Understory vegetation data handling

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```r
# setup ------------------------------------------------------------

library(tidyverse)
```

```
## -- Attaching core tidyverse packages ---------------------- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.6
## v forcats   1.0.1     v stringr   1.6.0
## v ggplot2   4.0.1     v tibble    3.3.0
## v lubridate 1.9.4     v tidyr     1.3.2
## v purrr     1.2.0
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(readxl)

# data import ------------------------------------------------------

read_me <- list.files(path="data/transects", full.names = TRUE)
read_me <- read_me[order(as.numeric(gsub("[^0-9]+", "", read_me)))]

#lists of T
read_me2 <- read_me |>
  basename() |>
  tools::file_path_sans_ext()

#species names
specieslookup <- read_csv("data/specieslookup_harm.csv", show_col_types = F)


## transect data ---------------------------------------------------

dat <- vector(mode = "list", length = length(read_me2))
for(i in seq_along(read_me2)){
  df <- read_csv(read_me[i], trim_ws = T, show_col_types = F) |> #header cut off already
    select(!2) |>
    rename(X=1) |>
    mutate(across(where(is.character), toupper)) |>
    mutate(across(where(is.character), function(x) gsub("\\s+", "", x))) |>
    mutate(across(where(is.character), function(x) gsub("(PL)","", x, fixed = TRUE))) |>
```

```r
    pivot_longer(cols = !1, names_to = NULL, values_to = "code", values_drop_na = T) |>
    filter(!code %in% c("MOSS", "TRUNK", "FERN", "D", "R","B", "ROOT", "")) |>
    left_join(specieslookup, by = "code")
  dat[[i]] <- df
  names(dat)[i] <- read_me2[i]
}
rm(df, i, specieslookup)

#remove sites without structural and canopy data
dat[c("T15", "T16", "T17", "T32")] <- NULL

#check records without species names
NAs <- dat |>
  lapply(function (x) filter(x, is.na(species))) |>
  bind_rows()

NAs |>
  distinct(code) #all "sp."
```

```
## # A tibble: 4 x 1
##   code
##   <chr>
## 1 HSP
## 2 CASP
## 3 TAR
## 4 ROX
```

```r
#remove those few genus-level records
dat <- dat |>
  lapply(function (x) filter(x, !is.na(species)))

rm(NAs)

## species frequencies -------------------------------------------------

#by plot
speciesfreqs_plot <- lapply(dat, function(x) count(x, code, species, family, sort = T)) |>
  bind_rows(.id = "Plot")

#overall
speciesfreqs_all <- speciesfreqs_plot |>
  count(code, species, family, wt = n, sort = T)

#clean dat
dat <- map(dat, ~select(.x, 1, 3))

# trait DB ----------------------------------------------------------------

##aboveground traits Diaz et al. 2022-----
gspff <- read_excel("data/GSPFF_enhanced/Species_mean_traits.xlsx", sheet = 1,
                    col_types = "text") |>
  select(2, 16, 18, 20, 22, 24, 31) |>
  rename(species=`Species name standardized against TPL`) |>
```

```r
  mutate(across(!species, as.numeric)) |>
  mutate(presentgspff = T) |>
  janitor::clean_names()

#synonyms
GSPFF_syno <- read_csv("data/synonyms_forGSPFF.txt", show_col_types = F) |>
  filter(!is.na(`DB name`)) |>
  rename(species = `DB name`)
GSPFF_syno <- setNames(GSPFF_syno$`Our name`, GSPFF_syno$species)

gspff <- gspff |>
  mutate(species = recode(species, !!!GSPFF_syno))
rm(GSPFF_syno)

##clonal from CLO-PLA---------
clopla <- read.csv("data/CLO-PLA-traits.txt", sep = "\t") |>
  mutate(Species_name = gsub("\"","", .data$Species_name)) |>
  slice(-113) |> #allium urs. subsp., multiple match
  mutate(Species_name = word(.data$Species_name, 1, 2)) |>
  rename(species=Species_name) |>
  mutate(presentclo = T) |>
  select(species, presentclo, clonal, BBRsize, persistence, offspring, spread) |>
  mutate(clonal = as.logical(clonal))

