

Environmental filtering and habitat (mis)matching of riverine invertebrate communities

NRSA DisEQ-Figures

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```
## Load the tidyverse
library(tidyverse)
library(reshape2)

## Load vegan for the ordination
library(vegan)

## Packages for figures
library(ggpubr)
library(grid)
library(gridExtra)
library(scales)
library(viridis)
library(viridisLite)

## Packages for the site map
library(ggspn)
library(mapdata)
library(rgdal)
```

```

## Load the reduced workspace
load("data_analysis/2-DisEQ_analyses/2-DisEQ_analyses-Reduced_Workspace.RData")

## Reorder trait variables for plotting
trait.axis.limits <- c(
  "dispersal.low", "dispersal.high",
  "flying.strength.none", "flying.strength.weak", "flying.strength.strong",
  "size.small", "size.medium", "size.large",
  "depositional", "depositional.erosional", "erosional",
  "cold", "cool.warm", "warm",
  "sensitive", "medium", "tolerant",
  "CG", "CF", "HB", "PR"
)
)

## Rename trait variables for plotting
trait.axis.labels <- c(
  "dispersal.low" = "Low Dispersal", "dispersal.high" = "High Dispersal",
  "flying.strength.none" = "Nonflyer", "flying.strength.weak" = "Weak Flyer",
  "flying.strength.strong" = "Strong Flyer",
  "size.small" = "Small Size", "size.medium" = "Medium Size", "size.large" = "Large Size",
  "depositional" = "Depositional", "depositional.erosional" = "Depo-Eros", "erosional" = "Erosional",
  "cold" = "Cold", "cool.warm" = "Cool-Warm", "warm" = "Warm",
  "sensitive" = "Sensitive", "medium" = "Intermediate", "tolerant" = "Tolerant",
  "CG" = "CG", "CF" = "CF", "HB" = "HB", "PR" = "PR"
)

```

Site Map

```
## Figure was created by evaluating the supplementary R code and data
## provided by King et al. 2019 (Ecological Applications), deposited by
## Katelyn King on Zenodo at:

# https://zenodo.org/record/3246537#.XgDUKRdKhSw

## Set base projection and site locations
usa <- map_data("usa") # pull out the USA map
base.map <- ggplot(data = usa) +
  geom_polygon(aes(x = long, y = lat, group = group),
               fill = "white", color = "black") +
  coord_fixed(1.3)
points <- select(final.data, site.long, site.lat, ecoregion)

## Add points to the US map
site.map <- base.map +
  geom_point(data = points, size = 2,
             aes(x = site.long, y = site.lat, colour = ecoregion, shape = ecoregion)) +
  scale_colour_manual(values = viridis(n = 9), name = "Ecoregion") +
  scale_shape_manual(values = c(0:8), name = "Ecoregion") +
  north(data = usa, symbol = 3, scale = 0.1, location = "bottomright",
        anchor = c(x = -120, y = 27)) +
  ggsn::scalebar(data = usa, dist = 500, dist_unit = "km", transform = TRUE, model = "WGS84",
                 st.size = 2, location = "bottomleft") +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line.x = element_blank(),
        axis.title.x = element_blank(),
        axis.ticks.x = element_blank(),
        axis.text.x = element_blank(),
        axis.line.y = element_blank(),
        axis.title.y = element_blank(),
        axis.ticks.y = element_blank(),
        axis.text.y = element_blank(),
        panel.background = element_blank()) +
  theme(legend.position = c(0.88, 0.20), legend.text = element_text(size = 9)) +
  theme(legend.text = element_text(size = 9))
```

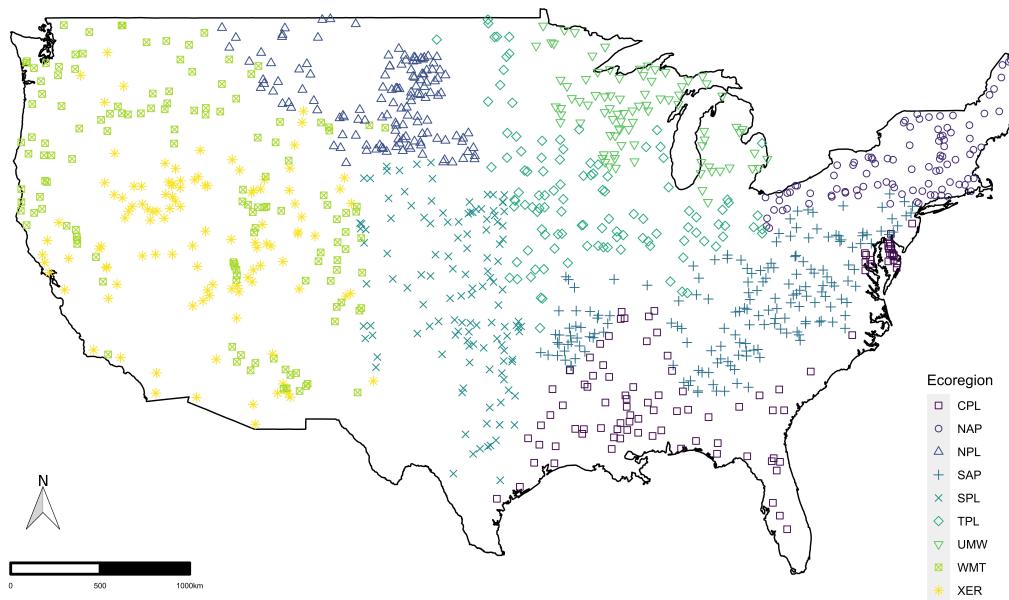


Figure 1: Map of all 1078 sites included in the study.

Filtering & Niche Mismatch ANOVAs

```
## Filtering and niche mismatch data management for plotting
DisEQ.data.wide <- final.DisEQ.data %>%
  select(UID, ecoregion, filtering.scaled, mismatch.scaled)

DisEQ.data.long <- DisEQ.data.wide %>%
  gather(DisEQ.metric, measurement, filtering.scaled:mismatch.scaled, factor_key = TRUE) %>%
  na.omit

