

How Prevalent is Archaeological Garden Hunting?

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1/24/2022

Libraries

```
library(SIBER)
library(tidyverse)
library(cowplot)
library(broom)
library(car)
```

Figure 1

Plant genera reported by Scribner and Krysel (1982) were assigned a photosynthetic pathway from the following sources: Basinger and Robertson (1997), Bruhl and Wilson (2007), Danneberger (1999), Giussani et al. (2001), Kocacinar and Sage (2003), Nelson (2012), Osborne et al. (2014), and Syvertsen et al. (1976).

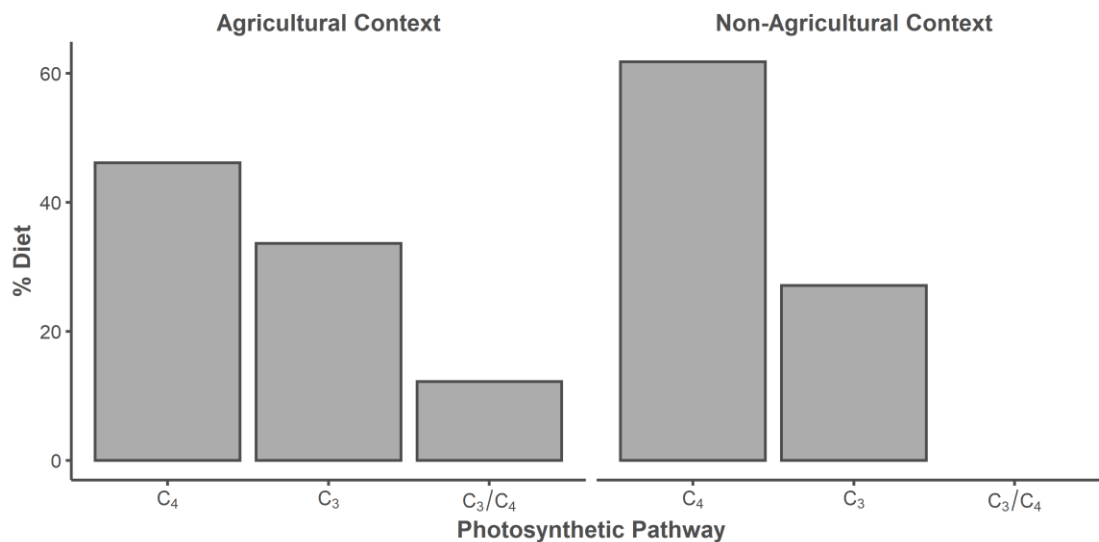
```
Table_2 <- read.csv("Scribner and Krysl_Table 2/Table 2.csv", header = TRUE)

Pathway <- Table_2 %>%
  select(Environmental.Context, Photosynthetic.pathway, DF....) %>%
  group_by(Environmental.Context, Photosynthetic.pathway) %>%
  summarize(sum_DF = sum(DF....), .groups = "keep")

labels <- c("Agricultural Playa Basins" = "Agricultural Context",
            "Playa Basins" = "Non-Agricultural Context")

Pathway %>%
ggplot(aes(x = reorder(Photosynthetic.pathway, -sum_DF), y = sum_DF)) +
  geom_bar(stat = "identity", size = 0.75, alpha = 0.5, color = "#4d4d4d") +
  facet_wrap(~ Environmental.Context, ncol = 2,
            labeller = labeller(Environmental.Context = labels)) +
  scale_x_discrete(labels = parse(text = c("C[4]", "C[3]", "C[3]/C[4]"))) +
  theme_classic() +
  theme(legend.position="none",
        strip.background = element_blank(),
        strip.text.x = element_text(color = "#4d4d4d", size = 12,
                                     face = "bold"),
        axis.line = element_line(color = "#4d4d4d", size = 0.75),
        axis.text.x = element_text(color = "#4d4d4d", size = 10),
```

```
axis.text.y = element_text(color = "#4d4d4d", size = 10),
axis.title.x = element_text(color = "#4d4d4d", size = 12,
                             face = "bold"),
axis.title.y = element_text(color = "#4d4d4d", size = 12,
                             face = "bold"),
axis.ticks.x = element_line(color = "#4d4d4d", size = 0.75),
axis.ticks.y = element_line(color = "#4d4d4d", size = 0.75)) +
labs(x = "Photosynthetic Pathway", y = "% Diet")
```



Isotope Data

Bone from the archaeo dataset was demineralized in 0.5 N hydrochloric acid, lipids were removed using 2:1 chloroform:methanol, and the resulting collagen pseudomorph was freeze-dried overnight. Between 0.5 and 0.6 mg of collagen was weighed out for the analysis of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$. All seeds from the seeds dataset were purchased from Native seeds/SEARCH. Between 5.0 and 6.0 mg of ground corn and 2.0 and 2.5 mg of ground bean/squash was weighed out for the analysis of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$. $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ were measured at the University of New Mexico Center for Stable Isotopes (UNM CSI, Albuquerque, NM) on a Thermo Scientific Delta V isotope ratio mass spectrometer (IRMS) with a dual inlet and Conflo IV interface coupled to a Costech 4010 elemental analyzer (EA). Stable isotope values are reported as parts per mil (‰).

