

Herbivory Plots

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January 12, 2021

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DATA INPUT: Clean & plot herb csv from the shared Google drive

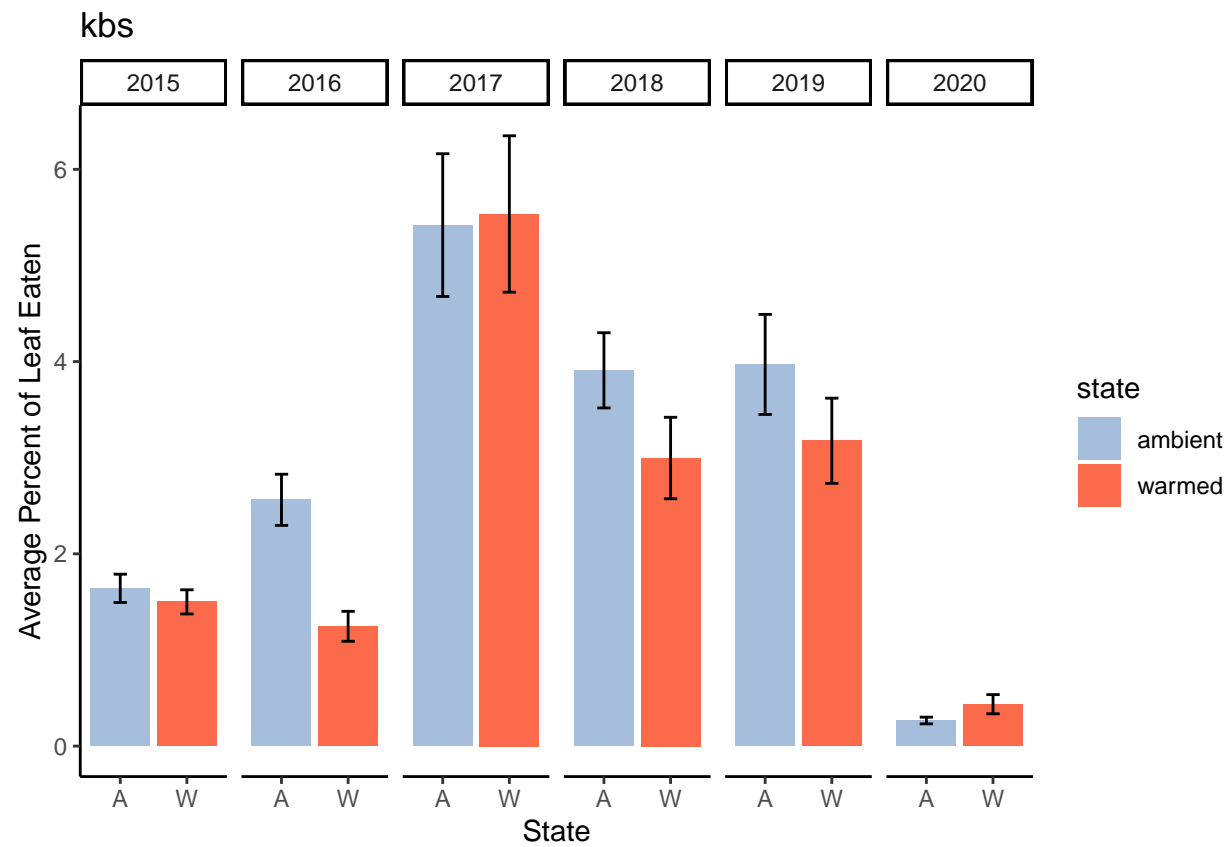
DATA OUTPUT: Code and Rmd are in the scripts folder in Github

