

Generating figures visualizing the match between sPlot 2.1 and TRY 3.0

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Abstract

This document describes the workflow of generating some figures that visualize the match between (i) global vegetation plot database sPlot version 2.1 and (ii) the global plant trait data base TRY version 3.

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1 Load required packages

```
library(ggplot2)
library(plyr)
library(dplyr)
library(reshape)
library(foreach)
```

2 Loading Data

2.1 sPlot species data

Loading a reduced version of 'splot_20161025_species', DT2_small, that just contains the columns 'PlotObservationID', 'species' and 'Relative.cover':

```
load("/home/oliver/Dokumente/PhD/PostPhD/IDiv/sDiv/sPlot/Analyses/Data/Species/sPlot/sPlot_2017_08_04/splot_20161025_species_small.Rdata")
gc()
```

```
dim(DT2_small)
```

```
## [1] 22195966      3
```

```
head(DT2_small)
```

```
##   PlotObservationID      species Relative.cover
## 1                15 Festuca brachyphylla  0.20000000
## 2                15  Potentilla elegans  0.75000000
## 3                15 Saxifraga serpyllifolia 0.05000000
## 4                16 Festuca brachyphylla  0.27777778
## 5                16  Potentilla elegans  0.69444444
## 6                16 Saxifraga serpyllifolia 0.02777778
```

2.2 Header data

Includes a reduced version of 'splot_20161124_header', mainly containing the biome-affiliation and the X-Y-coordinates of each plot:

```
load("/home/oliver/Dokumente/PhD/PostPhD/IDiv/sDiv/sPlot/Analyses/Data/Species/sPlot/sPlot_2017_08_04/splot_20161124_header_small.Rdata")
gc()
```

```
coord.biome <- header_small
```

2.3 Trait data

Loading the gapfilled trait data from TRY 3.0:

```
try3gapfilled <- read.csv("/home/oliver/Dokumente/PhD/PostPhD/IDiv/sDiv/sPlot/Analyses/Data/Traits/TRY_3.0_gapfilled/Export_sPlot_2016_09_12.csv", stringsAsFactors = F)
gc()
```

```
dim(try3gapfilled)
```

```
## [1] 632938      34
```

```
names(try3gapfilled)
```

```
## [1] "ObservationID"      "X1"
## [3] "X4"                  "X11"
## [5] "X13"                 "X14"
## [7] "X15"                 "X18"
## [9] "X26"                 "X27"
## [11] "X47"                 "X50"
```

```
## [13] "X56" "X78"
## [15] "X138" "X163"
## [17] "X169" "X237"
## [19] "X282" "ObservationID.2"
## [21] "AccSpeciesID" "Species"
## [23] "Genus" "Family"
## [25] "PhylogeneticGroup" "Exposition"
## [27] "Maturity" "PlantGrowthForm"
## [29] "LeafType" "LeafCompoundness"
## [31] "TypicalNumberOfLeaflets" "DbComment"
## [33] "ObservationID.1" "name.short.correct"
```

2.4 Taxonomic backbone

```
load("/home/oliver/Dokumente/PhD/PostPhD/IDiv/sDiv/sPlot/Analyses/Code/
backbone.splot2.1.try3.is.vascular.Rdata")
gc()
```

3 Matching species with biomes

```
DTMatch <- dplyr::left_join(DT2_small, coord.biome[,c(1,5)], by = "PlotObservationID")
```

```
head(DTMatch)
```

##	PlotObservationID	species	Relative.cover	Biome
## 1	15	Festuca brachyphylla	0.20000000	Boreal zone
## 2	15	Potentilla elegans	0.75000000	Boreal zone
## 3	15	Saxifraga serpyllifolia	0.05000000	Boreal zone
## 4	16	Festuca brachyphylla	0.27777778	Boreal zone
## 5	16	Potentilla elegans	0.69444444	Boreal zone
## 6	16	Saxifraga serpyllifolia	0.02777778	Boreal zone

```
table(DTMatch$Biome)
```

##	Alpine	Boreal zone
##	422923	417748
##	Dry midlatitudes	Dry tropics and subtropics
##	491939	318004
##	Polar and subpolar zone	Subtrop. with year-round rain
##	44738	666686
##	Subtropics with winter rain	Temperate midlatitudes
##	2189688	17061718
##	Tropics with summer rain	Tropics with year-round rain
##	341649	229810