#synonyms
clopla_syno <- read_csv("data/synonyms_forCLOPLA.txt", show_col_types = F) |>
  filter(!is.na(`DB name`)) |>
  rename(species = `DB name`)
clopla_syno <- setNames(clopla_syno$`Our name`, clopla_syno$species)

clopla <- clopla |>
  mutate(species = recode(species, !!!clopla_syno))
rm(clopla_syno)

##join aboveground----
speciestraits <- left_join(speciesfreqs_all, gspff) |>
  mutate(presentgspff = if_else(is.na(.data$presentgspff), F, T)) |>
  relocate(presentgspff, .after=4)
```

```
## Joining with `by = join_by(species)`
```

```r
#which species have height > 1.3 m?
tall <- speciestraits |>
  filter(!plant_height_m < 1.3) |>
  pull(species)

tall
```

```
##  [1] "Fagus sylvatica"    "Abies alba"           "Pteridium aquilinum"
##  [4] "Rubus hirtus"       "Acer pseudoplatanus"  "Hedera helix"
##  [7] "Cytisus scoparius"  "Fraxinus excelsior"   "Prunus avium"
## [10] "Calystegia sepium"  "Acer platanoides"     "Sambucus nigra"
## [13] "Euonymus latifolius" "Laburnum alpinum"    "Acer opalus"
```

```
## [16] "Clematis vitalba"     "Crataegus monogyna"   "Sorbus aria"
## [19] "Sorbus aucuparia"      "Quercus cerris"       "Tilia platyphyllos"
```

```r
#how many records?
speciesfreqs_all |>
  filter(species %in% tall) |>
  print(n = 50)
```

```
## # A tibble: 21 x 4
##    code  species              family               n
##    <chr> <chr>                <chr>            <int>
##  1 FA    Fagus sylvatica      Fagaceae           650
##  2 AB    Abies alba           Pinaceae           195
##  3 PT    Pteridium aquilinum  Dennstaedtiaceae   122
##  4 RU    Rubus hirtus         Rosaceae            74
##  5 PSE   Acer pseudoplatanus  Sapindaceae         72
##  6 HEX   Hedera helix         Araliaceae          67
##  7 CY    Cytisus scoparius    Fabaceae            34
##  8 FRAX  Fraxinus excelsior   Oleaceae            30
##  9 AVI   Prunus avium         Rosaceae            16
## 10 COS   Calystegia sepium    Convolvulaceae      11
## 11 PLA   Acer platanoides     Sapindaceae          9
## 12 SAM   Sambucus nigra       Viburnaceae          9
## 13 ELA   Euonymus latifolius  Celastraceae         6
## 14 LAB   Laburnum alpinum     Fabaceae             5
## 15 ACE   Acer opalus          Sapindaceae          4
## 16 CLE   Clematis vitalba     Ranunculaceae        3
## 17 CRA   Crataegus monogyna   Rosaceae             3
## 18 SOR   Sorbus aria          Rosaceae             2
## 19 AUC   Sorbus aucuparia     Rosaceae             1
## 20 QU    Quercus cerris       Fagaceae             1
## 21 TIG   Tilia platyphyllos   Malvaceae            1
```

```r
rm(tall)

#remove seedlings/juveniles (above 1.3 m)
speciestraits <- speciestraits |>
  filter(plant_height_m < 1.3 | is.na(plant_height_m))

##join clonal----
speciestraits <- left_join(speciestraits, clopla) |>
  mutate(presentclo = if_else(is.na(.data$presentclo), F, T)) |>
  relocate(presentclo, clonal, .after=5)
```

```
## Joining with `by = join_by(species)`
```

```r
##join measured LS----
#Viola reichenbachiana and Euphorbia amygdaloides have measured LS

measured <- read_csv('data/measured_LS.csv') |>
  select(2,3) |>
  rename(LS = 2) |>
```

