Biomass Plots

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TITLE: Biomass plots

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DATA INPUT: Data imported as csv files from shared Google drive L0 folder

DATA OUTPUT: Visualizations of biomass data

PROJECT: warmXtrophic

DATE: March 2022

```r
# Clear all existing data
rm(list=ls())

#Load packages
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.3     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(plotrix)
library(ggpubr)
library(emmeans)

# Get data
Sys.getenv("L1DIR")
```

```
## [1] "/Volumes/GoogleDrive-117472253521803368412/Shared drives/SpaCE_Lab_warmXtrophic/data/L1/"
```

```r
L1_dir<-Sys.getenv("L1DIR")
list.files(L1_dir)
```

```
##  [1] "ANPP"            "climate_data"      "CN"
##  [4] "Greenness"       "herbivory"         "HOBO_data"
```

```
##  [7] "PAR"                "phenology"         "plant_composition"
## [10] "SLA"
kbs_biomass_21 <- read.csv(file.path(L1_dir, "ANPP/kbs_biomass_2021_L1.csv"))
umbs_biomass_21 <- read.csv(file.path(L1_dir, "ANPP/umbs_biomass_2021_L1.csv"))
kbs_biomass_21 <- kbs_biomass_21 %>% dplyr::select(-X) # get rid of "X" column that shows up (could fix
umbs_biomass_21 <- umbs_biomass_21 %>% dplyr::select(-X)

# making separate dataframe for biomass - easier in plots
kbs_biomass_only <- kbs_biomass_21 %>%
        select(-cover) %>%
        drop_na(weight_g)
umbs_biomass_only <- umbs_biomass_21 %>%
        select(-cover) %>%
        drop_na(weight_g)

# remove uninformative species
kbs_biomass_live <- kbs_biomass_only[!grepl("Litter", kbs_biomass_only$species),]
kbs_biomass_live <- kbs_biomass_live[!grepl("Umsp", kbs_biomass_live$species),]
umbs_biomass_live <- umbs_biomass_only[!grepl("Litter", umbs_biomass_only$species),]
umbs_biomass_live <- umbs_biomass_live[!grepl("Standing_Dead", umbs_biomass_live$species),]
umbs_biomass_live <- umbs_biomass_live[!grepl("Surface_Litter", umbs_biomass_live$species),]
umbs_biomass_live <- umbs_biomass_live[!grepl("Lisp", umbs_biomass_live$species),]
umbs_biomass_live <- umbs_biomass_live[!grepl("Umsp", umbs_biomass_live$species),]

# keeping species found only in w and a
kbs_biomass_live2 <- kbs_biomass_live %>%
        group_by(species) %>%
        filter(all(c('warmed', 'ambient') %in% state))
umbs_biomass_live2 <- umbs_biomass_live %>%
        group_by(species) %>%
        filter(all(c('warmed', 'ambient') %in% state))

# clean insecticide labels for plotting
insect_labels <- c("insects" = "Herbivory", "no_insects" = "Reduced Herbivory")

### Overall averages btwn treatments - barplot
# plot level KBS
biomass_sum_k2 <- kbs_biomass_live %>%
        group_by(plot, state, insecticide) %>%
        summarize(avg_weight = sum(weight_g, na.rm = TRUE))

## `summarise()` regrouping output by 'plot', 'state' (override with `.groups` argument)

biomass_sum_k3 <- biomass_sum_k2 %>%
        group_by(state, insecticide) %>%
        summarize(average_weight = mean(avg_weight, na.rm = TRUE),
                  se = std.error(avg_weight, na.rm = TRUE))

## `summarise()` regrouping output by 'state' (override with `.groups` argument)

kbs_bio <- ggplot(biomass_sum_k3, aes(x = state, y = average_weight, fill = state)) +
        facet_grid(.~insecticide, labeller = as_labeller(insect_labels)) +
        geom_bar(position = "identity", stat = "identity", col = "black") +
        geom_errorbar(aes(ymin = average_weight - se, ymax = average_weight + se), width = 0.2,
                      position = "identity") +
```

```r
        labs(title="KBS", y="", x="") +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_x_discrete(labels=c("ambient" = "", "warmed" = "")) +
        theme_classic()

# plot level UMBS
biomass_sum_u2 <- umbs_biomass_live %>%
        group_by(plot, state, insecticide) %>%
        summarize(avg_weight = sum(weight_g, na.rm = TRUE))
```

`summarise()` regrouping output by 'plot', 'state' (override with `.groups` argument)

```r
biomass_sum_u3 <- biomass_sum_u2 %>%
        group_by(state, insecticide) %>%
        summarize(average_weight = mean(avg_weight, na.rm = TRUE),
                  se = std.error(avg_weight, na.rm = TRUE))
```

`summarise()` regrouping output by 'state' (override with `.groups` argument)

```r
umbs_bio <- ggplot(biomass_sum_u3, aes(x = state, y = average_weight, fill = state)) +
        facet_grid(.~insecticide, labeller = as_labeller(insect_labels)) +
        geom_bar(position = "identity", stat = "identity", col = "black") +
        geom_errorbar(aes(ymin = average_weight - se, ymax = average_weight + se), width = 0.2,
                  position = "identity") +
        labs(title="UMBS", y="", x="")+
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
        theme_classic()

biomass_comb <- ggpubr::ggarrange(kbs_bio, umbs_bio,
                                  nrow = 2, common.legend = T, legend="none")
#png("biomass_plots_L2_barplot.png", units="in", width=8, height=8, res=300)
annotate_figure(biomass_comb,
                left = text_grob("Plant Biomass (g)", color = "black", rot = 90),
                bottom = text_grob("Treatment", color = "black"))
```