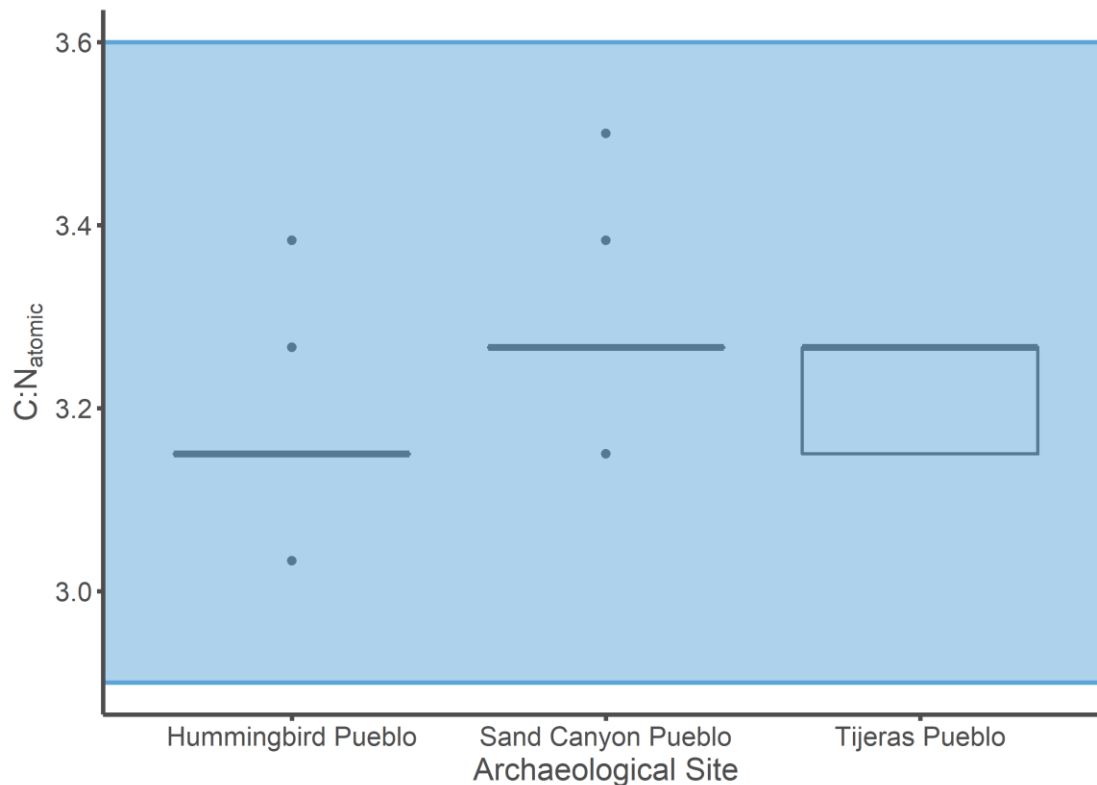
The humans and turkeys isotope values come from the following sources: Chisholm and Matson (1994), Coltrain et al. (2007), Conrad et al. (2016), Jones et al. (2016), Kellner et al. (2010), Kennett et al. (2017), Martin (1999), McCaffery et al. (2014), and Rawlings and Driver (2010).

```
archaeo <- read.csv("archaeological.csv", header = TRUE)
seeds <- read.csv("modern seeds.csv", header = TRUE)
turkeys <- read.csv("turkeys.csv", header = TRUE)
humans <- read.csv("humans.csv", header = TRUE)
```

Assessing Collagen Purity

Boxplots of C:N_{atomic} values of archaeological leporid collagen per site. The blue box represents the acceptable range of collagen purity (2.9-3.6) reported by Ambrose (1990).

```
archaeo %>%
  mutate(CNatomic = CN * (14/12)) %>%
  ggplot(mapping = aes(y = CNatomic, x = Site.Name, group = Site.Name)) +
  geom_boxplot(color = "#4d4d4d", size = 0.75) +
  labs(y = expression("C:N"[atomic]), x = "Archaeological Site") +
  theme_classic() +
  theme(legend.position="none",
        axis.line = element_line(color = "#4d4d4d", size = 1),
        axis.text.x = element_text(color = "#4d4d4d", size = 12),
        axis.text.y = element_text(color = "#4d4d4d", size = 12),
        axis.title.x = element_text(color = "#4d4d4d", size = 14),
        axis.title.y = element_text(color = "#4d4d4d", size = 14),
        axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
        axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_y_continuous(limits=c(2.9, 3.6)) +
  annotate(geom = "rect", xmin = -Inf, xmax = Inf, ymin = 2.9, ymax = 3.6,
         color = "#5da5da", fill = "#5da5da", alpha = 0.5, size = 1)
```



Data Wrangling

A ^{13}C Suess correction of 2.0‰ was applied to the modern seed data (Dombrosky 2020).

```
seeds <- seeds %>%
  mutate(d13Csuess = d13C + 2)

archaeo_SIBER <- archaeo %>%
  unite(group, Site.Name, Genus, sep = " ") %>%
  select(group, d13C, d15N)

seeds_SIBER <- seeds %>%
  select(Comparative.Group, d13Csuess, d15N) %>%
  rename(group = Comparative.Group,
         d13C = d13Csuess)

turkeys_SIBER <- turkeys %>%
  mutate(animal = "Turkey") %>%
  unite(group, Diet.Type, animal, sep = " ") %>%
  select(group, d13C, d15N)

humans_SIBER <- humans %>%
  mutate(group = "Humans") %>%
  select(group, d13C, d15N)

SIBER_data <- rbind(archaeo_SIBER, seeds_SIBER, turkeys_SIBER, humans_SIBER)
```