```r
  group_by(Species) |>
  summarise(LS = mean(LS))
```

```
## New names:
## Rows: 5 Columns: 13
## -- Column specification
## ----------------------------------------------------------- Delimiter: "," chr
## (1): Species dbl (12): Transect, Spacers length (cm) average, ...4, ...5, ...6,
## ...7, ......
## 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.
## * `` -> `...4`
## * `` -> `...5`
## * `` -> `...6`
## * `` -> `...7`
## * `` -> `...8`
## * `` -> `...9`
## * `` -> `...10`
## * `` -> `...11`
## * `` -> `...12`
## * `` -> `...13`
```

```r
speciestraits <- speciestraits |>
  left_join(measured, by = join_by(species == Species)) |>
  mutate(spread = if_else(!is.na(spread), spread, LS)) |>
  select(!LS)

#two measured species that are actually clonal

speciestraits[speciestraits$species %in% measured$Species, "clonal"] <- T

rm(gspff,clopla, speciesfreqs_plot, speciesfreqs_all, measured)

##set species known as clonal if missing----

clonals <- c("Geranium nodosum", "Arisarum proboscideum", "Clinopodium nepeta")
speciestraits[speciestraits$species %in% clonals, "clonal"] <- T
rm(clonals)

##and species known as not clonal----

speciestraits <- speciestraits |>
  mutate(clonal = if_else(is.na(clonal), F, clonal))

##set clonal traits at 0 if not clonal----

speciestraits <- speciestraits |>
  mutate(across(persistence:spread, ~if_else(condition = !clonal & is.na(.x), true = 0, false = .x)))

# missingness -------------------------------------------------------------

# incomplete cases
```

```r
sum(!complete.cases(speciestraits)) #26/83 overall
```

```
## [1] 26
```

```r
sum(!complete.cases(speciestraits[8:13])) #22 for gspff
```

```
## [1] 22
```

```r
sum(!complete.cases(speciestraits[14:17])) #9 for clo-pla
```

```
## [1] 9
```

```r
# missing species gspff
speciestraits |>
  filter(presentgspff==F) |>
  pull(species)
```

```
## [1] "Cardamine chelidonia"  "Arisarum proboscideum"
```

```r
# missing species clo-pla
speciestraits|>
  filter(presentclo==F) |>
  pull(species)
```

```
## [1] "Geranium nodosum"      "Daphne laureola"        "Cardamine chelidonia"
## [4] "Rosa arvensis"         "Arisarum proboscideum" "Hypericum androsaemum"
## [7] "Clinopodium nepeta"
```

```r
## empty cells for present species----

#gspff
speciestraits |>
  filter(if_any(8:13, ~is.na(.) & presentgspff == T)) |>
  select(leaf_area_mm2:ssd_combined_mg_mm3) |>
  print(n =50)
```

```
## # A tibble: 20 x 6
##     leaf_area_mm2 nmass_mg_g lma_g_m2 plant_height_m diaspore_mass_mg
##             <dbl>      <dbl>    <dbl>          <dbl>            <dbl>
## 1           4067.         NA     26.0          0.307           0.4
## 2          27262          NA     89.2          0.264          11.6
## 3           1518.       24.6    108.           0.793          49.0
## 4            110          NA     22.3          0.176           0.78
## 5          24165.         NA     74.0          0.811           0.0000194
## 6             NA          NA      NA           0.206           1.64
## 7             NA          NA      NA           0.179          NA
## 8             NA        22.2     34.6          0.687           0.0000368
## 9            239          NA     29.6          0.394           0.256
## 10            NA        21.1     51.9          0.799           0.0000194
```