KBS

UMBS

Treatment

Plant Biomass (g)
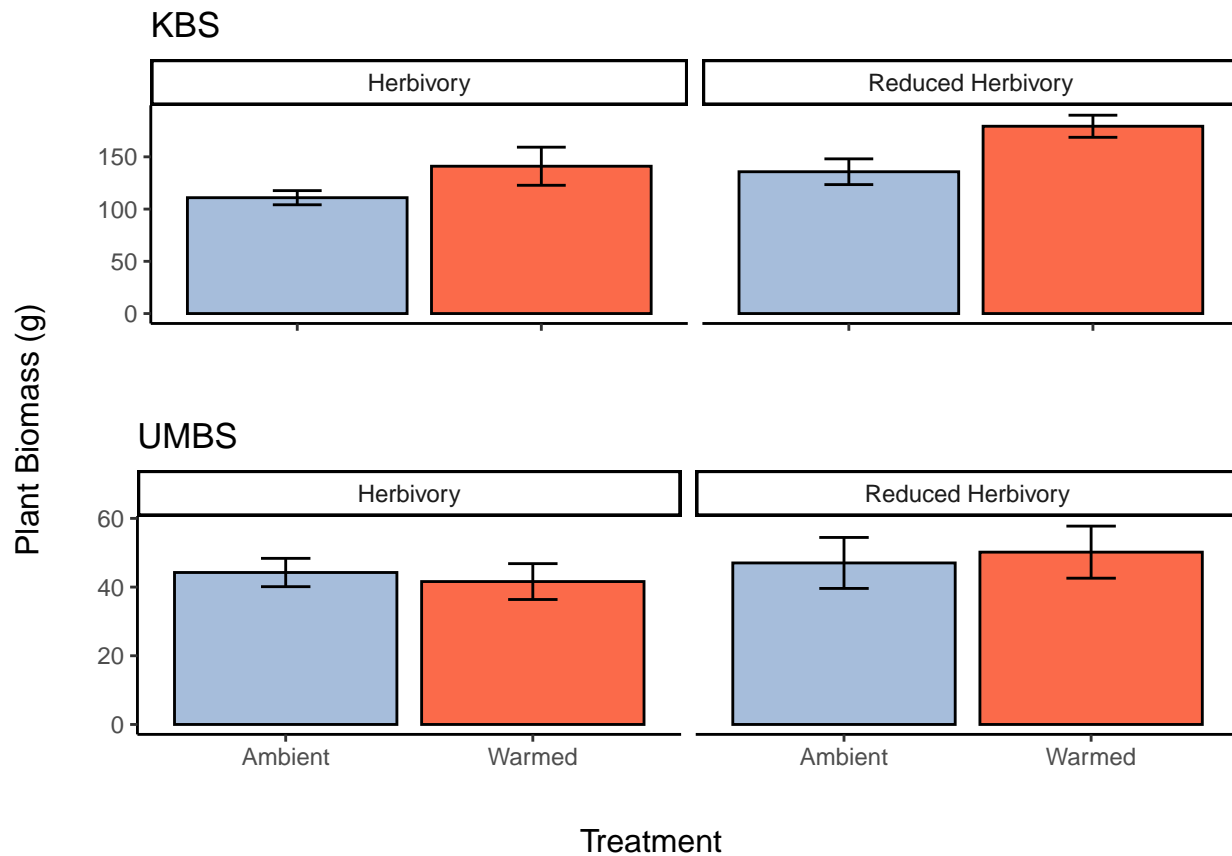
```
#dev.off()

### Overall averages btwn treatments - boxplot
# species level KBS
ggplot(kbs_biomass_live, aes(x = state, y = weight_g, fill=state)) +
        geom_boxplot(outlier.shape=NA, alpha=0.7) +
        geom_jitter(aes(alpha=0.6, color=state, fill=state), shape=16, size=2) +
        scale_color_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        labs(title="KBS - species level")+
        scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
        theme_classic()
```

KBS – species level
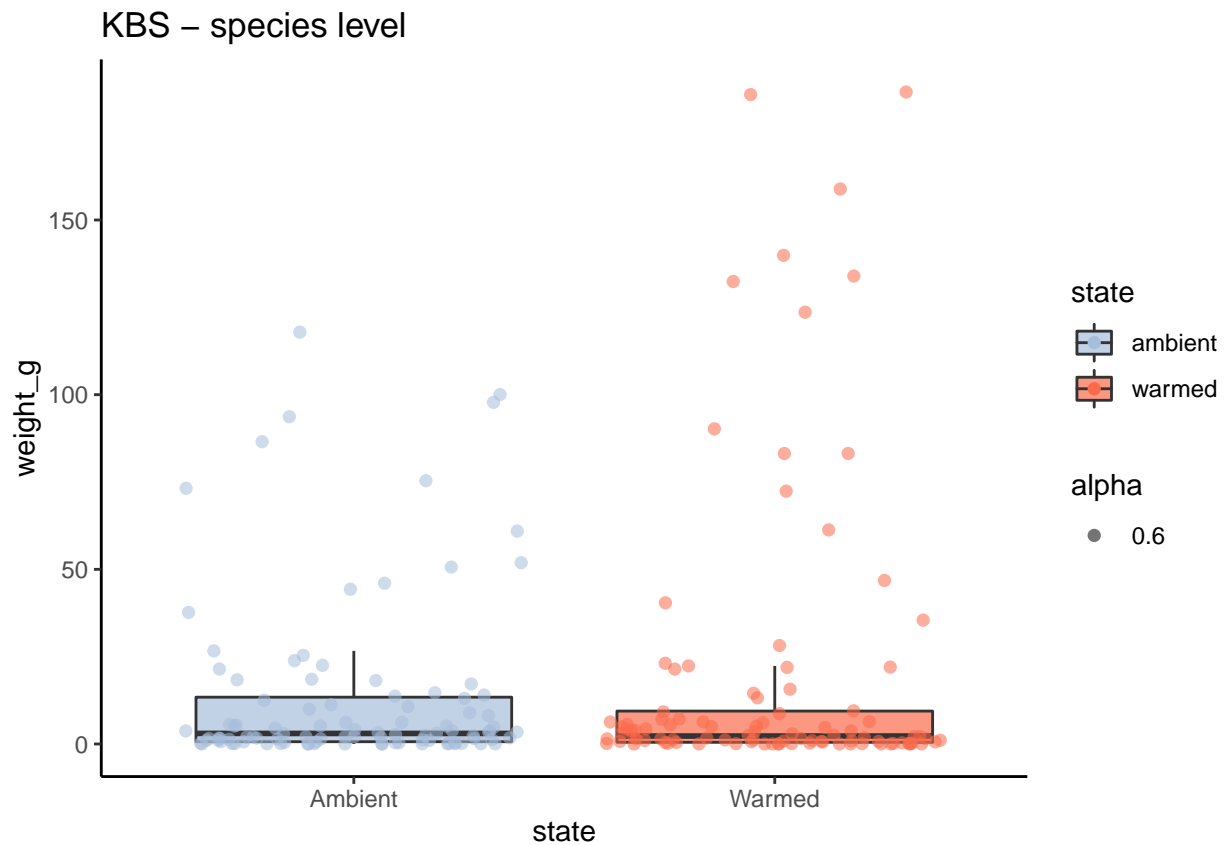
```r
# plot level KBS
ggplot(biomass_sum_k2, aes(x = state, y = avg_weight, fill=state)) +
        geom_boxplot(outlier.shape=NA, alpha=0.7) +
        geom_jitter(aes(alpha=0.6, color=state, fill=state), shape=16, size=2) +
        scale_color_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        labs(title="KBS - plot level")+
        scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
        theme_classic()
```

