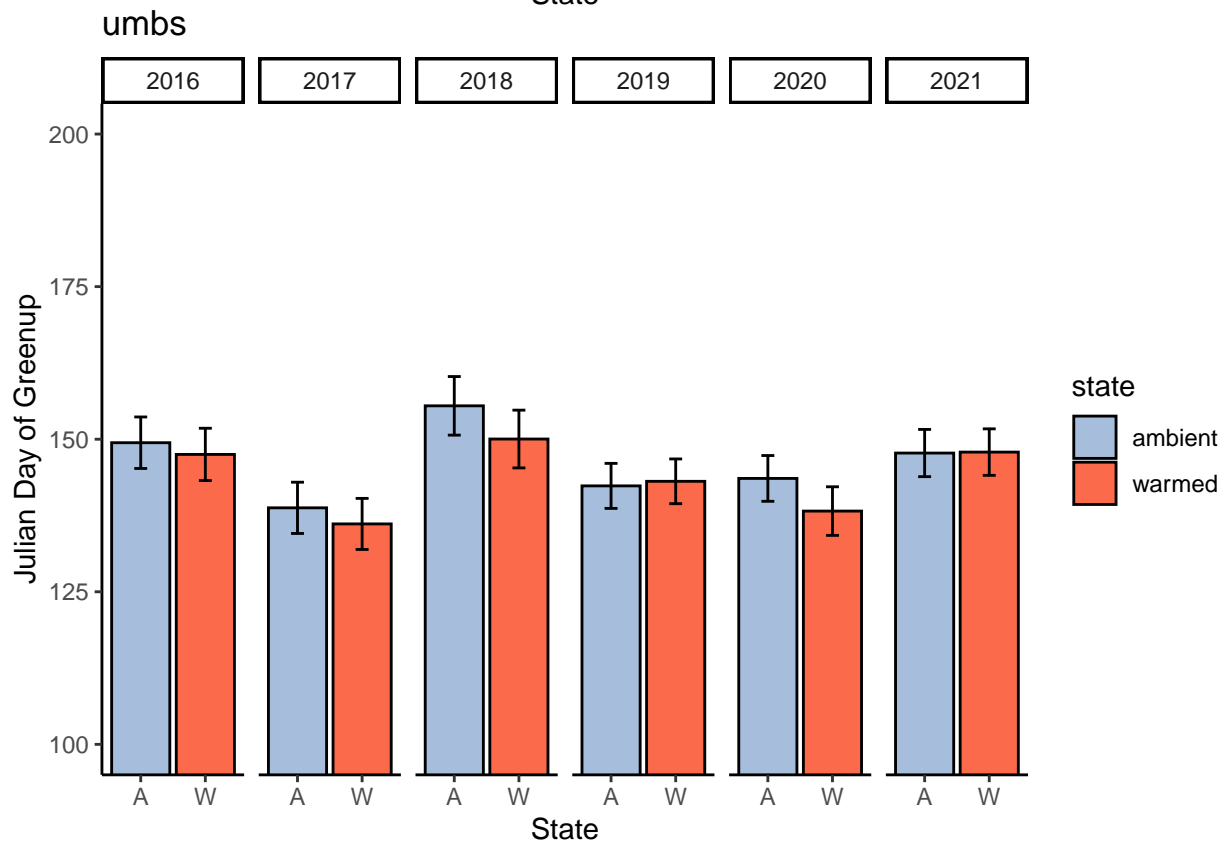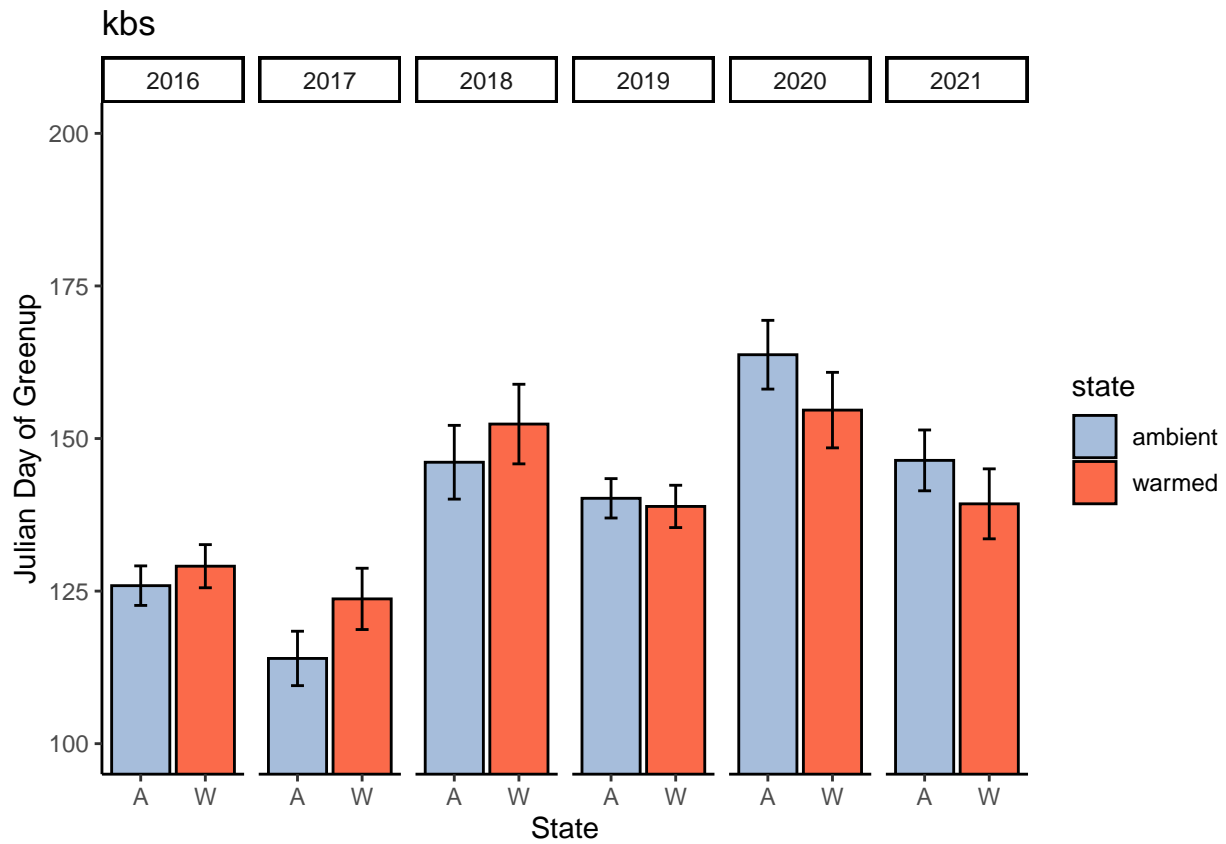# Greenup Plots