```
## 11          302.      24.3    45.4        1.16        10.8
## 12         3647        NA     42.6       0.404       0.146
## 13         2121.       NA     36.9       0.393       0.121
## 14           NA      19.7     31.0       0.160        1.39
## 15         2198.      23.3    45.6       0.940        1.77
## 16           NA        NA       NA       0.354          NA
## 17           NA        NA       NA       0.182        4.49
## 18          675        NA       NA       0.654        0.07
## 19        12698.       NA     76.0       0.296    0.000022
## 20           NA        NA       NA       0.828          NA
## # i 1 more variable: ssd_combined_mg_mm3 <dbl>
```

```r
#clonals
#these are the two species with measured LS and the three species added as clonal
speciestraits |>
  filter(if_any(14:17, ~is.na(.)) & clonal == T) |>
  select(species, presentclo, clonal, BBRsize:spread)
```

```
## # A tibble: 5 x 7
##   species               presentclo clonal BBRsize persistence offspring spread
##   <chr>                 <lgl>      <lgl>    <dbl>       <dbl>     <dbl>  <dbl>
## 1 Viola reichenbachiana TRUE       TRUE      40          NA        NA   1.16
## 2 Geranium nodosum      FALSE      TRUE      NA          NA        NA NA
## 3 Euphorbia amygdaloides TRUE      TRUE     31.8         NA        NA   1.08
## 4 Arisarum proboscideum FALSE      TRUE      NA          NA        NA NA
## 5 Clinopodium nepeta    FALSE      TRUE      NA          NA        NA NA
```

```r
#overall
speciestraits |>
  group_by(presentgspff, presentclo) |>
  summarise(across(where(is.numeric) & !n, ~ sum(is.na(.)))) |>
  glimpse()
```

```
## `summarise()` has grouped output by 'presentgspff'. You can override using the
## `.groups` argument.
```

```
## Rows: 3
## Columns: 12
## Groups: presentgspff [2]
## $ presentgspff        <lgl> FALSE, TRUE, TRUE
## $ presentclo          <lgl> FALSE, FALSE, TRUE
## $ leaf_area_mm2       <int> 2, 0, 8
## $ nmass_mg_g          <int> 2, 1, 13
## $ lma_g_m2            <int> 2, 1, 5
## $ plant_height_m      <int> 2, 0, 0
## $ diaspore_mass_mg    <int> 2, 0, 3
## $ ssd_combined_mg_mm3 <int> 2, 3, 10
## $ BBRsize             <int> 2, 5, 0
## $ persistence         <int> 1, 2, 2
## $ offspring           <int> 1, 2, 2
## $ spread              <int> 1, 2, 0
```

```r
## percent completeness----

onlytraits <- speciestraits |>
  select(where(is.numeric)&!n)

#overall
100-sum(is.na(onlytraits))/prod(dim(onlytraits))*100
```

```
## [1] 90.84337
```

```r
#gspff
100-sum(is.na(onlytraits[1:6]))/prod(dim(onlytraits[1:6]))*100
```

```
## [1] 88.75502
```

```r
#clo-pla
100-sum(is.na(onlytraits[7:10]))/prod(dim(onlytraits[7:10]))*100
```

```
## [1] 93.9759
```

```r
#by trait
onlytraits |>
  summarise(across(everything(), ~ 100-sum(is.na(.x))/n()*100)) |>
  glimpse()
```

```
## Rows: 1
## Columns: 10
## $ leaf_area_mm2      <dbl> 87.95181
## $ nmass_mg_g         <dbl> 80.72289
## $ lma_g_m2           <dbl> 90.36145
## $ plant_height_m     <dbl> 97.59036
## $ diaspore_mass_mg   <dbl> 93.9759
## $ ssd_combined_mg_mm3 <dbl> 81.92771
## $ BBRsize            <dbl> 91.56627
## $ persistence        <dbl> 93.9759
## $ offspring          <dbl> 93.9759
## $ spread             <dbl> 96.38554
```

```r
# imputation ----------------------------------------------------------------
#devtools::install_github("jinyizju/V.PhyloMaker2")
library(V.PhyloMaker2)
```

```
## Loading required package: ape
##
## Attaching package: 'ape'
##
## The following object is masked from 'package:dplyr':
##
##     where
```

```r
library(funspace)