KBS – plot level
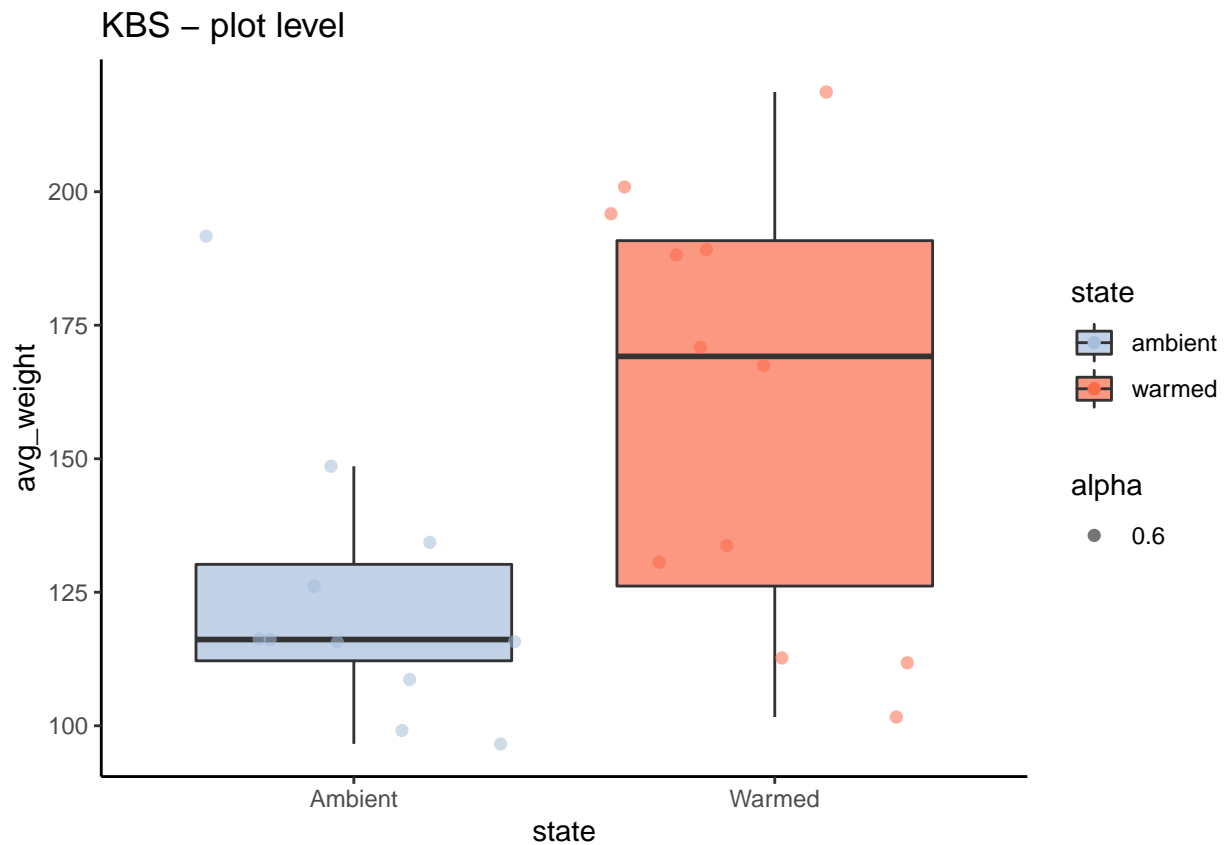
```r
# species level UMBS
ggplot(umbs_biomass_live, aes(x = state, y = weight_g, fill=state)) +
    geom_boxplot(outlier.shape=NA, alpha=0.7) +
    geom_jitter(aes(alpha=0.6, color=state, fill=state), shape=16, size=2) +
    scale_color_manual(values = c("#a6bddb", "#fb6a4a")) +
    scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
    labs(title="UMBS")+
    scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
    theme_classic()
```
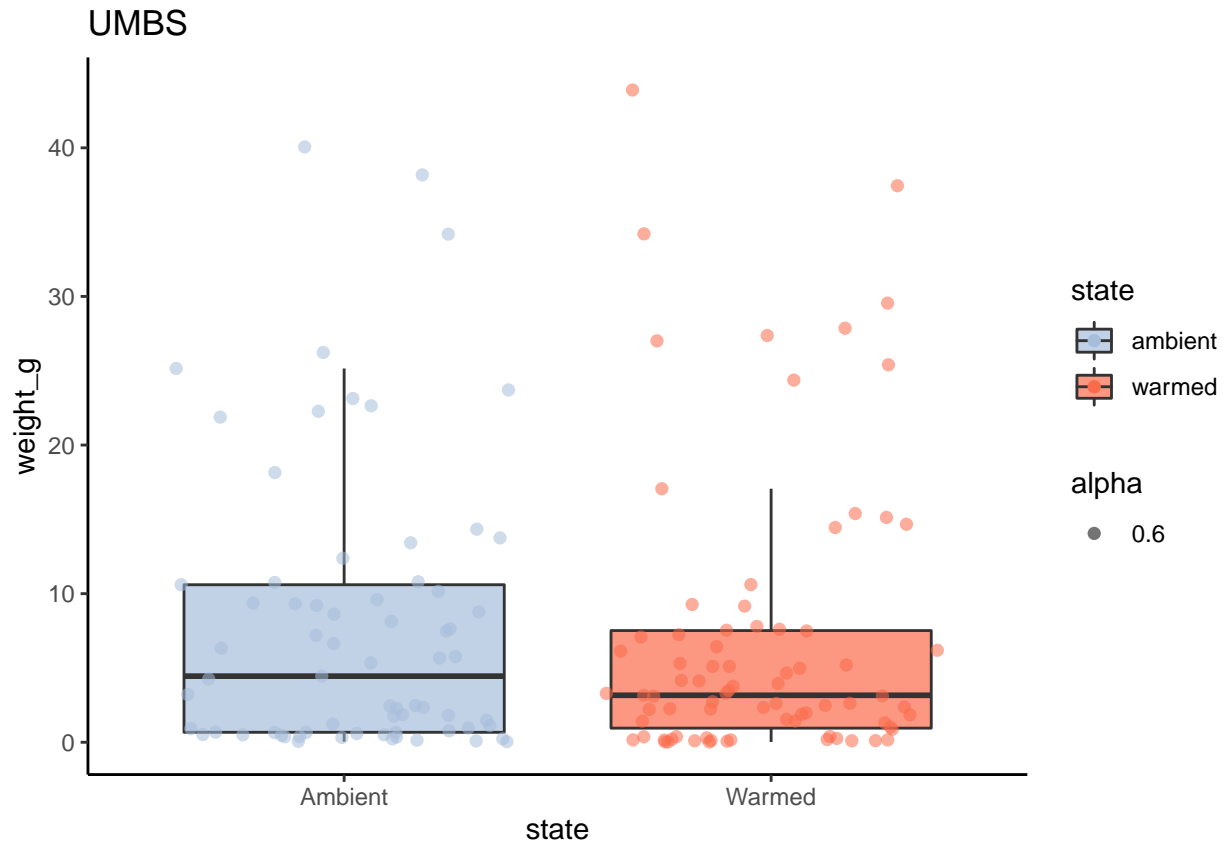
```
