

Biomass Plots

Kara Dobson

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TITLE: Biomass plots

AUTHORS: Kara Dobson

COLLABORATORS: Phoebe Zarnetske, Moriah Young, Mark Hammond, Pat Bills

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

DATA OUTPUT: Visualizations of biomass data

PROJECT: warmXtrophic

DATE: March 2022

```
# 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()
```

```
library(plotrix)  
library(ggpubr)
```

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

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

```

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

## [1] "ANPP"           "climate_data"      "CN"
## [4] "Greenness"      "herbivory"         "HOB0_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$species),]
umbs_biomass_live <- umbs_biomass_only[!grepl("Litter", umbs_biomass_only$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),]

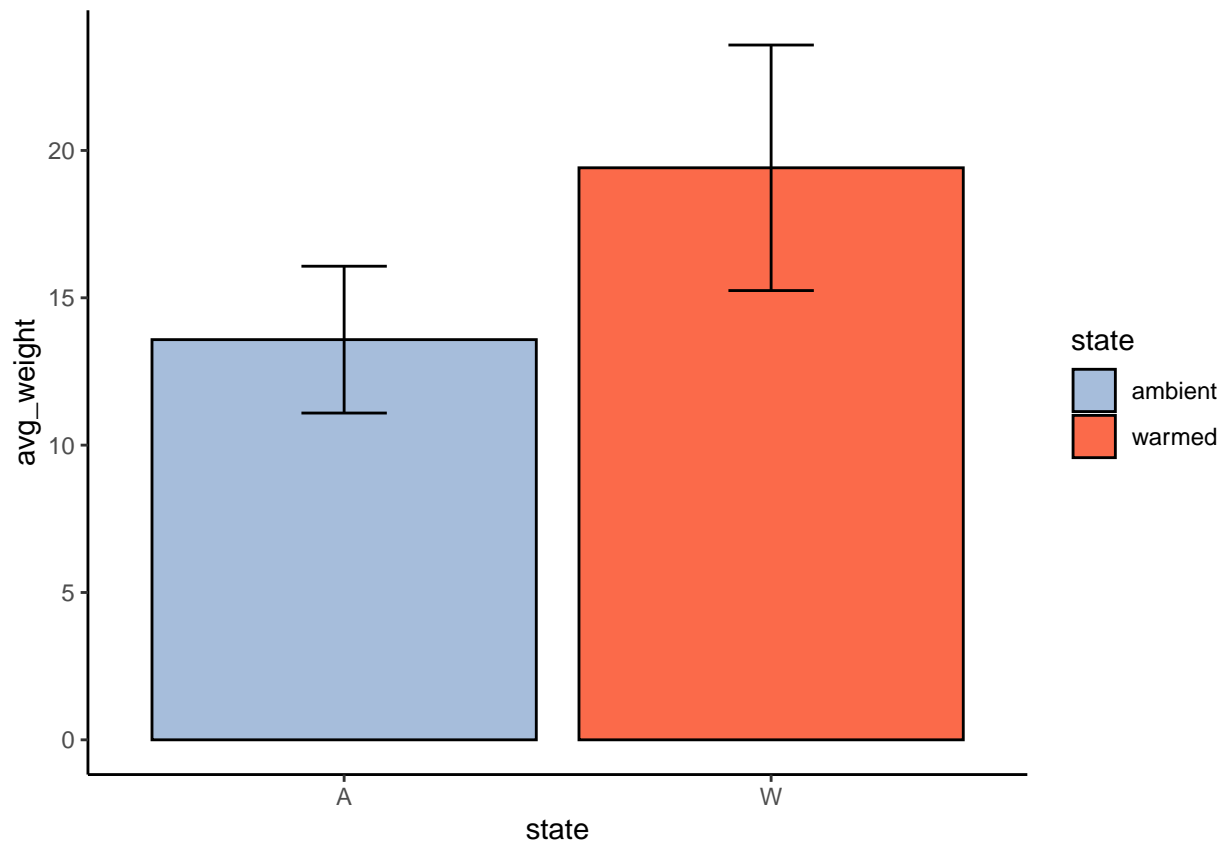
