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

NRSA DisEQ-Figures

Contents

```r
## 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"
    )

## Ecoregion labels (remove acronyms)
ecoregion.labels <- c(
    "CPL" = "Coastal Plain", "NAP" = "Northern Appalachians", "NPL" = "Northern Plains",
    "SAP" = "Southern Appalachians", "SPL" = "Southern Plains", "TPL" = "Temperate Plains",
    "UMW" = "Upper Midwest", "WMT" = "Western Mountains", "XER" = "Xeric"
    )
```

```r
## Ecoregion----------------------------------------------------------------#
## Set colour palette (viridis)
viridis.continuous <- viridis(n = 9)

# View the colour palette
#show_col(viridis.continuous)

# Set the ecoregion palette
viridis.ecoregion <- viridis.continuous[c(9, 7, 3, 8, 4, 5, 6, 1, 2)]

# Alphabetical --> Geographical
# CPL (1-9), NAP (2-7), NPL (3-3), SAP (4-8), SPL (5-4), TPL (6-5), UMW (7-6), WMT (8-1), XER (9-2)

# Reordered
# WMT, XER, NPL, SPL, TPL, UMW, NAP, SAP, CPL


## Functional Traits--------------------------------------------------------#
## Set colour palette (magma)
magma.continuous <- magma(n = 16)

# View the colour palette
#show_col(magma.continuous)

# Set the functional traits palette
magma.functional.traits <- magma.continuous[c(3, 8, 13)]


## Environmental Predictors-------------------------------------------------#
## Set colour palette (plasma)
plasma.continuous <- plasma(n = 16)

# View the colour palette
#show_col(plasma.continuous)

# Set the environ palette
plasma.environmental.predictors <- plasma.continuous[c(1, 9, 14)]
```

Site Map

```r
## 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

## Reorder ecoregions for plotting
final.data$ecoregion <- fct_relevel(
    final.data$ecoregion,
    levels = c("WMT", "XER", "NPL", "SPL", "TPL", "UMW", "NAP", "SAP", "CPL")
    )

## 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.ecoregion, 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))
```
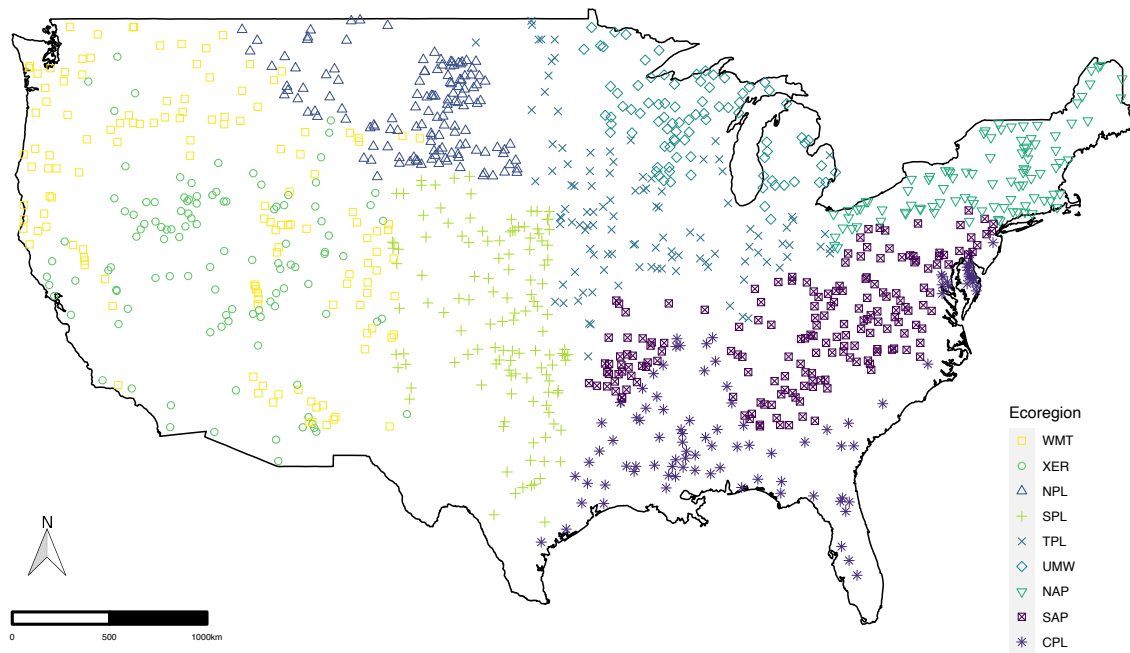
Figure 1: Map of all 1078 sites included in the study.

Filtering & Habitat Matching ANOVAs

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

DisEQ.data.long <- DisEQ.data.wide %>%
    pivot_longer(!ecoregion, names_to = "DisEQ.metric", values_to = "measurement") %>%
    na.omit()
```

