

Rscript03: Analysis microbial performance at biome level

Angel Rain

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1 Load data

1.1 Load packages

```
knitr::opts_chunk$set(dev = "cairo_pdf")
rm(list=ls())
library(readxl)
library(ggplot2)
library(stringr)
library(dplyr)
library(ggrepel)
library(rstatix)
library(ggfortify)
library(cowplot)
library(tidyr)
library(scales)
library(ggbreak)
library(moments)
library(dendextend)
library(ggExtra)
library(purrr)
library(ggtext)
library(kableExtra)
library(FSA)      # install.packages("FSA") if needed

cbp1 <- c("red", "#E69F00", "#0072B2", "#009E73", "#56B4E9", "#FOE442", "#100000")
```

1.2 Load Rating-data from Rscript02

```
load(file = "../Scripts/Elo_MAPdata_from_Script02.RData")
str(df_MAP_Elo)

## 'data.frame': 1816294 obs. of 5 variables:
## $ player_id : chr "90_1;96_1;97_1;98_1;99_1" "90_1;96_1;97_1;98_1;99_1" "90_1;96_1;97_1;98_1;99_1"
## $ biome     : chr "animal.3" "plant.2" "freshwater.3" "freshwater.2" ...
## $ Category   : chr "Corrected" "Classic" "Corrected" "Classic" ...
## $ mean_rating: num 802 1000 794 1000 1000 ...
## $ sd_rating  : num 8.089 0.028 6.7699 0.0505 0.0473 ...

tibble(df_MAP_Elo)

## # A tibble: 1,816,294 x 5
##   player_id          biome    Category  mean_rating sd_rating
##   <chr>            <chr>    <chr>        <dbl>      <dbl>
## 1 90_1;96_1;97_1;98_1;99_1 animal.3 Corrected     802.     8.09
## 2 90_1;96_1;97_1;98_1;99_1 plant.2   Classic      1000.    0.0280
## 3 90_1;96_1;97_1;98_1;99_1 freshwater.3 Corrected     794.     6.77
## 4 90_1;96_1;97_1;98_1;99_1 freshwater.2 Classic      1000.    0.0505
## 5 90_1;96_1;97_1;98_1;99_1 freshwater.1 Classic      1000.    0.0473
```

```

## 6 90_1;96_1;97_1;98_1;99_1 animal.2      Classic      1000.  0.0179
## 7 90_1;96_1;97_1;98_1;99_1 freshwater.1 Corrected     869.   8.93
## 8 90_1;96_1;97_1;98_1;99_1 plant.3       Classic      1000.  0.0536
## 9 90_1;96_1;97_1;98_1;99_1 plant.2       Corrected     702.  11.7
## 10 90_1;96_1;97_1;98_1;99_1 freshwater.2 Corrected     812.   9.64
## # i 1,816,284 more rows

```

1.2.1 Cheching results

```
print (paste("Number of unique OTUs =",length(unique(df_MAP_Elo$player_id))))
```

```
## [1] "Number of unique OTUs = 124772"
```

1.3 Load metadata

```

df.elo.diversity<-read_xlsx("../data/Supplementary_tables_ms.xlsx",
                           sheet="Table S2",skip=1)

tibble(df.elo.diversity)

```

```

## # A tibble: 24 x 10
##   `#` MAP_biomes Life.Style MAP_biomesFullName n.samples.initial
##   <dbl> <chr>      <chr>                <dbl>
## 1 1    airborne.1 Free-living  airborne            1595
## 2 2    animal.1   Host-associated animal-urogenital 29317
## 3 3    animal.2   Host-associated animal-proximalgut 180797
## 4 4    animal.3   Host-associated animal-distalgut  125143
## 5 5    animal.4   Host-associated animal-oral        37433
## 6 6    animal.5   Host-associated animal-skin       40488
## 7 7    animal.6   Host-associated animal-respiratory 10360
## 8 8    freshwater.1 Free-living   freshwater-sediments 19946
## 9 9    freshwater.2 Free-living   freshwater-water    46327
## 10 10   freshwater.3 Free-living   freshwater-biofilm  5067
## # i 14 more rows
## # i 5 more variables: n.samples.1000reads.3OTUS <dbl>, gamma.diversity <dbl>,
## #   'Elo.coeffcient (a)' <dbl>, 'Elo.coeffcient (a).error' <dbl>,
## #   'Elo.coeffcient (a).pvalue' <dbl>

```

1.4 Load alpha diversity data

```

#Load files per biome
diversity.files<-list.files(path="../data/Diversity_alpha/",pattern="AlphaRaw.*")

list.tmp<-list()

for (i in 1:length(diversity.files)){
  df.tmp<-read.csv(paste0("../data/Diversity_alpha/",diversity.files[i]))
}