# plot level UMBS
ggplot(biomass_sum_u2, aes(x = state, y = avg_weight, fill=state)) +
        geom_boxplot(outlier.shape=NA, alpha=0.7) +
        geom_jitter(aes(alpha=0.6, color=state, fill=state), shape=16, size=2) +
        scale_color_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        labs(title="UMBS")+
        scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
        theme_classic()
```
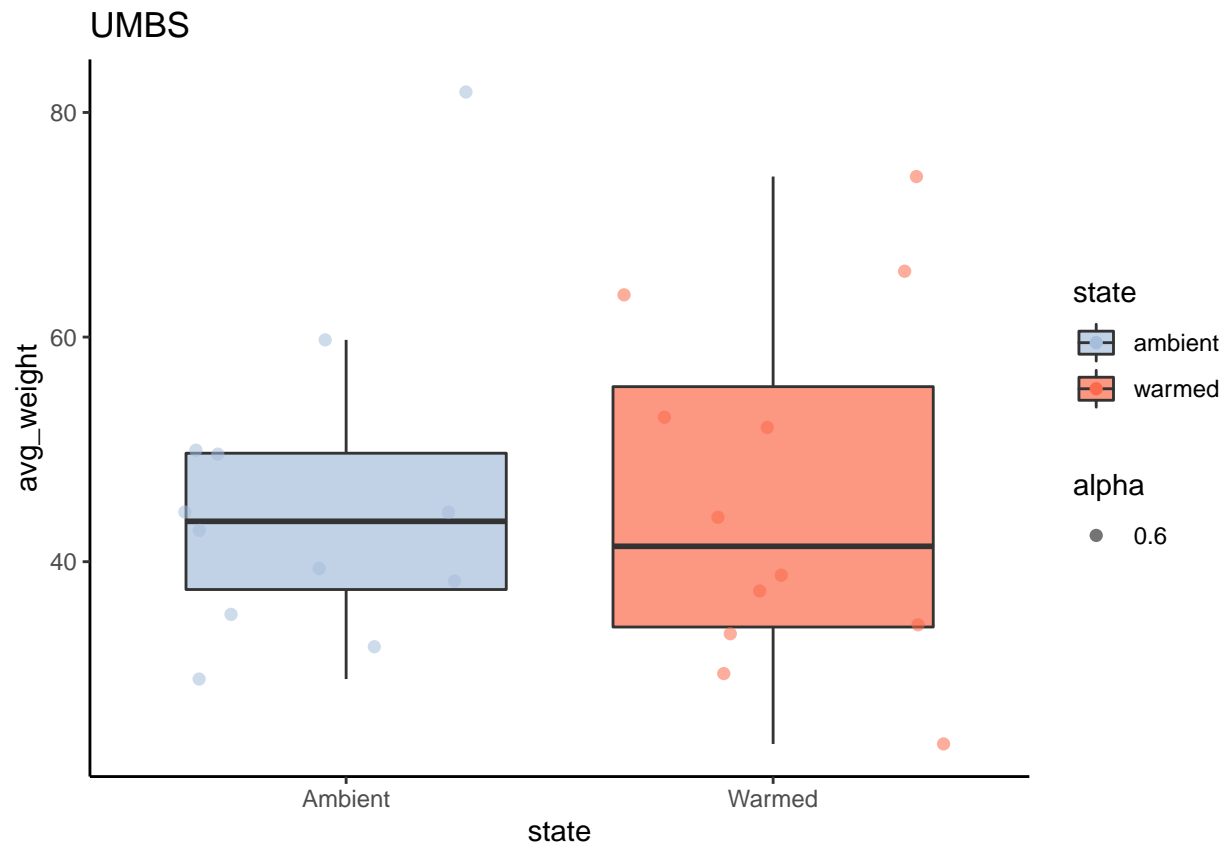
```
### Line plot of species responses to warming
mod11_k <- lm(log(weight_g) ~ state * species, kbs_biomass_live2)
emmip(mod11_k, species~state) +