PROJECT: warmXtrophic

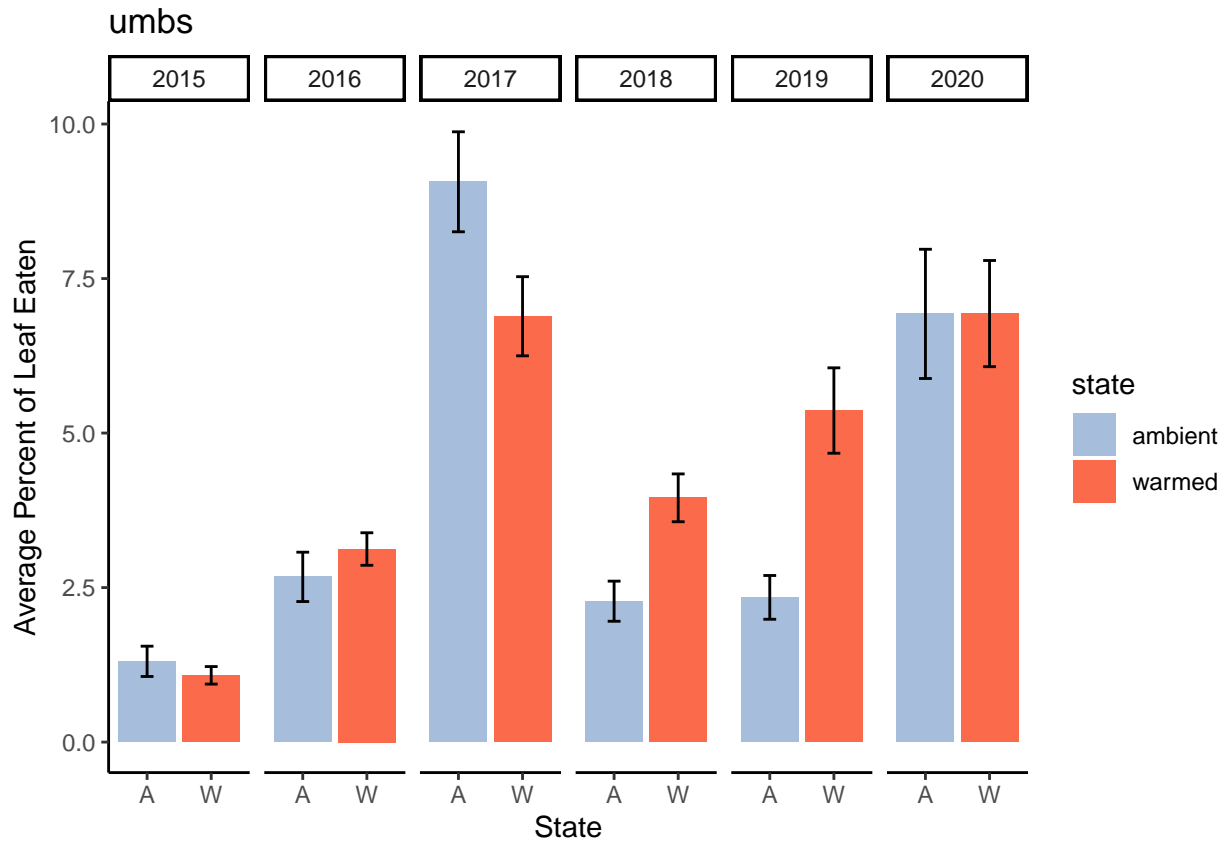
- Still working on plots with insecticide included as a factor *

Makes a plot for a given site

```
herb_plot_all <- function(loc) {  
  herb_spp <- subset(sum_herb_all, site == loc)  
  return(ggplot(herb_spp, aes(x = state, y = avg_eaten, fill = state)) +  
    facet_grid(.~year) +  
    geom_bar(position = "identity", stat = "identity") +  
    geom_errorbar(aes(ymin = avg_eaten - se, ymax = avg_eaten + se), width = 0.2,  
      position = "identity") +  
    labs(x = "State", y = "Average Percent of Leaf Eaten", title = loc) +  
    scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +  
    scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +  
    theme_classic()  
}  
herb_plot_all("kbs")
```