Kara Dobson

January 28, 2022

COLLABORATORS: Phoebe Zarnetske, Mark Hammond, Pat Bills, Moriah Young
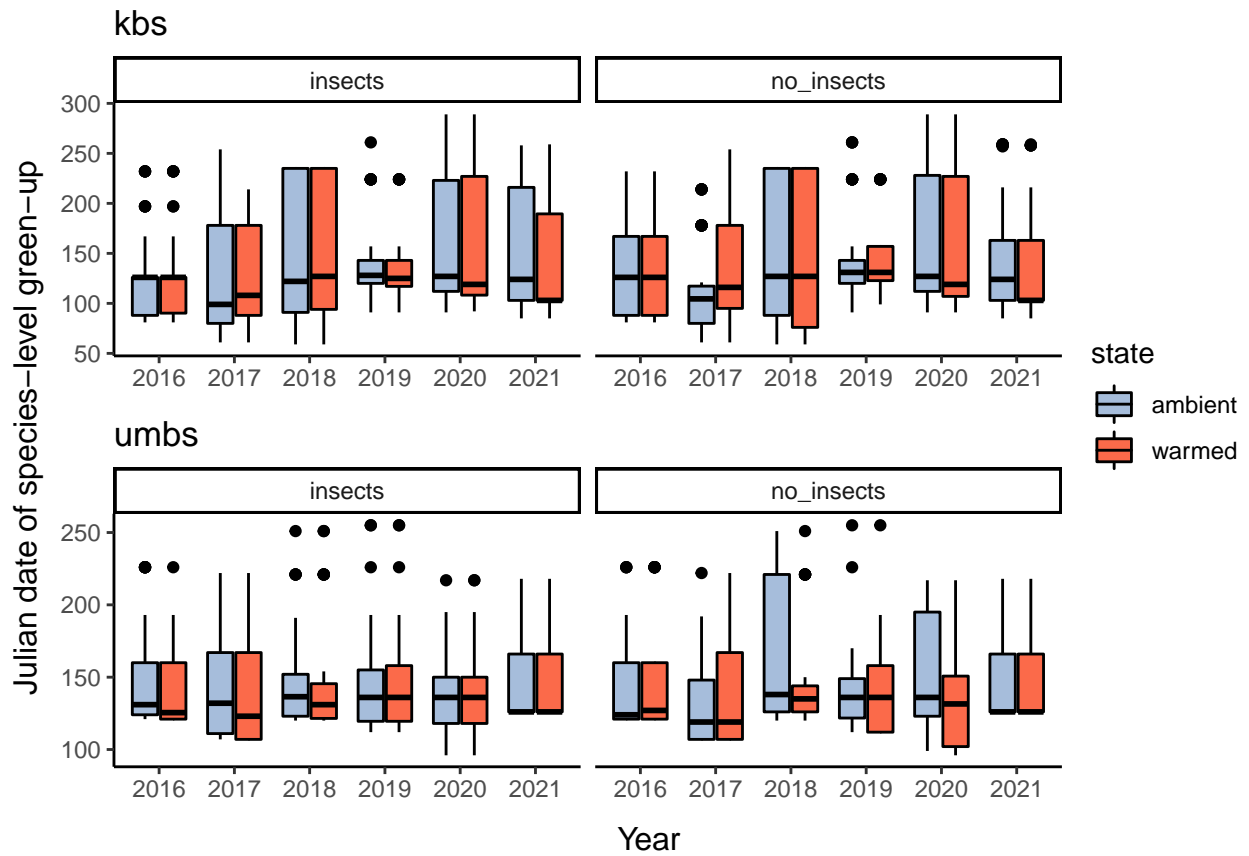DATA INPUT: Plot and species level greenup files from warmX Google drive
DATA OUTPUT: Plots of greenup at KBS and UMBS - Rmd and PDF located in Github folder PROJECT: warmXtrophic
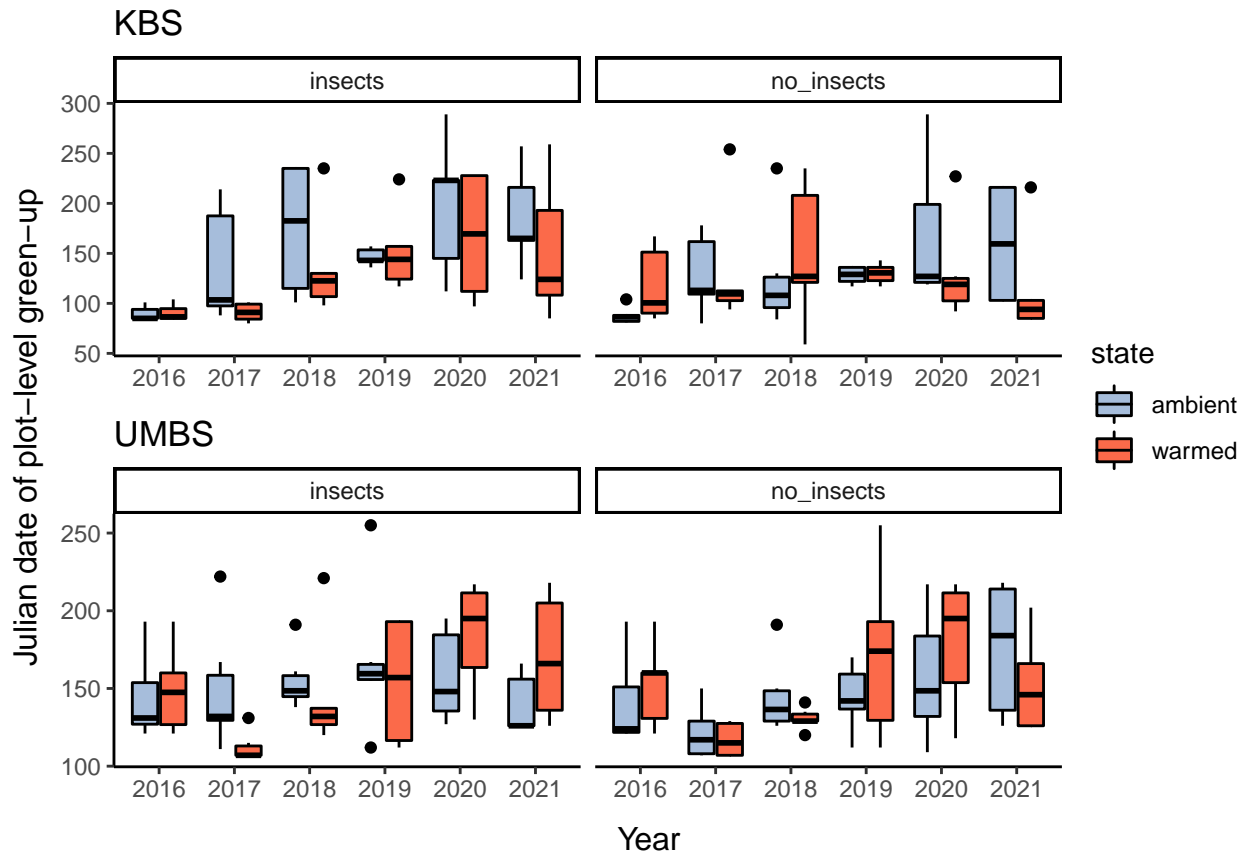
Bar plot for greenup for KBS and UMBS - Species half cover date

Box plot for greenup for KBS and UMBS - Species half cover date

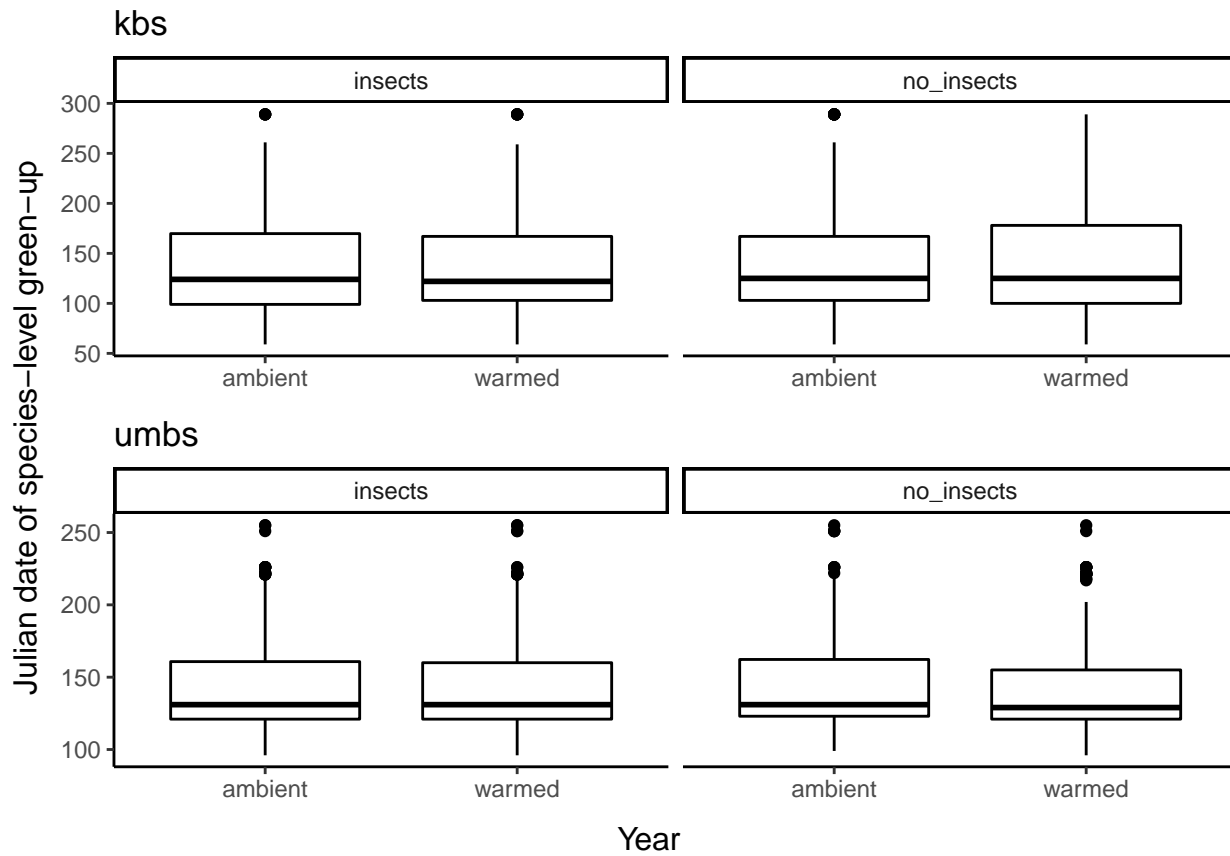**Box plot for greenup for KBS and UMBS - Plot half cover date**

