Plant Composition Diversity Plots

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DATA INPUT: Plant composition diversity measures from warmX Google drive L2 folder DATA OUTPUT:
Plots of Plant composition diversity at KBS and UMBS - Rmd and PDF located in Github folder PROJECT:
warmXtrophic

```
## [1] "ambient" "warmed"
```

```
## [1] "warmed"  "ambient"
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## [1] "ambient" "warmed"
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## [1] "warmed"  "ambient"
```
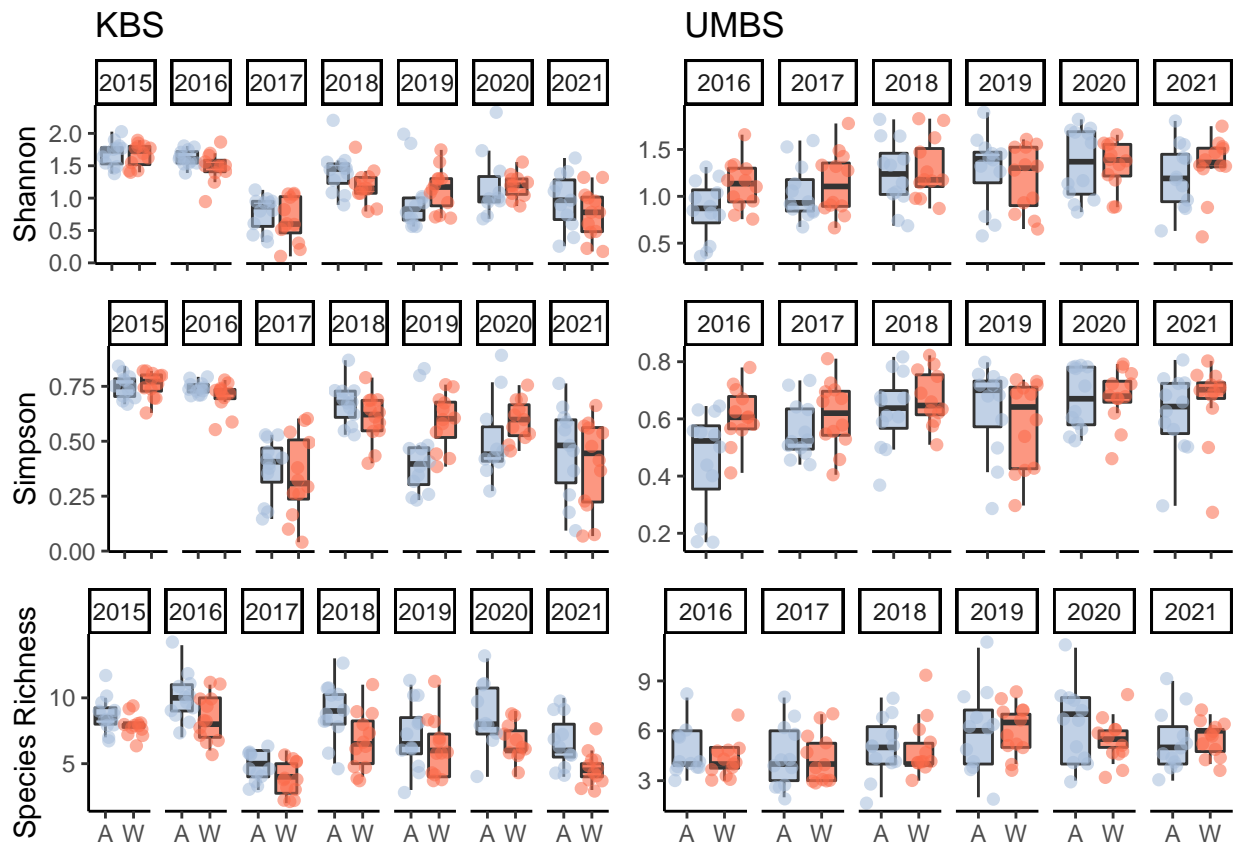
```
## [1] "ambient" "warmed"
```

```
## [1] "warmed"  "ambient"
```

Combining diversity indices - state only
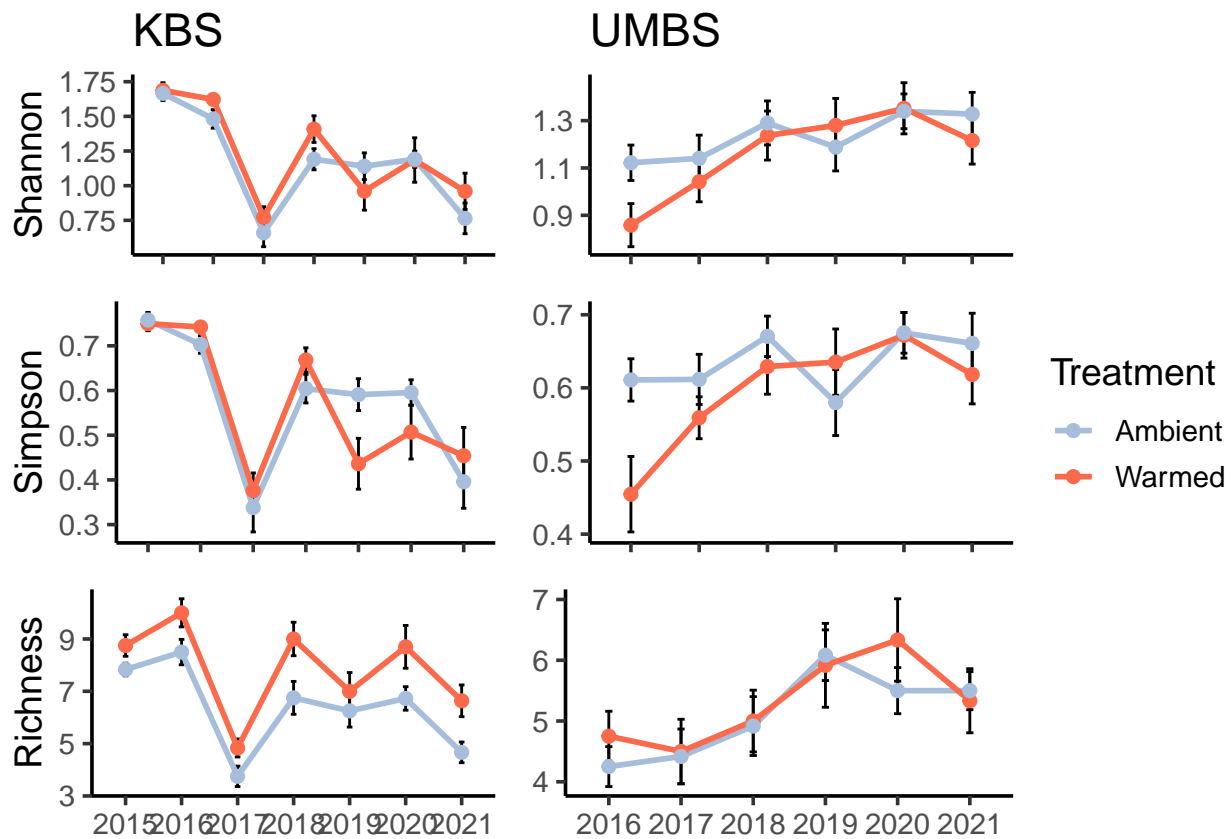
Boxplot


```
## pdf
##    2
```

Combining diversity indices - state only

Line plot


```
## pdf
##    2
```

Combining diversity indices - all treatments

Line plot with insecticide - code from Kara

```
# Shannon
sum_shannon_i$year <- as.factor(sum_shannon_i$year)
sum_shannon_i$full_treat <- paste(sum_shannon_i$state, sum_shannon_i$insecticide, sep="_")
sum_shannon_line_i <- function(loc) {
        shannon_plot <- subset(sum_shannon_i, site == loc)
        return(ggplot(shannon_plot, aes(x = year, y = avg_shannon, group=full_treat, linetype=full_trea
                        geom_errorbar(aes(ymin=avg_shannon-se, ymax=avg_shannon+se), width=.1) +
                        geom_line(size = 1) +
                        geom_point(size = 2) +
                        scale_color_manual(name="Treatment",