## make phylogenetic tree----

for_phylo <- speciestraits |>
  select(species, family) |>
  mutate(genus = word(species), .after = 1)
for_phylo[for_phylo$genus == "Adoxa", "family"] <- "Adoxaceae"   #old family used by phylo

tree <- phylo.maker(for_phylo)
```
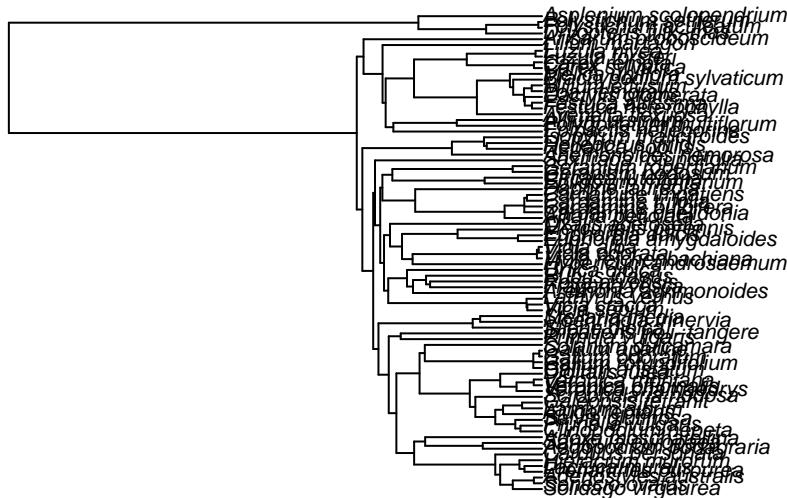
```
## Warning: Setting row names on a tibble is deprecated.
## Setting row names on a tibble is deprecated.
```

```r
table(tree$species.list$status) #13 bind, 70 prune
```

```
##
##  bind prune
##    13    70
```

```r
#check the phylogenetic tree
plot(tree$scenario.3, type = "phylogram", cex = 0.7)
```

```r
rm(for_phylo)

#add status to traits
speciestraits <- tree$species.list |>
  select(species, status) |>
  right_join(speciestraits) |>
  relocate(status, .after = presentclo)
```

Joining with `by = join_by(species)`

```r
## imputation -----------------------------------------------------------

#save traits before imputation

saveRDS(speciestraits, file = 'traits_noimp.rds')

#dataframe for imputation
imputation <- speciestraits |>
  mutate(species = str_replace_all(species, " ", "_")) |>
  select(!2:7) |>
  mutate(clonal = as.factor(clonal)) |>
  column_to_rownames(var = "species")

#impute missing traits
imputed <- impute(as.data.frame(imputation), phylo = tree$scenario.3)

imputed <- imputed$imputed |>
  rownames_to_column("species") |>
  mutate(species = str_replace_all(species, "_", " "))

#check imputed values

if (sum(!complete.cases(imputed)) != 0){
warning("There are still missing values after imputation!")
}


#add imputed values

speciestraits <- speciestraits |>
  select(species:status) |>
  left_join(imputed)
```

Joining with `by = join_by(species)`

```r
speciestraits |>
  select(!5:8) |>
  print(n = 100)
```

```
## # A tibble: 83 x 14
##    species  code  family     n leaf_area_mm2 nmass_mg_g lma_g_m2 plant_height_m
##    <chr>    <chr> <chr> <int>         <dbl>      <dbl>    <dbl>          <dbl>
```