```

```

df.tmp$biome<-str_split_fixed(str_remove_all(diversity.files[i], ".csv"), "[.]", 2)[,2]
df.tmp<-df.tmp[,c(1:6)]
names(df.tmp)<-c("sample","richness","shannon","pielou","simpson","biome")
list.tmp[[i]]<-df.tmp
rm(df.tmp) # save some memory
}

#Combine datasets
df.diversity<-do.call(rbind,list.tmp)
rm(list.tmp,diversity.files) #Remove unused files

```

1.5 Setting rating data.frame

```

# Add full names here:
df_MAP_Elo<-merge(df.elo.diversity,df_MAP_Elo,by.x="MAP_biomes",by="biome")
df_MAP_Elo$MAP_biomesFullName<-as.factor(df_MAP_Elo$MAP_biomesFullName)
str(df_MAP_Elo)

## 'data.frame': 1816294 obs. of 14 variables:
## $ MAP_biomes : chr "airborne.1" "airborne.1" "airborne.1" "airborne.1" ...
## $ # : num 1 1 1 1 1 1 1 1 1 ...
## $ Life.Style : chr "Free-living" "Free-living" "Free-living" "Free-living" ...
## $ MAP_biomesFullName : Factor w/ 24 levels "airborne","animal-distalgut",...: 1 1 1 1 1 1 1 ...
## $ n.samples.initial : num 1595 1595 1595 1595 1595 ...
## $ n.samples.1000reads.3OTUS: num 1449 1449 1449 1449 1449 ...
## $ gamma.diversity : num 24141 24141 24141 24141 24141 ...
## $ Elo.coeffcient (a) : num 1.02 1.02 1.02 1.02 1.02 ...
## $ Elo.coeffcient (a).error : num 0.00012 0.00012 0.00012 0.00012 0.00012 0.00012 0.00012 0.00012 ...
## $ Elo.coeffcient (a).pvalue: num 0 0 0 0 0 0 0 0 ...
## $ player_id : chr "90_602;96_5854;97_7045;98_8712;99_11631" "90_1728;96_20467;97_25...
## $ Category : chr "Classic" "Corrected" "Classic" "Classic" ...
## $ mean_rating : num 1000 866 1000 1000 866 ...
## $ sd_rating : num 0.0837 3.1459 0.0219 0.2918 3.1449 ...

#Re-order biome names
levels_sorted<-c("animal-urogenital","animal-proximalgut","animal-distalgut","animal-oral","animal-skin",
               "plant-rhizosphere","plant-phyllosphere","plant-endosphere","plant-spermophore",
               "airborne","freshwater-sediments","freshwater-water","freshwater-biofilm",
               "freshwater-peatlands(peat/bog)","freshwater-peatlands(water)",
               "saline-sediments","saline-water","saline-biofilm",
               "soil-agricultural","soil-desert","soil-tundra","soil-forest","soil-grassland")

#Set biome full names as a factor
df_MAP_Elo$MAP_biomesFullName<-factor(df_MAP_Elo$MAP_biomesFullName,levels_sorted)

```

2 OTUs ratings description at biome level

```

# 1) define your color map for Life.Style
style_cols <- c(`Free-living` = "blue2", `Host-associated` = "red3")

# 2) build a named vector of HTML-wrapped labels
label_vec <- with(df_MAP_Elo, setNames(
  sprintf("<span style='color:%s;'>%s</span>",
    style_cols[Life.Style],
    MAP_biomesFullName), MAP_biomesFullName))

## Setting plot for absence corrected rating or BB-score
plot.descriptive.corrected.Elo<-df_MAP_Elo[df_MAP_Elo$Category=="Corrected",] %>%
  ggplot(aes(x = MAP_biomesFullName, y = (mean_rating))) +
  geom_point(stat = "identity", shape=20, size=0.5, alpha=0.75,
             position = position_dodge2(0.5), aes(colour=Life.Style)) +
  stat_summary(fun="mean", size=0.8, geom="point") +
  coord_flip() +
  theme_bw() + theme(panel.grid.major= element_blank(), panel.grid.minor= element_blank()) +
  theme(text = element_text(size=11)) +
  labs(title="A", x = NULL, y = "BB-score") +
  scale_x_discrete(labels = label_vec) +
  theme(panel.grid      = element_blank(),
        text           = element_text(size = 11),
        axis.text.y    = element_markdown(),           # render the <span> tags
        legend.position = "none") +
  scale_colour_manual(values=c("blue2", "red3")) +
  theme(plot.title = element_text(face="bold", vjust=-4, hjust=0.01, size=12)) +
  theme(plot.margin = margin(t=-4, r=6, l=1, 0),
        plot.title= element_text(margin = margin(t = 0, b=0)))

## Setting plot for Elo-rating
plot.descriptive.classic.Elo<-df_MAP_Elo[df_MAP_Elo$Category=="Classic",] %>%
  ggplot(aes(x = MAP_biomesFullName, y = (mean_rating))) +
  geom_point(stat = "identity", shape=20, size=0.5, alpha=0.75,
             position = position_dodge2(0.5), aes(colour=Life.Style)) +
  stat_summary(fun="mean", size=0.8, geom="point") +
  coord_flip() +
  theme_bw() + theme(panel.grid.major= element_blank(), panel.grid.minor= element_blank()) +
  theme(text = element_text(size=11)) +
  labs(title="", x = NULL, y = "Classic Elo-Rating") +
  scale_x_discrete(labels = label_vec) +
  theme(panel.grid      = element_blank(),
        text           = element_text(size = 11),
        axis.text.y    = element_markdown(),           # render the <span> tags
        legend.position = "none") +
  scale_colour_manual(values=c("blue2", "red3")) +
  scale_y_continuous(limits=c(900,1250))   # keep numeric labels