                                        values = c("#a6bddb", "#a6bddb", "#fb6a4a", "#fb6a4a"),
                                        labels=c("Ambient + Herbivory","Ambient + Reduced Herbivory",
                        scale_linetype_manual(name="Treatment",
```

```
                                                values = c("solid", "dashed", "solid", "dashed"),
                                                labels=c("Ambient + Herbivory","Ambient + Reduced Herbivory
                        labs(x = NULL, y = "Shannon", title = loc) +
                        theme_bw(14))
}
sum_shannon_line_i_kbs <- sum_shannon_line_i("KBS")
sum_shannon_line_i_kbs <- sum_shannon_line_i_kbs + theme(axis.text.x=element_blank())
sum_shannon_line_i_umbs <- sum_shannon_line_i("UMBS")
sum_shannon_line_i_umbs <- sum_shannon_line_i_umbs + labs(y=NULL) + theme(axis.text.x=element_blank())

#Simpson
sum_simpson_i$year <- as.factor(sum_simpson_i$year)
sum_simpson_i$full_treat <- paste(sum_simpson_i$state, sum_simpson_i$insecticide, sep="_")
sum_simpson_line_i <- function(loc) {
        simpson_plot <- subset(sum_simpson_i, site == loc)
        return(ggplot(simpson_plot, aes(x = year, y = avg_simpson, group=full_treat, linetype=full_treat
                        geom_errorbar(aes(ymin=avg_simpson-se, ymax=avg_simpson+se), width=.1) +
                        geom_line(size = 1) +
                        geom_point(size = 2) +
                        scale_color_manual(name="Treatment",