Figure 2

Sand Canyon Pueblo Figures

[illegible]

```

"Maize-fed Turkey", "Bean", "Squash",
"Corn"))

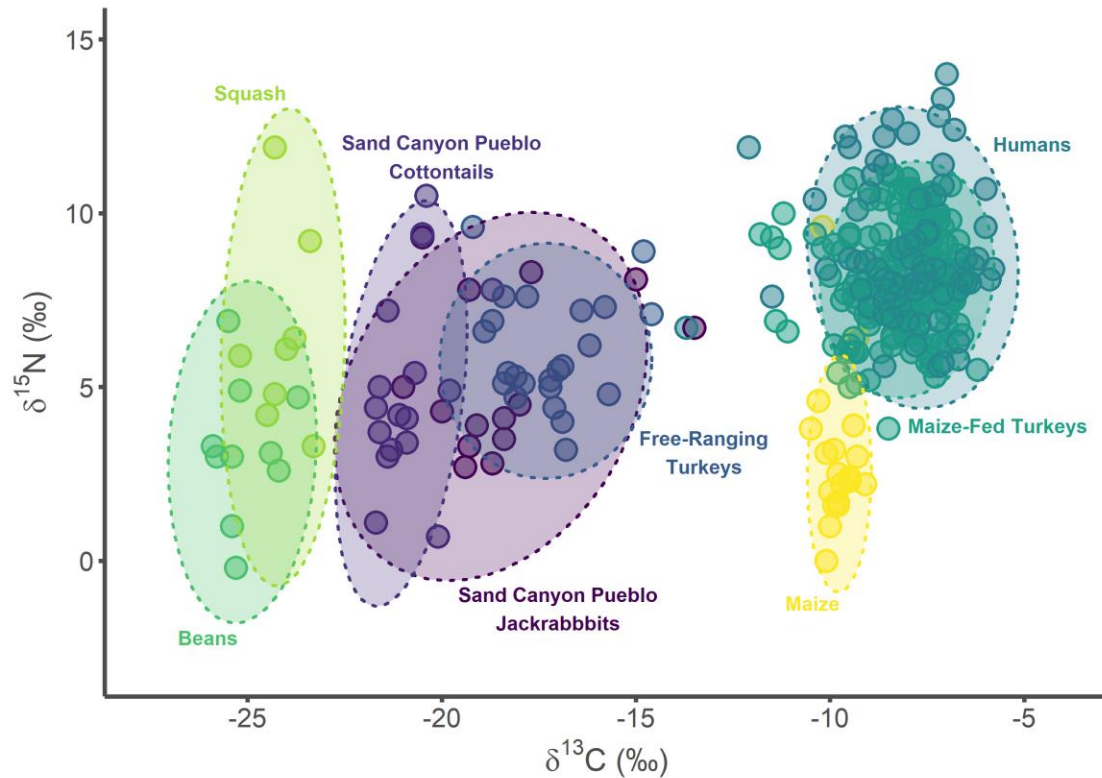
sand_plot <- SIBER_data %>%
  filter(group %in% c("Sand Canyon Pueblo Lepus",
    "Sand Canyon Pueblo Sylvilagus",
    "Bean", "Corn", "Squash", "Free-ranging Turkey",
    "Maize-fed Turkey", "Humans"))

sand_plot$group <- factor(sand_plot$group,
  levels = c("Sand Canyon Pueblo Lepus",
    "Sand Canyon Pueblo Sylvilagus",
    "Free-ranging Turkey", "Humans",
    "Maize-fed Turkey", "Bean", "Squash",
    "Corn"))

sand_p1 <- ggplot(sand_plot, aes(x = d13C, y = d15N)) +
  geom_point(aes(fill = group, color = group), stroke = 1, size = 4,
    alpha = 0.5, shape = 21) +
  geom_point(aes(color = group), fill = NA, stroke = 1, size = 4,
    shape = 21) +
  ylab(expression(paste(delta^{15}, "N (\u2030)"))) +
  xlab(expression(paste(delta^{13}, "C (\u2030)"))) +
  theme_classic() +
  theme(legend.position = "none",
    axis.line = element_line(color = "#4d4d4d", size = 1),
    axis.text.x = element_text(color = "#4d4d4d", size = 12),
    axis.text.y = element_text(color = "#4d4d4d", size = 12),
    axis.title.x = element_text(color = "#4d4d4d", size = 14,
      face = "bold"),
    axis.title.y = element_text(color = "#4d4d4d", size = 14,
      face = "bold"),
    axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
    axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_color_viridis_d() +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
    alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,
    type = "t", geom = "polygon") +
  geom_text(data = sand_label_df, aes(x = d13C, y = d15N,
    label = label, color = group, hjust = hjust,
    vjust = vjust),
    size = 9/.pt, fontface = "bold") +
  scale_fill_viridis_d() +
  scale_x_continuous(limits=c(-27.5, -4),
    breaks = c(-25, -20, -15, -10, -5)) +
  scale_y_continuous(limits=c(-3, 15))

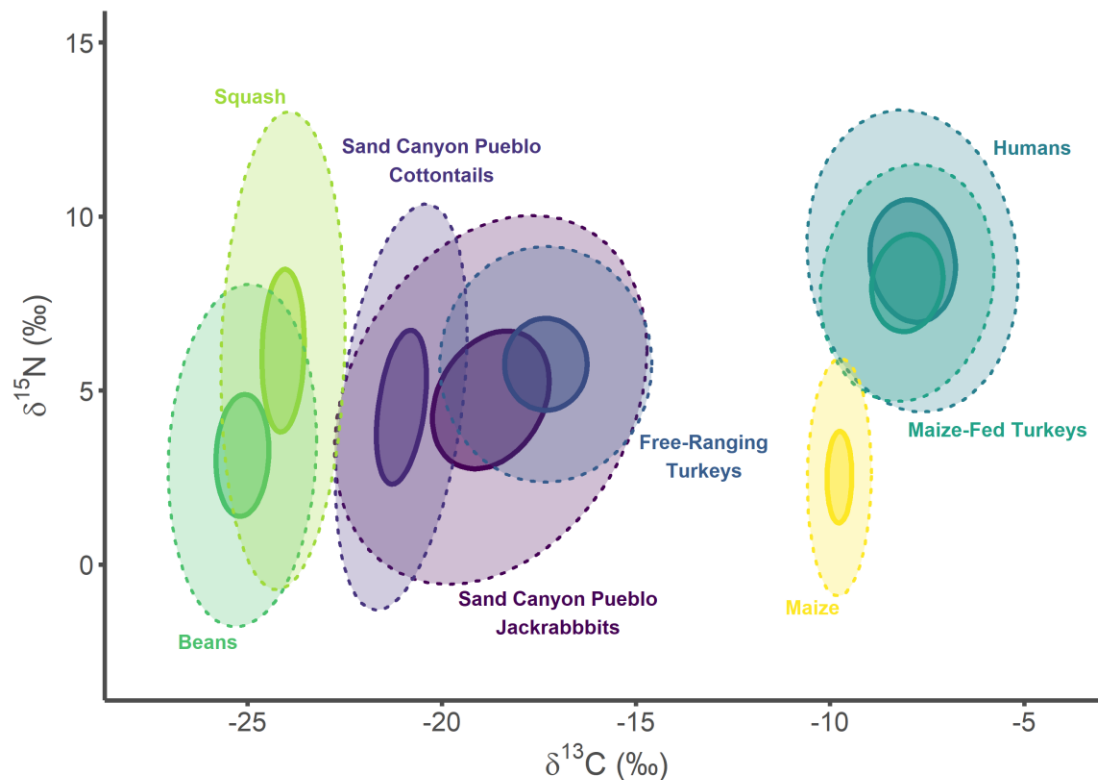
sand_p1