```
##  1 Sanicula~ SAN   Apiac~ 1855    2700.     21.9    28.1    0.298
##  2 Galium o~ G     Rubia~ 1796     192.     24.2    24.3    0.267
##  3 Melica u~ MEL   Poace~  680     454.     19.6    28.6    0.362
##  4 Oxalis a~ O     Oxali~  622     146.     27.0    16.2    0.0910
##  5 Viola re~ VR    Viola~  612     488.     23.4    33.3    0.136
##  6 Brachypo~ BRA   Poace~  490    2195.     21.6    23.1    0.662
##  7 Luzula n~ NIV   Junca~  481     589.     24.9    40.2    0.616
##  8 Festuca ~ FE    Poace~  480     285.     28.0    33.0    0.566
##  9 Mercuria~ ME    Eupho~  418    1890.     32.3    38.3    0.273
## 10 Hieraciu~ H     Aster~  357    4067.     29.5    26.0    0.307
## 11 Veronica~ VE    Plant~  288     458      20.0    30.3    0.268
## 12 Geranium~ NOD   Geran~  266    7445.     19.6    23.5    0.226
## 13 Cardamin~ BUL   Brass~  263    2207.     36.1    24.8    0.425
## 14 Carex sy~ CAR   Cyper~  250     677      21.8    38.3    0.451
## 15 Geranium~ ROB   Geran~  250    1069.     25.8    30.5    0.276
## 16 Milium e~ MIL   Poace~  231    1621.     23.1    29.2    0.843
## 17 Hellebor~ HEL   Ranun~  201   27262      24.0    89.2    0.264
## 18 Daphne l~ DA    Thyme~  192    1518.     24.6    108.    0.793
## 19 Stellari~ STE   Caryo~  129     263.     33.6    20.6    0.152
## 20 Euphorbi~ EU    Eupho~  124     313.     28.1    41.6    0.406
## 21 Galium r~ ROT   Rubia~  121     110      27.0    22.3    0.176
## 22 Lactuca ~ MY    Aster~  112    2002.     25.3    16.0    0.508
## 23 Cardamin~ CHE   Brass~  103    1793.     32.3    33.8    0.440
## 24 Circaea ~ CIR   Onagr~   90    2313.     23.7    22.2    0.335
## 25 Alliaria~ AL    Brass~   85    2958.     42.4    23.2    0.438
## 26 Senecio ~ S     Aster~   80    7780.     29.9    36.1    0.985
## 27 Avenella~ AVE   Poace~   69      50.8    18.4    38.4    0.301
## 28 Moehring~ STEX  Caryo~   66      77.4    26.6    28.1    0.154
## 29 Luzula f~ LU    Junca~   59     339.     20.3    46.4    0.176
## 30 Salvia g~ GLU   Lamia~   57   11483.     39.2    18.6    0.544
## 31 Polystic~ POLY  Dryop~   54   24165.     24.0    74.0    0.811
## 32 Anemonoi~ ANE   Ranun~   53    2924.     29.4    35.5    0.183
## 33 Cardamin~ TRI   Brass~   52    1437.     28.1    33.9    0.206
## 34 Adenosty~ AUS   Aster~   48   18139.     26.2    49.6    0.512
## 35 Aremonia~ A     Rosac~   43    1602.     26.4    33.9    0.179
## 36 Dryopter~ DRY   Dryop~   43    6532.     22.2    34.6    0.687
## 37 Cardamin~ CIMP  Brass~   41     239      30.3    29.6    0.394
## 38 Galium a~ APA   Rubia~   39     159.     25.7    25.9    0.390
## 39 Galeopsi~ GT    Lamia~   38     857.     30.8    31.7    0.366
## 40 Polystic~ SET   Dryop~   37    9356.     21.1    51.9    0.799
## 41 Epipacti~ EPI   Orchi~   31    1617.     34.3    33.3    0.505
## 42 Rosa arv~ RO    Rosac~   30     302.     24.3    45.4    1.16
## 43 Saxifrag~ SAX   Saxif~   30    1876.     17.9    52.3    0.263
## 44 Prenanth~ PRE   Aster~   27    2945.     30      15.2    0.789
## 45 Adoxa mo~ ADO   Vibur~   25    1808.     37.2    26.1    0.0847
## 46 Carex re~ CRE   Cyper~   22     302.     16.3    36.3    0.433
## 47 Dactylis~ DAC   Poace~   22    1457.     21.0    44.3    0.691
## 48 Digitali~ DIG   Plant~   22    3647      26.6    42.6    0.404
## 49 Primula ~ P     Primu~   21    4278.     23.9    30.7    0.0973
## 50 Allium u~ URS   Amary~   21    6409.     36.9    27.6    0.306
## 51 Polygona~ MUL   Aspar~   20    1607.     30      22.8    0.423
## 52 Urtica d~ U     Urtic~   17    1553.     42.9    34.6    0.883
## 53 Silene d~ SIL   Caryo~   14    3533      30.1    27.7    0.556
## 54 Hepatica~ HEP   Ranun~   13    2885.     18.8    36.2    0.100
```