DisEQ.figure <- ggerrorplot(
  data = DisEQ.data.long,
  x = "ecoregion",
  y = "measurement",
  size = 1.25,
  width = 1.5,
  desc_stat = "mean",
  color = "ecoregion",
  xlab = "Ecoregion",
  ylab = "Measurement",
  title = "DisEQ by Ecoregion",
  palette = viridis(n = 9),
  add = "boxplot",
  ggtheme = theme_pubr(),
  legend = "right"
) %>%
  facet(
    facet.by = "DisEQ.metric",
    nrow = 2,
    ncol = 1,
    scales = "free_y"
  ) +
  scale_x_discrete(limits = c("WMT", "XER", "NPL", "SPL", "TPL", "UMW", "NAP", "SAP", "CPL")) +
  geom_hline(yintercept = 0, linetype = 3, size = 1, colour = "gray20") +
  font("xlab", size = 16, color = "gray0") +
  font("ylab", size = 16, color = "gray0") +
  font("xy.text", size = 12, color = "gray20")
```

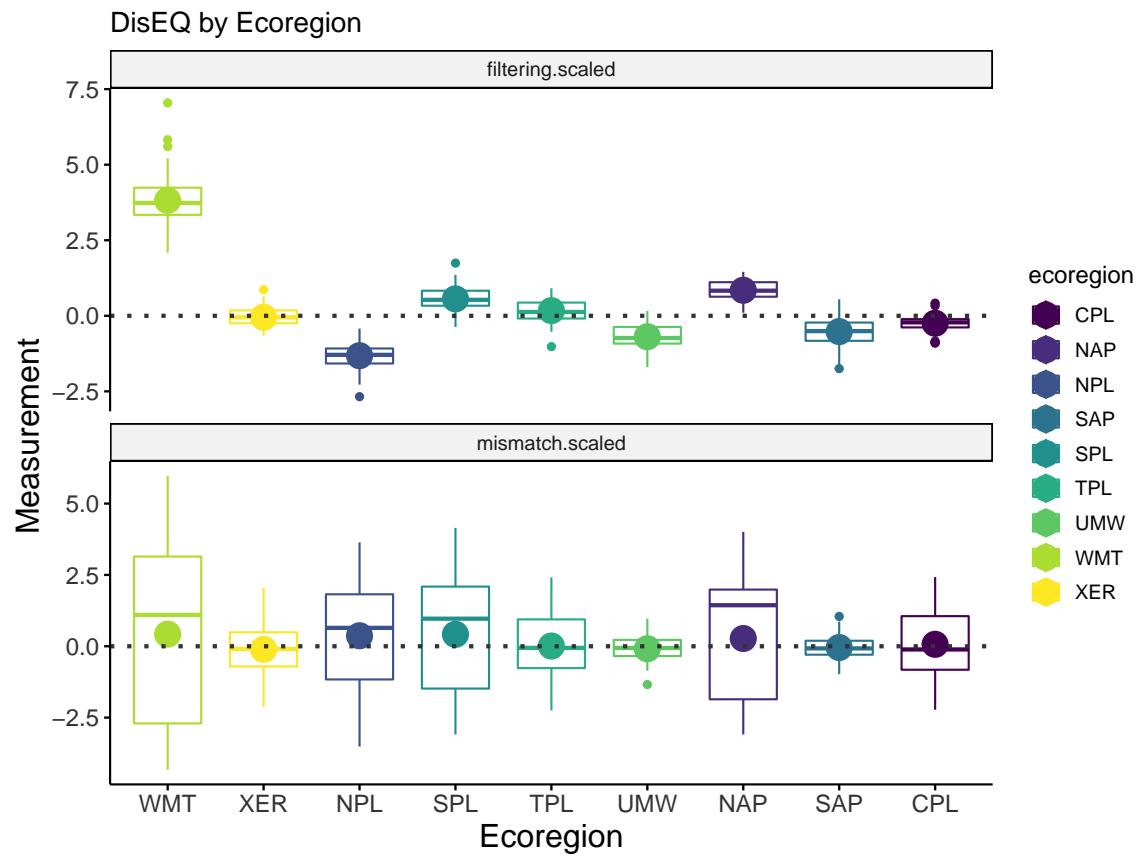


Figure 2: Plots of environmental filtering and niche mismatch by ecoregion.

Habitat Matching & Mismatch Vector Component ANOVAs

```
## Vector component data management for plotting
vector.component.wide <- final.DisEQ.data %>%
  select(UID, ecoregion, Tmax.direction, Tmin.direction, pH.direction, cond.direction)

vector.component.long <- vector.component.wide %>%
  gather(vector.component, measurement, Tmax.direction:cond.direction, factor_key = TRUE) %>%
  na.omit

vector.component.figure <- ggerrorplot(
  data = vector.component.long,
  x = "ecoregion",
  y = "measurement",
  size = 1.25,
  width = 1.5,
  desc_stat = "mean",
  color = "ecoregion",
  xlab = "Ecoregion",
  ylab = "Measurement",
  title = "Vector Component",
  palette = viridis(n = 9),
  add = "boxplot",
  ggtheme = theme_pubr(),
  legend = "right"
) %>%
  facet(
    facet.by = "vector.component",
    nrow = 2,
    ncol = 2,
    scales = "free_y"
  ) +
  scale_x_discrete(limits = c("WMT", "XER", "NPL", "SPL", "TPL", "UMW", "NAP", "SAP", "CPL")) +
  font("xlab", size = 16, color = "gray0") +
  font("ylab", size = 16, color = "gray0") +
  font("xy.text", size = 12, color = "gray20")
```

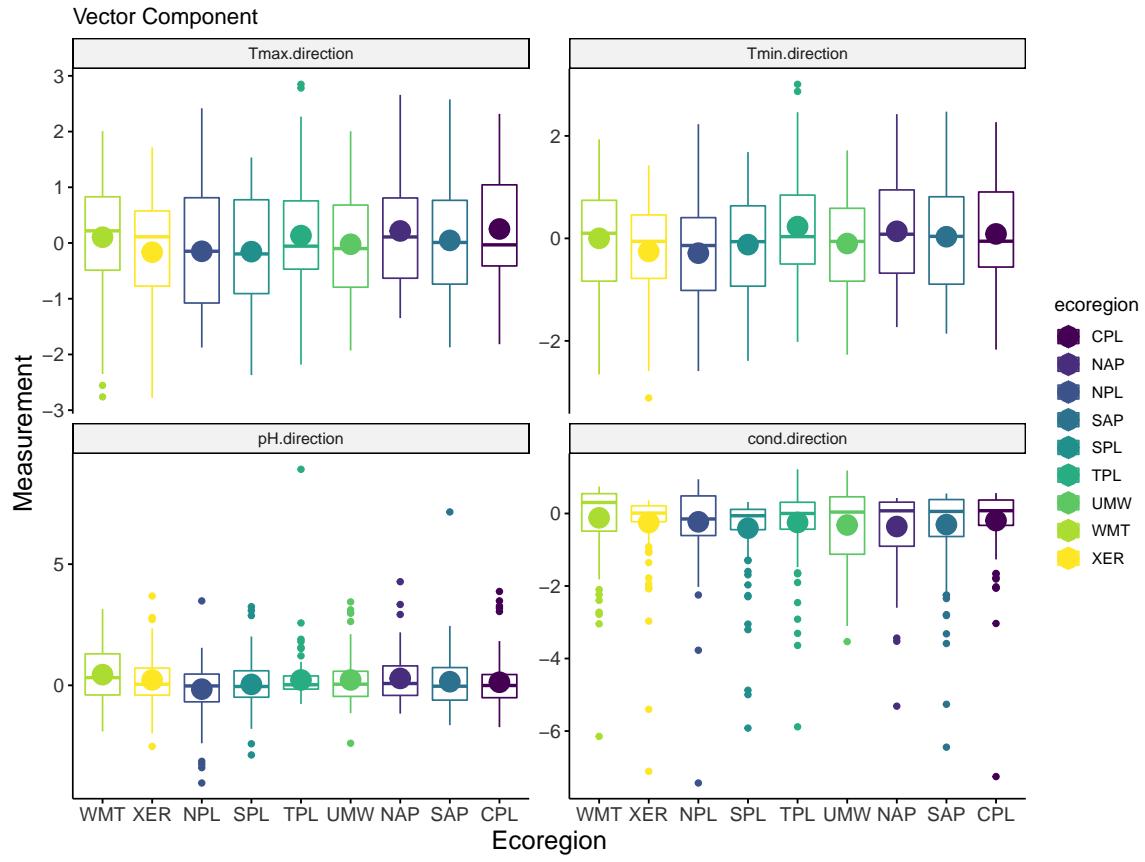


Figure 3: Plots of vector components of habitat matching and mismatch.

Functional Trait Diversity ANOVAs

