Herbivory Plots

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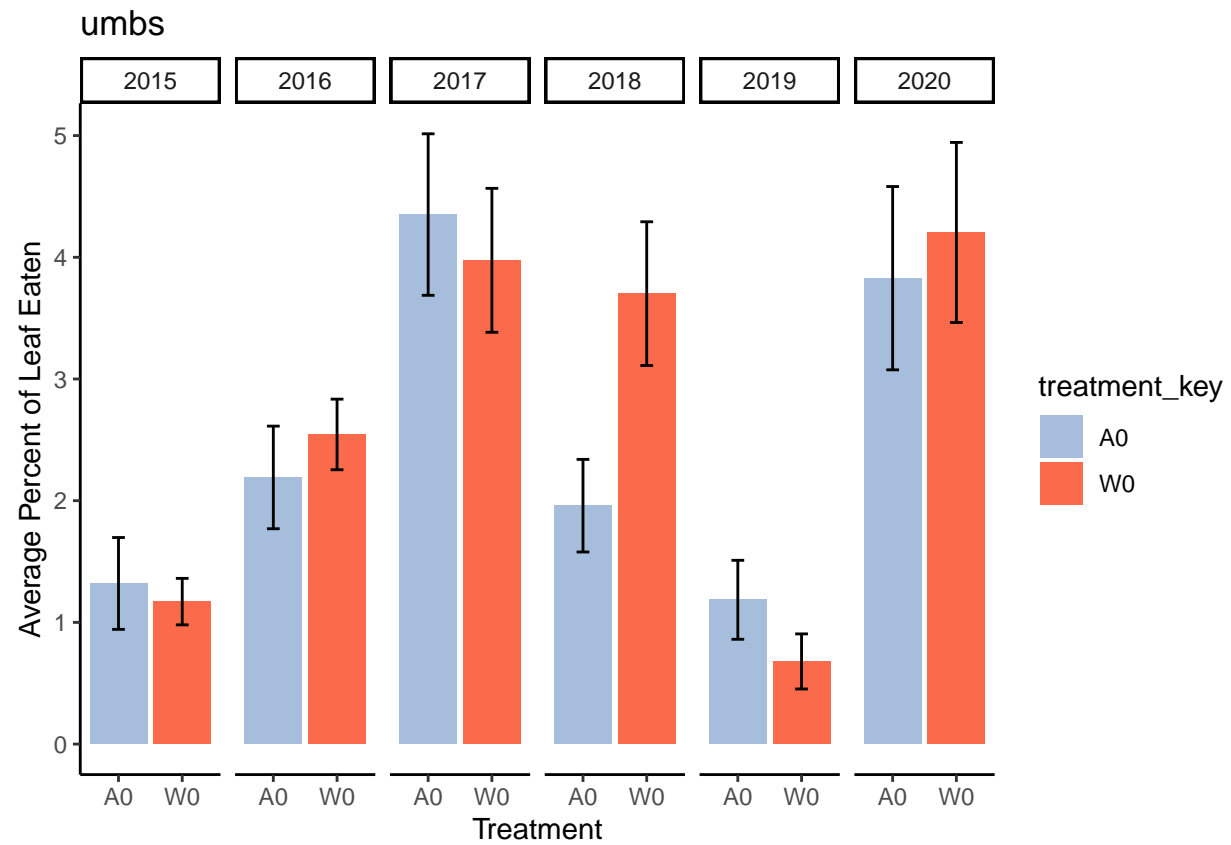COLLABORATORS: Phoebe Zarnetske, Mark Hammond, Pat Bills, Moriah Young
DATA INPUT: Clean & plot herb csv from the shared Google drive
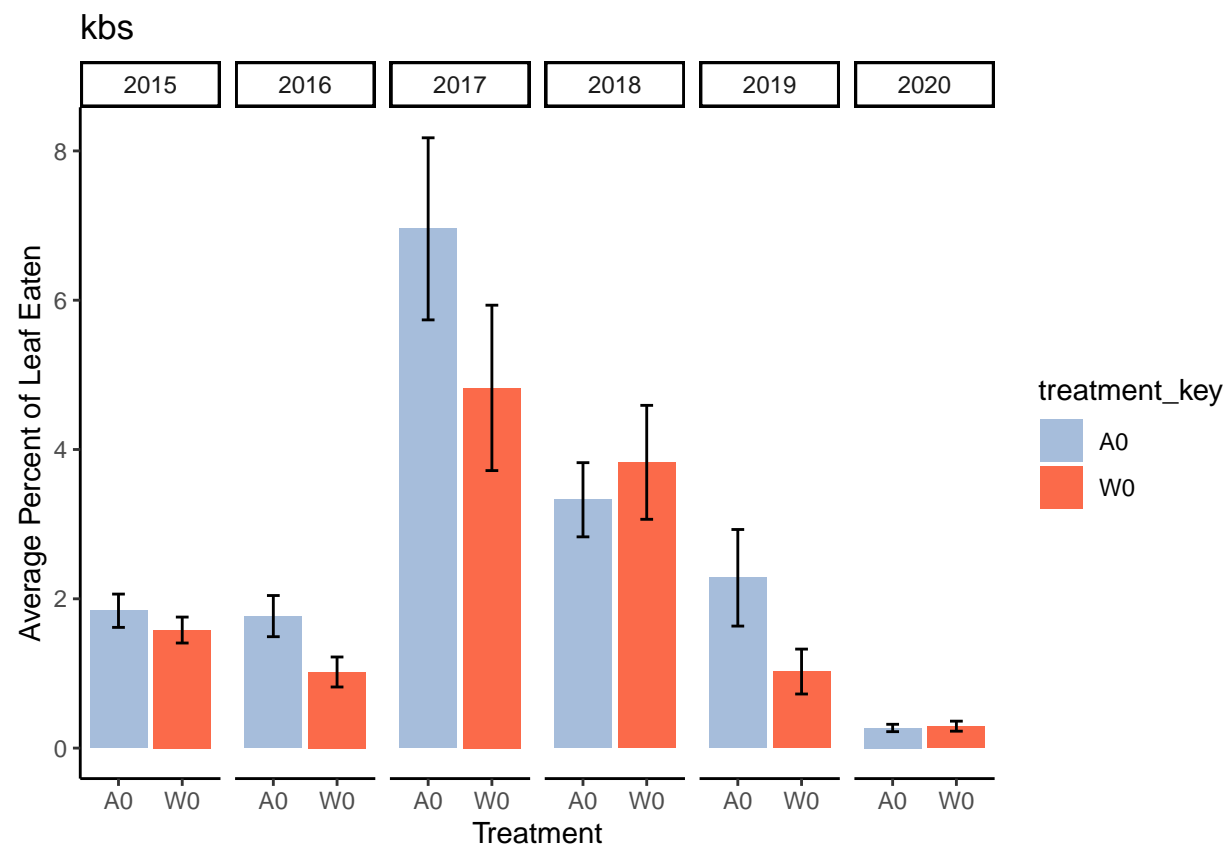DATA OUTPUT: Code and Rmd are in the scripts folder in Github
PROJECT: warmXtrophic