```r
DisEQ.figure <- ggerrorplot(
    data = DisEQ.data.long,
    x = "ecoregion",
    y = "measurement",
    size = 1.5,
    width = 1.5,
    desc_stat = "mean",
    color = "ecoregion",
    xlab = "Ecoregion",
    ylab = "Measurement",
    title = "DisEQ by Ecoregion",
    palette = viridis.ecoregion,
    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"),
                                labels = ecoregion.labels) +
    rotate_x_text(angle = 45) +
    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")
```
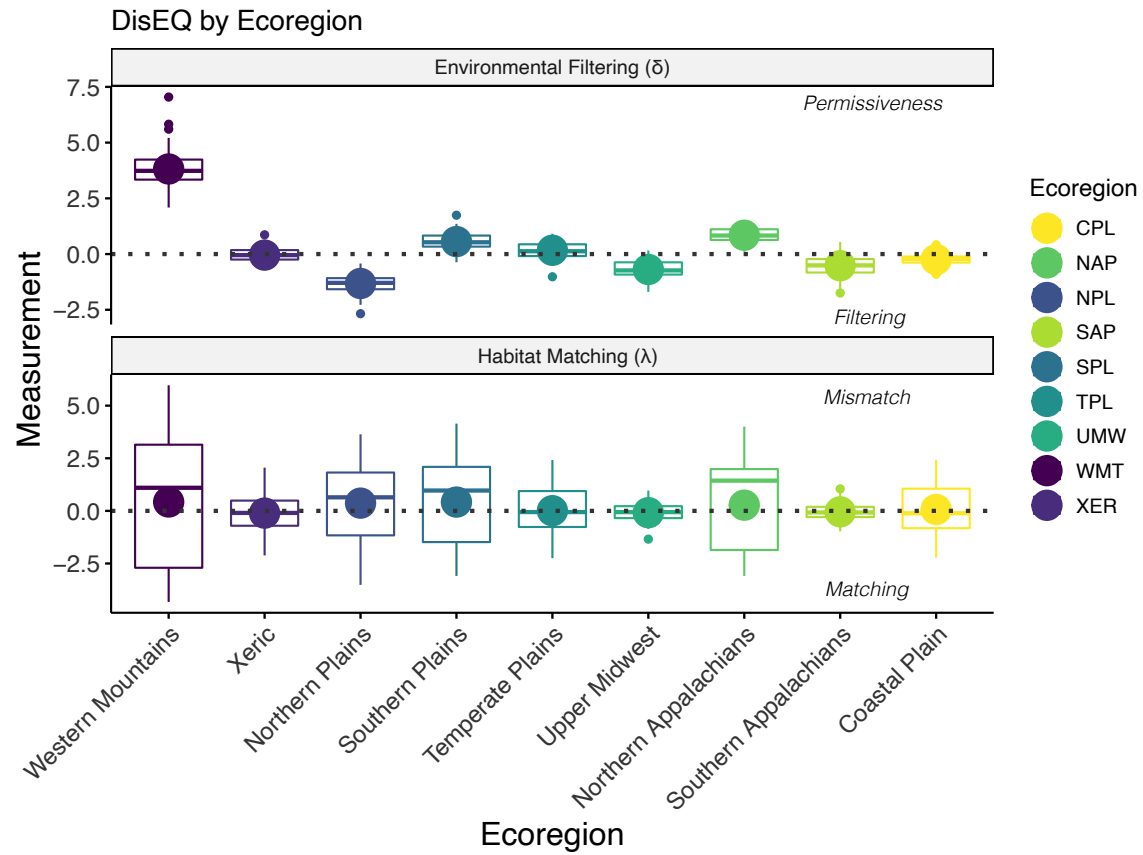
Figure 2: Plots of environmental filtering and habitat matching by ecoregion.

Habitat Matching & Mismatch Vector Component ANOVAs

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

vector.component.long <- vector.component.wide %>%
    pivot_longer(!ecoregion, names_to = "vector.component", values_to = "measurement") %>%
    na.omit()

## Re-order variables for the facet plots
vector.component.long$vector.component <- fct_relevel(
    vector.component.long$vector.component,
    levels = c("Tmax.direction", "Tmin.direction", "pH.direction", "cond.direction")
    )
```

```
vector.component.figure <- ggerrorplot(
    data = vector.component.long,
    x = "ecoregion",
    y = "measurement",
    size = 1.5,
    width = 1.5,
    desc_stat = "mean",
    color = "ecoregion",
    xlab = "Ecoregion",
    ylab = "Measurement",
    title = "Vector Components",
    palette = viridis.ecoregion,
    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"),
                                labels = ecoregion.labels) +
    rotate_x_text(angle = 60) +
    font("xlab", size = 16, color = "gray0") +
    font("ylab", size = 16, color = "gray0") +
    font("xy.text", size = 12, color = "gray20")
```
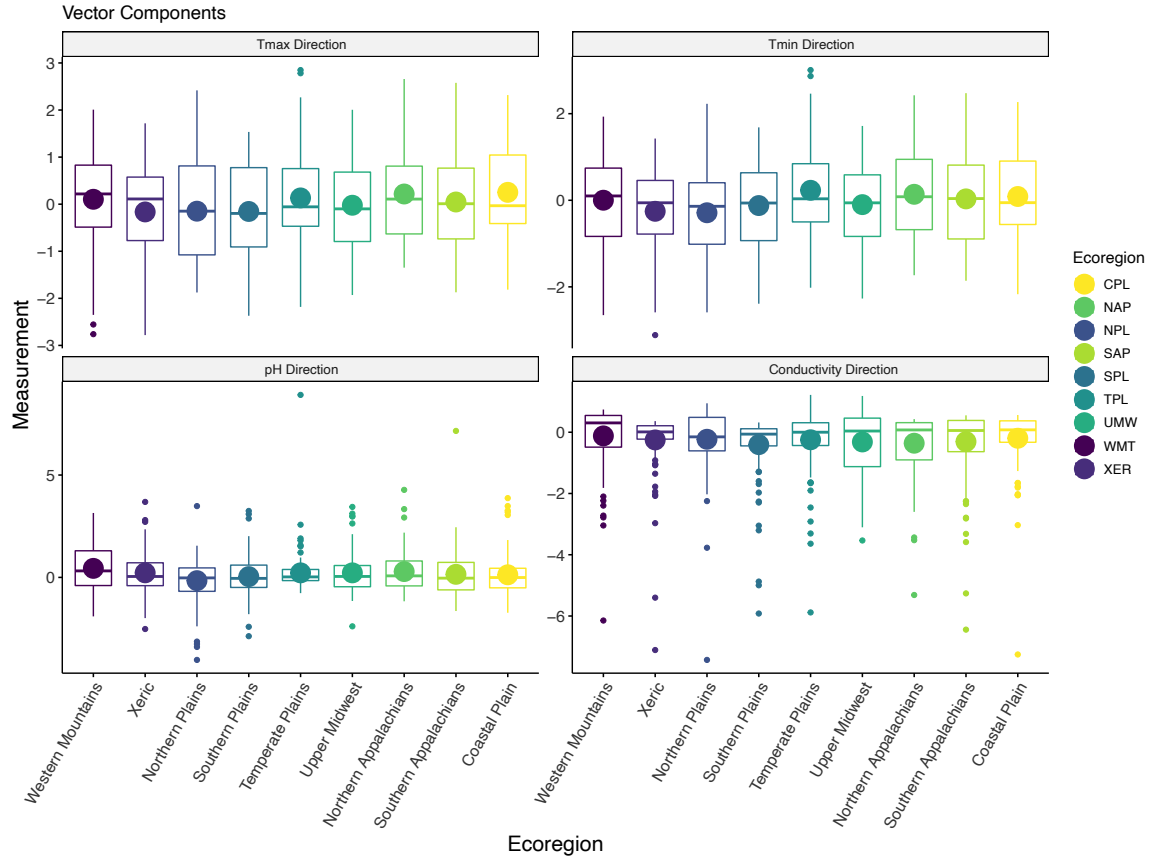
Figure 3: Plots of vector components of habitat matching and mismatch.