```
## Trait diversity data management for plotting
trait.diversity.wide <- final.DiseQ.data %>%
  select(UID, ecoregion, FRic, FEve, FDiv, FDis)

trait.diversity.long <- trait.diversity.wide %>%
  gather(diversity.measure, measurement, FRic:FDis, factor_key = TRUE) %>%
  na.omit

trait.diversity.figure <- ggerrorplot(
  data = trait.diversity.long,
  x = "ecoregion",
  y = "measurement",
  size = 1.25,
  width = 1.5,
  desc_stat = "mean",
  color = "ecoregion",
  xlab = "Ecoregion",
  ylab = "Measurement",
  title = "Trait Diversity",
  palette = viridis(n = 9),
  add = "boxplot",
  ggtheme = theme_pubr(),
  legend = "right"
) %>%
  facet(
    facet.by = "diversity.measure",
    nrow = 2,
    ncol = 2,
    scales = "free_y"
  ) +
  scale_x_discrete(limits = c("WMT", "XER", "NPL", "SPL", "TPL", "UMW", "NAP", "SAP", "CPL")) +
  font("xlab", size = 16, color = "gray0") +
  font("ylab", size = 16, color = "gray0") +
  font("xy.text", size = 12, color = "gray20")
```

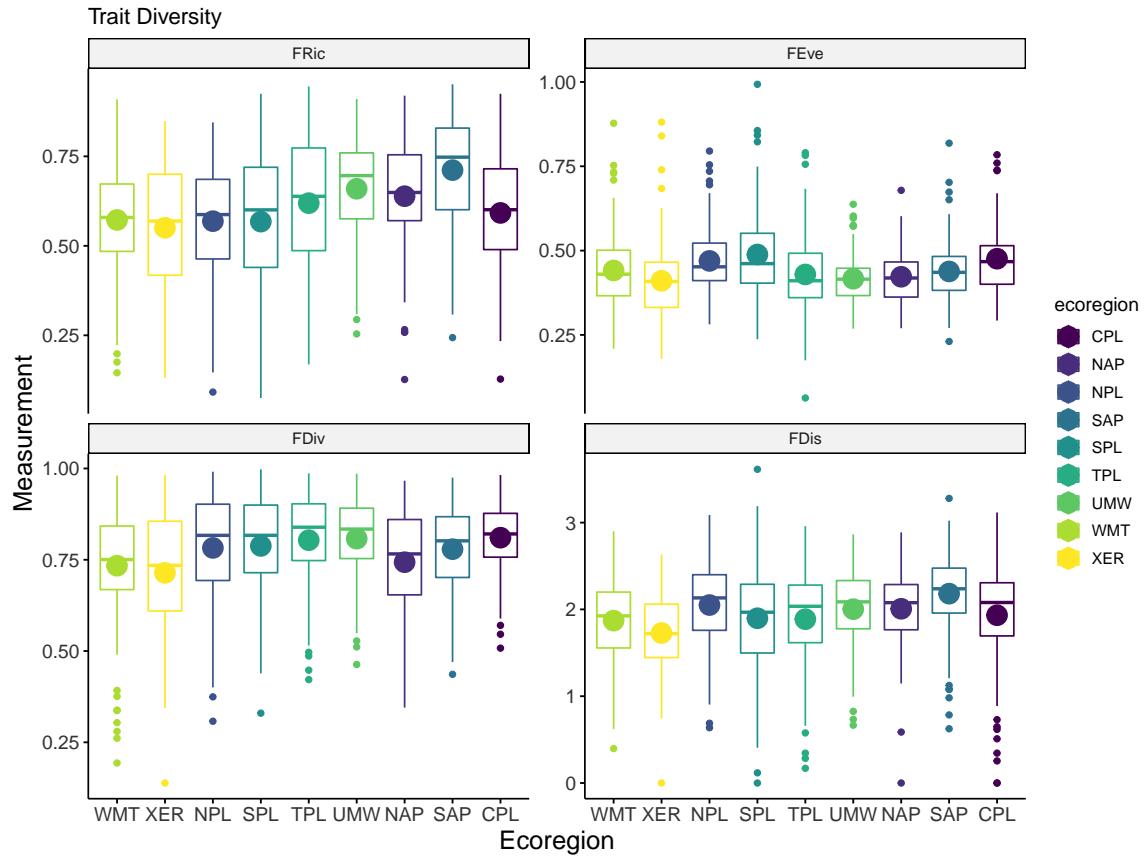


Figure 4: Plots of FRic, FEve, FDiv, and FDis by ecoregion.

DisEQ-by-Traits

Filtering-by-Traits Figure

```
## Re-order ecoregion for facet plots
filtering.by.trait.BRT.results$ecoregion <- factor(
  filtering.by.trait.BRT.results$ecoregion,
  levels = c("WMT", "UMW", "NAP", "XER", "NPL", "SAP", "SPL", "TPL", "CPL")
)