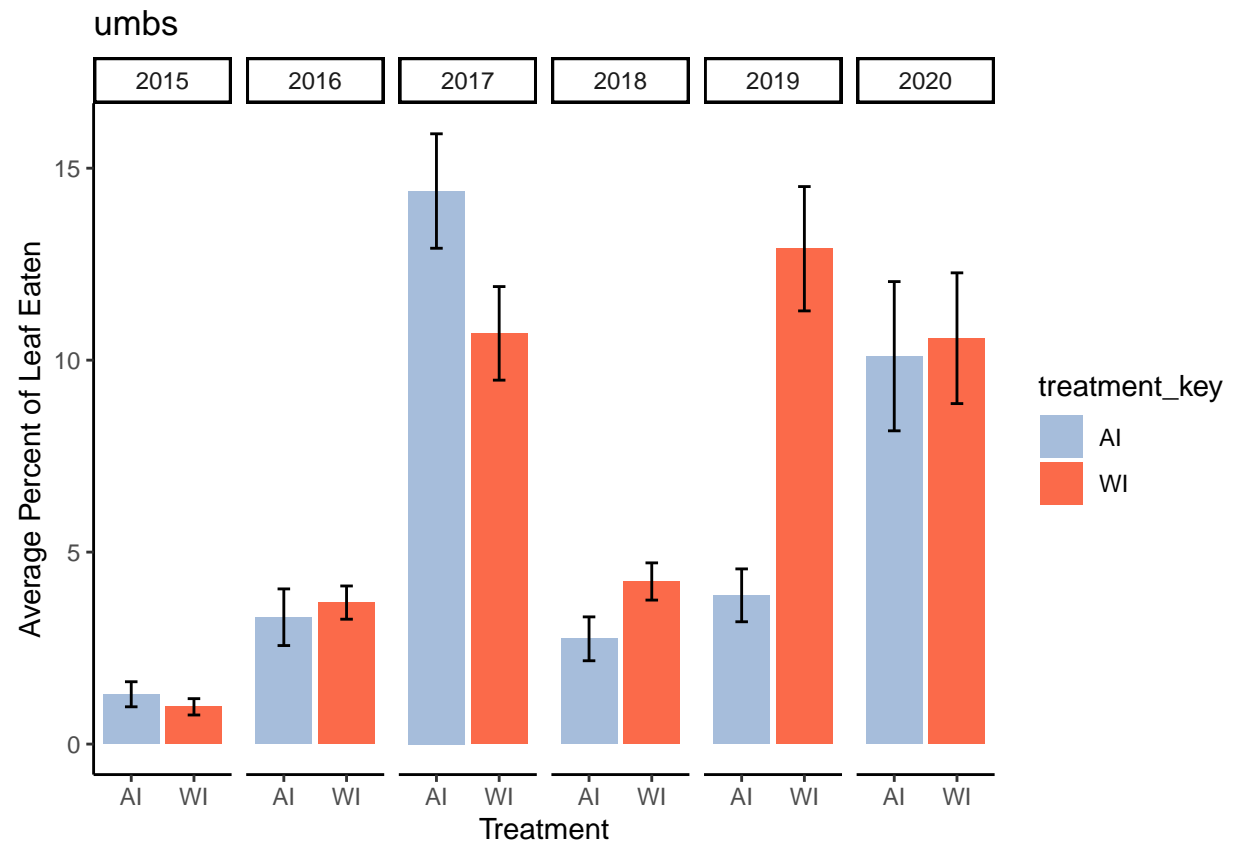**Makes a plot for each site with and without insecticide treatment**

```r
herb_plot_in <- function(loc, key, key2) {
  herb_spp <- subset(sum_herb_in, site == loc & treatment_key == key | site== loc & treatment_key == key
  return(ggplot(herb_spp, aes(x = treatment_key, y = avg_eaten, fill = treatment_key)) +