        labs(title="KBS")
```
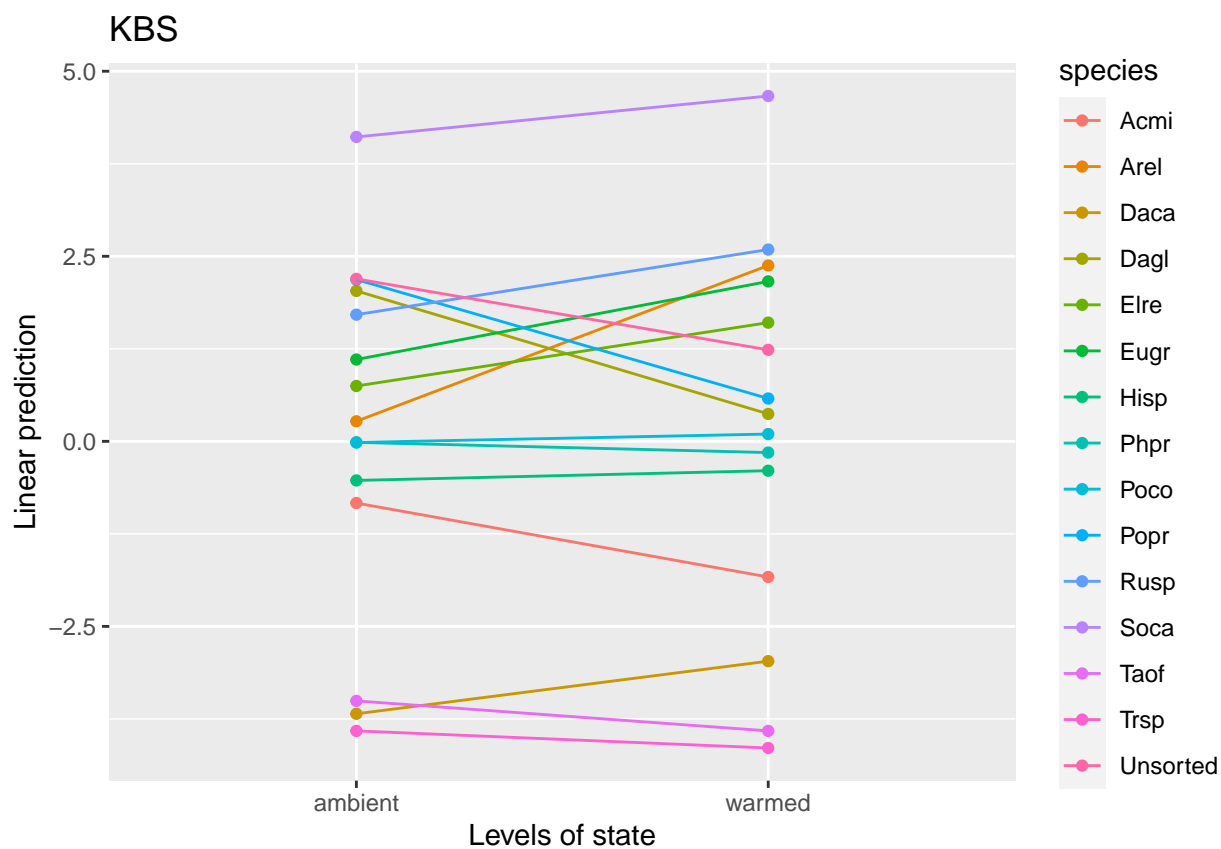
```
mod11_u <- lm(log(weight_g) ~ state * species, umbs_biomass_live2)
emmip(mod11_u, species~state)+
        labs(title="UMBS")
```
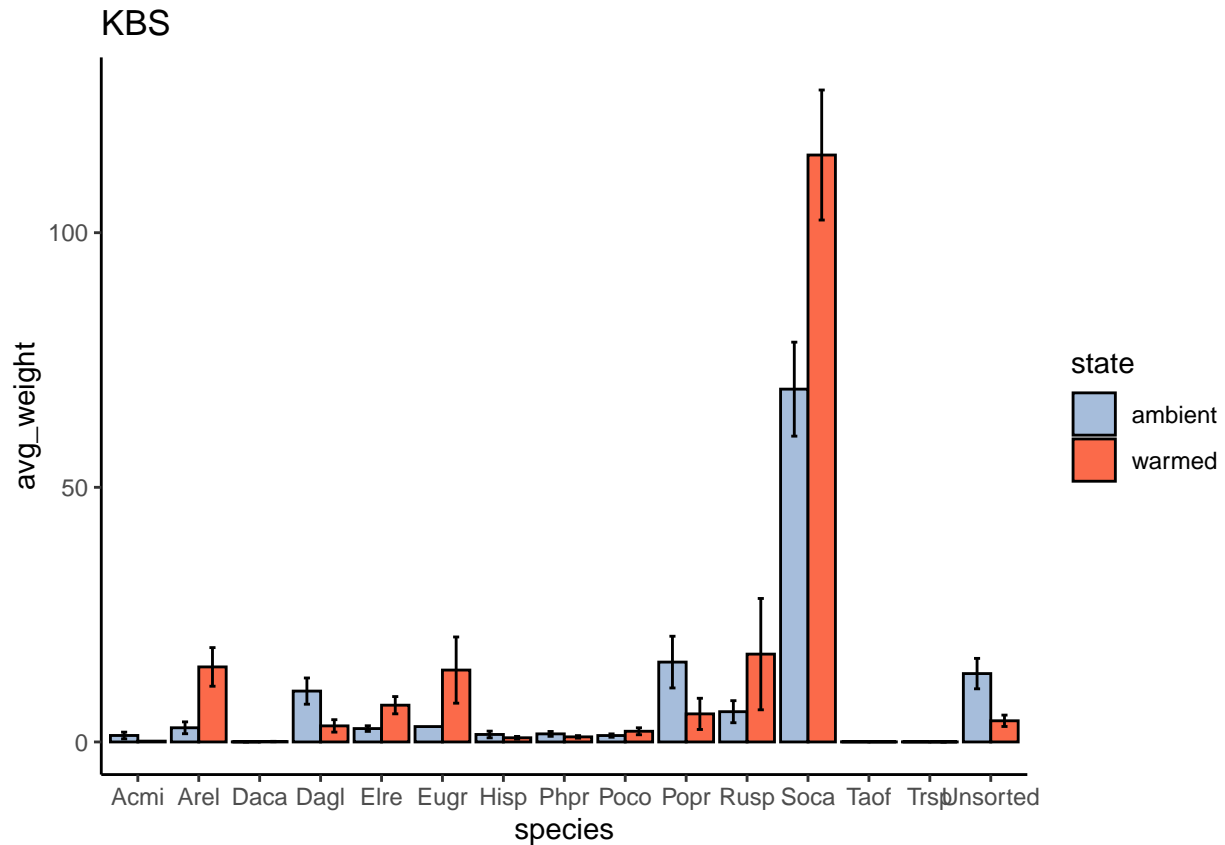
UMBS
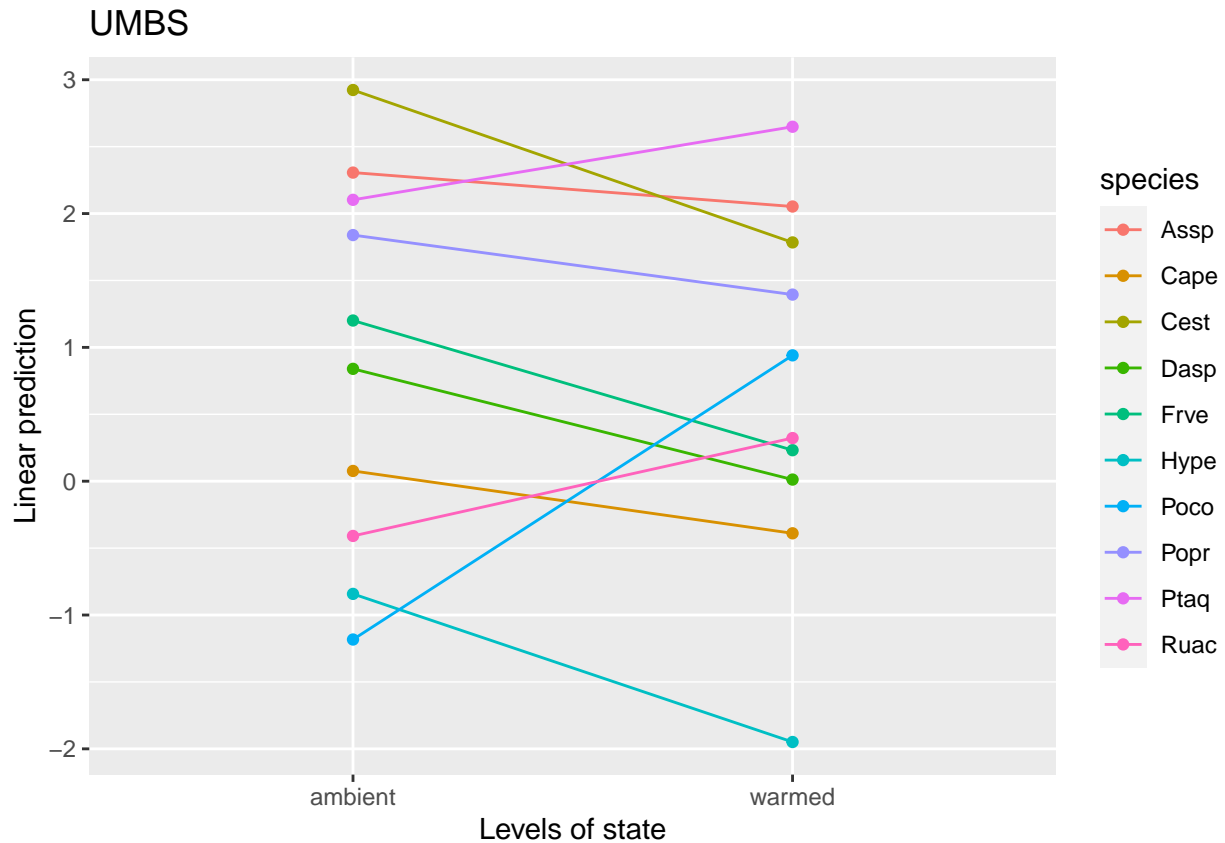
```
### Differences between warmed and ambient at a species level
biomass_spp_k <- kbs_biomass_live2 %>%
        group_by(species, state) %>%
        summarize(avg_weight = mean(weight_g, na.rm = TRUE),
                  se = std.error(weight_g, na.rm = TRUE))
```