4 Summarizing species information

4.1 Calculating species frequency and average cover

```
spec.group <- group_by(DTMatch, species)
spec.agg.splot2.vasc <- summarise(spec.group, count.spec = n(),
                                   Avg_Cover_Perc = mean(Relative.cover))
```

4.2 Classify species according to frequency and dominance

Assigning frequency classes:

```
quantile(spec.agg.splot2.vasc$count.spec, (0:4)/4)
```

```
##      0%      25%      50%      75%     100%
##       1       3      13      55  128942
```

```
fac1 <- cut(as.numeric(spec.agg.splot2.vasc$count.spec),
            quantile(spec.agg.splot2.vasc$count.spec, (0:4)/4),
            labels=c("Low", "Medium", "High", "Highest"))
```

Assigning dominance classes:

```
quantile(spec.agg.splot2.vasc$Avg_Cover_Perc, (0:4)/4)
```

```
##           0%           25%           50%           75%           100%
## 2.099379e-06 9.660214e-03 1.963825e-02 3.998146e-02 1.000000e+00
```

```
fac2 <- cut(as.numeric(spec.agg.splot2.vasc$Avg_Cover_Perc),
            quantile(spec.agg.splot2.vasc$Avg_Cover_Perc, (0:4)/4),
            labels=c("Low", "Medium", "High", "Highest"))
spec.agg.splot2.vasc$count.fac <- fac1
spec.agg.splot2.vasc$cover.fac <- fac2
```

Because we are interested in percentiles of the whole population of the 50,000+ species, I calculate 5% percentiles based on species ranks instead of their actual values:

```
spec.count.rank<-rank(spec.agg.splot2.vasc$count.spec, ties.method = "first")
fac1 <- cut(spec.count.rank, quantile(spec.count.rank, probs=0:20/20), include.lowest=TRUE,
            labels=1:20)
table(fac1)
```

```
## fac1
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15
## 2904 2903 2903 2903 2904 2903 2903 2903 2903 2904 2903 2903 2903 2903 2904
##   16  17  18  19  20
## 2903 2903 2903 2903 2904
```

```
spec.cover.rank<-rank(spec.agg.splot2.vasc$Avg_Cover_Perc, ties.method = "first")
fac2 <- cut(spec.cover.rank, quantile(spec.cover.rank, probs=0:20/20), include.lowest=TRUE,
            labels=1:20)
table(fac2)
```

```
## fac2
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15
## 2904 2903 2903 2903 2904 2903 2903 2903 2903 2904 2903 2903 2903 2903 2904
```

```
## 16 17 18 19 20
## 2903 2903 2903 2903 2904

spec.agg.splot2.vasc$count.fac.20 <- fac1
spec.agg.splot2.vasc$cover.fac.20 <- fac2
```