           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 = "Treatment", y = "Average Percent of Leaf Eaten", title = loc) +
           scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
           theme_classic())
}
herb_plot_in("umbs", "A0", "W0")
```
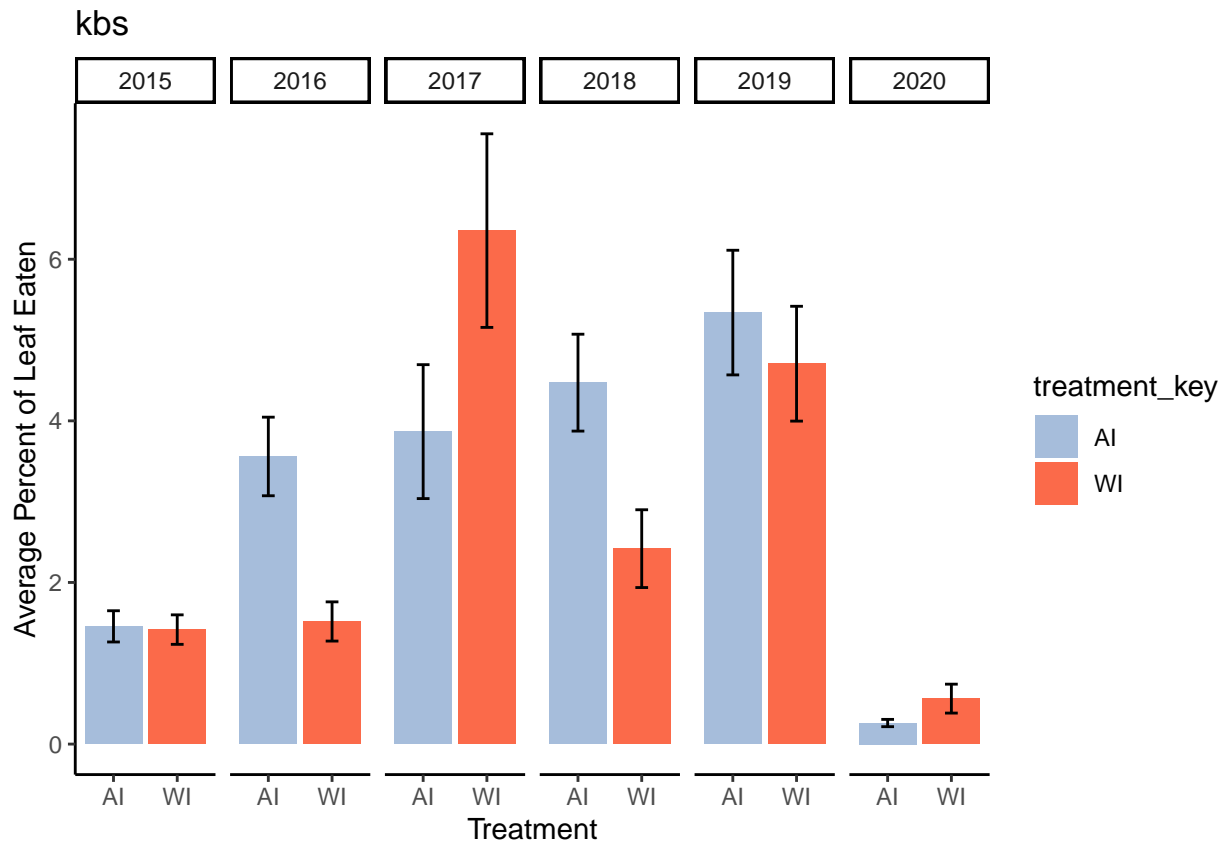
umbs


```
herb_plot_in("kbs", "A0", "W0")
```