```
## 55 Lathyrus~ LAT   Fabac~    13    1504.      38.6     24.5       0.270
## 56 Viola od~ V      Viola~    13    1827.      17.1     39.1       0.0895
## 57 Epilobiu~ MONT   Onagr~    12    2121.      25.5     36.9       0.393
## 58 Euphorbi~ EDU    Eupho~    10     420       41.0     30.1       0.310
## 59 Festuca ~ FX     Poace~    10    2404.      22.7     35.6       0.790
## 60 Ajuga re~ AJU    Lamia~     9    1817.      19.7     31.0       0.160
## 61 Impatien~ IMP    Balsa~     9    1578.      39.8     22.2       0.585
## 62 Solanum ~ SOL    Solan~     8    1408.      39.6     28.7       1.01
## 63 Arisarum~ ARP    Arace~     7    4242.      31.5     34.9       0.439
## 64 Rubus id~ IDE    Rosac~     7    2198.      23.3     45.6       0.940
## 65 Aegopodi~ AEG    Apiac~     6    2762.      27.5     35.3       0.621
## 66 Galium a~ GAR    Rubia~     5    2066.      29.3     26.8       0.354
## 67 Isopyrum~ CORY   Ranun~     4    5700.      23.7     44.3       0.182
## 68 Lamium a~ LAM    Lamia~     4    1886.      42.3     28.5       0.319
## 69 Lilium m~ LIL    Lilia~     4    3363.      37.6     38.5       0.583
## 70 Poa nemo~ POA    Poace~     4     527.      22.1     28.3       0.461
## 71 Prunella~ PRU    Lamia~     4     473.      19.2     34.9       0.145
## 72 Veronica~ VC     Plant~     4     300.      21.6     34.4       0.200
## 73 Hypericu~ AND    Hyper~     3     675       26.7     36.4       0.654
## 74 Clinopod~ CLI    Lamia~     3     108       26.6     39.7       0.312
## 75 Scrophul~ SCRO   Scrop~     3    5821.      28.8     33.5       0.750
## 76 Vicia cr~ VCR    Fabac~     3     714.      39.2     44.0       0.626
## 77 Aspleniu~ PHY    Asple~     2   12698.      23.0     76.0       0.296
## 78 Vicia se~ VIC    Fabac~     2      59.1     46       25.6       0.445
## 79 Veronica~ VO     Plant~     2      87.3     18.3     39.3       0.126
## 80 Carduus ~ CARD   Aster~     1    4304.      27.1     39.3       0.828
## 81 Fragaria~ FRA    Rosac~     1    1112.      18.4     45.3       0.114
## 82 Solidago~ SOV    Aster~     1     984.      28.3     43.4       0.508
## 83 Viola al~ VA     Viola~     1     920.      17.3     44.7       0.0705
## # i 6 more variables: diaspore_mass_mg <dbl>, ssd_combined_mg_mm3 <dbl>,
## #   BBRsize <dbl>, persistence <dbl>, offspring <dbl>, spread <dbl>
```

```r
rm(imputation, tree, imputed)


# save data -------------------------------------------------------------

saveRDS(speciestraits, file = "traits_imputation.rds")
saveRDS(dat, file = "transect_data.rds")