```



```
sand_p2 <- ggplot(sand_plot, aes(x = d13C, y = d15N)) +
  ylab(expression(paste(delta^{15}, "N (\u2030)"))) +
  xlab(expression(paste(delta^{13}, "C (\u2030)"))) +
  theme_classic() +
  theme(legend.position = "none",
        axis.line = element_line(color = "#4d4d4d", size = 1),
        axis.text.x = element_text(color = "#4d4d4d", size = 12),
        axis.text.y = element_text(color = "#4d4d4d", size = 12),
        axis.title.x = element_text(color = "#4d4d4d", size = 14,
                                     face = "bold"),
        axis.title.y = element_text(color = "#4d4d4d", size = 14,
                                     face = "bold"),
        axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
        axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_color_viridis_d() +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
              alpha = 0.5, size = 1.1, linetype = 1, level = 0.40,
              type = "t", geom = "polygon") +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
              alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,
              type = "t", geom = "polygon") +
  geom_text(data = sand_label_df, aes(x = d13C, y = d15N,
                                     label = label, color = group, hjust = hjust,
                                     vjust = vjust),
            size = 9/.pt, fontface = "bold") +
  scale_fill_viridis_d() +
```

sand_p2



```
hum_label_df <- data.frame(
  group = c("Hummingbird Pueblo Lepus", "Hummingbird Pueblo Sylvilagus",
    "Free-ranging Turkey", "Humans", "Maize-fed Turkey", "Bean",
    "Squash", "Corn"),
  label = c("Hummingbird Pueblo\nJackrabbbits",
    "Hummingbird Pueblo\nCottontails",
    "Free-Ranging\nTurkeys", "Humans", "Maize-Fed Turkeys", "Beans",
    "Squash", "Maize"),
  d13C = c(-20, -14.25, -20, -5.8, -8, -25.25, -24, -9.75),
  d15N = c(1.5, -1.25, 10, 12.2, 4.1, -2, 13.25, -1),
  hjust = c(0.5, 0.5, 0.5, 0, 0, 1, 1, 1),
  vjust = c(1, 0, 0, 1, 1, 1, 0, 1))

hum_label_df$group <- factor(hum_label_df$group,
  levels = c("Hummingbird Pueblo Lepus",
    "Hummingbird Pueblo Sylvilagus",
    "Free-ranging Turkey", "Humans",
    "Maize-fed Turkey", "Bean", "Squash",
```

```

      "Corn"))

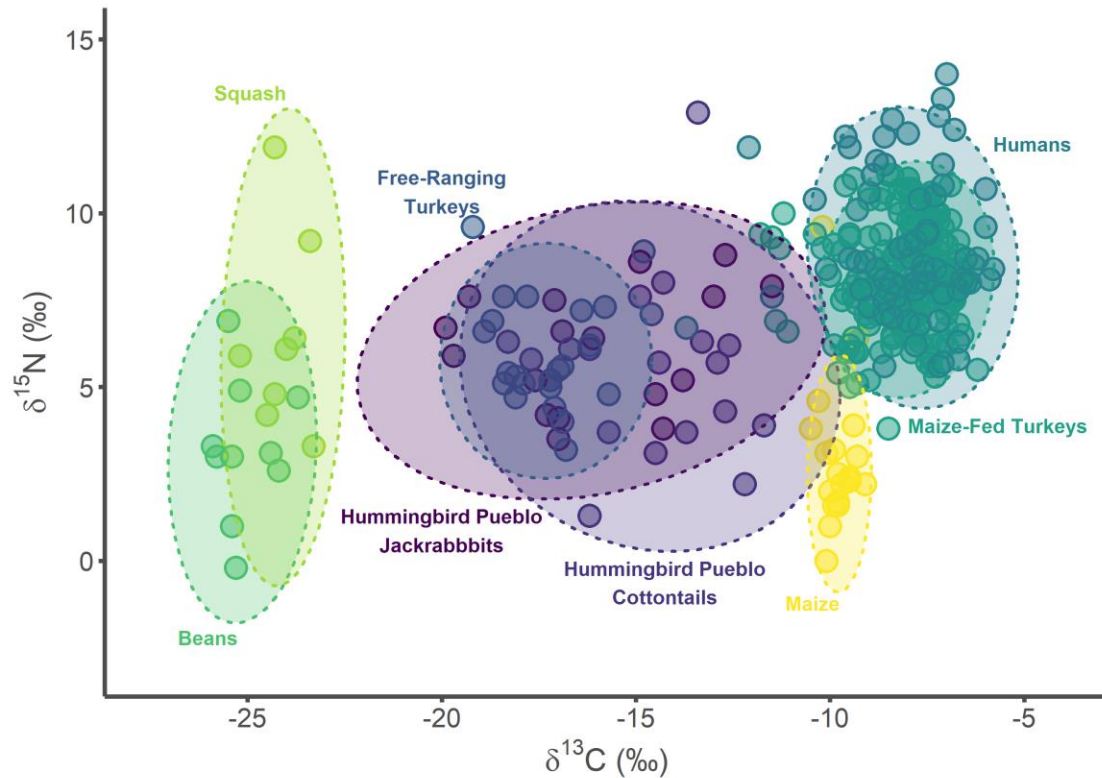
hum_plot <- SIBER_data %>%
  filter(group %in% c("Hummingbird Pueblo Lepus",
    "Hummingbird Pueblo Sylvilagus",
    "Bean", "Corn", "Squash", "Free-ranging Turkey",
    "Maize-fed Turkey", "Humans"))

hum_plot$group <- factor(hum_plot$group,
  levels = c("Hummingbird Pueblo Lepus",
    "Hummingbird Pueblo Sylvilagus",
    "Free-ranging Turkey", "Humans",
    "Maize-fed Turkey", "Bean", "Squash",
    "Corn"))

hum_p1 <- ggplot(hum_plot, aes(x = d13C, y = d15N)) +
  geom_point(aes(fill = group, color = group), stroke = 1, size = 4,
    alpha = 0.5, shape = 21) +
  geom_point(aes(color = group), fill = NA, stroke = 1, size = 4,
    shape = 21) +
  ylab(expression(paste(delta^{15}, "N (\u2030)"))) +
  xlab(expression(paste(delta^{13}, "C (\u2030)"))) +
  theme_classic() +
  theme(legend.position = "none",
    axis.line = element_line(color = "#4d4d4d", size = 1),
    axis.text.x = element_text(color = "#4d4d4d", size = 12),
    axis.text.y = element_text(color = "#4d4d4d", size = 12),
    axis.title.x = element_text(color = "#4d4d4d", size = 14,
      face = "bold"),
    axis.title.y = element_text(color = "#4d4d4d", size = 14,
      face = "bold"),
    axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
    axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_color_viridis_d() +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
    alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,
    type = "t", geom = "polygon") +
  geom_text(data = hum_label_df, aes(x = d13C, y = d15N,
    label = label, color = group, hjust = hjust,
    vjust = vjust),
    size = 9/.pt, fontface = "bold") +
  scale_fill_viridis_d() +
  scale_x_continuous(limits=c(-27.5, -4),
    breaks = c(-25, -20, -15, -10, -5)) +
  scale_y_continuous(limits=c(-3, 15))

hum_p1