filtering.by.traits.figure <- ggbarplot(
  data = filtering.by.trait.BRT.results,
  x = "var",
  y = "rel.inf",
  fill = "predictor.type",
  xlab = "Trait",
  ylab = "Relative Influence",
  title = "Filtering by Traits",
  facet.by = "ecoregion",
  palette = plasma(n = 3),
  ggtheme = theme_pubr(),
  legend = "right"
) +
  scale_x_discrete(
    limits = trait.axis.limits,
    labels = trait.axis.labels
  ) +
  scale_y_continuous(breaks = c(0, 5, 10), limits = c(0, 11.25)) +
  rotate_x_text(angle = 90) +
  font("xlab", size = 16, color = "gray0") +
  font("ylab", size = 16, color = "gray0") +
  font("xy.text", size = 12, color = "gray20")
```

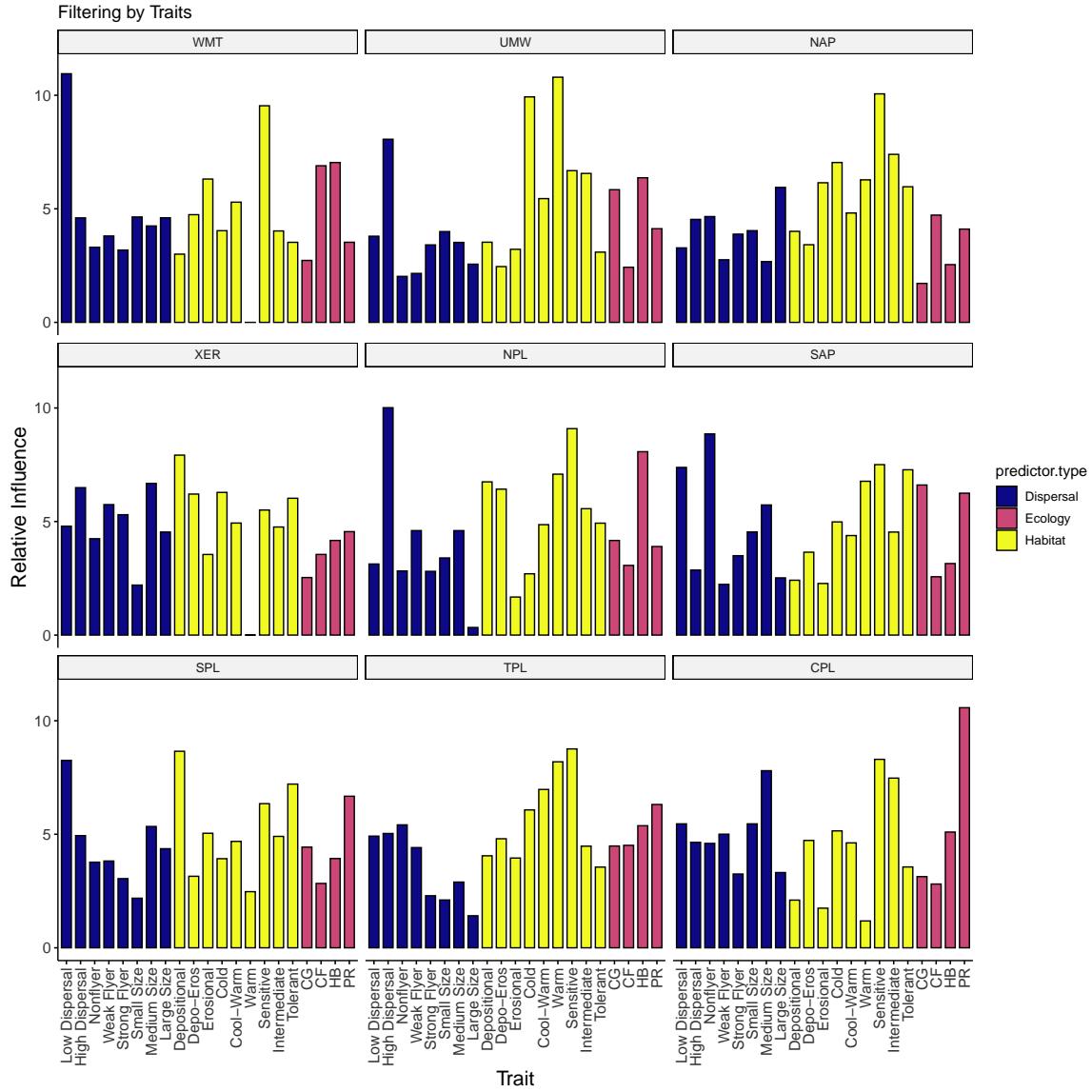


Figure 5: Plots of relative influence for each of 21 traits across ecoregions

Mismatch-by-Traits Figure

```
## Re-order ecoregion for facet plots
mismatch.by.trait.BRT.results$ecoregion <- factor(
  mismatch.by.trait.BRT.results$ecoregion,
  levels = c("WMT", "UMW", "NAP", "XER", "NPL", "SAP", "SPL", "TPL", "CPL")
)

mismatch.by.traits.figure <- ggbarplot(
  data = mismatch.by.trait.BRT.results,
  x = "var",
  y = "rel.inf",
  fill = "predictor.type",
  xlab = "Trait",
  ylab = "Relative Influence",
  title = "Habitat Matching by Traits",
  facet.by = "ecoregion",
  palette = plasma(n = 3),
  ggtheme = theme_pubr(),
  legend = "right"
) +
  scale_x_discrete(
    limits = trait.axis.limits,
    labels = trait.axis.labels) +
  rotate_x_text(angle = 90) +
  font("xlab", size = 16, color = "gray0") +
  font("ylab", size = 16, color = "gray0") +
  font("xy.text", size = 12, color = "gray20")
```

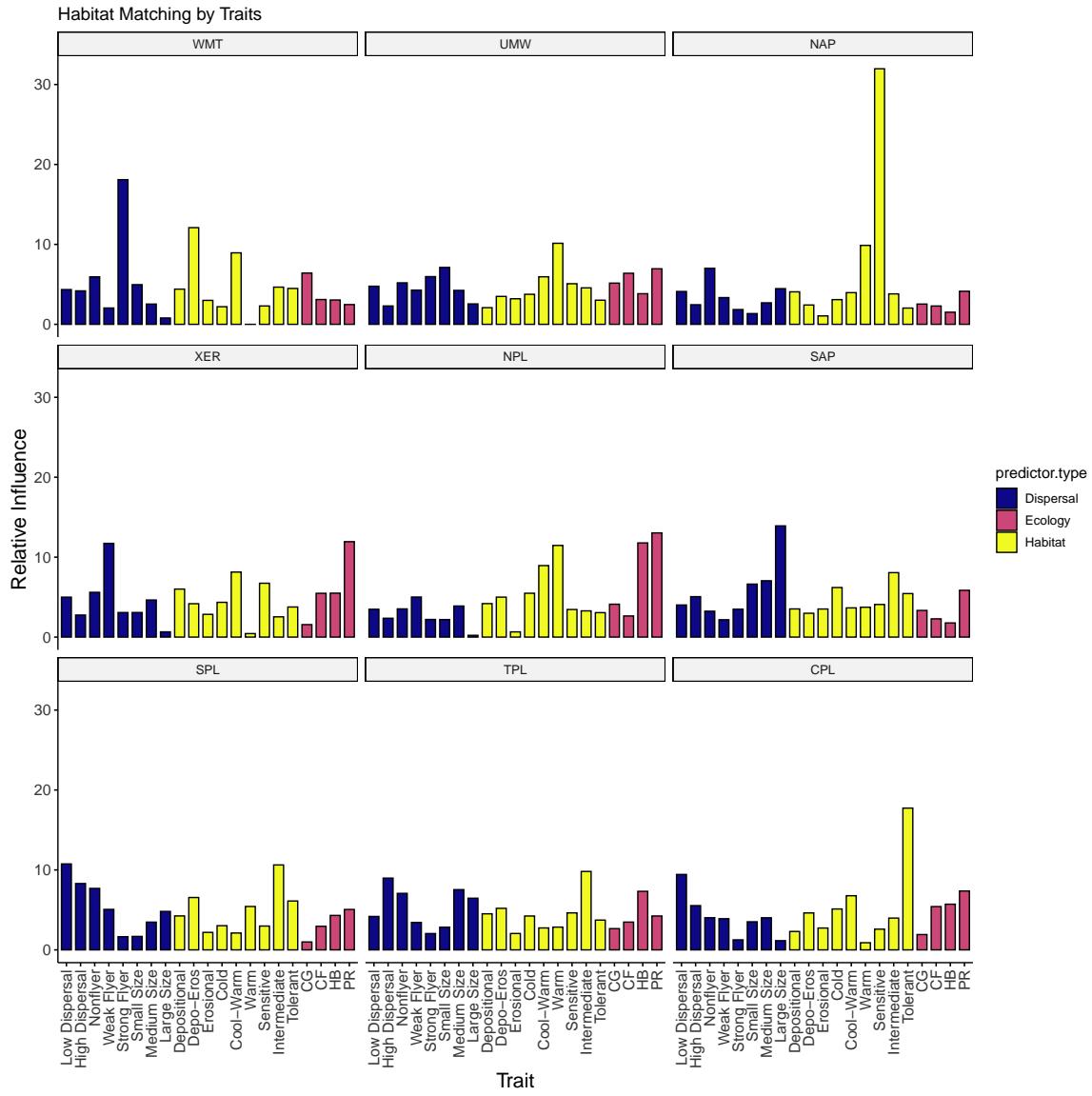


Figure 6: Plots of relative influence by dispersal, ecology, and habitat traits for each of 21 traits across all 9 ecoregions

Traits-by-Environment