`summarise()` regrouping output by 'species' (override with `.groups` argument)

```
ggplot(biomass_spp_k, aes(x = species, y = avg_weight, fill = state)) +
        geom_bar(position = "dodge", stat = "identity", col = "black") +
        geom_errorbar(aes(ymin = avg_weight - se, ymax = avg_weight + se), width = 0.2,
                  position = position_dodge(0.9)) +
        labs(title="KBS") +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +
        theme_classic()
```

KBS

```
biomass_spp_u <- umbs_biomass_live2 %>%
        group_by(species, state) %>%
        summarize(avg_weight = mean(weight_g, na.rm = TRUE),
                  se = std.error(weight_g, na.rm = TRUE))
```

`summarise()` regrouping output by 'species' (override with `.groups` argument)

```
ggplot(biomass_spp_u, aes(x = species, y = avg_weight, fill = state)) +
        geom_bar(position = "dodge", stat = "identity", col = "black") +
        geom_errorbar(aes(ymin = avg_weight - se, ymax = avg_weight + se), width = 0.2,
                      position = position_dodge(0.9)) +
        labs(title="UMBS") +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +
        theme_classic()
```
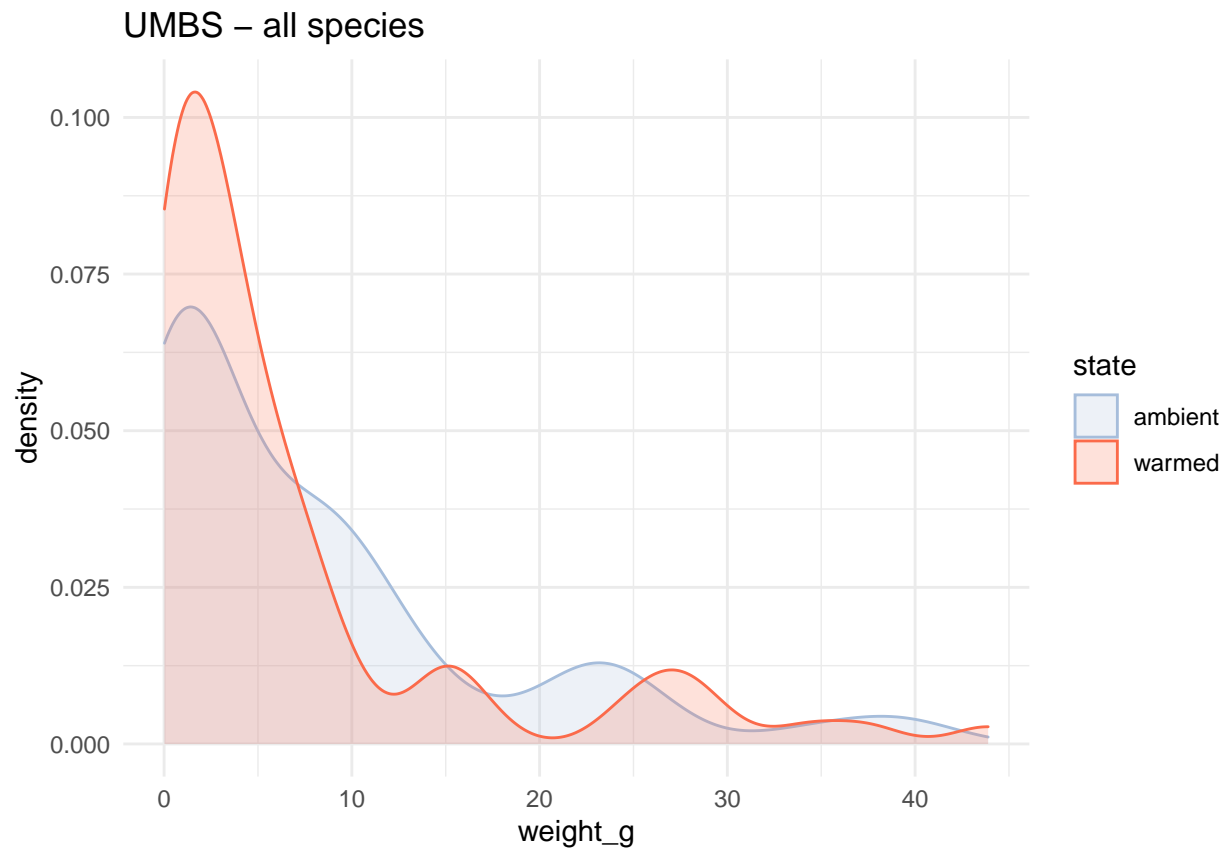
UMBS
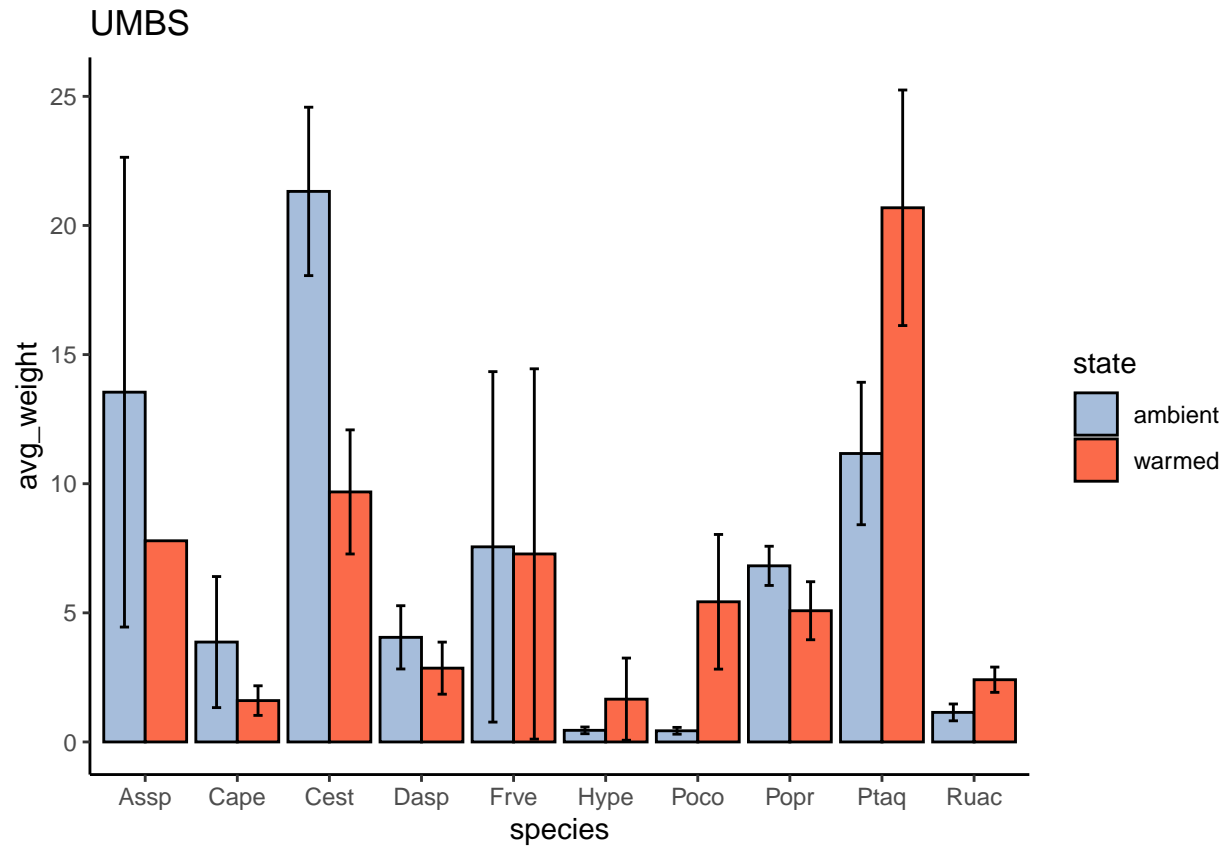
```
# Density histogram
ggplot(kbs_biomass_live, aes(weight_g, fill = state, colour = state)) +
    geom_density(alpha = 0.2) +
    labs(title="KBS - all species") +
    scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
    scale_colour_manual(values = c("#a6bddb", "#fb6a4a")) +
    theme_minimal()
```