Averaging greenup over all years - plot level

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

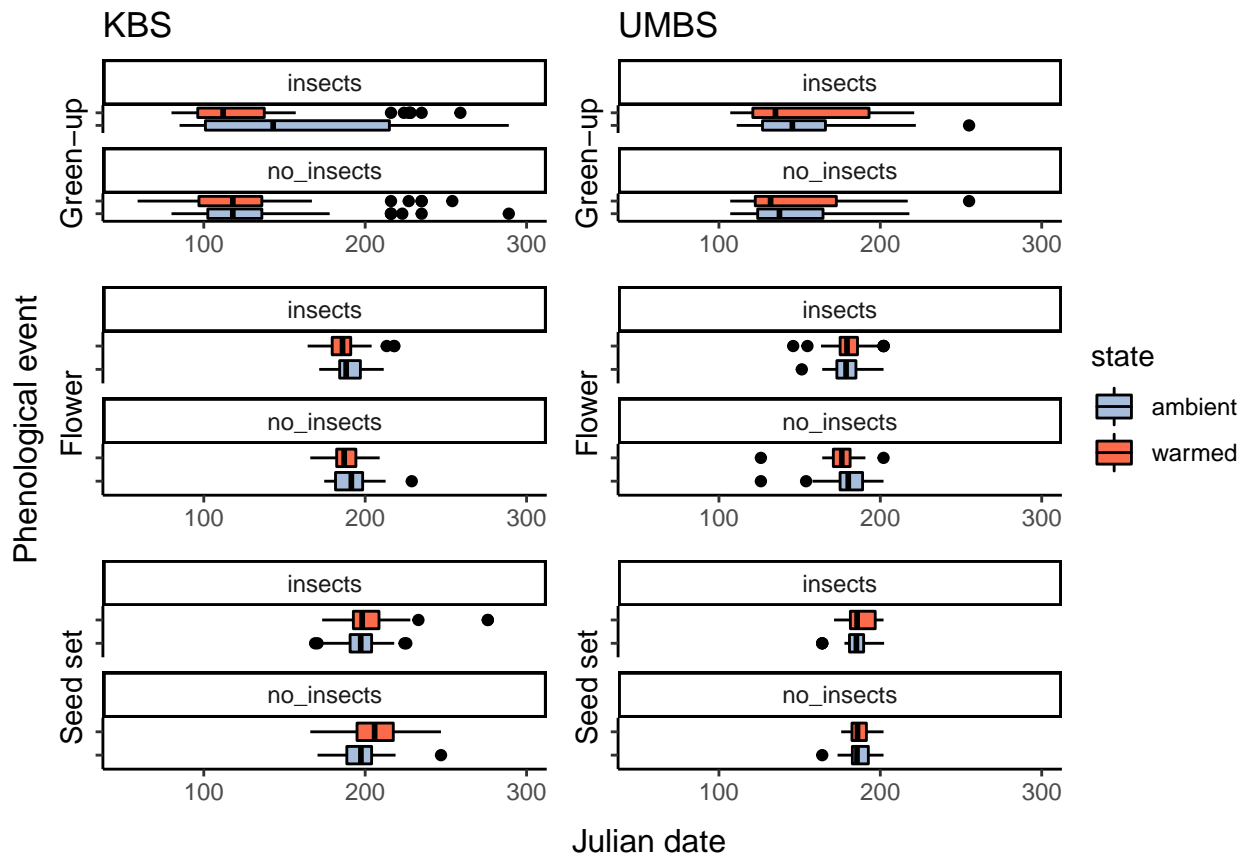**Averaging greenup over all years - species level**

Combining greenup, flower, and seed into one figure - plot level
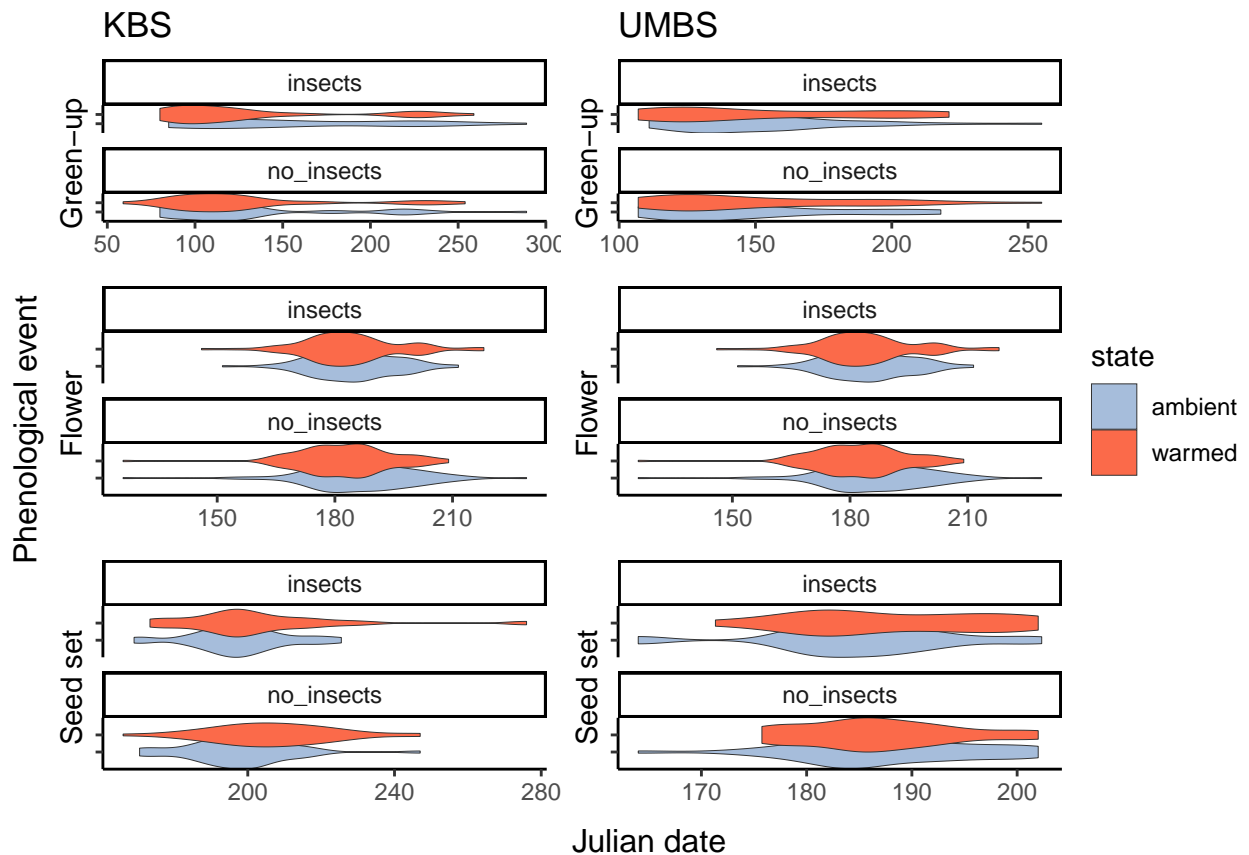
```
## pdf
##   2
```