```

```
hum_p2 <- ggplot(hum_plot, aes(x = d13C, y = d15N)) +
  ylab(expression(paste(delta^{15}, "N (\u2030)"))) +
  xlab(expression(paste(delta^{13}, "C (\u2030)"))) +
  theme_classic() +
  theme(legend.position = "none",
        axis.line = element_line(color = "#4d4d4d", size = 1),
        axis.text.x = element_text(color = "#4d4d4d", size = 12),
        axis.text.y = element_text(color = "#4d4d4d", size = 12),
        axis.title.x = element_text(color = "#4d4d4d", size = 14,
                                     face = "bold"),
        axis.title.y = element_text(color = "#4d4d4d", size = 14,
                                     face = "bold"),
        axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
        axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_color_viridis_d() +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
              alpha = 0.5, size = 1.1, linetype = 1, level = 0.40, type =
"t",
              geom = "polygon") +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
              alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,
              type = "t", geom = "polygon") +
  geom_text(data = hum_label_df, aes(x = d13C, y = d15N,
                                     label = label, color = group, hjust = hjust,
                                     vjust = vjust),
            size = 9/.pt, fontface = "bold") +
```

hum_p2

[illegible]

```

"Maize-fed Turkey", "Bean", "Squash",
"Corn"))

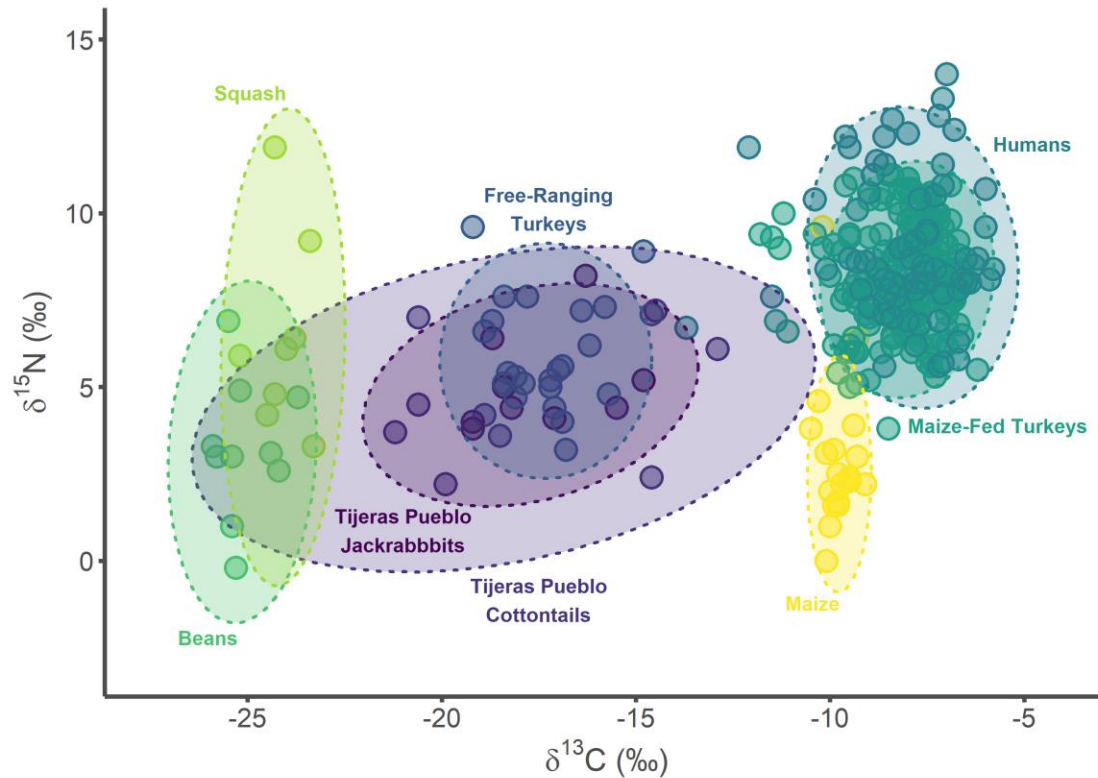
tij_plot <- SIBER_data %>%
  filter(group %in% c("Tijeras Pueblo Lepus",
    "Tijeras Pueblo Sylvilagus",
    "Bean", "Corn", "Squash", "Free-ranging Turkey",
    "Maize-fed Turkey", "Humans"))

tij_plot$group <- factor(tij_plot$group,
  levels = c("Tijeras Pueblo Lepus",
    "Tijeras Pueblo Sylvilagus",
    "Free-ranging Turkey", "Humans",
    "Maize-fed Turkey", "Bean", "Squash",
    "Corn"))

tij_p1 <- ggplot(tij_plot, aes(x = d13C, y = d15N)) +
  geom_point(aes(fill = group, color = group), stroke = 1, size = 4,
    alpha = 0.5, shape = 21) +
  geom_point(aes(color = group), fill = NA, stroke = 1, size = 4,
    shape = 21) +
  ylab(expression(paste(delta^{15}, "N (\u2030)"))) +
  xlab(expression(paste(delta^{13}, "C (\u2030)"))) +
  theme_classic() +
  theme(legend.position = "none",
    axis.line = element_line(color = "#4d4d4d", size = 1),
    axis.text.x = element_text(color = "#4d4d4d", size = 12),