                                           values = c("#a6bddb", "#a6bddb", "#fb6a4a", "#fb6a4a"),
                                           labels=c("Ambient + Herbivory","Ambient + Reduced Herbivory",
                        scale_linetype_manual(name="Treatment",
                                              values = c("solid", "dashed", "solid", "dashed"),
                                              labels=c("Ambient + Herbivory","Ambient + Reduced Herbivory
                        labs(x = NULL, y = "Simpson", title = loc) +
                        theme_bw(14))
}
sum_simpson_line_i_kbs <- sum_simpson_line_i("KBS")
sum_simpson_line_i_kbs <- sum_simpson_line_i_kbs + theme(axis.text.x=element_blank()) + labs(title=NULL)
sum_simpson_line_i_umbs <- sum_simpson_line_i("UMBS")
sum_simpson_line_i_umbs <- sum_simpson_line_i_umbs + labs(y=NULL, title=NULL) + theme(axis.text.x=elemen

#Richness
sum_richness_i$year <- as.factor(sum_richness_i$year)
sum_richness_i$full_treat <- paste(sum_richness_i$state, sum_richness_i$insecticide, sep="_")
sum_richness_line_i <- function(loc) {
        richness_plot <- subset(sum_richness_i, site == loc)
        return(ggplot(richness_plot, aes(x = year, y = avg_richness, group=full_treat, linetype=full_tre
                        geom_errorbar(aes(ymin=avg_richness-se, ymax=avg_richness+se), width=.1) +
                        geom_line(size = 1) +
                        geom_point(size = 2) +
                        scale_color_manual(name="Treatment",