kbs


```
herb_plot_in("umbs", "AI", "WI")
```
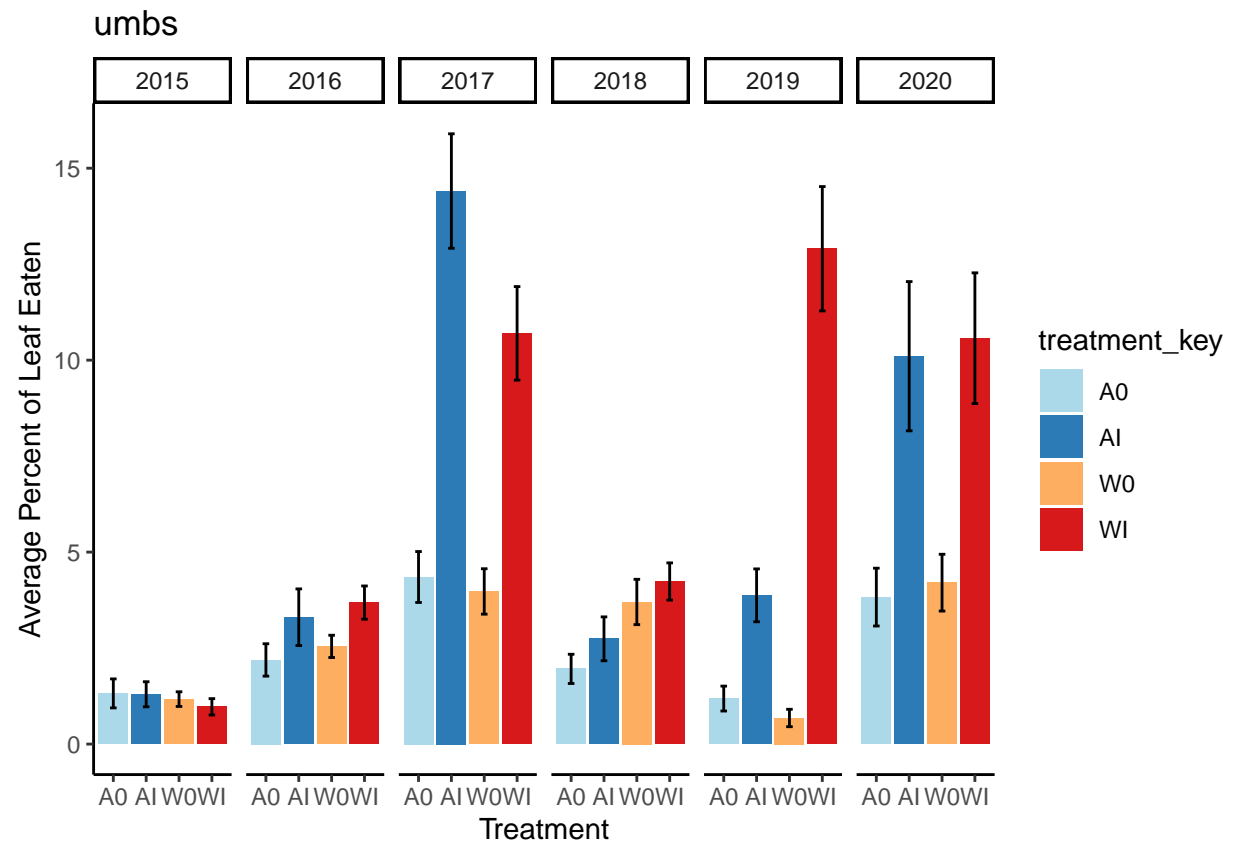
umbs


```
herb_plot_in("kbs", "AI", "WI")
```
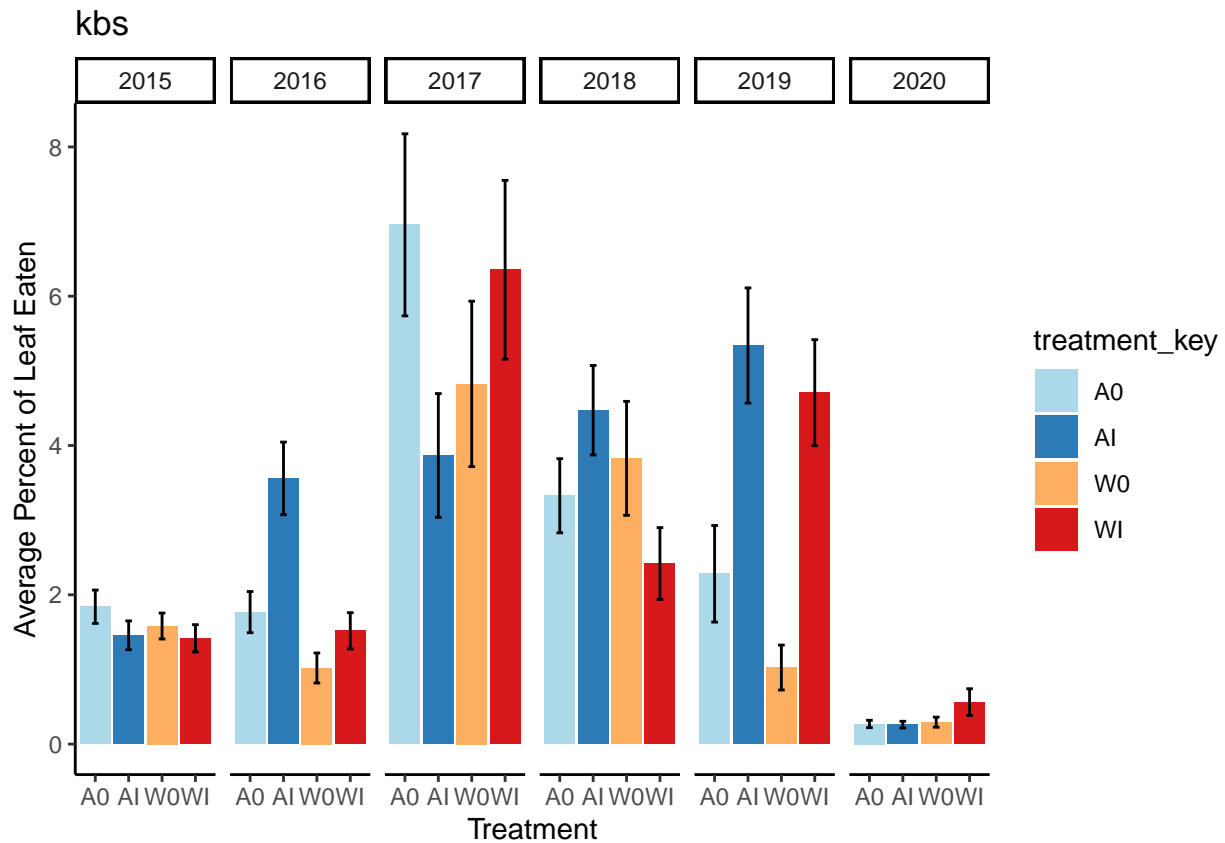
kbs

Makes a plot for a given site

```
herb_plot_in <- function(loc) {
  herb_spp <- subset(sum_herb_in, site == loc)
  return(ggplot(herb_spp, aes(x = treatment_key, y = avg_eaten, fill = treatment_key)) +
           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 = "Treatment", y = "Average Percent of Leaf Eaten", title = loc) +
           scale_fill_manual(values = c("#abd9e9", "#2c7bb6", "#fdae61", "#d7191c")) +
           theme_classic())
}
herb_plot_in("umbs")
```

umbs


```
herb_plot_in("kbs")
```

kbs

Makes a plot for a given species and site

Ex: Popr at kbs, Eugr at kbs

```r
herb_plot <- function(spp, loc) {
  herb_spp <- subset(sum_herb, species == spp & site == loc)
  return(ggplot(herb_spp, aes(x = treatment_key, y = avg_eaten, fill = treatment_key)) +
         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")
```

Soca