Functional Trait Diversity ANOVAs

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

trait.diversity.long <- trait.diversity.wide%>%
    pivot_longer(!ecoregion, names_to = "diversity.measure", values_to = "measurement") %>%
    na.omit()
```

```r
trait.diversity.figure <- ggerrorplot(
    data = trait.diversity.long,
    x = "ecoregion",
    y = "measurement",
    size = 1.5,
    width = 1.5,
    desc_stat = "mean",
    color = "ecoregion",
    xlab = "Ecoregion",
    ylab = "Measurement",
    title = "Trait Diversity",
    palette = viridis.ecoregion,
    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"),
                                labels = ecoregion.labels) +
    rotate_x_text(angle = 60) +
    font("xlab", size = 16, color = "gray0") +
    font("ylab", size = 16, color = "gray0") +
    font("xy.text", size = 12, color = "gray20")
```
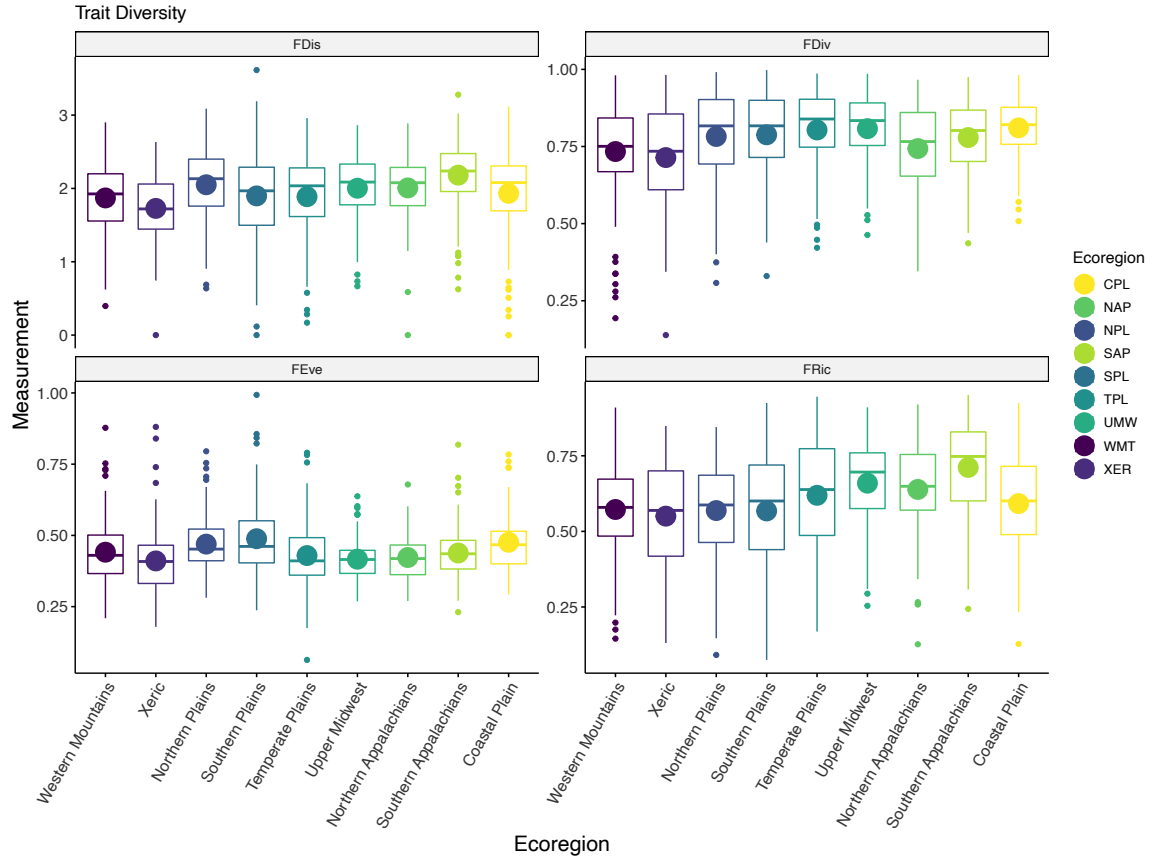
Figure 4: Plots of FRic, FEve, FDiv, and FDis by ecoregion.

DisEQ-by-Traits

Filtering-by-Traits Figure