5 TRY species list

Match names in TRY with the backbone and generate a list of unique, resolved names of original (partly unresolved) names in TRY:

```
index2 <- match(try3gapfilled$Species, backbone.splot2.1.try3$names.sPlot.TRY)
try3gapfilled$name.short.correct <- backbone.splot2.1.try3$name.short.correct[index2]
```

```
str(try3gapfilled)
```

```
## 'data.frame': 632938 obs. of 34 variables:
## $ ObservationID : num 15472 15473 15474 15475 15476 ...
## $ X1 : num 2520 8500 7122 4917 2587 ...
## $ X4 : num 0.607 0.567 0.511 0.52 0.47 ...
## $ X11 : num 18 21.6 15.3 14 16.7 ...
## $ X13 : num 468 478 471 478 477 ...
## $ X14 : num 19.2 20.5 22.5 22.2 27.6 ...
## $ X15 : num 1.87 1.9 2.13 1.52 2 ...
## $ X18 : num 8.96 19.15 24.27 23.01 15.26 ...
## $ X26 : num 17.766 64.555 49.765 7190.923 0.914 ...
## $ X27 : num 14.23 18.58 18.96 33.89 2.51 ...
## $ X47 : num 0.255 0.349 0.34 0.294 0.299 ...
## $ X50 : num 1.24 0.937 1.508 1.633 1.622 ...
## $ X56 : num 8.99 11.24 11.73 15.23 12.41 ...
## $ X78 : num 1.494 5.805 4.072 0.837 1.117 ...
## $ X138 : num 67.66 1.65 132.23 32.09 48.35 ...
## $ X163 : num 0.428 1.272 1.6 5.514 0.427 ...
## $ X169 : num 77.6 239.5 149.7 93.5 98 ...
## $ X237 : num 12.43 26.62 25.18 33.77 2.73 ...
## $ X282 : num 725 237 227 615 512 ...
## $ ObservationID.2 : int 15472 15473 15474 15475 15476 15477 15478 15479 15480 15481 ...
## $ AccSpeciesID : int 797 854 855 1571 2710 2736 3184 4447 6088 7230 ...
## $ Species : chr "Acer campestre" "Acer platanoides" "Acer pseudoplatanus" "Aesculus
## $ Genus : chr "Acer" "Acer" "Acer" "Aesculus" ...
## $ Family : chr "Aceraceae" "Aceraceae" "Aceraceae" "Hippocastanaceae" ...
## $ PhylogeneticGroup : chr "Angiosperm_Eudicotyl" "Angiosperm_Eudicotyl" "Angiosperm_Eudicotyl
## $ Exposition : chr "" "" "" "" ...
## $ Maturity : chr "" "" "" "" ...
## $ PlantGrowthForm : chr "tree" "tree" "tree" "tree" ...
## $ LeafType : chr "broadleaved" "broadleaved" "broadleaved" "broadleaved" ...
## $ LeafCompoundness : chr "simple" "simple" "simple" "compound" ...
## $ TypicalNumberOfLeaflets: int 1 1 1 6 1 1 1 1 1 1 ...
## $ DbComment : chr "" "" "" "" ...
## $ ObservationID.1 : int 15472 15473 15474 15475 15476 15477 15478 15479 15480 15481 ...
## $ name.short.correct : chr "Acer campestre" "Acer platanoides" "Acer pseudoplatanus" "Aesculus
```

Generate a list of unique, resolved names of original (partly unresolved) names in TRY:

```
names.try <- unique(try3gapfilled$name.short.correct)
length(names.try)
```

```
## [1] 52033
```

There are 52033 unique resolved species in TRY.

```
length(unique(try3gapfilled$Species))
```

```
## [1] 59319
```

There are 59319 unique but partly unresolved species in TRY. Means that 12.3% of the gapfilled species in TRY3.0 are Synonyms (or to a small extent species where no suitable name matches were found).

6 Calculate match between sPlot and TRY

```
biome.group <- group_by(DTMatch, Biome)

biome.trait.match.freq.dom <- foreach(i = 6:7, .combine = rbind) %:%
  foreach(j = 2:20, .combine = cbind) %do% {
    index3 <- which(spec.agg.splot2.vasc[,i] == j)
    names.freq.dom <- unique(spec.agg.splot2.vasc$species[index3])
    biome.group.small <- biome.group[which(biome.group$species %in% names.freq.dom), ]
    x <- dplyr::summarise(biome.group.small,
      match.splot.try =
        100*(length(unique(species)
          [which(unique(species) %in%
            names.try)])/length(unique(species))))[,2]
    x
  }

gc()
```

6.1 Assign names to match stats

Take the nineteen 5% percentiles as colnames. Skip the lowest percentile as it could not be calculated for the some of the biomes.

```
a <- seq(6, 100, 5)
b <- seq(10, 100, 5)
nam <- paste(a,b, sep = "-")
colnames(biome.trait.match.freq.dom) <- nam
```