KBS – all species
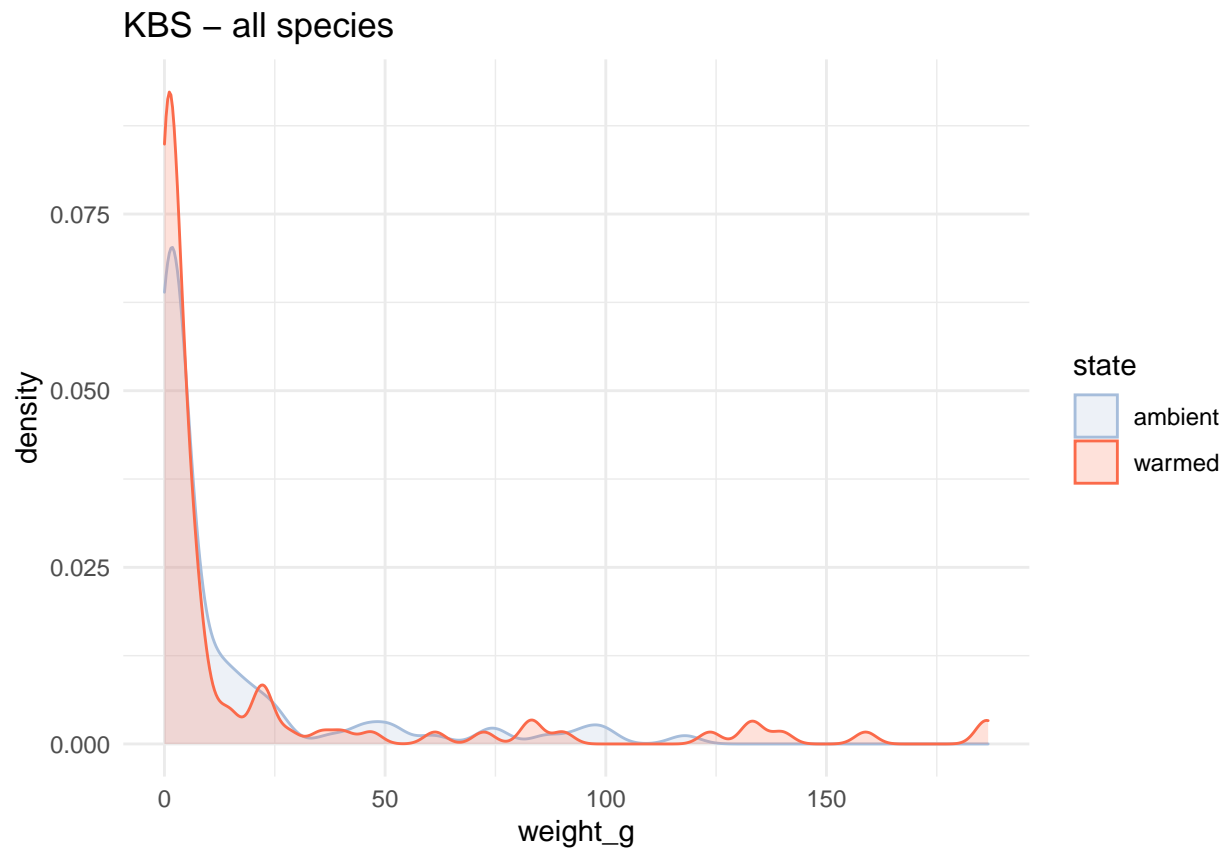

```
ggplot(biomass_sum_k2, aes(avg_weight, fill = state, colour = state)) +
    geom_density(alpha = 0.2) +
    labs(title="KBS - plot level") +
    scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
    scale_colour_manual(values = c("#a6bddb", "#fb6a4a")) +
    theme_minimal()
```

KBS – plot level
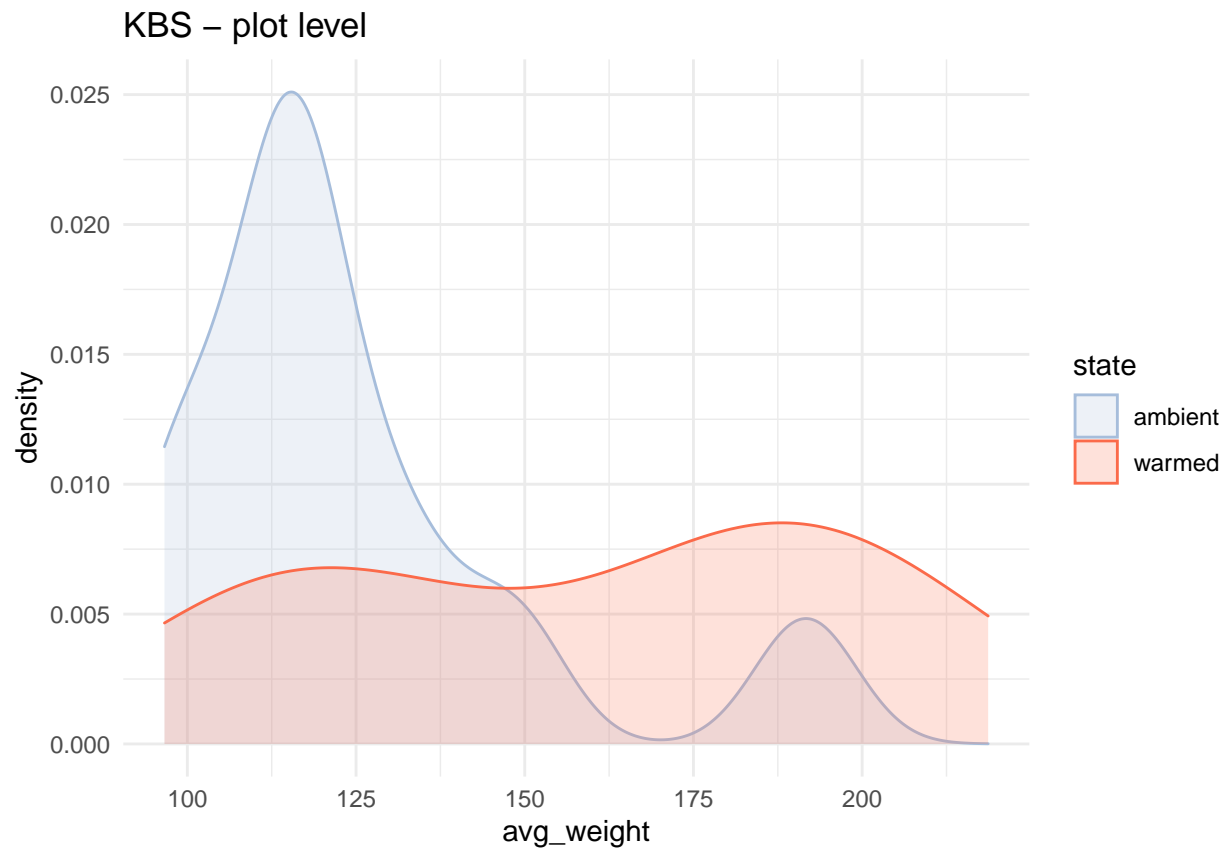
```
ggplot(umbs_biomass_live, aes(weight_g, fill = state, colour = state)) +
        geom_density(alpha = 0.2) +
        labs(title="UMBS - all species") +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_colour_manual(values = c("#a6bddb", "#fb6a4a")) +
        theme_minimal()
```

UMBS – all species


```
ggplot(biomass_sum_u2, aes(avg_weight, fill = state, colour = state)) +
        geom_density(alpha = 0.2) +
        labs(title="UMBS - plot level") +
        scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
        scale_colour_manual(values = c("#a6bddb", "#fb6a4a")) +
        theme_minimal()
```