# session info ----------------------------------------------------------

sessionInfo()
```

```
## R version 4.5.2 (2025-10-31)
## Platform: x86_64-redhat-linux-gnu
## Running under: Nobara Linux 43 (KDE Plasma Desktop Edition)
##
## Matrix products: default
## BLAS/LAPACK: FlexiBLAS OPENBLAS-OPENMP;  LAPACK version 3.12.1
##
## locale:
##  [1] LC_CTYPE=it_IT.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=it_IT.utf8         LC_COLLATE=it_IT.UTF-8
```

```
##  [5] LC_MONETARY=it_IT.utf8    LC_MESSAGES=it_IT.UTF-8
##  [7] LC_PAPER=it_IT.utf8       LC_NAME=C
##  [9] LC_ADDRESS=C              LC_TELEPHONE=C
## [11] LC_MEASUREMENT=it_IT.utf8 LC_IDENTIFICATION=C
##
## time zone: Europe/Rome
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats     graphics  grDevices datasets  utils     methods   base
##
## other attached packages:
##  [1] funspace_0.2.2      V.PhyloMaker2_0.1.0 ape_5.8-1
##  [4] readxl_1.4.5        lubridate_1.9.4     forcats_1.0.1
##  [7] stringr_1.6.0       dplyr_1.1.4         purrr_1.2.0
## [10] readr_2.1.6         tidyr_1.3.2         tibble_3.3.0
## [13] ggplot2_4.0.1       tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] Rdpack_2.6.4           mnormt_2.1.1           gridExtra_2.3
##  [4] phangorn_2.12.1        permute_0.9-8          rlang_1.1.6
##  [7] magrittr_2.0.4         ade4_1.7-23            snakecase_0.11.1
## [10] compiler_4.5.2         mgcv_1.9-4             vctrs_0.6.5
## [13] maps_3.4.3             combinat_0.0-8         quadprog_1.5-8
## [16] pkgconfig_2.0.3        crayon_1.5.3           fastmap_1.2.0
## [19] utf8_1.2.6             CoprManager_0.5.7      rmarkdown_2.30
## [22] tzdb_0.5.0             pracma_2.4.6           itertools_0.1-3
## [25] bit_4.6.0              xfun_0.55              randomForest_4.7-1.2
## [28] clusterGeneration_1.3.8 parallel_4.5.2        cluster_2.1.8.1
## [31] R6_2.6.1               stringi_1.8.7          RColorBrewer_1.1-3
## [34] ranger_0.17.0          cellranger_1.1.0       numDeriv_2016.8-1.1
## [37] Rcpp_1.1.0             iterators_1.0.14       knitr_1.50
## [40] optimParallel_1.0-2    Matrix_1.7-4           splines_4.5.2
## [43] igraph_2.2.1           timechange_0.3.0       tidyselect_1.2.1
## [46] rstudioapi_0.17.1      yaml_2.3.12            viridis_0.6.5
## [49] vegan_2.7-2            doParallel_1.0.17      codetools_0.2-20
## [52] doRNG_1.8.6.2          lattice_0.22-7         ks_1.15.1
## [55] withr_3.0.2            S7_0.2.1               coda_0.19-4.1
## [58] evaluate_1.0.5         phytools_2.5-2         mclust_6.1.2
## [61] pillar_1.11.1          rngtools_1.5.2         KernSmooth_2.23-26
## [64] foreach_1.5.2          generics_0.1.4         vroom_1.6.7
## [67] hms_1.1.4              scales_1.4.0           glue_1.8.0
## [70] janitor_2.2.1          scatterplot3d_0.3-44   tools_4.5.2
## [73] paran_1.5.4            mvtnorm_1.3-3          fastmatch_1.1-6
## [76] grid_4.5.2             missForest_1.6.1       rbibutils_2.4
## [79] nlme_3.1-168           cli_3.6.5              DEoptim_2.2-8
## [82] expm_1.0-0             viridisLite_0.4.2      gtable_0.3.6
## [85] digest_0.6.39          farver_2.1.2           htmltools_0.5.9
## [88] lifecycle_1.0.4        bit64_4.6.0-1          MASS_7.3-65
```