```
## Re-order ecoregion for facet plots
filtering.by.trait.BRT.results$ecoregion <- fct_relevel(
    filtering.by.trait.BRT.results$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 = magma.functional.traits,
    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) +
    geom_hline(yintercept = 5, 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")
```
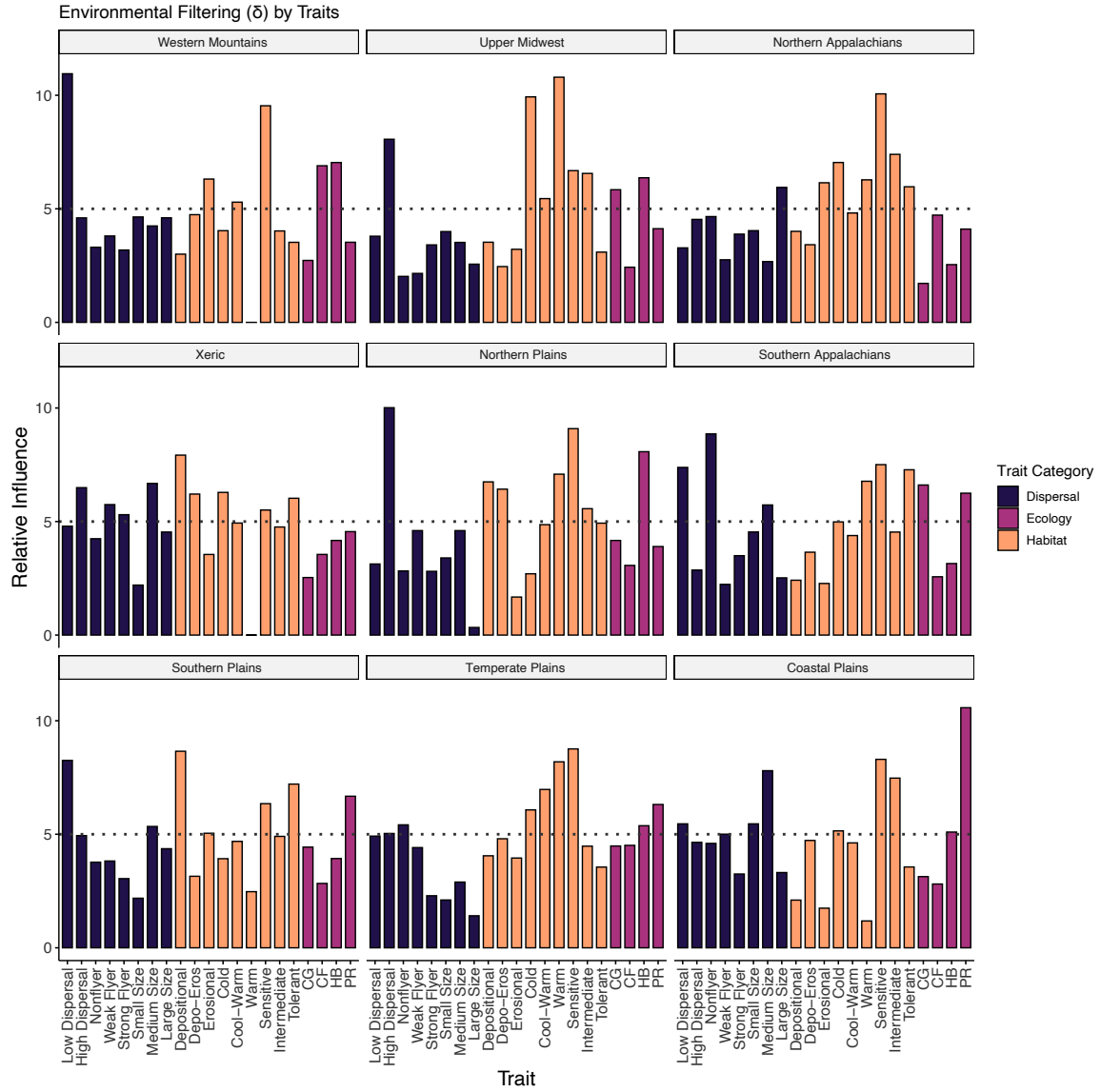
Figure 5: Plots of relative influence for each of 21 traits across ecoregions

Mismatch-by-Traits Figure

```
## Re-order ecoregion for facet plots
mismatch.by.trait.BRT.results$ecoregion <- fct_relevel(
    mismatch.by.trait.BRT.results$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 = magma.functional.traits,
    ggtheme = theme_pubr(),
    legend = "right"
    ) +
    scale_x_discrete(
        limits = trait.axis.limits,
        labels = trait.axis.labels) +
    rotate_x_text(angle = 90) +
    geom_hline(yintercept = 5, 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")
```
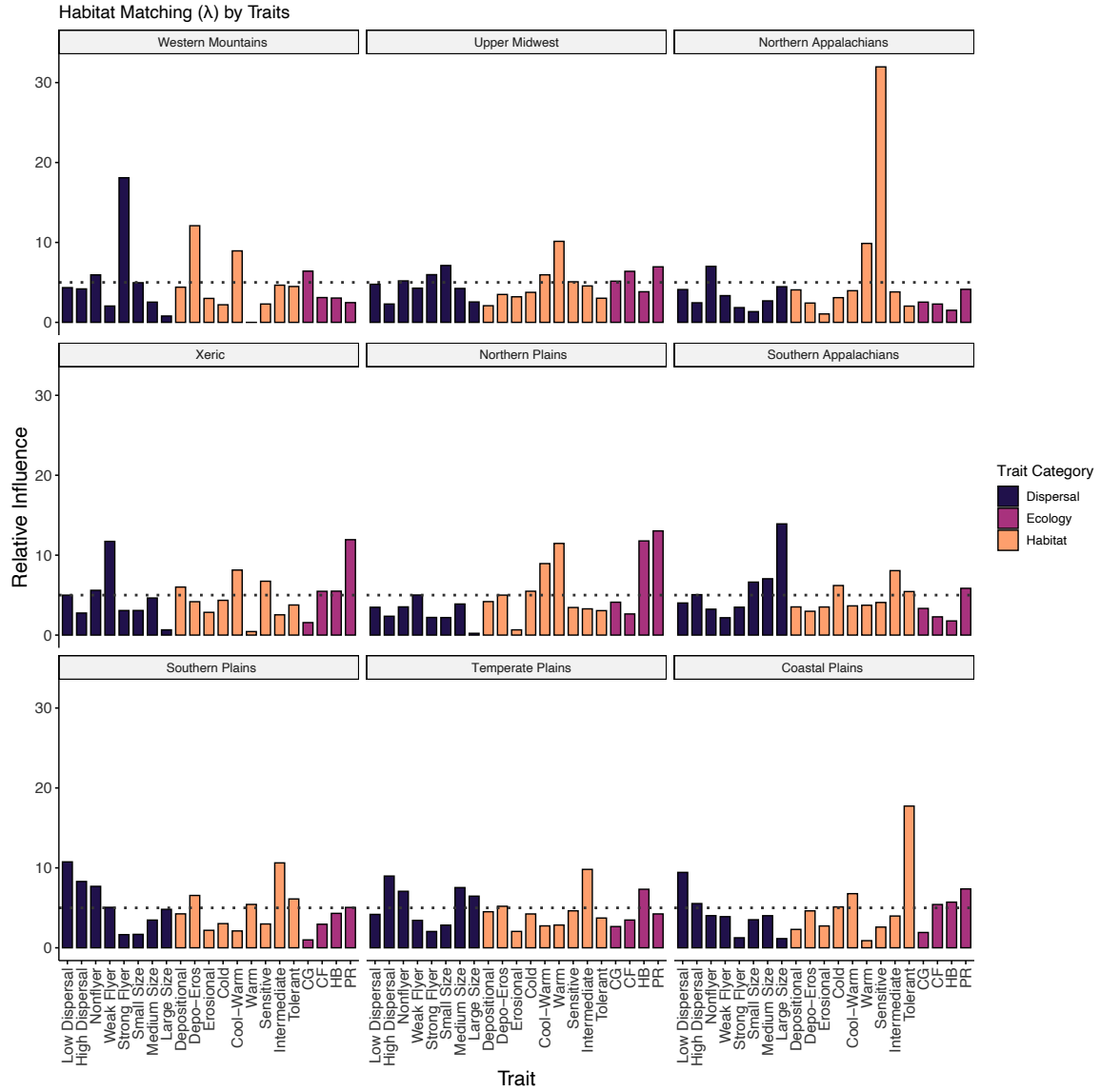
Figure 6: Plots of relative influence by dispersal, ecology, and habitat traits for each of 21 traits across all 9 ecoregions

Traits-by-Environment

