??

df\_qpyr7 <- df\_tree\_sel %>%   
 filter(sp == "Qpyr") %>%   
 filter(dbh < 7) %>%   
 group\_by(code) %>%   
 count()

## filter: removed 77 rows (2%), 3,082 rows remaining

## filter: removed 2,130 rows (69%), 952 rows remaining

## group\_by: one grouping variable (code)

## count: now 36 rows and 2 columns, one group variable remaining (code)

## *Quercus ilex*

Fuente: Ruiz-Peinado, Montero, and Del Rio (2012)

* Stem
* Thick branches:
  + If then ; If then
* Medium branches
* Thin branches
* Roots

Ojo aquellos ind que no tengan d > 12.5, no se considera la fracción thick branches.

biomassQilex <- function(d, h, ...){  
 # aboveground biomass   
 # nota: no he incluido la parte de thick branches   
  
 ws <- 0.143 \* d^2  
 wb7 <- ifelse(d > 12.5, 0.0684 \* ((d - 12.5)^2) \* h, NA)  
 wb27 <- 0.0898 \* d^2  
 wb2 <- 0.0824 \* d^2  
 wr <- 0.254 \* d^2  
   
 out <- data.frame(ws, wb7, wb27, wb2, wr)  
 return(out)  
}

df\_qilex <- df\_tree\_sel %>%   
 filter(sp == "Qilex") %>%   
 bind\_cols(map2\_dfr(.$dbh, .$h, biomassQilex))

## filter: removed 3,156 rows (>99%), 3 rows remaining

w\_qilex <- df\_qilex %>%   
 group\_by(code) %>%   
 summarise\_at(vars(starts\_with("w")), sum)

## group\_by: one grouping variable (code)

## summarise\_at: now one row and 6 columns, ungrouped

## Otras especies

### Pistacia therebinthus

Fuente: Oyonarte and Cerrillo (2003) para datos de arbustos de Andalucía

siendo la fitomasa, el volumen. Se han calculado para arbustos, determinando el volumen con dos morfotipos:

Limitaciones: - es la media del Crown diameter mayor y menor - Solamente aboveground biomass - No fraccionados los componentes de la biomasa

### Crataegus monogyna

Fuente: Oyonarte and Cerrillo (2003) para datos de arbustos de Andalucía

siendo la fitomasa, el volumen. Se han calculado para arbustos, determinando el volumen con el morfotipo:

Limitaciones: - es la media del Crown diameter mayor y menor - Solamente aboveground biomass - No fraccionados los componentes de la biomasa

## Adenocarpus decorticans

Fuente: Robles et al. (2006) para matorrales de Sierra Nevada

siendo la fitomasa, el volumen. Se han calculado para arbustos, determinando el volumen con el morfotipo cilindro circular:

siendo el diámetro (crow diameter)

## Acer opalus granatensis

## Prunus dulcis / avium

## Sorbus aria

Oyonarte, P. Blanco, and R. Navarro Cerrillo. 2003. “Aboveground Phytomass Models for Major Species in Shrub Ecosystems of Western Andalusia.” *Forest Systems* 12 (3): 47–55. <https://doi.org/10.5424/1078>.

Robles, A. B., P. Fern’andez, J. Ruiz-Mirazo, M. E. Ramos, C. B. Passera, and J. L. Gonz’alez-Rebollar. 2006. “Nine Native Leguminous Shrub Species: Allometric Regression Equations and Nutritive Values.” In *Sustainable Grassland Productivity: Proceedings of the 21st General Meeting of the European Grassland Federation, Badajoz, Spain, 3-6 April, 2006*, edited by J. Lloveras, A. Gonz’alez-Rodríguez, O. V’azquez-Yañez, J. Piñeiro, O. Santamar’ıa, L. Olea, and M. J. Poblaciones, 309–11. Madrid, Spain: Sociedad Española para el Estudio de los Pastos (SEEP).

Ruiz-Peinado, R., G. Montero, and M. Del Rio. 2012. “Biomass Models to Estimate Carbon Stocks for Hardwood Tree Species.” *Forest Systems* 21 (1): 42. <https://doi.org/10.5424/fs/2112211-02193>.