```
## Bind all BRT results into a long dataframe for plotting
trait.by.environment.long.bin.1 <- bind_rows(
  low.dispersal.environment.BRT.results, high.dispersal.environment.BRT.results,
  nonflyer.environment.BRT.results, weak.flyer.environment.BRT.results,
  strong.flyer.environment.BRT.results, small.size.environment.BRT.results,
  medium.size.environment.BRT.results, large.size.environment.BRT.results,
  depositional.environment.BRT.results, depositional.erosional.environment.BRT.results,
  erosional.environment.BRT.results, cold.water.environment.BRT.results,
  cool.warm.water.environment.BRT.results, warm.water.environment.BRT.results,
  sensitive.tolerance.environment.BRT.results, intermediate.tolerance.environment.BRT.results,
  tolerant.environment.BRT.results, CG.environment.BRT.results,
  CF.environment.BRT.results, HB.environment.BRT.results, PR.environment.BRT.results
)

## Add trait vector to the dataframe
trait.by.environment.long.bin.1$trait <- rep(
  c("Low Dispersal", "High Dispersal",
    "Nonflyer", "Weak Flyer", "Strong Flyer",
    "Small Size", "Medium Size", "Large Size",
    "Depositional", "Depo-Eros", "Erosional",
    "Cold", "Cool-Warm", "Warm",
    "Sensitive", "Intermediate", "Tolerant",
    "CG", "CF", "HB", "PR"),
  each = 162)

## Sum relative influence by predictor type and ecoregion for each trait
trait.by.environment.long <- aggregate(
  rel.inf ~ trait + ecoregion + predictor.type,
  data = trait.by.environment.long.bin.1,
  FUN = sum
)

## Re-order ecoregion for facet plots
trait.by.environment.long$ecoregion <- factor(
  trait.by.environment.long$ecoregion,
  levels = c("WMT", "UMW", "NAP", "XER", "NPL", "SAP", "SPL", "TPL", "CPL")
)

traits.by.environment.figure <- ggbarplot(
  data = trait.by.environment.long,
  x = "trait",
  y = "rel.inf",
  fill = "predictor.type",
  color = "predictor.type",
  xlab = "Trait",
  ylab = "Relative Influence",
  title = "Traits by Environment",
  facet.by = "ecoregion",
  palette = viridis(n = 3),
  ggtheme = theme_pubr(),
  legend = "right"
) +
```

```

scale_x_discrete(
  limits = c(
    "Low Dispersal", "High Dispersal", "Nonflyer", "Weak Flyer", "Strong Flyer",
    "Small Size", "Medium Size", "Large Size", "Depositional", "Depo-Eros", "Erosional",
    "Cold", "Cool-Warm", "Warm", "Sensitive", "Intermediate", "Tolerant",
    "CG", "CF", "HB", "PR"),
  labels = c(
    "Low Dispersal", "High Dispersal", "Nonflyer", "Weak Flyer", "Strong Flyer",
    "Small Size", "Medium Size", "Large Size", "Depositional", "Depo-Eros", "Erosional",
    "Cold", "Cool-Warm", "Warm", "Sensitive", "Intermediate", "Tolerant",
    "CG", "CF", "HB", "PR")
) +
rotate_x_text(angle = 90) +
font("xlab", size = 16, color = "gray0") +
font("ylab", size = 16, color = "gray0") +
font("xy.text", size = 12, color = "gray20")

```

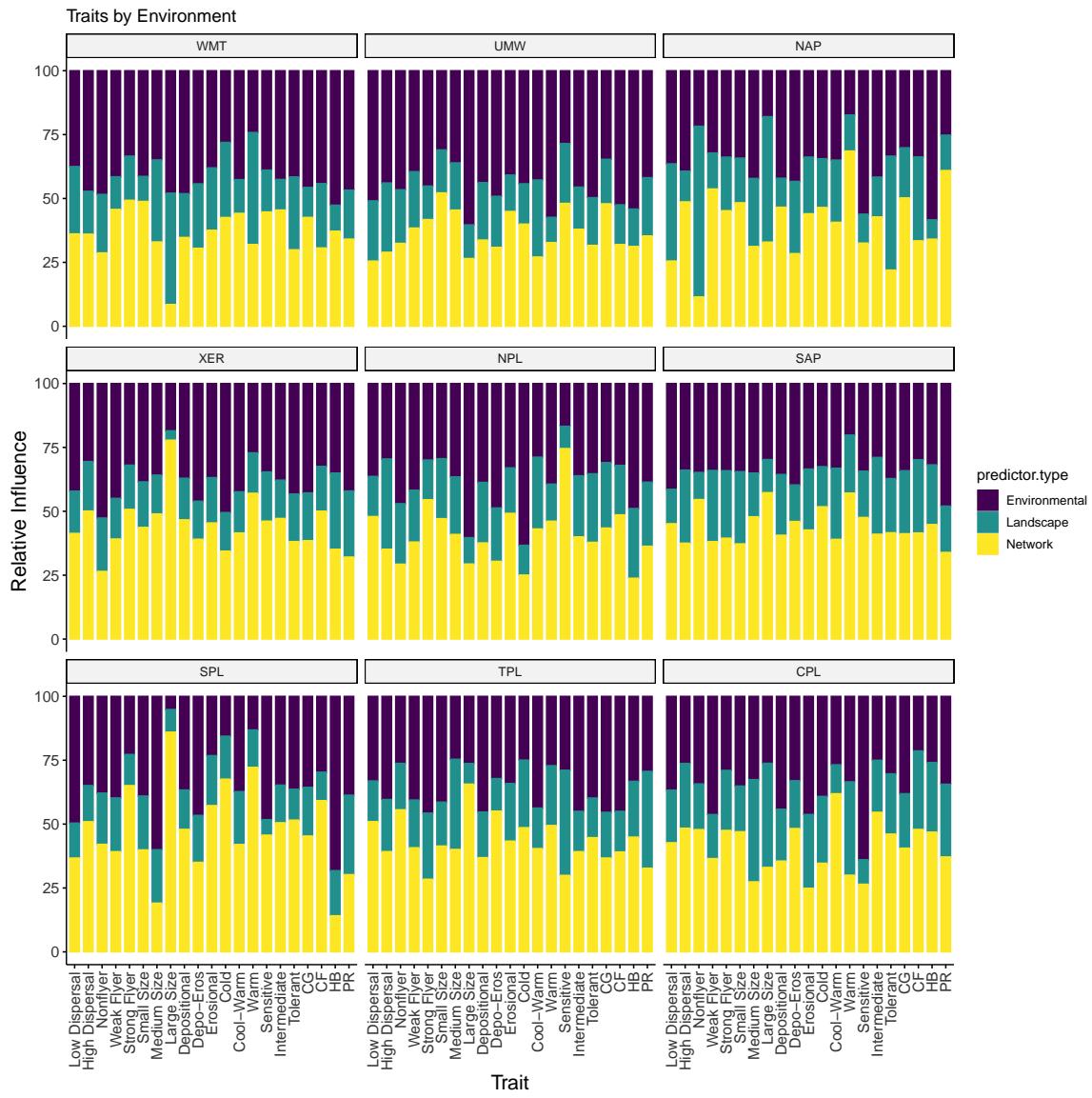


Figure 7: Plots of relative influence by environmental, landscape, and network predictors for each of 21 traits across all 9 ecoregions

DisEQ & Functional Diversity ANCOVAs