```r
## 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
    )

## Filter predictors with relative influence < 5.00
trait.by.environment.long.bin.2 <- trait.by.environment.long.bin.1 %>%
    filter(rel.inf > 5.00)

## 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.2,
    FUN = sum
    )

## Re-order ecoregion for facet plots
trait.by.environment.long$ecoregion <- fct_relevel(
    trait.by.environment.long$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 = plasma.environmental.predictors,
    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")
```
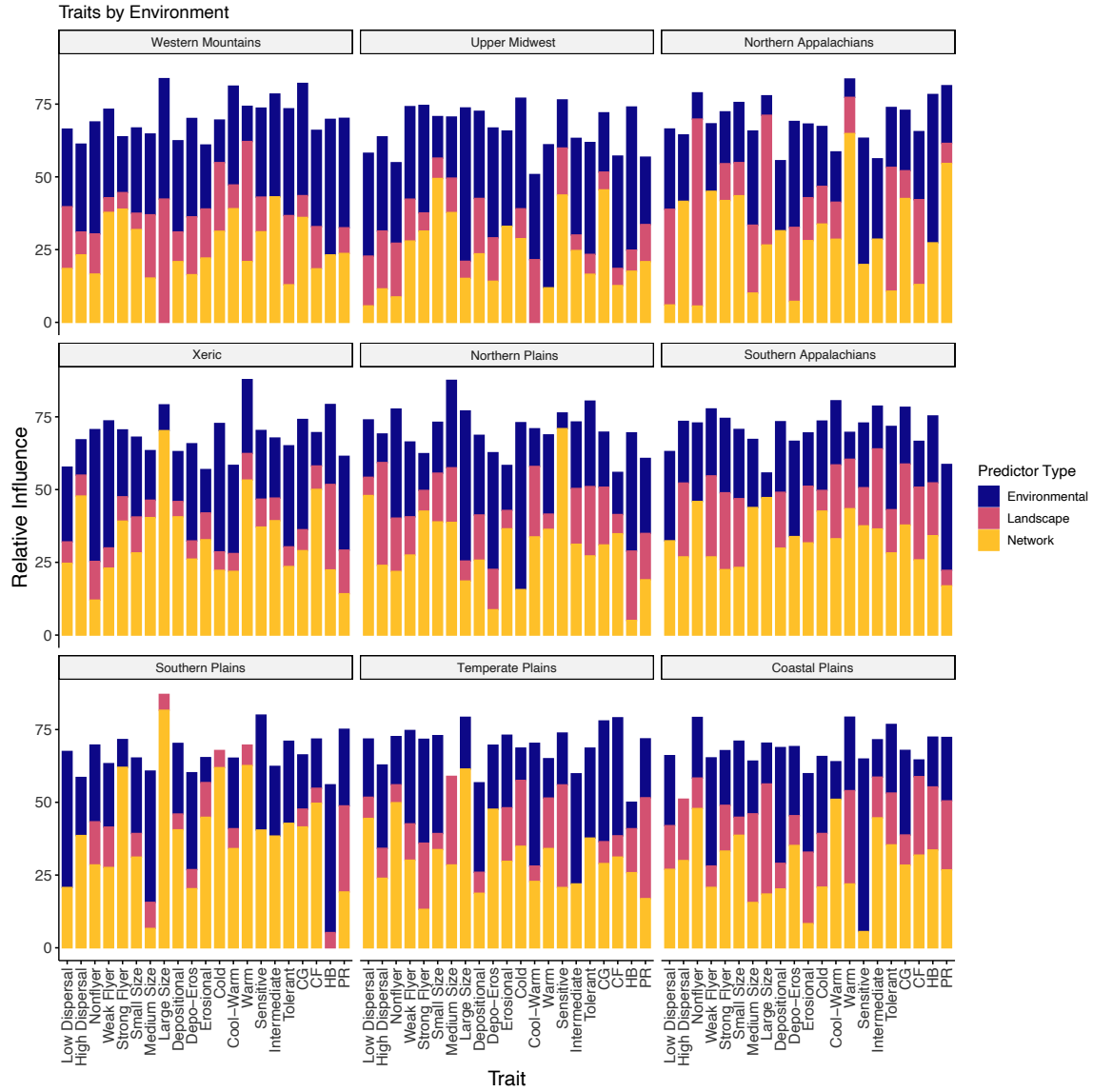
Figure 7: Plots of relative influence by environmental, landscape, and network predictors for each of 21 traits across all 9 ecoregions

DisEQ & Functional Diversity ANCOVAs

