
```
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```

#Foundation plants and avian community associations

A set of survey data to examine key desert plant species associations with avian community structure and composition.

Hypothesis:

There are associations between birds and foundation plant species such as shrubs and cacti, and these relationships change with phenology.

Predictions:

1. Abundance and diversity of birds is greater near foundation plant species.
2. Spring and summer seasons change the associations between the foundation plants and avian community.
3. Behaviour and functional diversity of the avian species also differ when in association with foundation plant species relative to open microsites.

#Data

```
` `{r, Data, warning=FALSE, include=FALSE, echo=FALSE}
library(tidyverse)
library(lubridate)
library(vegan)
data <- read_csv("~/Masters/Desert-Bird-Habitat-Use/data/line_transects_viz.csv")
tidy_data <- data %>%
  rename(rep = bird.id, survey = walk, long = lon, migratory_class =
migratory.class, guild = trophic.guild, behavior_simple = broad.behavior,
microhabitat = three.mesohabitat) %>%
  mutate(date = mdy(date)) %>%
  mutate(day = mday(date))
```

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#take a peek at tidy data then select key vectors
tidy_data <- tidy_data %>%
  select(rep, date, season, day, survey, microhabitat, family, species,
migratory_class, guild, behavior_simple, month.day.hour) %>%
  mutate(microhabitat = case_when(microhabitat == "other" ~ "open", TRUE ~
as.character(microhabitat)))
write_csv(tidy_data, "~/Masters/Desert-Bird-Habitat-Use/data/tidy_data.csv")
#weather data
weather <- read_csv("~/Masters/Desert-Bird-Habitat-Use/weather/weather.csv") %>%
  select(month.day.hour, Air.Temperature.Mean.Deg.F)
#join mean air temperature for the hour to tidy data
tidy_data <- left_join(tidy_data, weather, by = 'month.day.hour') %>%
  rename(temp = Air.Temperature.Mean.Deg.F)
#tidydata without BTSP
tidy_data_noBTSP <- tidy_data %>%
  select(rep, date, season, day, survey, microhabitat, family, species,
migratory_class, guild, behavior_simple, temp) %>%
  mutate(microhabitat = case_when(microhabitat == "other" ~ "open", TRUE ~
as.character(microhabitat))) %>%
  filter(species != "Black.throated Sparrow")
#taxonomic model datasets

data_species <- tidy_data %>%
  group_by(season, survey, microhabitat, species, temp) %>%
  summarise(counts = n())
data_richness <- data_species %>%
  group_by(season, survey, microhabitat, temp) %>%
  summarise(richness = n())
data_behavior <- tidy_data %>%
  group_by(season, survey, microhabitat, behavior_simple, temp) %>%
  summarise(totals = n())
div <- tidy_data %>%
  dplyr::select(season, survey, microhabitat, species)#pull season, walk,
microhabitat, and species
div_long <- as.data.frame(table(div)) #get freq of each species in long table with
walks as rep
div_wide <- div_long %>% spread(species, Freq) #get species into wide format
div_wide$survey <- as.numeric(div_wide$survey) #make walks numeric
div_wide <- filter(div_wide, (season == "spring" & survey < 27) | (season ==
"summer" & survey > 26))
data_div <- as.data.frame( diversity(div_wide[,4:45])) %>%
  rename(Shannon = "diversity(div_wide[, 4:45])")
data_wide <- div_wide %>% dplyr::select(season, survey, microhabitat)

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data_div <- bind_cols(data_wide, data_div)
weather_survey <- tidy_data %>% dplyr::select(survey, temp)
weather_survey <- aggregate(temp~survey, weather_survey, FUN=mean)

data_div <- left_join(data_div, weather_survey, by = "survey")
#trophic guild model dataset
data_trophic <- tidy_data %>%
  group_by(season, survey, microhabitat, guild, temp) %>%
  summarise(counts = n()) %>%
  filter(guild != 'Unknown') %>%
  filter(guild != "unknown")
#migratory class model dataset
data_migratory <- tidy_data %>%
  group_by(season, survey, microhabitat, migratory_class, temp) %>%
  summarise(counts = n()) %>%
  filter(migratory_class != "unknown")
#Black-throated Sparrow only
data_sparrow <- tidy_data %>%
  group_by(season, survey, microhabitat, species, behavior_simple, temp) %>%
  summarise(counts = n()) %>%
  filter(species == "Black.throated Sparrow")
#Black-throated Sparrow excluded
data_species_noBTSP <- tidy_data_noBTSP %>%
  group_by(season, survey, microhabitat, species, temp) %>%
  summarise(counts = n())
data_richness_noBTSP <- data_species_noBTSP %>%
  group_by(season, survey, microhabitat, temp) %>%
  summarise(richness = n())
data_behavior_noBTSP <- tidy_data_noBTSP %>%
  group_by(season, survey, microhabitat, behavior_simple, temp) %>%
  summarise(totals = n())
div_long_noBTSP <- as.data.frame(table(div)) %>%
  filter(species != "Black.throated Sparrow") #get freq of each species in long
table with walks as rep
div_wide_noBTSP <- div_long_noBTSP %>% spread(species, Freq) #get species into wide
format
div_wide_noBTSP$survey <- as.numeric(div_wide_noBTSP$survey) #make walks numeric
div_wide_noBTSP <- filter(div_wide_noBTSP, (season == "spring" & survey < 27) |
(season == "summer" & survey > 26))
data_div_noBTSP <- as.data.frame(diversity(div_wide_noBTSP[,4:45])) %>%
  rename(Shannon = "diversity(div_wide_noBTSP[, 4:45])")
div_wide_noBTSP <- div_wide_noBTSP %>% dplyr::select(season, survey, microhabitat)
data_div_noBTSP <- bind_cols(div_wide_noBTSP, data_div_noBTSP)