Combining greenup, flower, and seed into one figure - plot level

Swapping axis

Combining greenup, flower, and seed into one figure - plot level

Violin plot

Combining greenup, flower, and seed into one figure - plot level

Line plot - code from Moriah

```r
# greenup
sum_green_plot$year <- as.factor(sum_green_plot$year)
gr_line <- function(loc) {
  gr_plot <- subset(sum_green_plot, site == loc)
  return(ggplot(gr_plot, aes(x = year, y = avg_julian, group = state)) +
                geom_errorbar(aes(ymin=avg_julian-se, ymax=avg_julian+se), width=.1) +
          geom_line(aes(color=state), size = 1) +
          geom_point(aes(color=state), size = 2) +
          scale_color_manual(values = c("#a6bddb", "#fb6a4a"), labels=c("Ambient","Warmed")) +
          labs(x = NULL, y = "Green-up", title = loc, color="Treatment") +
          theme_bw(14))
}
gr_line_kbs <- gr_line("KBS")
gr_line_kbs <- gr_line_kbs + theme(axis.text.x=element_blank())
gr_line_umbs <- gr_line("UMBS")
gr_line_umbs <- gr_line_umbs + labs(y=NULL) + theme(axis.text.x=element_blank())

#flower
sum_flwr_plot$year <- as.factor(sum_flwr_plot$year)
```

```r
flwr_line <- function(loc) {
  flwr_plot <- subset(sum_flwr_plot, site == loc)
  return(ggplot(flwr_plot, aes(x = year, y = avg_julian, group = state)) +
                geom_errorbar(aes(ymin=avg_julian-se, ymax=avg_julian+se), width=.1) +
          geom_line(aes(color=state), size = 1) +
          geom_point(aes(color=state), size = 2) +
          scale_color_manual(values = c("#a6bddb", "#fb6a4a"), labels=c("Ambient","Warmed")) +
          labs(x = NULL, y = "Flowering", title=loc, color="Treatment") +
          theme_bw(14))
}
flwr_line_kbs <- flwr_line("KBS")
flwr_line_kbs <- flwr_line_kbs + theme(axis.text.x=element_blank()) + labs(title=NULL)
flwr_line_umbs <- flwr_line("UMBS")
flwr_line_umbs <- flwr_line_umbs + labs(y=NULL, title=NULL) + theme(axis.text.x=element_blank())

#seed
sum_sd_plot$year <- as.factor(sum_sd_plot$year)
sd_line <- function(loc) {
  sd_plot <- subset(sum_sd_plot, site == loc)
  return(ggplot(sd_plot, aes(x = year, y = avg_julian, group = state)) +
                geom_errorbar(aes(ymin=avg_julian-se, ymax=avg_julian+se), width=.1) +
          geom_line(aes(color=state), size = 1) +
          geom_point(aes(color=state), size = 2) +
          scale_color_manual(values = c("#a6bddb", "#fb6a4a"),labels=c("Ambient","Warmed")) +
          labs(x = NULL, y = "Seed set", title=loc, color="Treatment") +
          theme_bw(14))
}
sd_line_kbs <- sd_line("KBS")
sd_line_kbs <- sd_line_kbs + labs(title=NULL)
sd_line_umbs <- sd_line("UMBS")
sd_line_umbs <- sd_line_umbs + labs(y=NULL, title=NULL)

phen_line <- ggpubr::ggarrange(gr_line_kbs, gr_line_umbs,
                          flwr_line_kbs, flwr_line_umbs,
                          sd_line_kbs, sd_line_umbs,
                          nrow = 3, ncol = 2, common.legend = T, legend="right")
png("greenup_plots_L2_all_phenology_line.png", units="in", width=9, height=8, res=300)
annotate_figure(phen_line,
            left = text_grob("Phenological event julian date", color = "black", rot = 90, size=15),
            bottom = text_grob("Year", color = "black", size=15))
dev.off()
```