```r
## 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 %>%
    pivot_longer(cols = FRic:FDis, names_to = "trait.metric", values_to = "measurement") %>%
    na.omit()

## Reorder trait metrics for plotting
DisEQ.trait.diversity.long$trait.metric <- fct_relevel(
    DisEQ.trait.diversity.long$trait.metric,
    c("FRic", "FEve", "FDiv", "FDis")
    )
```

Filtering by Functional Diversity

```r
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.ecoregion,
    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

```r
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.ecoregion,
    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")
```
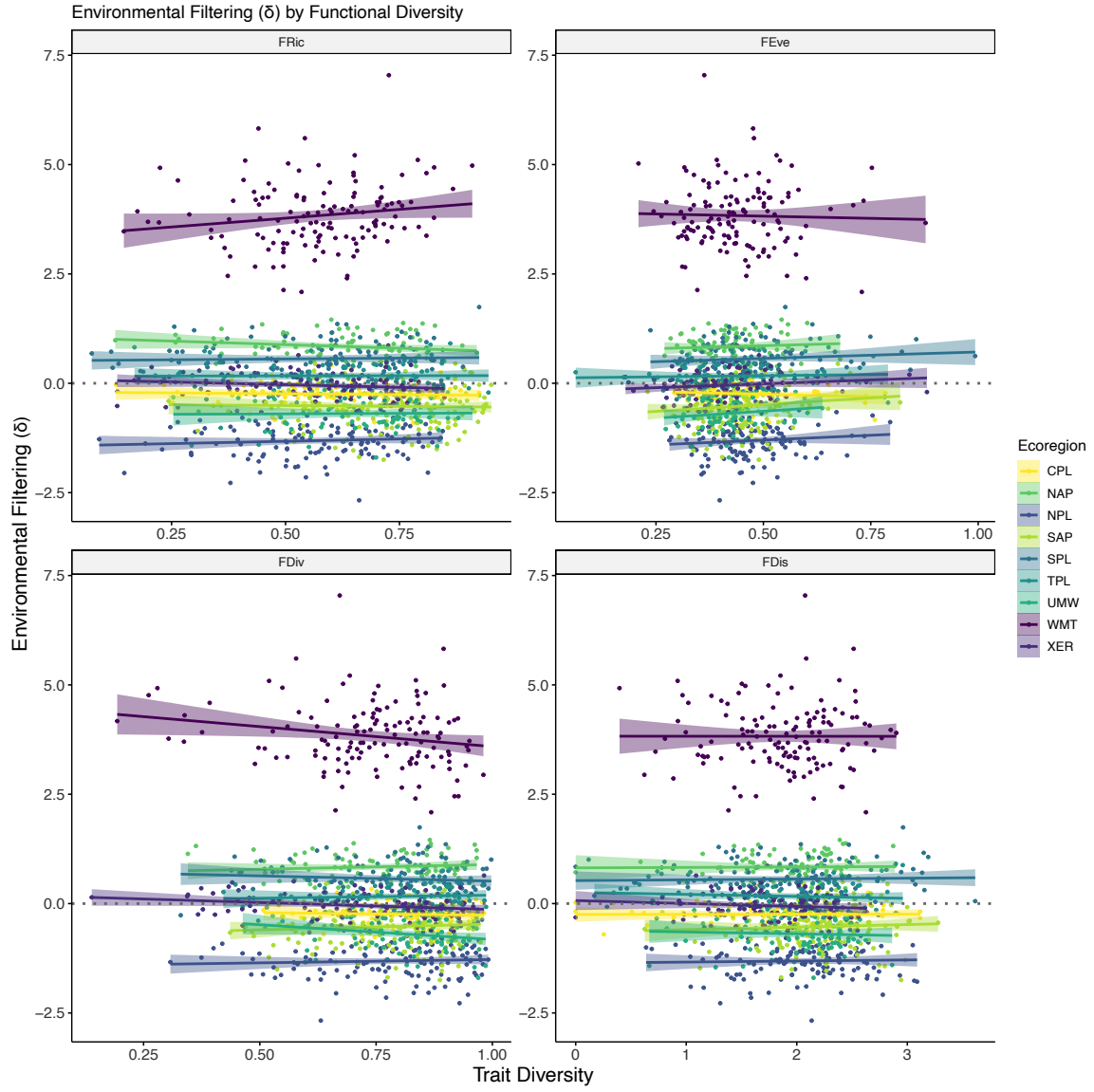
Figure 8: Plots of environmental filtering against measures of functional trait diversity.
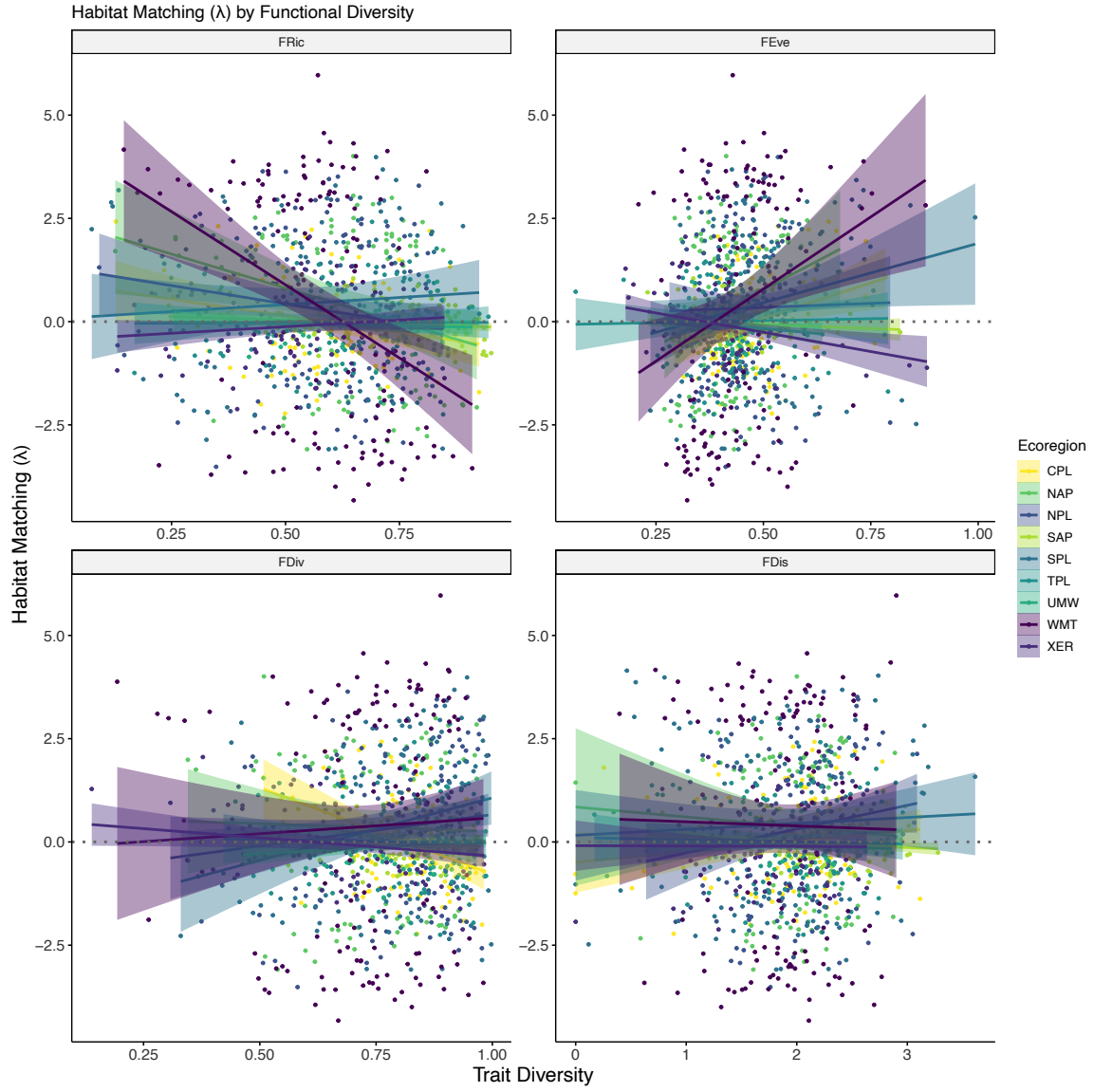
Figure 9: Plots of habitat matching against measures of functional trait diversity.