```

```
data_div_noBTSP <- left_join(data_div_noBTSP, weather_survey, by = "survey")
...
```

#Viz

```
`{r}
```

```
library(ggpubr)
```

```
box1 <- ggplot(data_species, aes(season, counts, color = microhabitat)) +
  geom_boxplot(aes(fill = microhabitat)) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_color_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y = "Species Abundance", x = " ", title = "A") +
  theme_classic(base_size = 15) +
  theme(legend.position = "none") +
  theme(axis.text=element_text(size=15)) +
  stat_summary(fun=mean, colour="#E77272", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
```

```
box2 <- ggplot(data_richness, aes(season, richness, color = microhabitat)) +
  geom_boxplot(aes(fill = microhabitat)) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_color_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y="Species Richness", x=" ", title = "B") +
  theme_classic(base_size = 15) +
  theme(legend.title = element_blank()) +
  theme(axis.text = element_text(size=15)) +
  theme(legend.position = "none") +
  stat_summary(fun=mean, colour="#E77272", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
```

```
box3 <- ggplot (data_div, aes(season, Shannon, color = microhabitat)) +
  geom_boxplot(aes(fill=microhabitat)) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_color_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y="Shannon Weaver Index", x=" ", title = "C") +
  theme_classic(base_size = 15) +
  theme(legend.title = element_blank()) +
  theme(legend.position = "none") +
  theme(axis.text = element_text(size=15)) +
  stat_summary(fun=mean, colour="#E77272", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
```

```
box4 <- ggplot(data_behavior, aes(behavior_simple, totals, color = microhabitat)) +
  geom_boxplot(aes(fill=microhabitat)) +
```

```

scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
scale_colour_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
facet_wrap(~season, ncol = 2) +
labs(y = "Species Frequency", x = " ") +
theme_classic(base_size = 15) +
theme(legend.position = "bottom") +
theme(axis.text.x = element_text(angle = 90)) +
theme(axis.text = element_text(size=15)) +
stat_summary(fun=mean, colour="#E77272", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
box4
box5 <- ggplot(data_trophic, aes(season, counts, color = microhabitat)) +
  geom_boxplot(aes(fill=microhabitat)) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_colour_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y = "Trophic Guild Abundance", x = " ", title = "D") +
  theme_classic(base_size = 15) +
  theme(legend.position = "none") +
  theme(axis.text = element_text(size=15)) +
  stat_summary(fun=mean, colour="#E77272", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
box6 <- ggplot(data_migratory, aes(season, counts, color = microhabitat)) +
  geom_boxplot(aes(fill=microhabitat)) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_colour_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y="Migratory Class Abundance", x="Season", title = "E") +
  theme_classic(base_size = 15) +
  theme(legend.title = element_blank()) +
  theme(axis.text = element_text(size=15)) +
  stat_summary(fun=mean, colour="#E77272", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
ggarrange(box1, box2, box3, box5, box6, ncol=3, nrow=2)
sparrow <- ggplot(data_sparrow, aes(season, counts, color = microhabitat)) +
  geom_boxplot(lwd=1.5) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_colour_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y="BTSP Abundance", x= "Season") +
  facet_wrap(~behavior_simple, ncol=2) +
  theme_classic(base_size = 15) +
  theme(legend.title = element_blank()) +
  theme(axis.text = element_text(size=15)) +
  stat_summary(fun=mean, colour="black", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))

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```

nosparrow <- ggplot(data_species_noBTSP, aes(season, counts, color = microhabitat))
+
  geom_boxplot(lwd=1.5) +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  scale_colour_manual(values=c("#6E6E6E", "#6E6E6E", "#6E6E6E")) +
  labs(y="BTSP exclusion Species Abundance", x= "Season") +
  theme_classic(base_size = 15) +
  theme(legend.title = element_blank()) +
  theme(axis.text = element_text(size=15)) +
  stat_summary(fun=mean, colour="black", aes(group=microhabitat), geom="point",
shape=18, size=3, position=position_dodge(.75))
nosparrow
sparrow
ggarrange(box1, box2, box3, box5, box6, ncol=3, row = 2)
#species stacked barchart
ggplot(data_species, aes(fill=microhabitat, y=counts, x=species)) +
  geom_bar(position="fill", stat="identity") +
  scale_fill_manual(values=c("#D5E5A8", "#A8E5D6", "#B8A8E5")) +
  facet_wrap(~season) +
  theme_classic() +
  coord_flip() +
  labs(y="Percent Abundance", x="Species") +
  theme(legend.title = element_blank())

...