# keeping species found only in w and a
kbs_biomass_live2 <- kbs_biomass_live %>%
  group_by(species) %>%
  filter(all(c('warmed', 'ambient') %in% state))
umbs_biomass_live2 <- umbs_biomass_live %>%
  group_by(species) %>%
  filter(all(c('warmed', 'ambient') %in% state))

### Overall averages btwn treatments - barplot
biomass_sum_k <- kbs_biomass_live %>%
  group_by(state) %>%
  summarize(avg_weight = mean(weight_g, na.rm = TRUE),
            se = std.error(weight_g, na.rm = TRUE))

## `summarise()` ungrouping output (override with `.groups` argument)

ggplot(biomass_sum_k, aes(x = state, y = avg_weight, fill = state)) +
  geom_bar(position = "identity", stat = "identity", col = "black") +
  geom_errorbar(aes(ymin = avg_weight - se, ymax = avg_weight + se), width = 0.2,
               position = "identity") +
  scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
  scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +
  theme_classic()

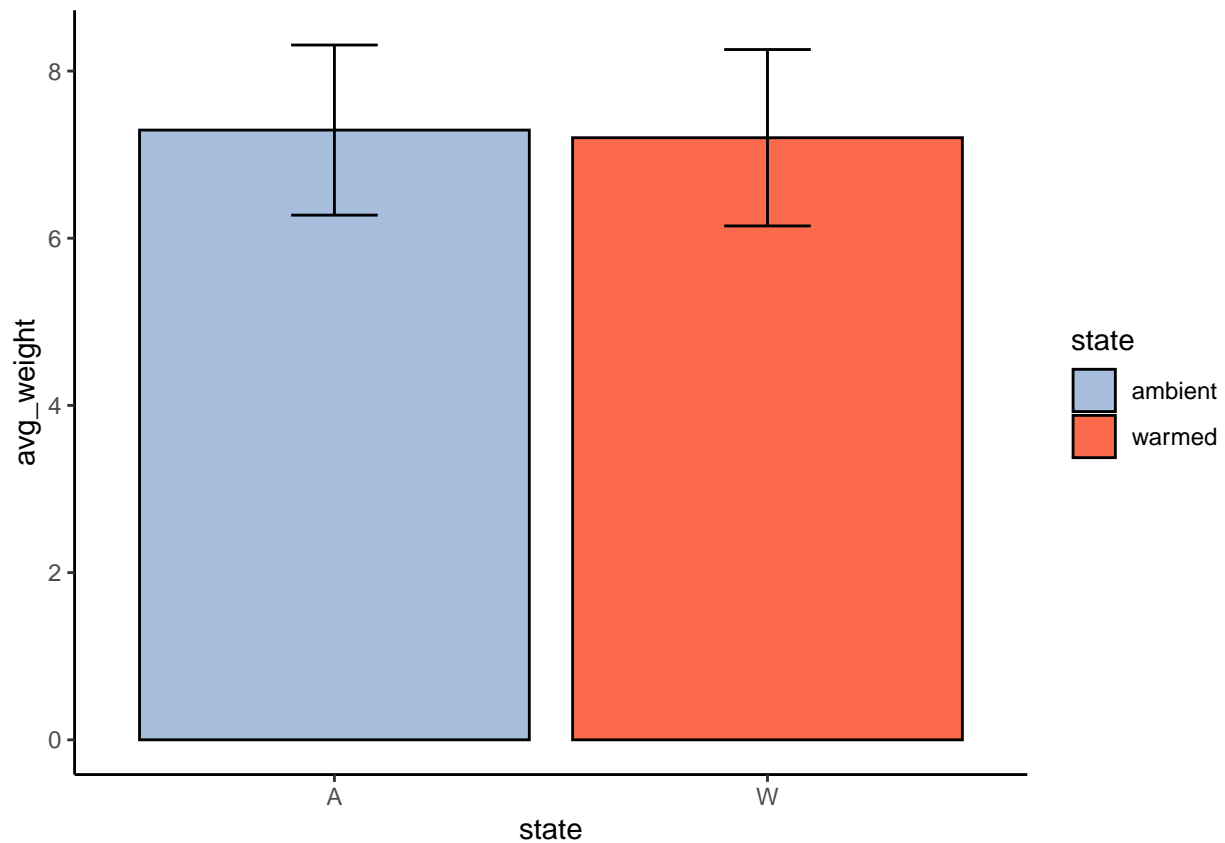
```