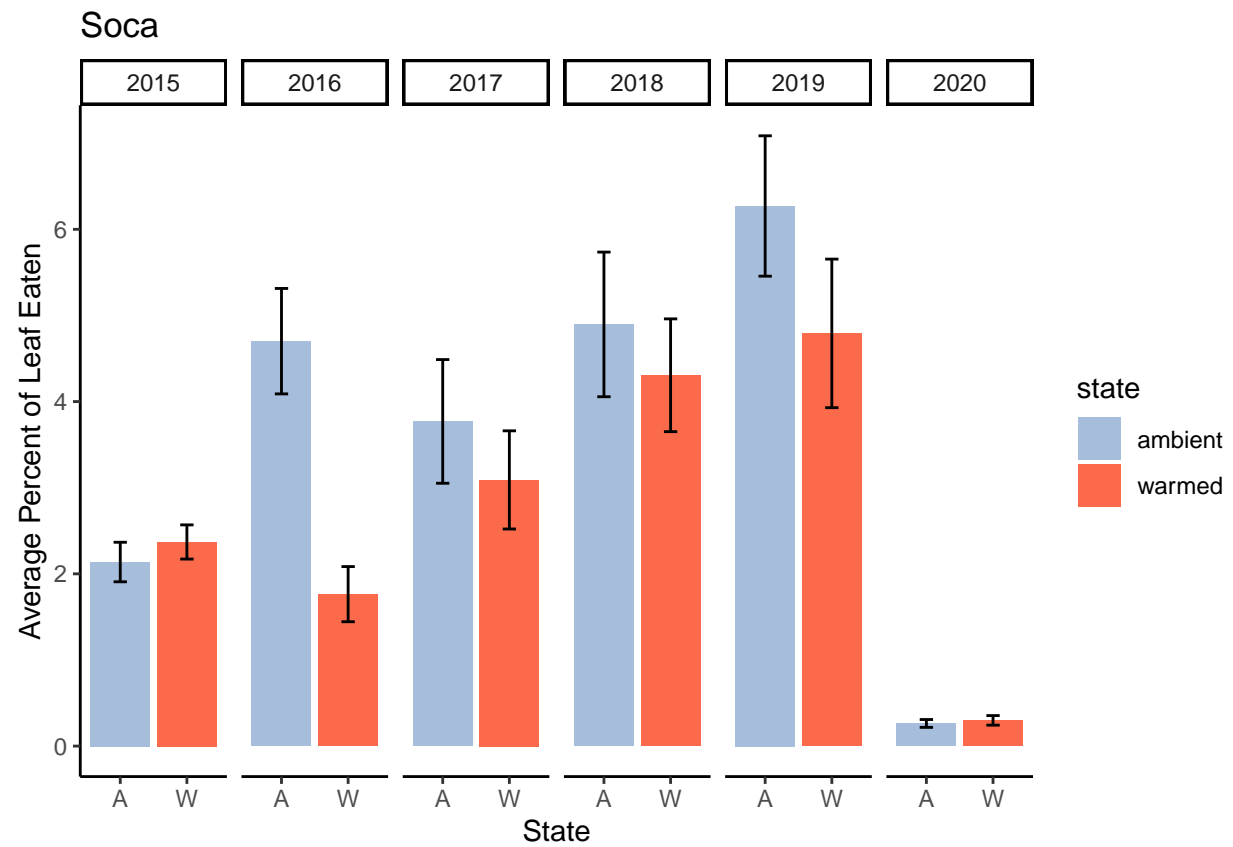
```
herb_plot_all("umbs")
```



Makes a plot for a given species and site

Ex: Popr at kbs, Eugr at kbs

```
herb_plot <- function(spp, loc) {
  herb_spp <- subset(sum_herb, species == spp & site == loc)
  return(ggplot(herb_spp, aes(x = state, y = avg_eaten, fill = state)) +
    facet_grid(.~year) +
    geom_bar(position = "identity", stat = "identity") +
    geom_errorbar(aes(ymin = avg_eaten - se, ymax = avg_eaten + se), width = 0.2,
      position = "identity") +
    labs(x = "State", y = "Average Percent of Leaf Eaten", title = spp) +
    scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
    scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +
    theme_classic())
}
herb_plot("Soca", "kbs")
```



```
herb_plot("Eugr", "kbs")
```