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

Combining greenup, flower, and seed into one figure - plot level

Line plot with insecticide - code from Moriah

note to self: left off here, go back up & re-summarize data with insecticide included

```r
# greenup
sum_green_plot_i$year <- as.factor(sum_green_plot_i$year)
sum_green_plot_i$full_treat <- paste(sum_green_plot_i$state, sum_green_plot_i$insecticide, sep="_")
```

```r
gr_line_i <- function(loc) {
        gr_plot <- subset(sum_green_plot_i, site == loc)
        return(ggplot(gr_plot, aes(x = year, y = avg_julian, group=full_treat, linetype=full_treat, col
                        geom_errorbar(aes(ymin=avg_julian-se, ymax=avg_julian+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 = "Green-up", title = loc) +
                        theme_bw(14))
}
gr_line_i_kbs <- gr_line_i("KBS")
gr_line_i_kbs <- gr_line_i_kbs + theme(axis.text.x=element_blank())
gr_line_i_umbs <- gr_line_i("UMBS")
gr_line_i_umbs <- gr_line_i_umbs + labs(y=NULL) + theme(axis.text.x=element_blank())

#flower
sum_flwr_plot_i$year <- as.factor(sum_flwr_plot_i$year)
sum_flwr_plot_i$full_treat <- paste(sum_flwr_plot_i$state, sum_flwr_plot_i$insecticide, sep="_")
flwr_line_i <- function(loc) {
        flwr_plot <- subset(sum_flwr_plot_i, site == loc)
        return(ggplot(flwr_plot, aes(x = year, y = avg_julian, group=full_treat, linetype=full_treat, co
                        geom_errorbar(aes(ymin=avg_julian-se, ymax=avg_julian+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 = "Flowering", title = loc) +
                        theme_bw(14))
}
flwr_line_i_kbs <- flwr_line_i("KBS")