                                           values = c("#a6bddb", "#a6bddb", "#fb6a4a", "#fb6a4a"),
                                           labels=c("Ambient + Herbivory","Ambient + Reduced Herbivory",
                        scale_linetype_manual(name="Treatment",
                                              values = c("solid", "dashed", "solid", "dashed"),
                                              labels=c("Ambient + Herbivory","Ambient + Reduced Herbivory
                        labs(x = NULL, y = "Species Richness", title = loc) +
                        theme_bw(14))
}
sum_richness_line_i_kbs <- sum_richness_line_i("KBS")
sum_richness_line_i_kbs <- sum_richness_line_i_kbs + labs(title=NULL)
```
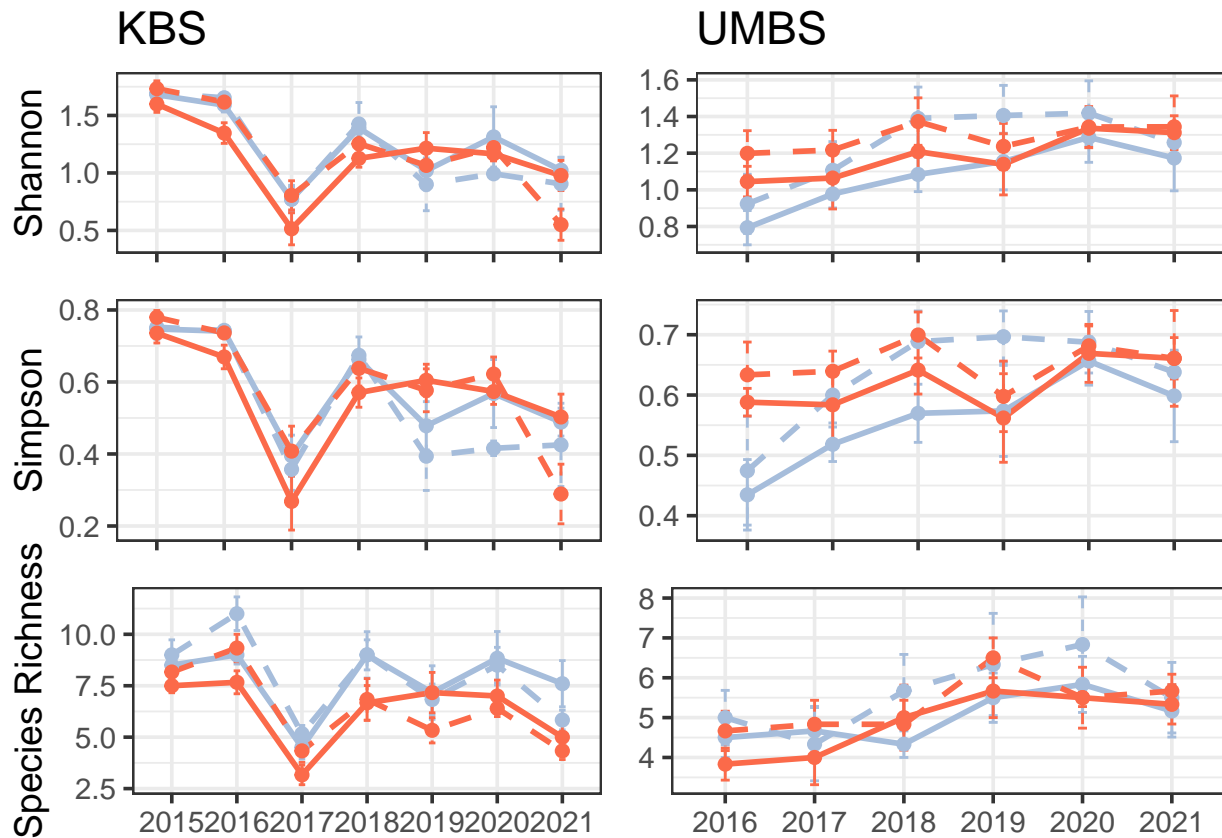
```
sum_richness_line_i_umbs <- sum_richness_line_i("UMBS")
sum_richness_line_i_umbs <- sum_richness_line_i_umbs + labs(y=NULL, title=NULL)

diversity_line_i <- ggpubr::ggarrange(sum_shannon_line_i_kbs, sum_shannon_line_i_umbs,
                        sum_simpson_line_i_kbs, sum_simpson_line_i_umbs,
                        sum_richness_line_i_kbs, sum_richness_line_i_umbs,
                        nrow = 3, ncol = 2, legend = "none")
diversity_line_i
```



```
png("plant_comp_diversity_plots_L2_all_diversity_lineplot_insect.png", units="in", width=11, height=8,
annotate_figure(diversity_line_i,
                left = text_grob("Ecological Diversity Indices", color = "black", rot = 90, size=15),
                bottom = text_grob("Year", color = "black", size=15))
dev.off()
```

```
## pdf
##   2
```