```

2.1 Display biome-level data from Elo-ratings estimations

```
#Calculate the average and standard deviation
tmp.av<-aggregate(mean_rating~MAP_biomesFullName,
```

MAP_biomesFullName	mean_rating	sd_rating
animal-urogenital	1000	2.5
animal-proximalgut	1000	0.5
animal-distalgut	1000	0.5
animal-oral	1000	1.2
animal-skin	1000	0.6
animal-respiratory	1000	1.1
plant-rhizosphere	1000	0.4
plant-phyllosphere	1000	0.6
plant-endosphere	1000	2.1
plant-spermophere	1000	1.4
airborne	1000	1.0
freshwater-sediments	1000	0.2
freshwater-water	1000	0.3
freshwater-biofilm	1000	0.5
freshwater-peatlands(peat/bog)	1000	3.5
freshwater-peatlands(water)	1000	0.6
saline-sediments	1000	0.4
saline-water	1000	0.5
saline-biofilm	1000	1.0
soil-agricultural	1000	0.4
soil-desert	1000	0.7
soil-tundra	1000	1.1
soil-forest	1000	0.7
soil-grassland	1000	0.6

```

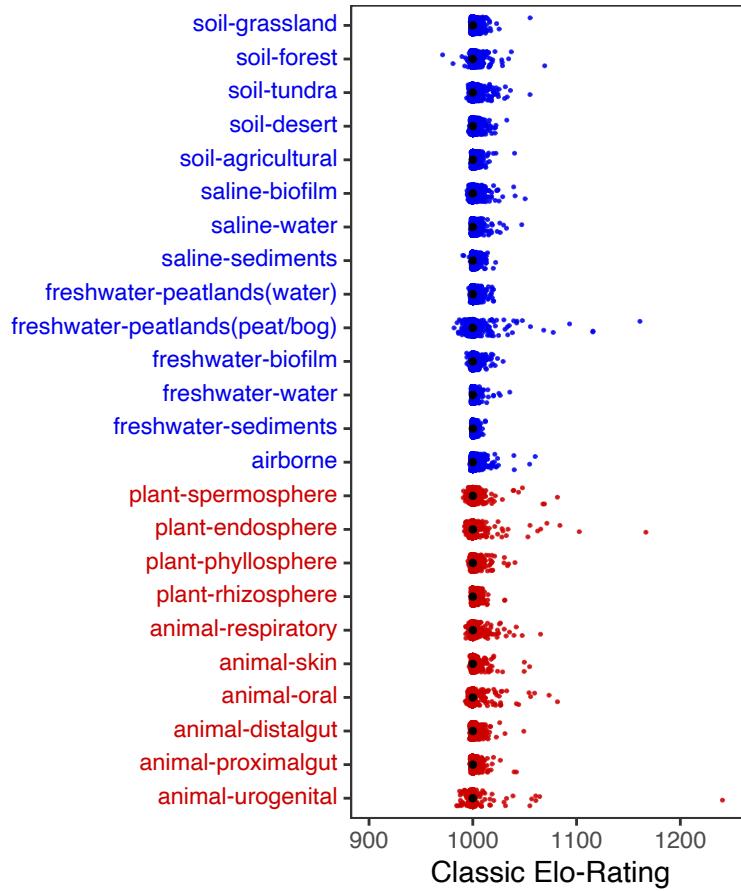
    data=df_MAP_Elo[df_MAP_Elo$Category=="Classic",],mean)
tmp.av$sd_rating<-aggregate(mean_rating~MAP_biomesFullName,
                                data=df_MAP_Elo[df_MAP_Elo$Category=="Classic",],sd) [,2]

tmp.av%>%
  kbl(digits=1)%>%
  kable_styling(full_width = FALSE, position = "center")