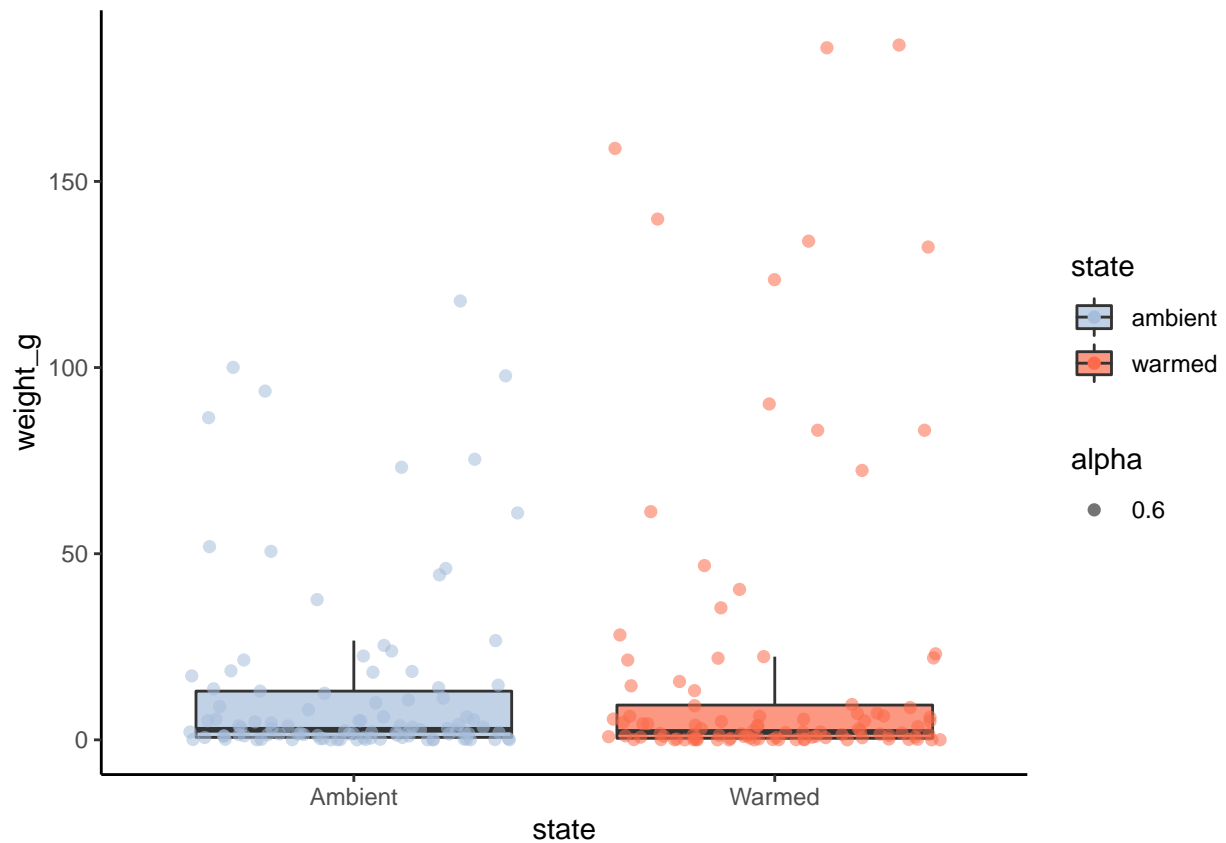
```
biomass_sum_u <- umbs_biomass_live %>%
  group_by(state) %>%
  summarize(avg_weight = mean(weight_g, na.rm = TRUE),
            se = std.error(weight_g, na.rm = TRUE))

## `summarise()` ungrouping output (override with `.groups` argument)

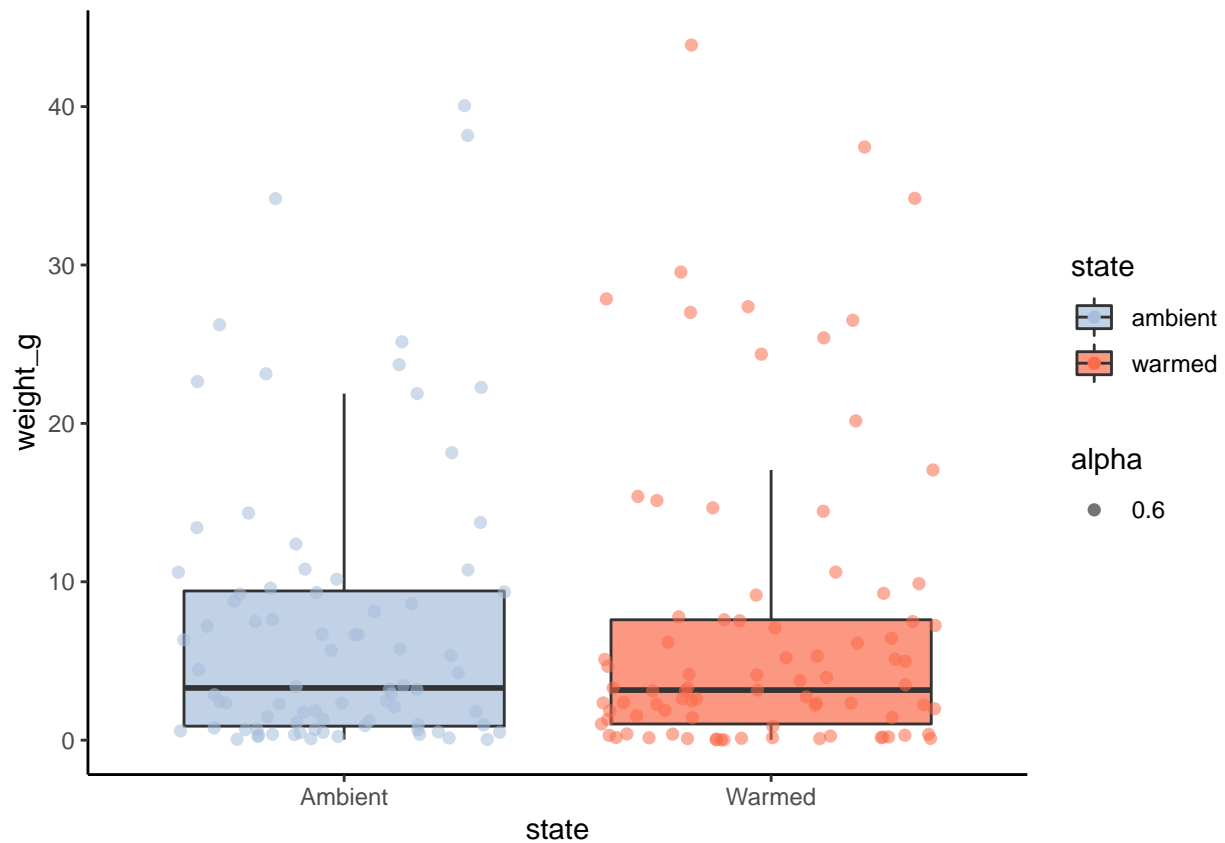
ggplot(biomass_sum_u, aes(x = state, y = avg_weight, fill = state)) +
  geom_bar(position = "identity", stat = "identity", col = "black") +
  geom_errorbar(aes(ymin = avg_weight - se, ymax = avg_weight + se), width = 0.2,
               position = "identity") +
  scale_fill_manual(values = c("#a6bddb",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