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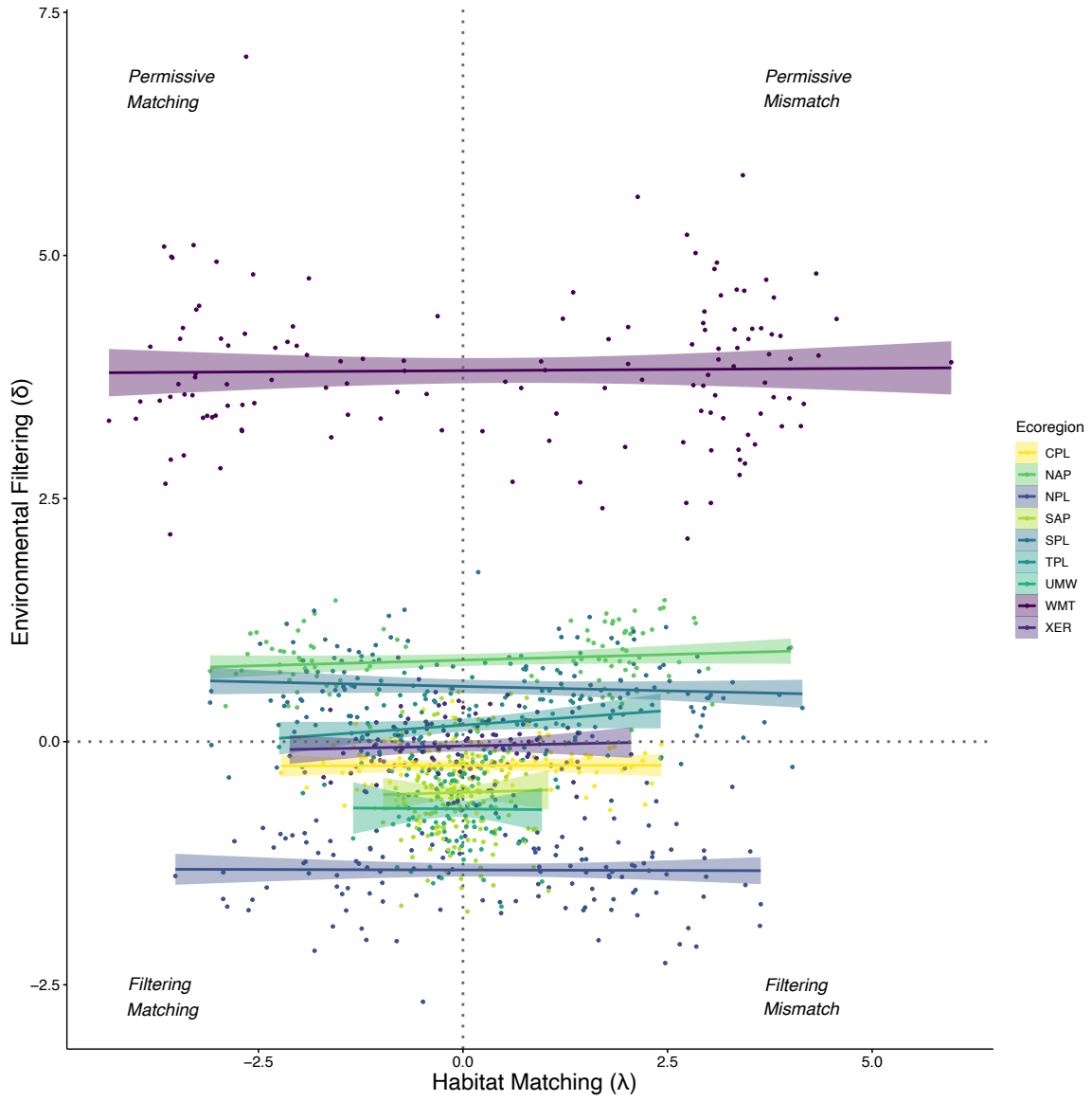
Figure 10: Plot of environmental filtering against habitat matching while controlling for the effect of ecoregion.

