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EEB 6485: Data Visualization

Week 8 Homework

For this week’s assignment, I originally found a GREAT example of confidence intervals (Figure 2) from Brandell et al. (2021) – it was model data using shaded polygons to depict 95% confidence intervals, with points layered on top. The paper also included Figure 4 with easily understandable 95% and 50% confidence intervals. So, I tried to replicate this with data from “Frugivore biodiversity and complementarity in interaction networks enhance landscape-scale dispersal function” (Garcia et al., 2018). After working with Jess and Cindy, we found that Figure 4 failed to investigate species-level effects, so I chose to investigate the abundance of plant species in a similar manner to the Brandell et al. I liked the horizontal boxplot visual, so I chose to do this with varying widths based on sample sizes.

Brandell, E. E., Cross, P. C., Craft, M. E., Smith, D. W., Dubovi, E. J., Gilbertson, M. L., ... & Hudson, P. J. (2021). Patterns and processes of pathogen exposure in gray wolves across North America. *Scientific reports*, *11*(1), 1-14.

<https://datadryad.org/stash/dataset/doi:10.5061/dryad.5hqbzkh51>

García, D., Donoso, I., & Rodríguez‐Pérez, J. (2018). Frugivore biodiversity and complementarity in interaction networks enhance landscape‐scale seed dispersal function. *Functional ecology*, *32*(12), 2742-2752.

<https://datadryad.org/stash/dataset/doi:10.5061/dryad.h748c88>

Chart

Description automatically generated

Graphical user interface, diagram, table

Description automatically generatedChart, box and whisker chart

Description automatically generated

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title: "EEB6485\_DataVis\_21\_03\_10"

output: word\_document

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```{r}

setwd("~/Desktop/EEB\_6485/Fig\_Week8")

plant.ab <- read.csv("EEB6485\_data\_210310.csv")

library(ggplot2)

```

```{r}

head(plant.ab)

#attempting to merge genus and species smh

library(dplyr)

plant.ab.c <- mutate(plant.ab, Plant = paste(Plant.Genus, Plant.Species))

head(plant.ab.c)

```

```{r}

plot <- ggplot(data=plant.ab.c, aes(x=Plant, y=Abundance, fill=Plant, color=Plant)) +

geom\_boxplot(varwidth = TRUE, alpha=0.2) +

scale\_y\_log10() +

theme(legend.position = "none", panel.grid = element\_blank(), panel.background = element\_blank(), axis.line = element\_line(color = "black")) +

coord\_flip()

plot(plot)

```