flwr_line_i_kbs <- flwr_line_i_kbs + theme(axis.text.x=element_blank()) + labs(title=NULL)
flwr_line_i_umbs <- flwr_line_i("UMBS")
flwr_line_i_umbs <- flwr_line_i_umbs + labs(y=NULL, title=NULL) + theme(axis.text.x=element_blank())

#seed
sum_sd_plot_i$year <- as.factor(sum_sd_plot_i$year)
sum_sd_plot_i$full_treat <- paste(sum_sd_plot_i$state, sum_sd_plot_i$insecticide, sep="_")
sd_line_i <- function(loc) {
        sd_plot <- subset(sum_sd_plot_i, site == loc)
        return(ggplot(sd_plot, aes(x = year, y = avg_julian, group=full_treat, linetype=full_treat, col
                        geom_errorbar(aes(ymin=avg_julian-se, ymax=avg_julian+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 Herbivor
                     labs(x = NULL, y = "Flowering", title = loc) +
                     theme_bw(14))
}
sd_line_i_kbs <- sd_line_i("KBS")
sd_line_i_kbs <- sd_line_i_kbs + labs(title=NULL)
sd_line_i_umbs <- sd_line_i("UMBS")
sd_line_i_umbs <- sd_line_i_umbs + labs(y=NULL, title=NULL)

phen_line_i <- ggpubr::ggarrange(gr_line_i_kbs, gr_line_i_umbs,
                     flwr_line_i_kbs, flwr_line_i_umbs,
                     sd_line_i_kbs, sd_line_i_umbs,
                     nrow = 3, ncol = 2, common.legend = T, legend="right")
#png("greenup_plots_L2_all_phenology_line_insect.png", units="in", width=9, height=8, res=300)
annotate_figure(phen_line_i,
               left = text_grob("Phenological event julian date", color = "black", rot = 90, size=15),
               bottom = text_grob("Year", color = "black", size=15))
```
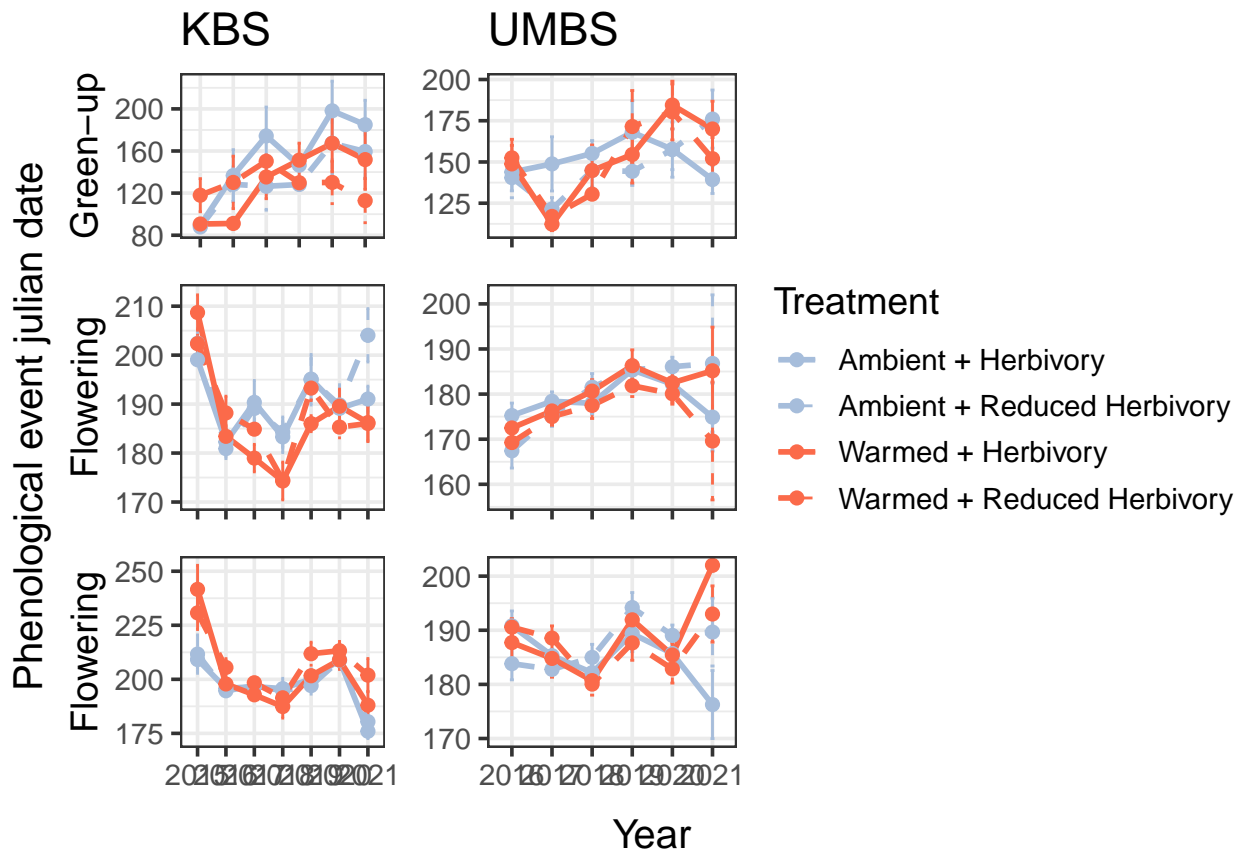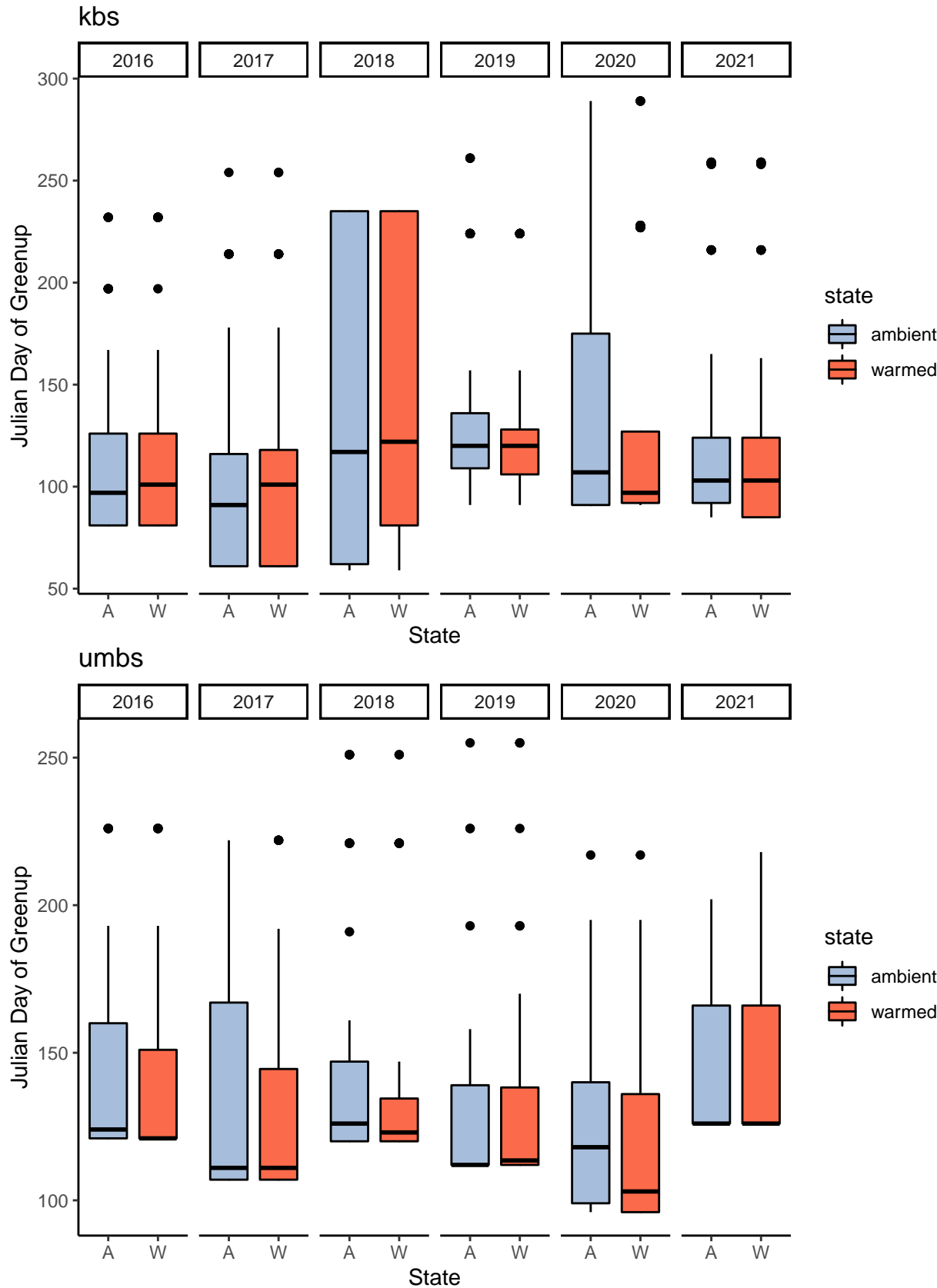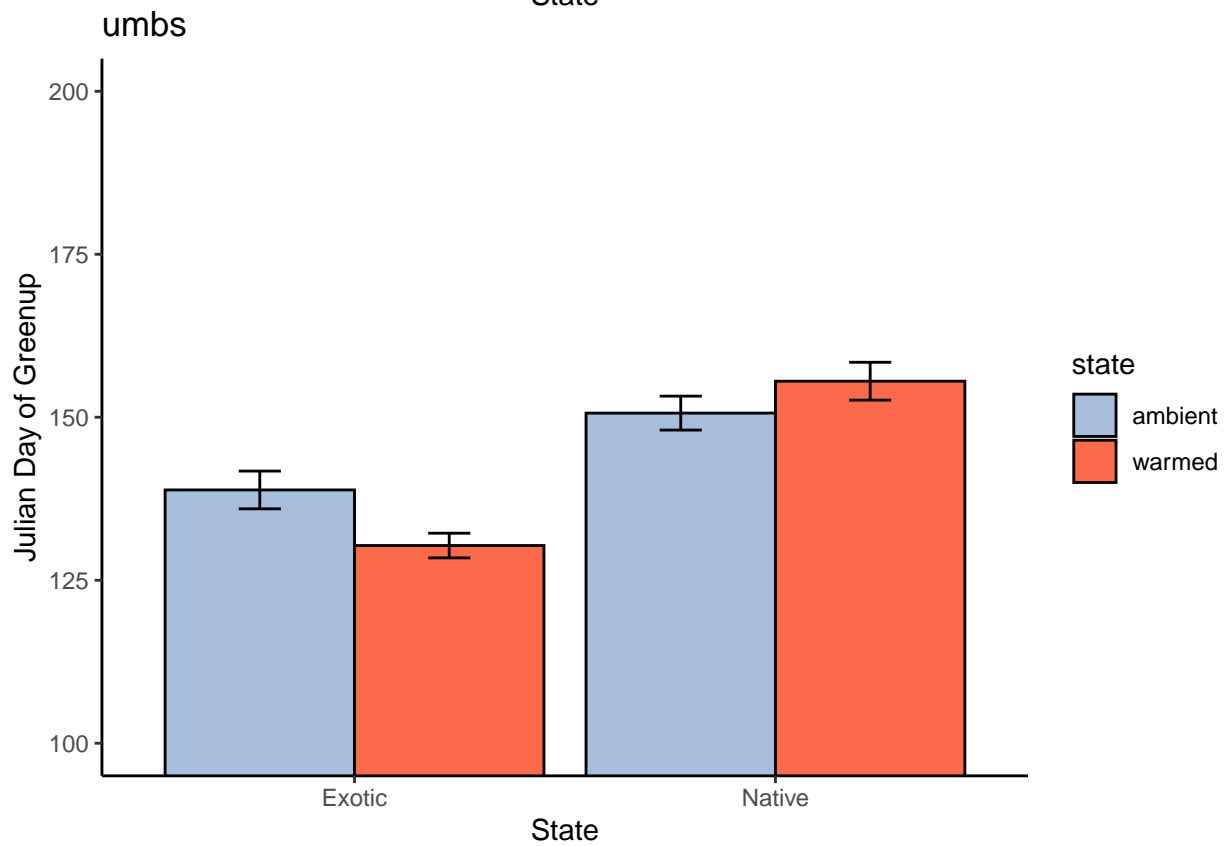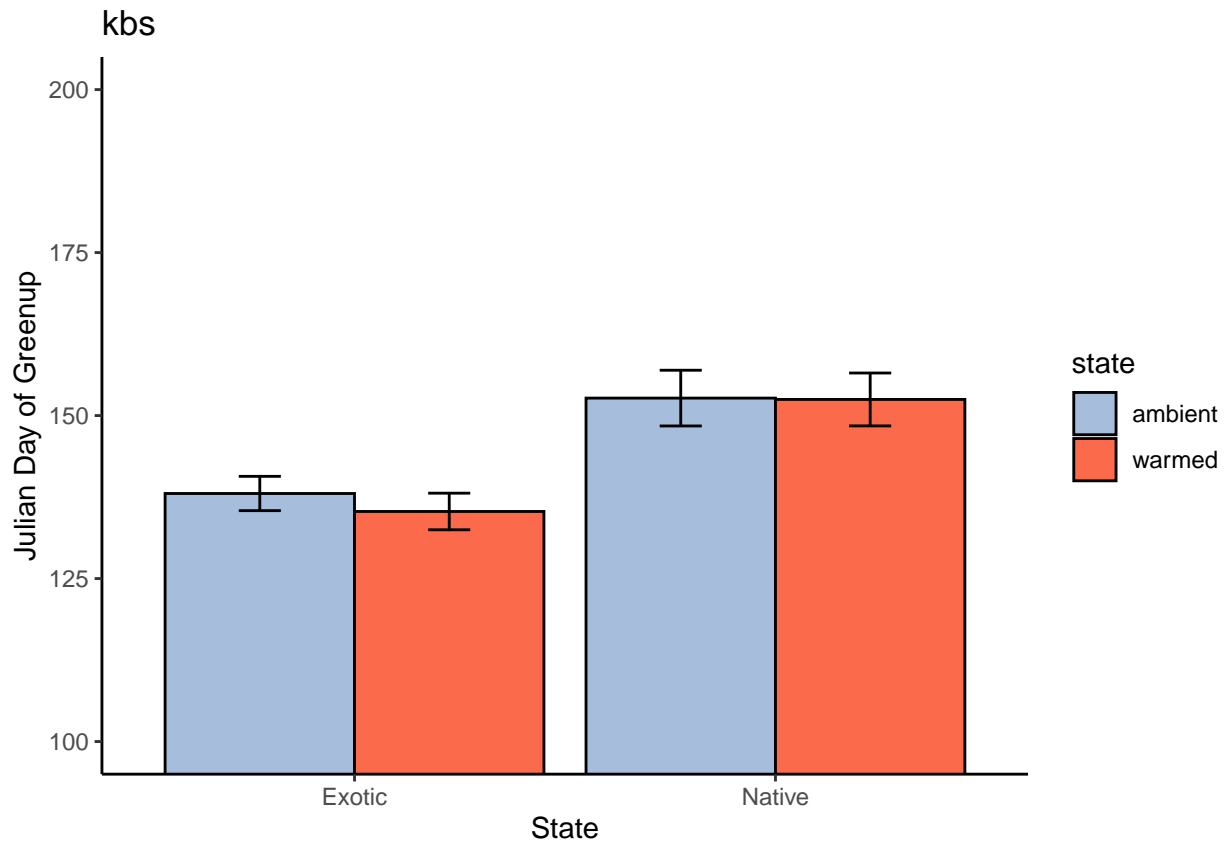


```
#dev.off()
```