    axis.text.y = element_text(color = "#4d4d4d", size = 12),
    axis.title.x = element_text(color = "#4d4d4d", size = 14,
      face = "bold"),
    axis.title.y = element_text(color = "#4d4d4d", size = 14,
      face = "bold"),
    axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
    axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_color_viridis_d() +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
    alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,
    type = "t", geom = "polygon") +
  geom_text(data = tij_label_df, aes(x = d13C, y = d15N,
    label = label, color = group, hjust = hjust,
    vjust = vjust),
    size = 9/.pt, fontface = "bold") +
  scale_fill_viridis_d() +
  scale_x_continuous(limits=c(-27.5, -4),
    breaks = c(-25, -20, -15, -10, -5)) +
  scale_y_continuous(limits=c(-3, 15))

tij_p1

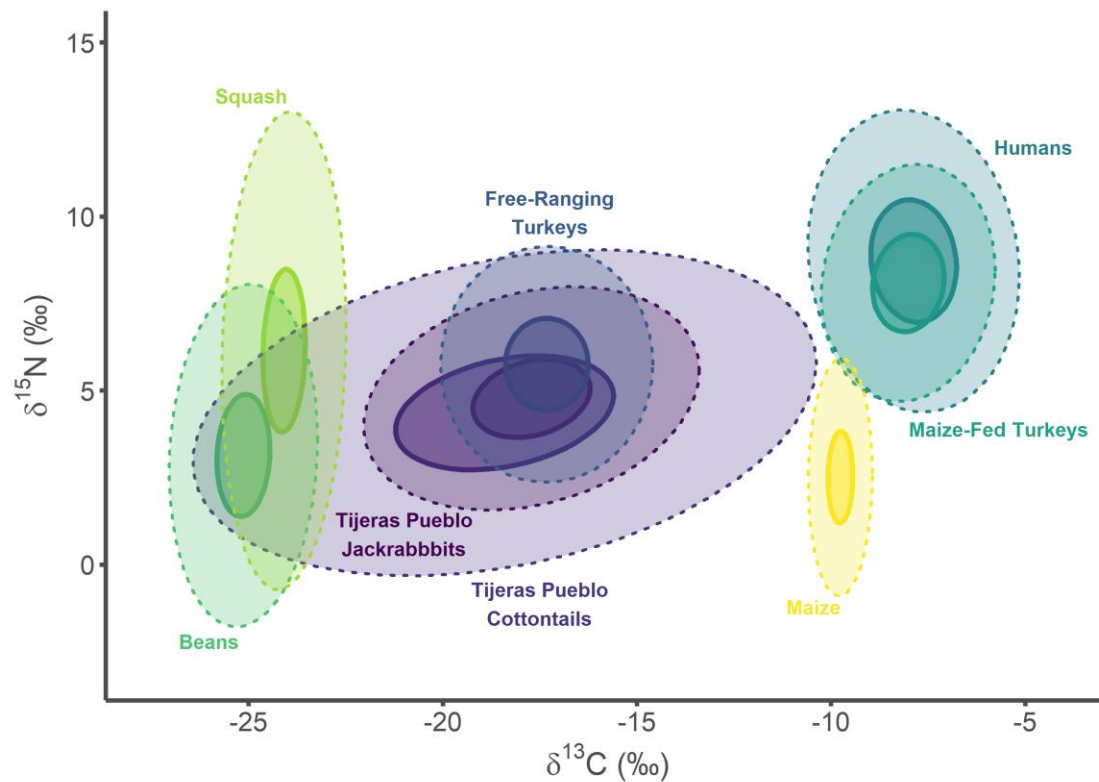
```



```
tij_p2 <- ggplot(tij_plot, aes(x = d13C, y = d15N)) +
  ylab(expression(paste(delta^{15}, "N (\u2030)"))) +
  xlab(expression(paste(delta^{13}, "C (\u2030)"))) +
  theme_classic() +
  theme(legend.position = "none",
        axis.line = element_line(color = "#4d4d4d", size = 1),
        axis.text.x = element_text(color = "#4d4d4d", size = 12),
        axis.text.y = element_text(color = "#4d4d4d", size = 12),
        axis.title.x = element_text(color = "#4d4d4d", size = 14,
                                     face = "bold"),
        axis.title.y = element_text(color = "#4d4d4d", size = 14,
                                     face = "bold"),
        axis.ticks.x = element_line(color = "#4d4d4d", size = 1),
        axis.ticks.y = element_line(color = "#4d4d4d", size = 1)) +
  scale_color_viridis_d() +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
              alpha = 0.5, size = 1.1, linetype = 1, level = 0.40,
              type = "t", geom = "polygon") +
  stat_ellipse(aes(group = interaction(group), color = group, fill = group),
              alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,
              type = "t", geom = "polygon") +
  geom_text(data = tij_label_df, aes(x = d13C, y = d15N,
                                     label = label, color = group, hjust = hjust,
                                     vjust = vjust),
            size = 9/.pt, fontface = "bold") +
  scale_fill_viridis_d() +
```

```
scale_x_continuous(limits=c(-27.5, -4),
                   breaks = c(-25, -20, -15, -10, -5)) +
scale_y_continuous(limits=c(-3, 15))
```