```

2.2 Classic Elo-rating Figure S1

Elo-ratings across biomes. Each dot represents the Elo-rating of an individual OTU across soil, freshwater, saline, plant-associated, and animal-associated biomes (blue: free-living; red: host-associated). The vertical line indicates the average Elo-ratings per biome, which converges at 1000 due to the zero-sum game property of Elo-ratings estimations, where per community gains by some OTUs are balanced by losses of others.



3 Diversity indices across biomes

Alpha- and gamma-diversity across biomes. (A) Sample-level richness (OTU count), (B) Shannon diversity, and (C) Pielou's evenness by biome. Boxplots show the median (center line) and the first and third quartiles (bottom and upper limits of boxes); whiskers span the 10th and 90th percentiles. Overlaid points represent the individual samples. (D) gamma-diversity (total OTUs observed across all samples within each biome)

```
# Add diversity indeces
df.diversity<-merge(df.diversity,df.elo.diversity[,c(2,3,4,7)],by.x="biome",by.y="MAP_biomes")

# Plot richness
plot.R<-df.diversity%>%
ggplot(aes(x=reorder(MAP_biomesFullName,-richness,median),richness))+
  geom_point(stat = "identity",shape=1,size=0.07,alpha=0.25,
             position = position_dodge2(0.5),aes(colour=Life.Style)) +
  geom_boxplot(outlier.shape = NA) +
  theme_bw() + theme(panel.grid.major = element_blank(),panel.grid.minor = element_blank()) +
  theme(text= element_text(size = 10),
        axis.text.x = element_blank(),
        legend.position = "none") +
  scale_colour_manual(values=c("blue2","red3"))+
```

```

  labs(y="Richness",x=NULL)

#Plot Shannon index
plot.H<-df.diversity%>%
ggplot(aes(x=reorder(MAP_biomesFullName,-richness,median),shannon))+
  geom_point(stat = "identity",shape=1,size=0.07,alpha=0.25,
             position = position_dodge2(0.5),aes(colour=Life.Style)) +
  geom_boxplot(outlier.shape = NA)+
  theme_bw() + theme(panel.grid.major = element_blank(),panel.grid.minor = element_blank())+
  theme(text= element_text(size = 10),
        axis.text.x = element_blank(),                      # render the <span> tags
        legend.position = "none")+
  scale_colour_manual(values=c("blue2","red3"))+
  labs(y="Shannon",x=NULL)

#Plot Pielou
plot.Pielou<-df.diversity%>%
ggplot(aes(x=reorder(MAP_biomesFullName,-richness,median),pielou))+
  geom_point(stat = "identity",shape=1,size=0.07,alpha=0.25,
             position = position_dodge2(0.5),aes(colour=Life.Style)) +
  geom_boxplot(outlier.shape = NA)+
  theme_bw() + theme(panel.grid.major = element_blank(),panel.grid.minor = element_blank())+
#  scale_x_discrete(labels = label_vec) +
  theme(text= element_text(size = 10),
        axis.text.x =element_blank(),                      # render the <span> tags
        legend.position = "none")+
  scale_colour_manual(values=c("blue2","red3"))+
  labs(y="Pielou",x=NULL)

#Plot gamma diversity (biome pool)
plot.gamma<-df.diversity%>%
ggplot(aes(x=reorder(MAP_biomesFullName,-richness,median),gamma.diversity))+
  stat_summary(fun = "mean",geom="point",shape=21,size=3,aes(fill=Life.Style)) +
  theme_bw() + theme(panel.grid.major = element_blank(),panel.grid.minor = element_blank())+
  scale_x_discrete(labels = label_vec) +
  theme(text= element_text(size = 10),
        axis.text.x = element_markdown(angle=60,hjust=1),      # render the <span> tag
        legend.position = "none")+
  scale_fill_manual(values=c("blue2","red3"))+
  scale_y_continuous(name="OTUs",
                     sec.axis = sec_axis(~./1247.72, name="% Total OTUs")) +
  labs(y="OTUs",x=NULL)