Bar plot for greenup for KBS and UMBS - Species min cover date
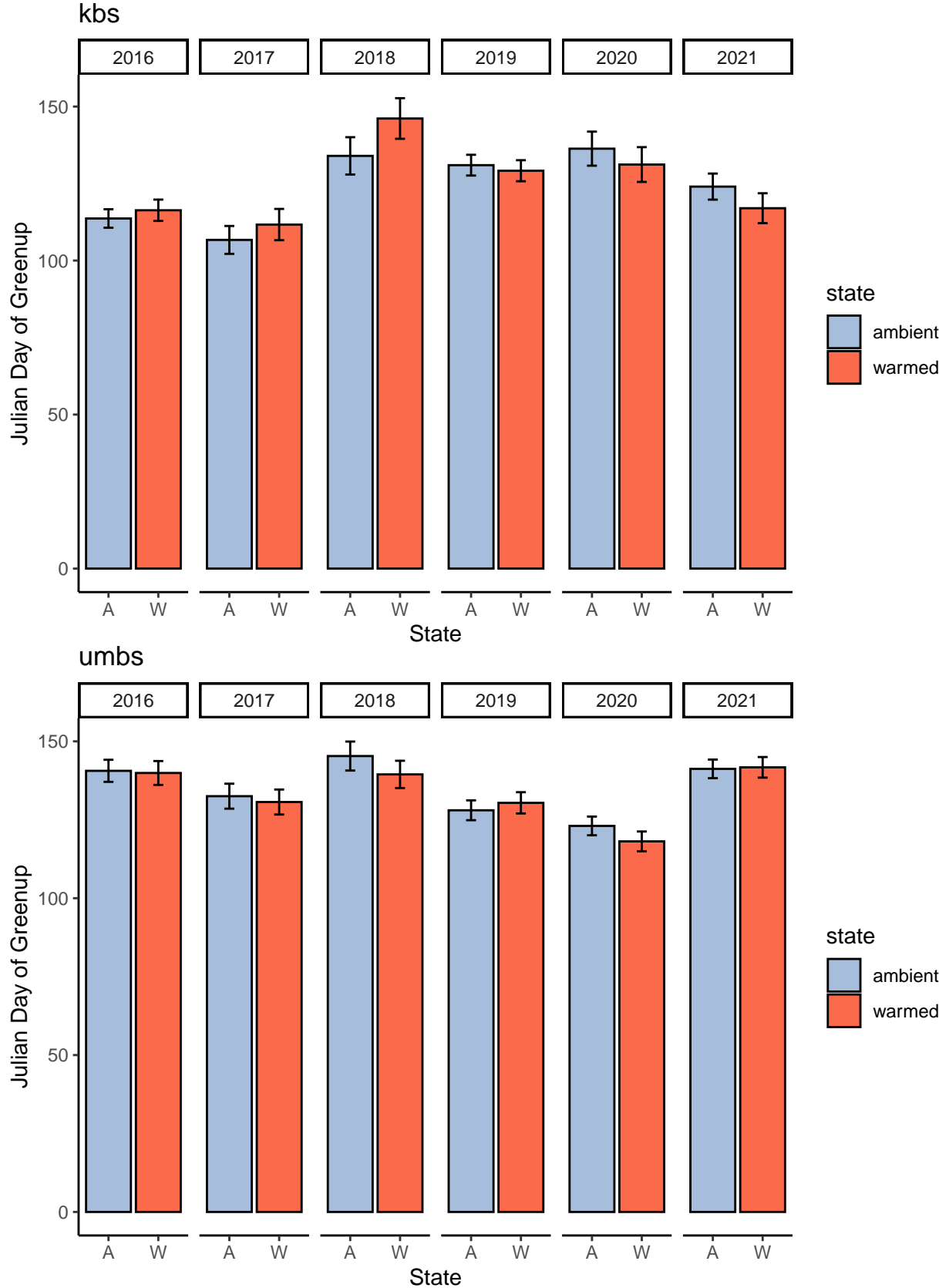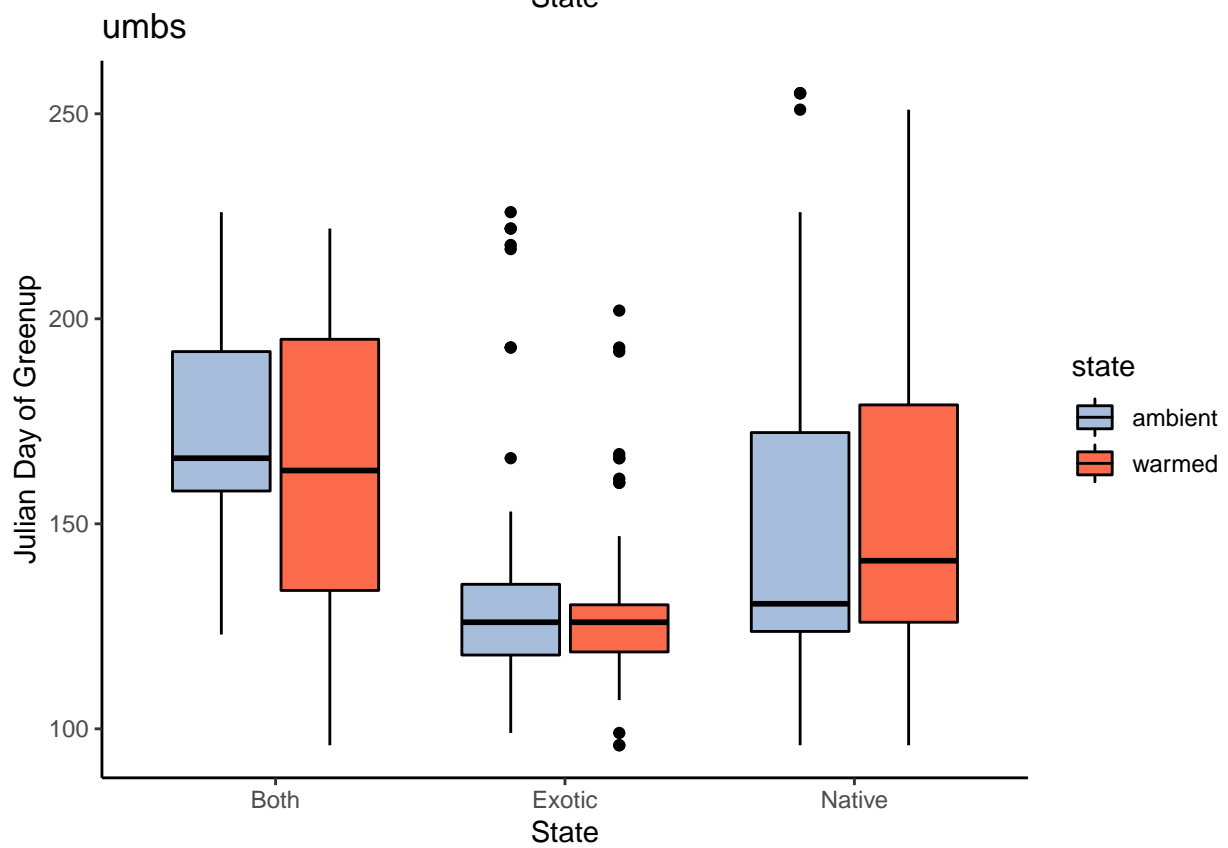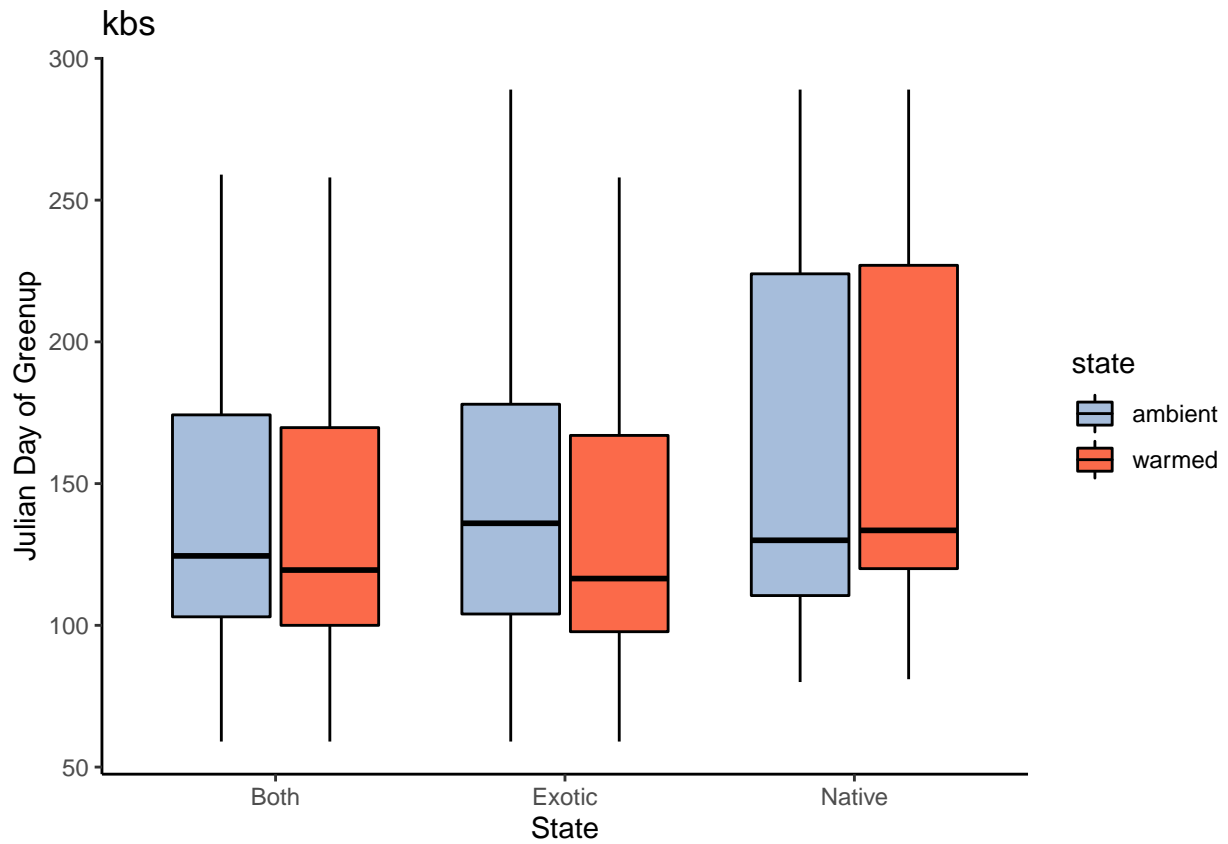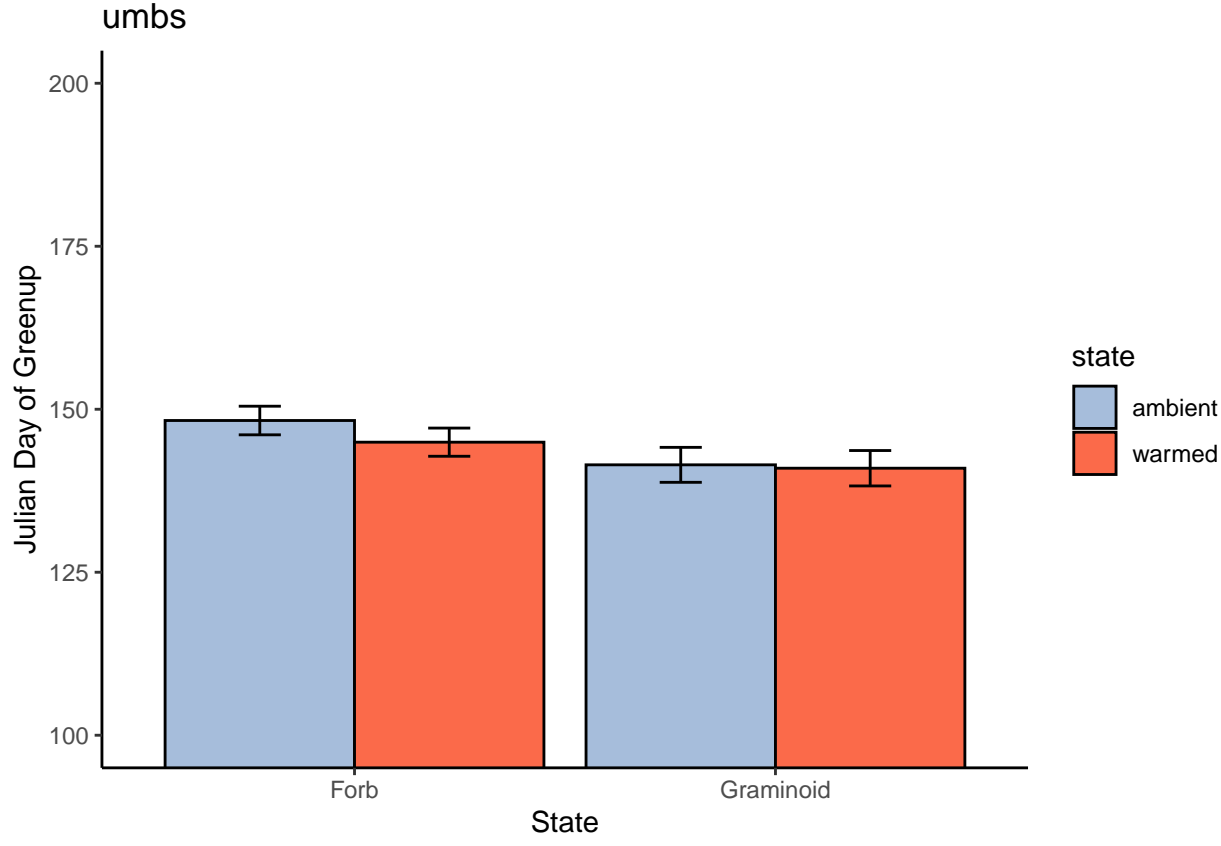
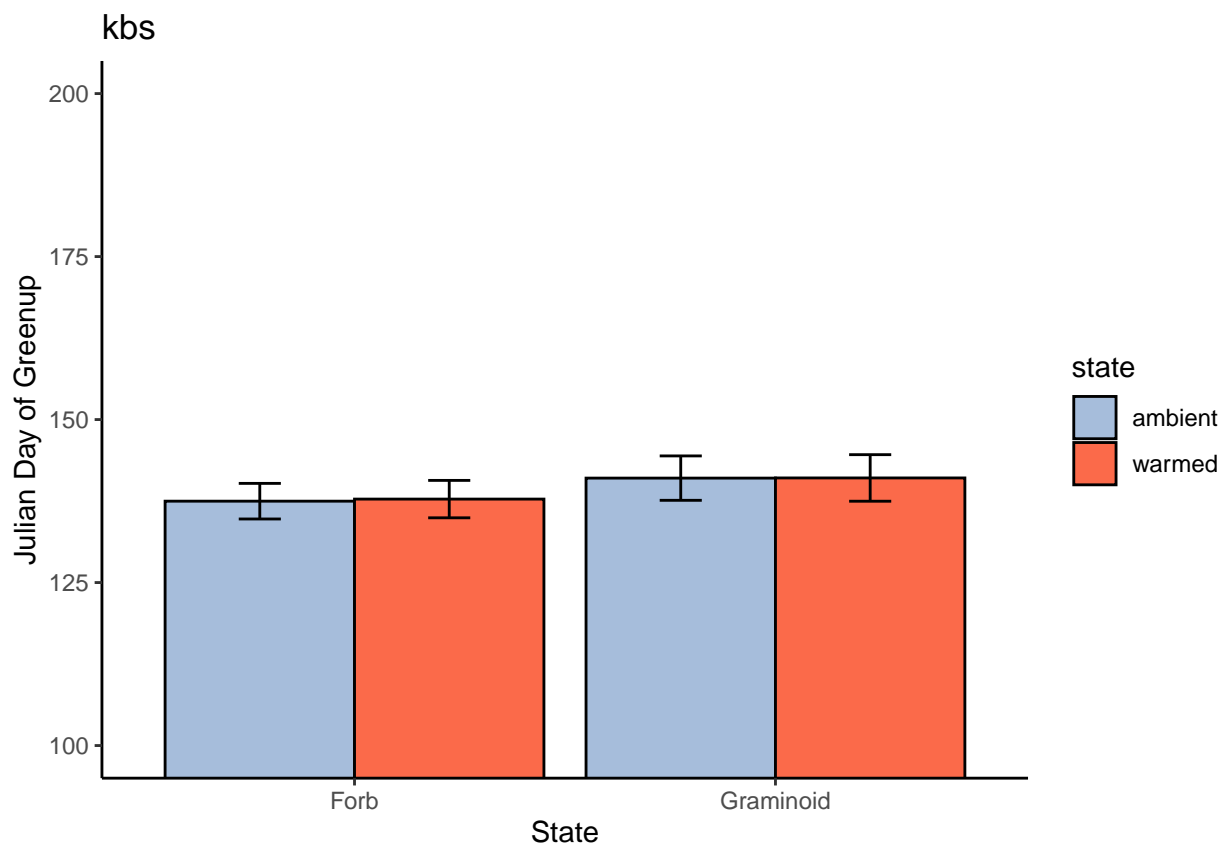**Box plot for greenup for KBS and UMBS - Species min cover date**