```
## DisEQ and trait diversity data management
# Wide format
DisEQ.trait.diversity.wide <- final.DisEQ.data %>%
  select(filtering.scaled, mismatch.scaled, ecoregion, FRic, FEve, FDiv, FDis)

# Switch from wide to long
DisEQ.trait.diversity.long <- DisEQ.trait.diversity.wide %>%
  gather(trait.metric, measurement, FRic:FDis, factor_key = TRUE) %>%
  na.omit
```

Filtering by Functional Diversity

```
filtering.by.trait.diversity.figure <- ggscatter(
  data = DisEQ.trait.diversity.long,
  x = "measurement",
  y = "filtering.scaled",
  size = 1,
  color = "ecoregion",
  xlab = "Trait Diversity",
  ylab = "Environmental Filtering",
  title = "Environmental Filtering by Functional Diversity",
  palette = viridis(n = 9),
  ggtheme = theme_pubr(),
  legend = "right",
  add = "reg.line",
  conf.int = TRUE
) %>%
  facet(
    facet.by = "trait.metric",
    nrow = 2,
    ncol = 2,
    scales = "free"
  ) +
  font("xlab", size = 16, color = "gray0") +
  font("ylab", size = 16, color = "gray0") +
  font("xy.text", size = 12, color = "gray20") +
  geom_hline(yintercept = 0, linetype = 3, size = 1, colour = "gray40")
```

Habitat Matching by Functional Diversity

```
mismatch.by.trait.diversity.figure <- ggscatter(  
  data = DisEQ.trait.diversity.long,  
  x = "measurement",  
  y = "mismatch.scaled",  
  size = 1,  
  color = "ecoregion",  
  xlab = "Trait Diversity",  
  ylab = "Habitat Matching",  
  title = "Habitat Matching by Functional Diversity",  
  palette = viridis(n = 9),  
  ggtheme = theme_pubr(),  
  legend = "right",  
  add = "reg.line",  
  conf.int = TRUE  
) %>%  
  facet(  
    facet.by = "trait.metric",  
    nrow = 2,  
    ncol = 2,  
    scales = "free"  
) +  
  font("xlab", size = 16, color = "gray0") +  
  font("ylab", size = 16, color = "gray0") +  
  font("xy.text", size = 12, color = "gray20") +  
  geom_hline(yintercept = 0, linetype = 3, size = 1, colour = "gray40")
```

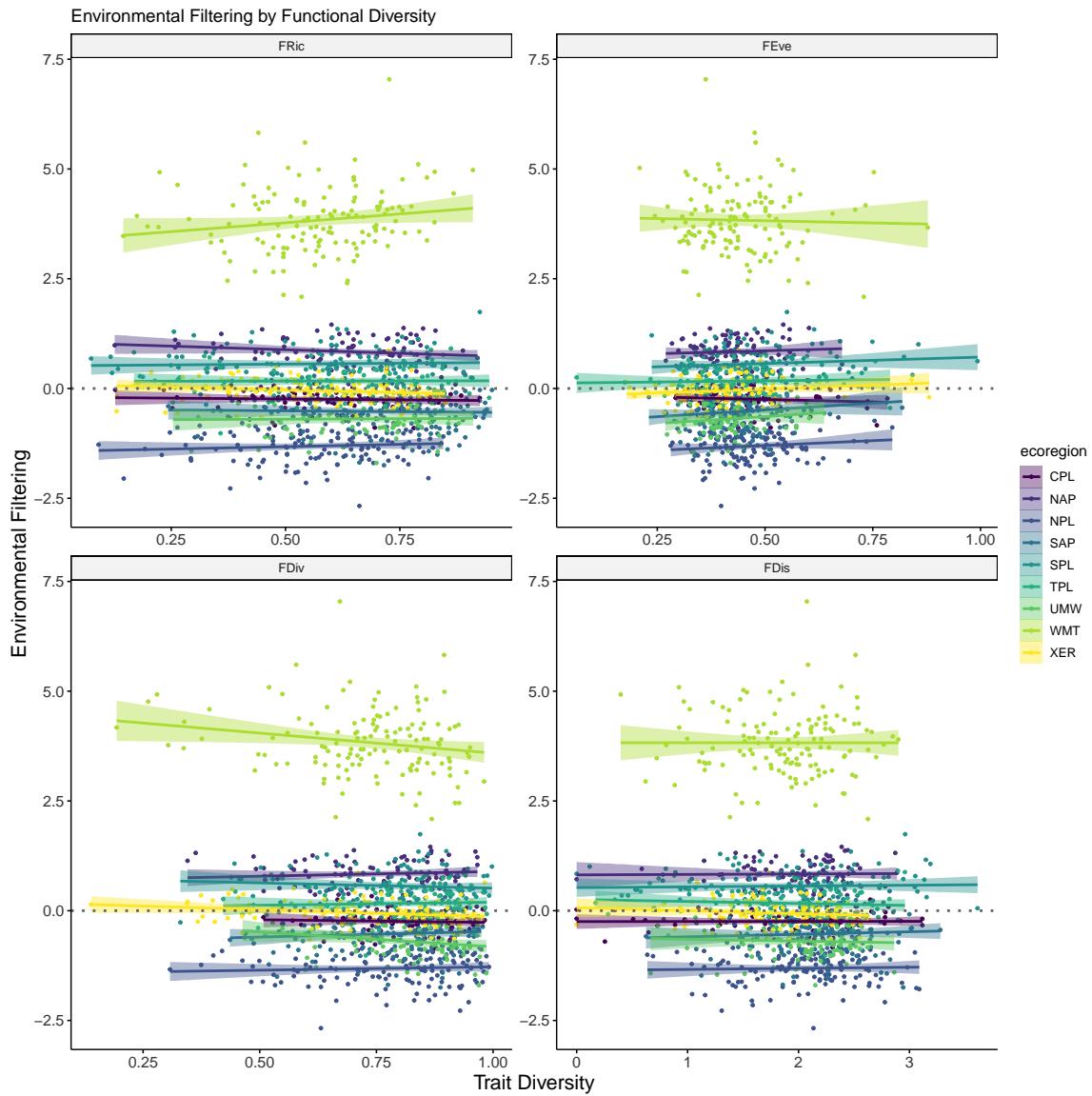


Figure 8: Plots of environmental filtering against measures of functional trait diversity.

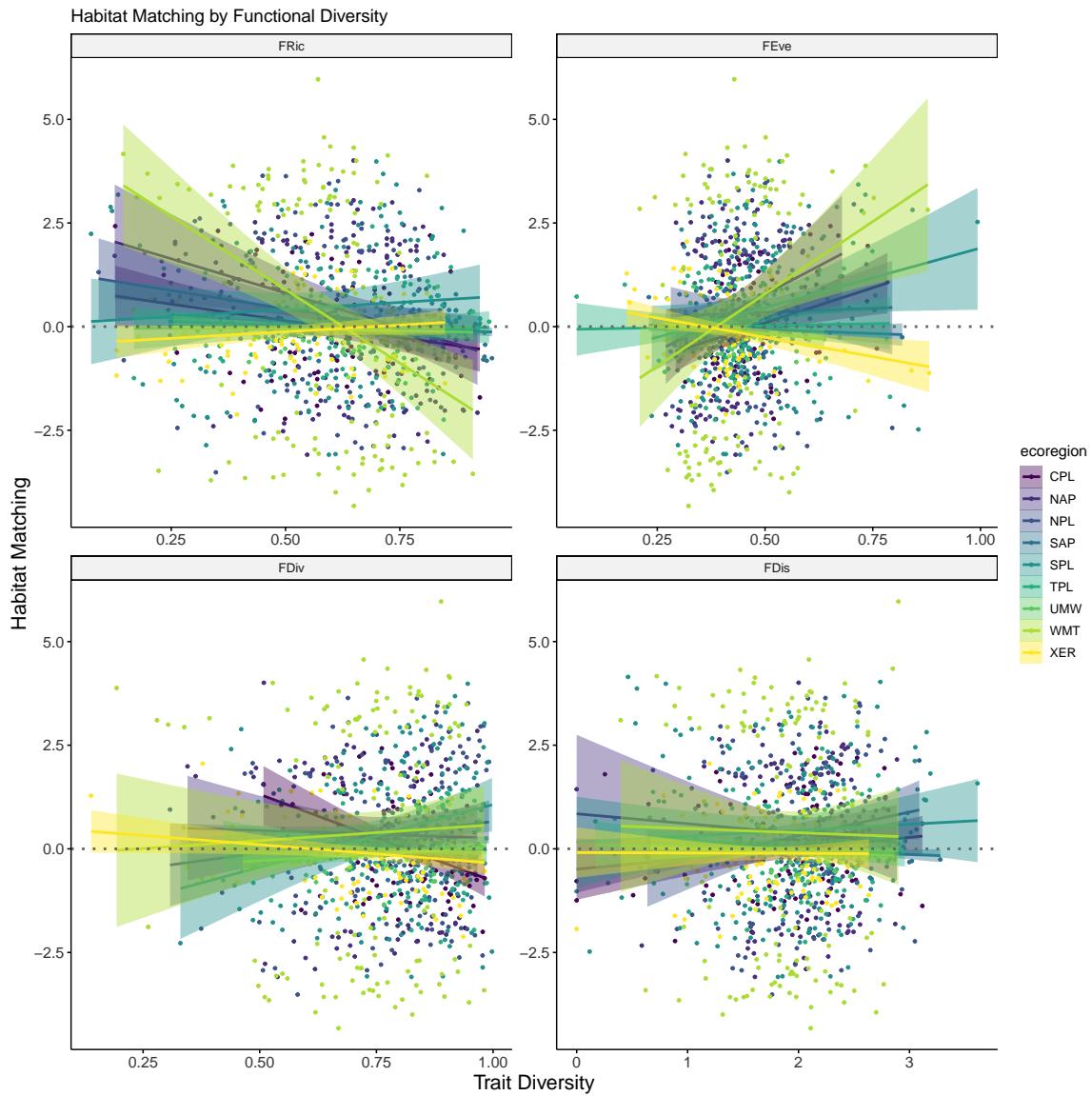


Figure 9: Plots of habitat matching against measures of functional trait diversity.

Environmental Filtering & Habitat Matching Model