Use the Biom in 'Schulz_Bio' as first column.

```
biome.trait.match.agg <-
  dplyr::summarise(biome.group,
    match.splot.try =
      100*(length(unique(species)[which(unique(species) %in%
        names.try)])/length(unique(species))))

biome.trait.match.freq.dom2 <- cbind(rep(biome.trait.match.agg$Biome, 2),
```

```

      biome.trait.match.freq.dom)
colnames(biome.trait.match.freq.dom2)[1] <- "Schulz_Bio"

biome.trait.match.3 <- biome.trait.match.freq.dom2 %>%
  dplyr::filter(!is.na(Schulz_Bio)) %>%
  dplyr::select(1:20) %>%
  reshape::melt("Schulz_Bio") %>%
  dplyr::mutate(freq.dom = rep(c("Frequency", "Dominance"), 19, each = 10))

head(biome.trait.match.3)

##           Schulz_Bio variable      value freq.dom
## 1             Alpine      6-10  8.333333 Frequency
## 2          Boreal zone      6-10  3.571429 Frequency
## 3    Dry midlatitudes      6-10 21.052632 Frequency
## 4 Dry tropics and subtropics      6-10 29.057592 Frequency
## 5    Polar and subpolar zone      6-10  0.000000 Frequency
## 6 Subtrop. with year-round rain      6-10 32.063492 Frequency

tail(biome.trait.match.3)

##           Schulz_Bio variable      value freq.dom
## 375    Polar and subpolar zone    96-100 76.92308 Dominance
## 376 Subtrop. with year-round rain    96-100 70.00000 Dominance
## 377 Subtropics with winter rain    96-100 60.63250 Dominance
## 378    Temperate midlatitudes    96-100 65.59140 Dominance
## 379    Tropics with summer rain    96-100 66.93712 Dominance
## 380 Tropics with year-round rain    96-100 63.01775 Dominance

Bring 'biomes names' and 'freq.dom' in a sensible order:

biome.trait.match.3$Schulz_Bio <-
  factor(biome.trait.match.3$Schulz_Bio, levels=c("Tropics with year-round rain",
      "Tropics with summer rain",
      "Dry tropics and subtropics",
      "Subtropics with winter rain",
      "Subtrop. with year-round rain",
      "Temperate midlatitudes",
      "Dry midlatitudes",
      "Boreal zone",
      "Polar and subpolar zone",
      "Alpine"))

biome.trait.match.3$freq.dom <- factor(biome.trait.match.3$freq.dom,
      levels=c("Frequency", "Dominance"))

```

7 Generate the Figure

```

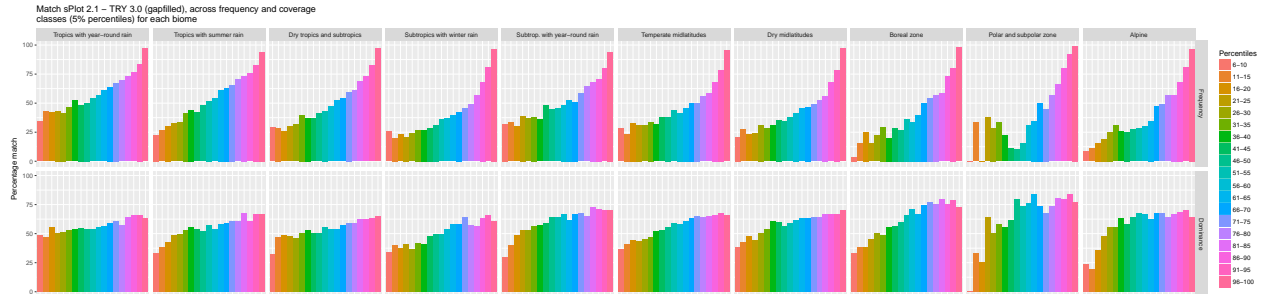
ggplot(biome.trait.match.3, aes(variable, value, fill=variable)) +
  geom_bar(stat="identity", position="dodge")+
  facet_grid(freq.dom ~ Schulz_Bio) +
  theme(axis.text.x=element_blank(),
        axis.ticks.x=element_blank(),
        axis.title.x=element_blank()) +

```

```

xlab("Biomes") +
ylab("Percentage match")+
guides(fill=guide_legend(title="Percentiles")) +
ggtitle("Match sPlot 2.1 - TRY 3.0 (gapfilled), across frequency and coverage
classes (5% percentiles) for each biome")

```



7.1 Save the figure

```

ggsave("Match TRY3-sPlot2.1.biome_Freq_Dom_5_perc.png", plot = last_plot(), device = "png",
path = NULL, scale = 1, width = 10, height = 5, units = c("mm"), dpi = 300,
limitsize = TRUE)

```