```
### Overall averages btwn treatments - boxplot
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")) +
  scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
  theme_classic()
```



```
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")) +
  scale_x_discrete(labels=c("ambient" = "Ambient", "warmed" = "Warmed")) +
  theme_classic()
```

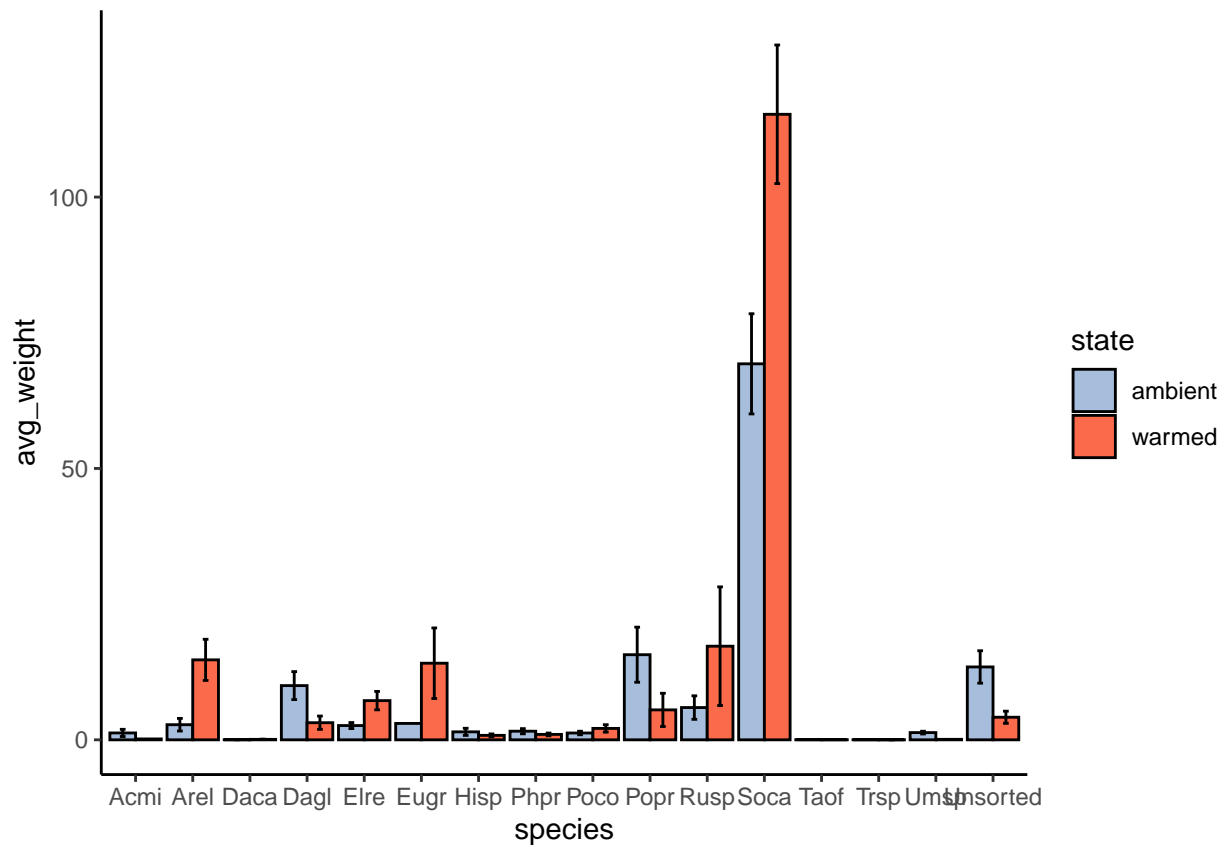


Differences between warmed and ambient at a species level

```
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)) +
  scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
  scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +
  theme_classic()
```



```
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)) +
  scale_fill_manual(values = c("#a6bddb", "#fb6a4a")) +
  scale_x_discrete(labels=c("ambient" = "A", "warmed" = "W")) +
  theme_classic()
```