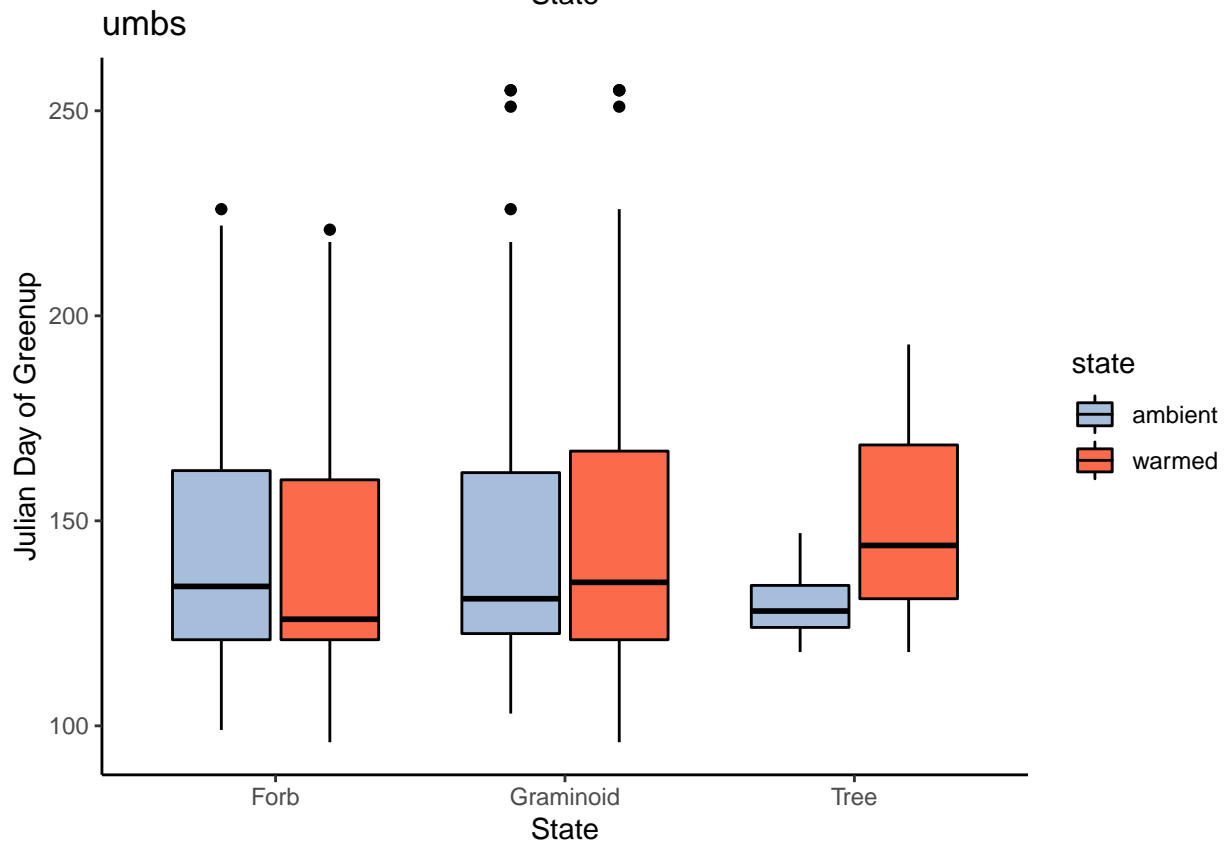**Plot for warmed vs ambient greenup between native and exotic - Species half cover date**
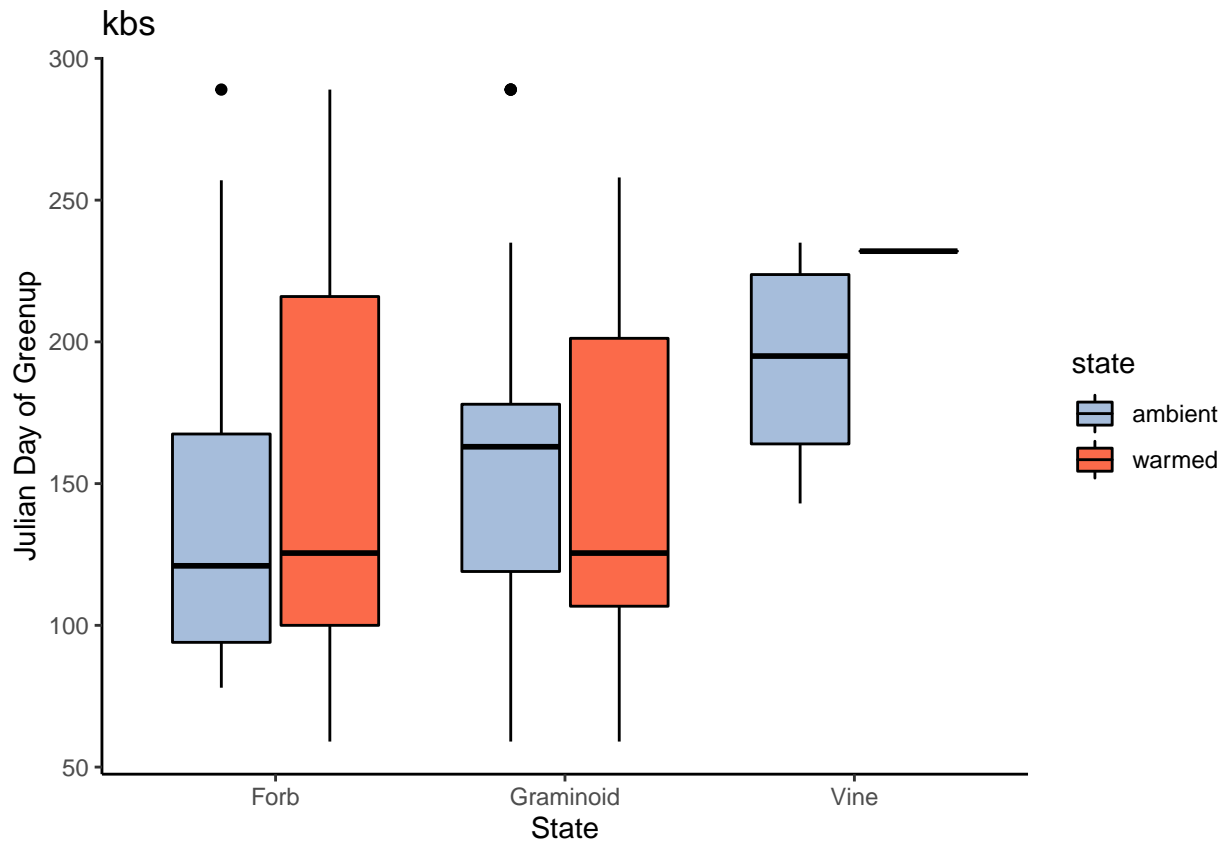
Plot for warmed vs ambient greenup between native and exotic - Plot half cover date

Plot for warmed vs ambient greenup between growth types - Species half cover date

Plot for warmed vs ambient greenup between growth types - Plot half cover date

kbs

umbs

Greenup plot for a given site and species - half cover date

Ex: Soca at KBS, Cest at UMBS

Soca

Cest