```

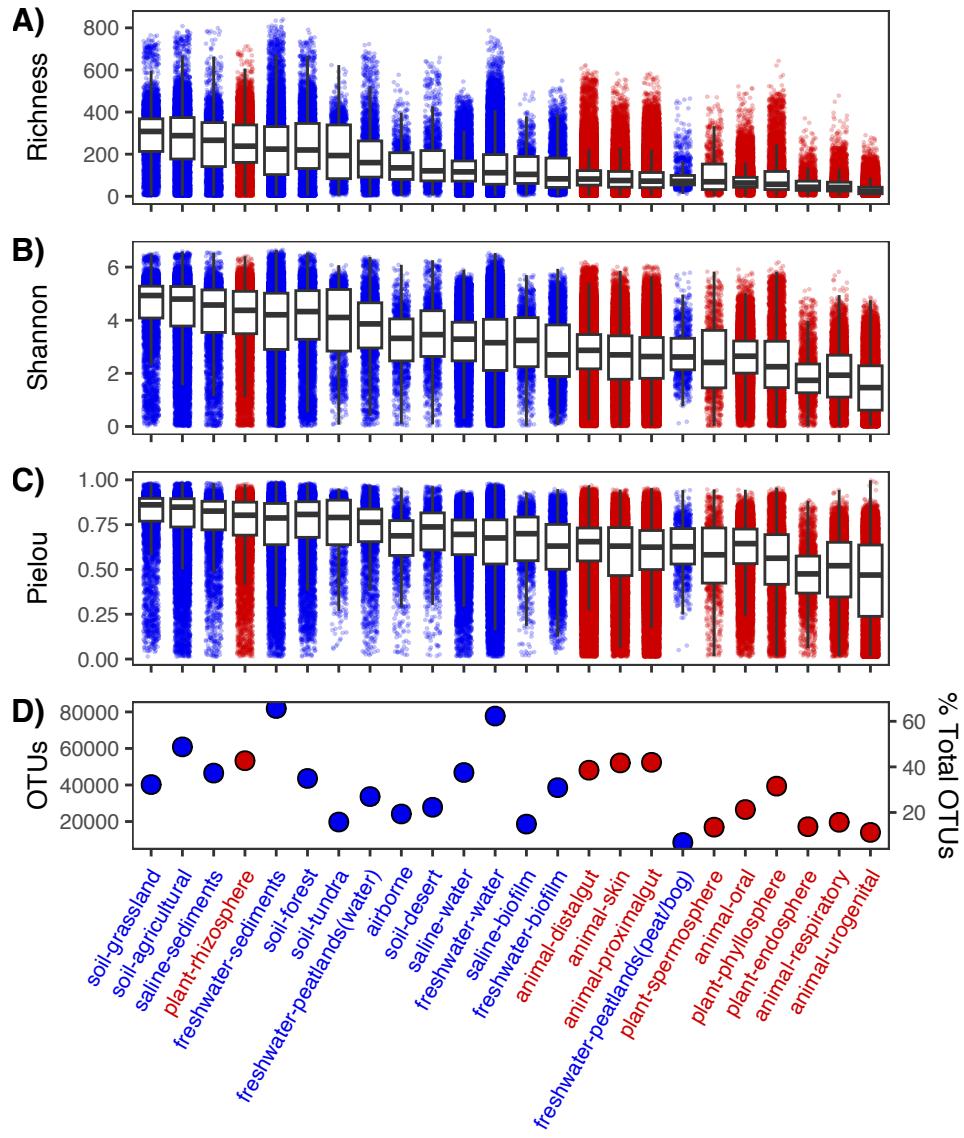
3.1 Diversity indeces Figure S2

Alpha- and gamma-diversity across biomes. (A) Sample-level richness (OTU count), (B) Shannon diversity, and (C) Pielou's evenness by biome. Boxplots show the median (center line) and the first and third quartiles (bottom and upper limits of boxes); whiskers span the 10th and 90th percentiles. Overlaid points represent the individual samples. (D) gamma-diversity (total OTUs observed across all samples within each biome); each point represents one biome.

```

## cairo_pdf
##          2

```



4 Summarize BB-score adata and diversity indices

5 Biome-level BB-score and diversity indices (Figure 3)

Baas Becking score (BB-score) across biomes and relationship with diversity metrics. (A) Distribution of BB-scores across soil, freshwater, saline, plant-associated, and animal-associated biomes (blue: free-living; red: host-associated). Correlations between mean BB-scores and community diversity metrics: species richness (B), Shannon index (C), Pielou's evenness (D), Simpson index (E), and gamma-diversity (F). Each point represents a biome mean; black lines show sign of correlation with Spearman's correlation coefficient and significance levels.