```
DisEQ.LMM.figure <- ggscatter(  
  data = final.DisEQ.data,  
  x = "mismatch.scaled",  
  y = "filtering.scaled",  
  size = 1,  
  color = "ecoregion",  
  xlab = "Habitat Matching",  
  ylab = "Environmental Filtering",  
  palette = viridis(n = 9),  
  ggtheme = theme_pubr(),  
  legend = "right",  
  add = "reg.line",  
  conf.int = TRUE  
) +  
  geom_hline(yintercept = 0, linetype = 3, size = 1, colour = "gray40") +  
  geom_vline(xintercept = 0, linetype = 3, size = 1, colour = "gray40")
```

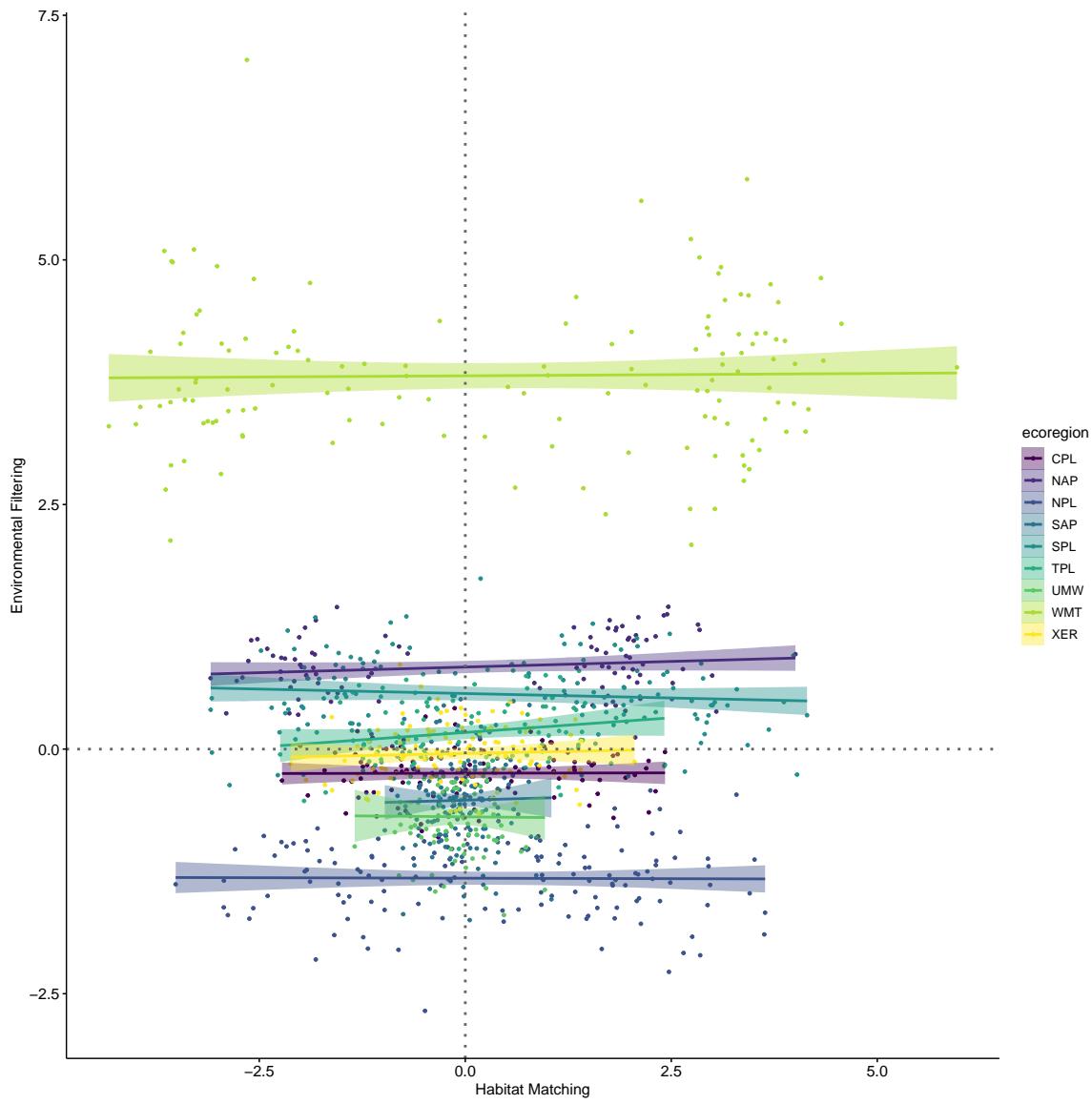


Figure 10: Plot of environmental filtering against habitat matching while controlling for the effect of ecoregion.

Community Composition