```

#Models

##Microhabitat, behavior, and season

```

```{r}
library(emmeans)
library(AER)
library(stats)
options(max.print = 99999999)
m1a <- glm(counts~microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_species)
anova(m1a, test = "Chisq")

```

```

aov(m1a)
summary(m1a) #not overdispersed when quasipoisson
dispersiontest(m1a, trafo=1) #overdispersed as poisson
anova(m1a)
c1a <- emmeans(m1a, pairwise~microhabitat*season)
c1a
m1b <- glm(counts~species*microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_species)
anova(m1b, test = "Chisq")
c1b <- emmeans(m1b, pairwise~species*microhabitat*season)
c1b
m1c <- glm(counts~microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_species_noBTSP)
anova(m1c, test = "Chisq")
summary(m1c) #not overdispersed when quasipoisson
c1c <- emmeans(m1c, pairwise~microhabitat*season)
c1c
m2 <- glm(richness~microhabitat*season + (1 |survey) + (1|temp), family = gaussian,
data = data_richness)
anova(m2, test = "Chisq")
summary(m2) #not overdispersed as gaussian
aov(m2)
c2 <- emmeans(m2, pairwise~microhabitat*season)
c2
m2b <- glm(richness~microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_richness_noBTSP)
anova(m2b, test = "Chisq")
summary(m2b) #not overdispersed as quasipoisson
c2b <- emmeans(m2b, pairwise~microhabitat*season)
c2b
m3 <- glm(totals~microhabitat*behavior_simple + (1|survey) + (temp), family =
quasipoisson, data = data_behavior)
anova(m3, test = "Chisq")
summary(m3) #not overdispersed as quasipoisson
c3 <- emmeans(m3, pairwise~microhabitat*behavior_simple)
c3
m3b <- glm(totals~microhabitat*season*behavior_simple + (1|survey) + (1|temp),
family = quasipoisson, data = data_behavior)
summary(m3b) #not overdispersed as quasipoisson
anova(m3b, test = "Chisq")
c3b <- emmeans(m3b, pairwise~microhabitat*season*behavior_simple)
c3b
#Trophic Guilds as diversity metrics

```

```

m4 <- glm(counts~microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_trophic)
summary(m4) #not overdispersed as quasipoisson
dispersiontest(m4, trafo=1) #overdispersed as poisson
anova(m4, test = "Chisq")
c4 <- emmeans(m4, pairwise~microhabitat*season)
c4

m4b <- glm(counts~guild*microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_trophic)
summary(m4b) #not overdispersed as quasipoisson
anova(m4b, test = "Chisq")
c4b <- emmeans(m4b, pairwise~guild*microhabitat*season)
c4b

#Migratory classes at diversity metrics
m5 <- glm(counts~microhabitat*season + (1 |survey) + (1|temp), family =
quasipoisson, data = data_migratory)
summary(m5) #not overdispersed as quasipoisson
anova(m5, test = "Chisq")
c5 <- emmeans(m5, pairwise~microhabitat*season)
c5

m5b <- glm(counts~migratory_class*microhabitat*season + (1 |survey) + (1|temp),
family = quasipoisson, data = data_migratory)
anova(m5b, test = "Chisq")
c5b <- emmeans(m5b, pairwise~migratory_class*microhabitat*season)
c5b

#Black-throated Sparrows only
m6 <- glm(counts~microhabitat*season*behavior_simple + (1|survey) + (1|temp),
family = quasipoisson, data = data_sparrow)
dispersiontest(m6)
summary(m6) #not overdispersed as quasipoisson
anova(m6, test = "Chisq")
c6 <- emmeans(m6, pairwise~microhabitat*season*behavior_simple)
c6

#Diversity
m7a <- glm(Shannon~microhabitat*season + (1|survey) + (1|temp), family =
quasipoisson, data = data_div)
anova(m7a, test = "Chisq")
summary(m7a) #not overdispersed as quasipoisson
c7a <- emmeans(m7a, pairwise~microhabitat*season)
c7a

m7b <- glm(Shannon~microhabitat*season + (1|survey) + (1|temp), family =
quasipoisson, data = data_div_noBTSP)
anova(m7b, test = "Chisq")

```



```
summary(m7b) #not overdispersed as quasipoisson
c7b <- emmeans(m7b, pairwise~microhabitat*season)
c7b
...
```