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/base/figure_S6A-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", ylal
ordiellipse(BC.NMDS, groups = NMDS.groups,
                        draw = "lines", col = viridis.ecoregion, 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.ecoregion)
## Export the figure
dev.off()


## Set figure dimensions
pdf("figures/base/figure_S6B-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", ylal
ordiellipse(axes.1_3, groups = NMDS.groups,
                        draw = "lines", col = viridis.ecoregion, label = FALSE, lwd = 5)
mtext(text = "(B)", side = 3, line = 1.75, adj = 0.025, cex = 1.25)

## Export the figure
dev.off()
```
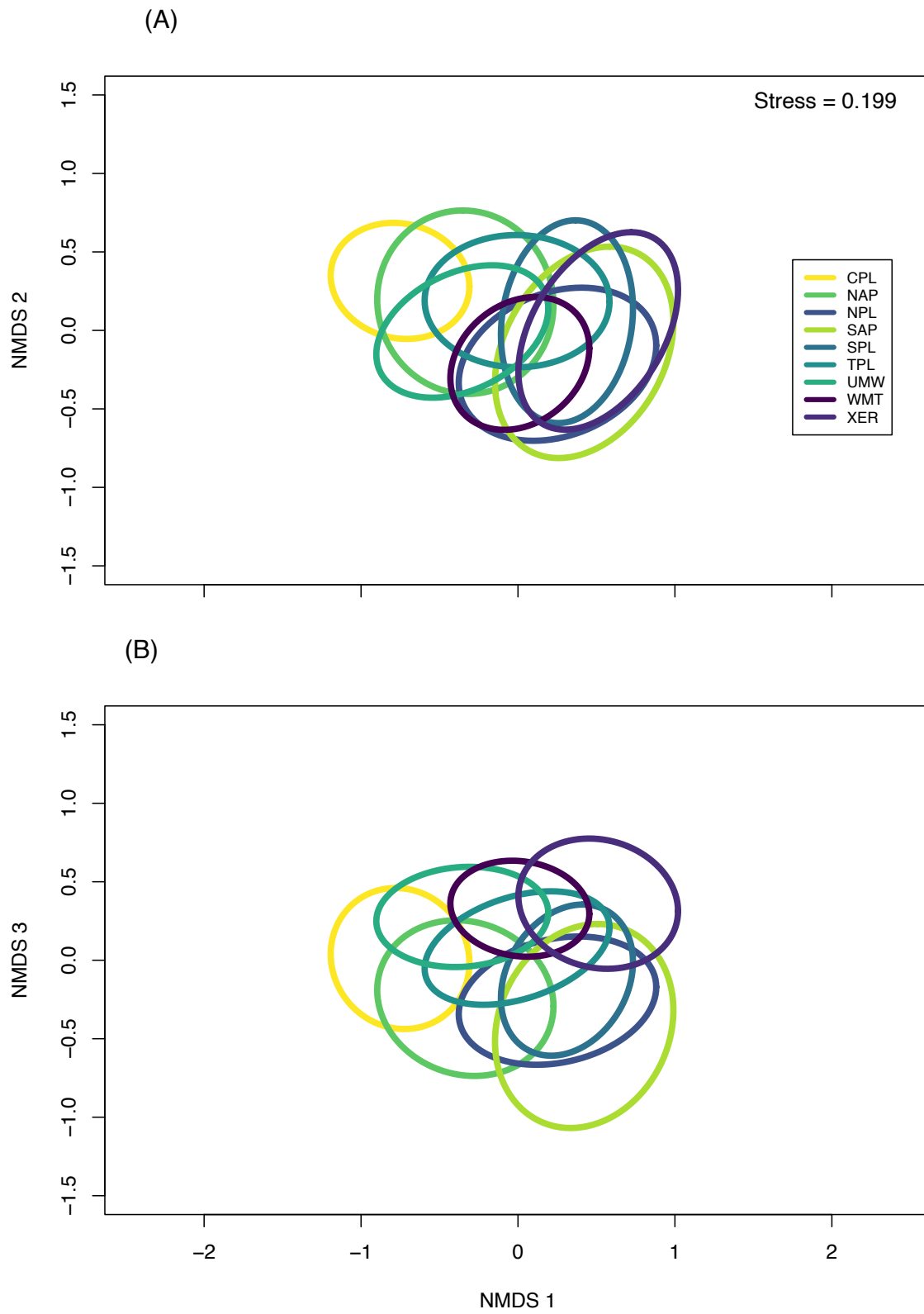
Figure 11: Plot of community composition by ecoregion.

R Session Information

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

Package	Loaded Version	Date
dplyr	1.0.9	2022-04-28
forcats	0.5.1	2021-01-27
ggplot2	3.3.6	2022-05-03
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	1.39	2022-04-26
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
rgdal	1.5-30	2022-04-08
scales	1.2.0	2022-04-13
sp	1.5-0	2022-06-05
stringr	1.4.0	2019-02-10
tibble	3.1.7	2022-05-03
tidyr	1.2.0	2022-02-01
tidyverse	1.3.1	2021-04-15
vegan	2.6-2	2022-04-17
viridis	0.6.2	2021-10-13
viridisLite	0.4.0	2021-04-13