```
## Make panel figure
par(mfrow = c(1, 1), mar = c(5, 5, 5, 5))

## Create identifier
NMDS.groups <- final.data[rowSums(final.data[, 67:142]) > 0, 25]

## Set figure dimensions
pdf("figures/Figure_S5A-community_composition-base.pdf", width = 8, height = 6)

## NMDS plot (axes 1 and 2)
axes.1_2 <- ordiplot(BC.NMDS, choices = c(1, 2), type = "none", display = "sites",
                      xlim = c(-1.5, 1.5), ylim = c(-1.5, 1.5), xlab = "NMDS 1", ylab =
ordielipse(BC.NMDS, groups = NMDS.groups,
           draw = "lines", col = viridis(n = 9), label = FALSE, lwd = 5)
mtext(text = "Stress = 0.199", side = 3, line = -1.5, adj = 0.95,
      cex = 1.05)
mtext(text = "(A)", side = 3, line = 1.75, adj = 0.05, cex = 1.25)
legend(1.75, 0.45, c("CPL", "NAP", "NPL", "SAP", "SPL", "TPL", "UMW", "WMT", "XER"),
       cex = 0.75, lty = 1, lwd = 4, x.intersp = 0.95, y.intersp = 0.95,
       col = viridis(n = 9))
## Export the figure
dev.off()

## Set figure dimensions
pdf("figures/Figure_S5B-community_composition-base.pdf", width = 8, height = 6)

## NMDS plot (axes 1 and 3)
axes.1_3 <- ordiplot(BC.NMDS, choices = c(1, 3), type = "none", display = "sites",
                      xlim = c(-1.5, 1.5), ylim = c(-1.5, 1.5), xlab = "NMDS 1", ylab =
ordielipse(axes.1_3, groups = NMDS.groups,
           draw = "lines", col = viridis(n = 9), label = FALSE, lwd = 5)
mtext(text = "(B)", side = 3, line = 1.75, adj = 0.025, cex = 1.25)

## Export the figure
dev.off()
```

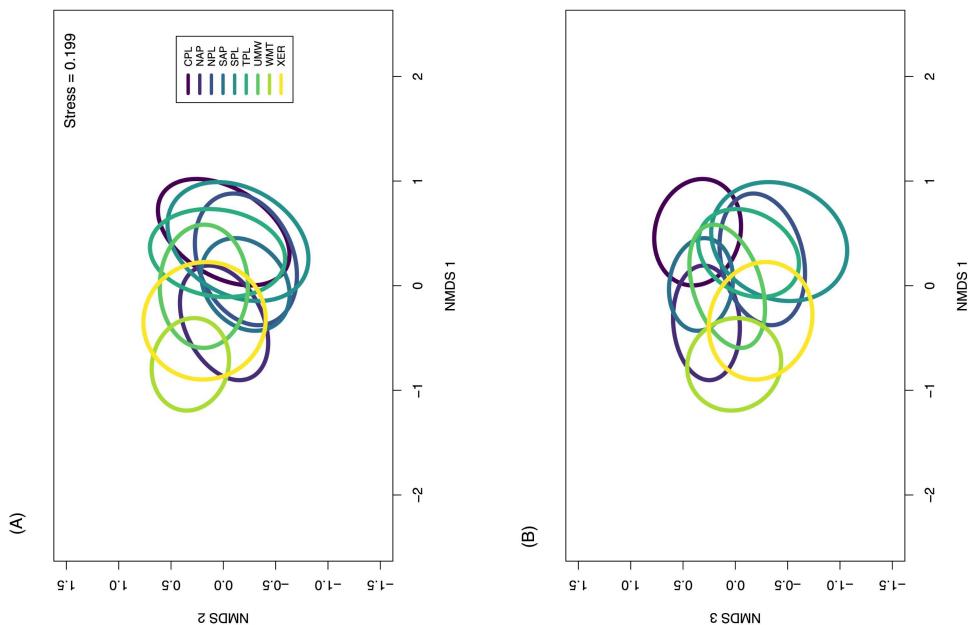


Figure 11: Plot of community composition by ecoregion.

R Session Information

Table 1: Packages required for data management and figure creation.

Package	Loaded	Version	Date
dplyr		1.0.8	2022-02-08
forcats		0.5.1	2021-01-27
ggplot2		3.3.5	2021-06-25
ggpubr		0.4.0	2020-06-27
ggsn		0.5.0	2019-02-18
gridExtra		2.3	2017-09-09
kableExtra		1.3.4	2021-02-20
knitr		1.38	2022-03-25
lattice		0.20-45	2021-09-22
mapdata		2.3.0	2018-03-30
maps		3.4.0	2021-09-25
permute		0.9-7	2022-01-27
purrr		0.3.4	2020-04-17
readr		2.1.2	2022-01-30
reshape2		1.4.4	2020-04-09
rgdal		1.5-28	2021-12-15
scales		1.1.1	2020-05-11
sp		1.4-6	2021-11-14
stringr		1.4.0	2019-02-10
tibble		3.1.6	2021-11-07
tidyverse		1.2.0	2022-02-01
tidyverse		1.3.1	2021-04-15
vegan		2.5-7	2020-11-28
viridis		0.6.2	2021-10-13
viridisLite		0.4.0	2021-04-13