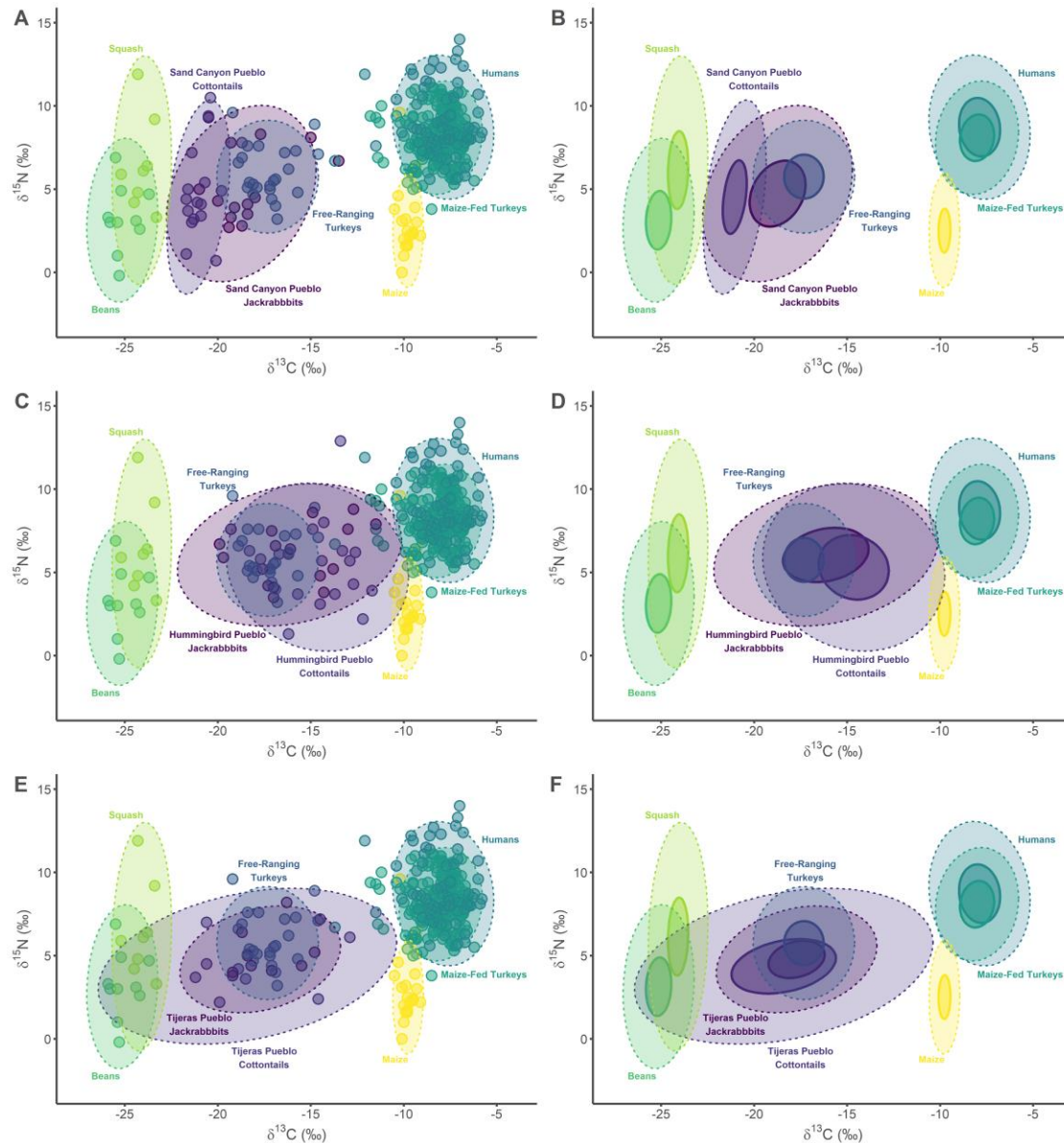
```
tij_p2
```



Combine Figures

```
all_plots <- plot_grid(sand_p1, sand_p2, hum_p1, hum_p2, tij_p1, tij_p2,
                       labels = "AUTO", label_colour = "#4d4d4d",
                       label_size = 20, ncol = 2, nrow = 3)
```

```
all_plots
```



```
ggsave("Figure 2.jpg", dpi = 300)
```

```
## Saving 14 x 15 in image
```

Test for Normality

Some isotope values per group are non-normal. Thus, ellipses in Figure 2 are visualized based on the t-distribution, which is also good for small sample sizes.

```
SIBER_data %>%
  group_by(group) %>%
  do(tidy(shapiro.test($.d13C)))
```

```
## # A tibble: 12 x 4
## # Groups:   group [12]
```


##	group	statistic	p.value	method
##	<chr>	<dbl>	<dbl>	<chr>
##	1 Bean	0.882	0.139	Shapiro-Wilk
	normality t~			
##	2 Corn	0.980	0.928	Shapiro-Wilk
	normality t~			
##	3 Free-ranging Turkey	0.960	0.462	Shapiro-Wilk
	normality t~			
##	4 Humans	0.914	0.000106	Shapiro-Wilk
	normality t~			
##	5 Hummingbird Pueblo Lepus	0.956	0.565	Shapiro-Wilk
	normality t~			
##	6 Hummingbird Pueblo Sylvilagus	0.956	0.502	Shapiro-Wilk
	normality t~			
##	7 Maize-fed Turkey	0.938	0.000000566	Shapiro-Wilk
	normality t~			
##	8 Sand Canyon Pueblo Lepus	0.862	0.0328	Shapiro-Wilk
	normality t~			
##	9 Sand Canyon Pueblo Sylvilagus	0.882	0.0415	Shapiro-Wilk
	normality t~			
##	10 Squash	0.958	0.788	Shapiro-Wilk
	normality t~			
##	11 Tijeras Pueblo Lepus	0.900	0.251	Shapiro-Wilk
	normality t~			
##	12 Tijeras Pueblo Sylvilagus	0.857	0.0878	Shapiro-Wilk
	normality t~			

```
SIBER_data %>%
  group_by(group) %>%
  do(tidy(shapiro.test(.$d15N)))
```