UMBS – plot level
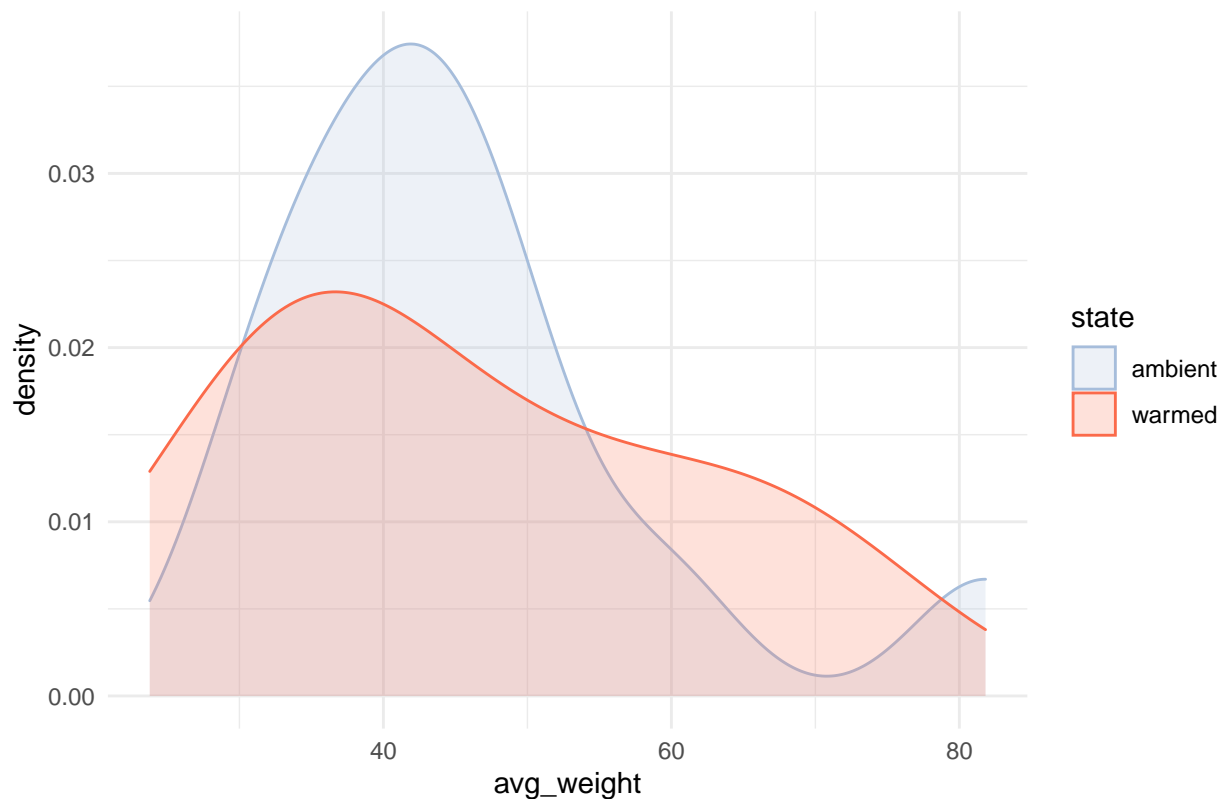

```r
## Regression between cover and biomass
# making a dataframe for regression between cover and biomass - removing uninformative species first
kbs_biomass_reg <- kbs_biomass_21[!grepl("Litter", kbs_biomass_21$species),]
kbs_biomass_reg <- kbs_biomass_reg[!grepl("Total Live", kbs_biomass_reg$species),]
kbs_biomass_reg <- kbs_biomass_reg[!grepl("Unknown", kbs_biomass_reg$species),]
kbs_biomass_reg <- kbs_biomass_reg[!grepl("Unsorted", kbs_biomass_reg$species),]
umbs_biomass_reg <- umbs_biomass_21[!grepl("Bare_Ground", umbs_biomass_21$species),]
umbs_biomass_reg <- umbs_biomass_reg[!grepl("Groundhog", umbs_biomass_reg$species),]
umbs_biomass_reg <- umbs_biomass_reg[!grepl("Litter", umbs_biomass_reg$species),]
umbs_biomass_reg <- umbs_biomass_reg[!grepl("Standing_Dead", umbs_biomass_reg$species),]
umbs_biomass_reg <- umbs_biomass_reg[!grepl("Surface_Litter", umbs_biomass_reg$species),]

# setting NA to 0 for cover or biomass for the regression
kbs_biomass_reg$cover[is.na(kbs_biomass_reg$cover)] <- 0
kbs_biomass_reg$weight_g[is.na(kbs_biomass_reg$weight_g)] <- 0
umbs_biomass_reg$cover[is.na(umbs_biomass_reg$cover)] <- 0
umbs_biomass_reg$weight_g[is.na(umbs_biomass_reg$weight_g)] <- 0

# fixing values listed as <1 for umbs
umbs_biomass_reg[umbs_biomass_reg=="<1"] <- 0
# making cover column numeric for umbs
umbs_biomass_reg$cover <- as.numeric(umbs_biomass_reg$cover)

# regression #
cor.test(kbs_biomass_reg$cover, kbs_biomass_reg$weight_g, method="pearson")

##
```
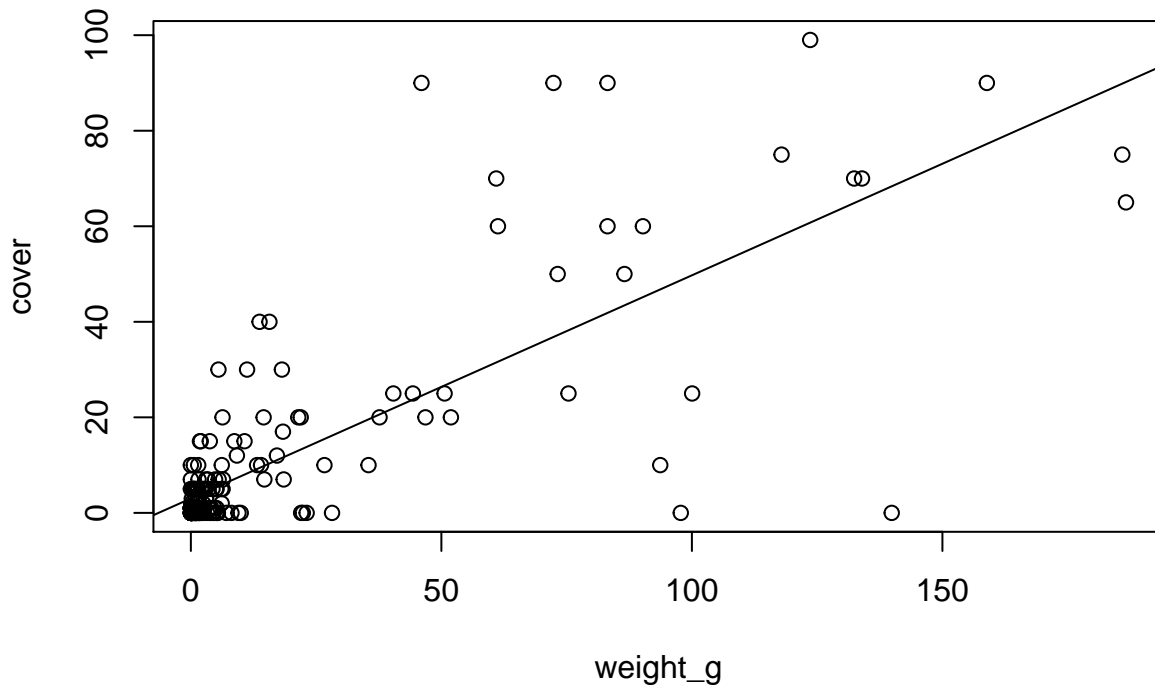
```
##  Pearson's product-moment correlation
##
## data:  kbs_biomass_reg$cover and kbs_biomass_reg$weight_g
## t = 17.401, df = 186, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.7257042 0.8360155
## sample estimates:
##       cor
## 0.7870724
```

```
lm1_k <- lm(cover ~ weight_g, data = kbs_biomass_reg)
plot(cover ~ weight_g, data = kbs_biomass_reg)
abline(lm1_k)
```



```
cor.test(umbs_biomass_reg$cover, umbs_biomass_reg$weight_g, method="pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  umbs_biomass_reg$cover and umbs_biomass_reg$weight_g
## t = 17.206, df = 172, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.7332977 0.8441927
## sample estimates:
##       cor
## 0.7953056
```

```
lm1_u <- lm(cover ~ weight_g, data = umbs_biomass_reg)
plot(cover ~ weight_g, data = umbs_biomass_reg)
abline(lm1_u)
```