##	# A tibble: 12 x 4	statistic	p.value	method
##	Groups: group [12]	<dbl>	<dbl>	<chr>
##	group			
##	<chr>			
##	1 Bean	0.958	0.766	Shapiro-Wilk normality
	test			
##	2 Corn	0.825	0.00206	Shapiro-Wilk normality
	test			
##	3 Free-ranging Turkey	0.960	0.462	Shapiro-Wilk normality
	test			
##	4 Humans	0.943	0.00241	Shapiro-Wilk normality
	test			
##	5 Hummingbird Pueblo Lepus	0.946	0.390	Shapiro-Wilk normality
	test			
##	6 Hummingbird Pueblo Sylvilagus	0.900	0.0496	Shapiro-Wilk normality
	test			
##	7 Maize-fed Turkey	0.986	0.0793	Shapiro-Wilk normality
	test			
##	8 Sand Canyon Pueblo Lepus	0.884	0.0664	Shapiro-Wilk normality

```

test
## 9 Sand Canyon Pueblo Sylvilagus      0.942 0.376   Shapiro-Wilk normality
test
## 10 Squash                             0.904 0.314   Shapiro-Wilk normality
test
## 11 Tijeras Pueblo Lepus               0.820 0.0348  Shapiro-Wilk normality
test
## 12 Tijeras Pueblo Sylvilagus          0.917 0.371   Shapiro-Wilk normality
test

```

SIBER Area Calculations

TA = Total Area, SEA = Standard Ellipse Area, and SEAc = Small Sample Size Corrected Standard Ellipse Area (see Jackson et al. 2011)

```

siber.example <- SIBER_data %>%
  select(d13C, d15N, group) %>%
  mutate(community = 1) %>%
  rename(iso1 = d13C,
         iso2 = d15N)

siber.example <- createSiberObject(siber.example)

group.ML1 <- data.frame(groupMetricsML(siber.example)) %>%
  rename("Hummingbird Jackrabbits" = X1.Hummingbird.Pueblo.Lepus,
        "Hummingbird Cottontails" = X1.Hummingbird.Pueblo.Sylvilagus,
        "Sand Canyon Jackrabbit" = X1.Sand.Canyon.Pueblo.Lepus,
        "Sand Canyon Cottontails" = X1.Sand.Canyon.Pueblo.Sylvilagus,
        "Tijeras Pueblo Jackrabbits" = X1.Tijeras.Pueblo.Lepus,
        "Tijeras Pueblo Cottontails" = X1.Tijeras.Pueblo.Sylvilagus,
        "Beans" = X1.Bean,
        "Maize" = X1.Corn,
        "Squash" = X1.Squash,
        "Free-ranging Turkey" = X1.Free.ranging.Turkey,
        "Maize-fed Turkey" = X1.Maize.fed.Turkey,
        "Humans" = X1.Humans) %>%
  t() %>%
  round(digits = 2)

group.ML1

```

##	TA	SEA	SEAc
## Hummingbird Jackrabbits	28.91	13.02	13.88
## Hummingbird Cottontails	44.81	15.47	16.38
## Sand Canyon Jackrabbit	29.74	13.82	14.97
## Sand Canyon Cottontails	18.75	6.43	6.89
## Tijeras Pueblo Cottontails	33.91	17.58	20.09
## Tijeras Pueblo Jackrabbits	11.71	7.01	8.01
## Beans	8.41	4.53	5.10

## Maize	8.21	2.40	2.53
## Squash	10.09	5.47	6.38
## Free-ranging Turkey	19.40	6.16	6.46
## Maize-fed Turkey	28.55	5.19	5.22
## Humans	46.75	8.81	8.93

SIBER Maximum Likelihood Overlap with Humans Calculations

```
results <- data.frame()
taxa <- c("1.Hummingbird Pueblo Lepus", "1.Hummingbird Pueblo Sylvilagus",
          "1.Sand Canyon Pueblo Lepus",
          "1.Sand Canyon Pueblo Sylvilagus",
          "1.Tijeras Pueblo Lepus",
          "1.Tijeras Pueblo Sylvilagus",
          "1.Maize-fed Turkey")

for (i in seq_along(taxa)) {

  sea.overlap <- maxLikOverlap(taxa[[i]], "1.Humans", siber.example,
                              p.interval = 0.95, n = 100)

  results[i, 1] <- taxa[[i]]
  results[i, 2] <- round(sea.overlap[[3]], digits = 2)
  results[i, 3] <- round(sea.overlap[[3]]/sea.overlap[[2]]*100, digits = 2)
  results[i, 4] <- round(sea.overlap[[3]]/sea.overlap[[1]]*100, digits = 2)
  results[i, 5] <- round(sea.overlap[[3]]/(sea.overlap[[2]] +
                                         sea.overlap[[1]] -
                                         sea.overlap[[3]])*100, digits =
2)
}

colnames(results) <- c("group", "overlap %", "% human niche", "% group
niche",
                      "% overlap")

results$group <- gsub("1.", "", as.character(results$group))
results$group <- gsub("Lepus", "Jackrabbits", as.character(results$group))
results$group <- gsub("Sylvilagus", "Cottontails",
as.character(results$group))

results

##              group overlap % % human niche % group niche
## 1 Hummingbird Pueblo Jackrabbits      4.55      8.50      5.47
## 2 Hummingbird Pueblo Cottontails      4.61      8.62      4.70
## 3 Sand Canyon Pueblo Jackrabbits      0.00      0.00      0.00
## 4 Sand Canyon Pueblo Cottontails      0.00      0.00      0.00
## 5      Tijeras Pueblo Jackrabbits      0.00      0.00      0.00
## 6      Tijeras Pueblo Cottontails      2.38      4.45      1.98
```

```
## 7          Maize-fed Turkey    31.23      58.39      100.00
## % overlap
## 1         3.44
## 2         3.14
## 3         0.00
## 4         0.00
## 5         0.00
## 6         1.39
## 7        58.39

round(mean(results$`% human niche`[1:6]), digits = 2)

## [1] 3.59

round(mean(results$`% group niche`[1:6]), digits = 2)

## [1] 2.02
```

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