Avoidance-Attraction Ratios in R

Avoidance-Attraction Ratios were first developed by Parsons et al. 2016 to investigate the effects of humans and their favorite companion, dogs, on wildlife. Since then Avoidance-Attraction Ratios have grown in popularity due to their ability to gain insights into species interactions at a fine temporal scale.

This guide will implement the functions in the AvoidAttract package and perform an analysis of species interactions using Avoidance-Attraction Ratios having bobcat (*Lynx rufus*), coyotes (*Canis latrans*), and swift fox (*Vulpes velox*) as the predator species. The data that we will use is integrated in the package and is from a camera trapping project in western Kansas, source: Palomo-Munoz et al. 2023.

Lets get started.

Package Install

```
# Install the package
# If needed install.package("devtools")
devtools::install_github("dpearcetamu/AvoidAttract", quiet = TRUE)
#> Warning: package 'AvoidAttract' is in use and will not be installed

# Load the package
library(AvoidAttract)
```

Now that the package is installed and loaded, let's take a look at the data.

Exploring the Data

```
# If you want to take a closer look use this code to read the dataset documentation,
# ?KScams_dat
```

Okay, now that we've seen the details of the camera trapping data, lets load it into the environment and take a closer look.

```
# Reading in the data
data("KScams_dat")

# Let's take a look
head(KScams_dat)
#>   General_project    Class        Order      Family   Genus Species
#> 1    Wkansas_2019 Mammalia    Carnivora Mustelidae Taxidea   taxus
#> 2    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison
#> 3    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison
#> 4    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison
#> 5    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison
```

```
#> 6    Wkansas_2019 Mammalia Artiodactyla    Bovidae    Bison    bison
#>        Binomial     Common_name Year Site        DateTime     Date
#> 1 Taxidea taxus American badger 2019    0 9/1/2019 5:30:38 9/1/2019
#> 2   Bison bison  American bison 2019    0 9/3/2019 2:20:50 9/3/2019
#> 3   Bison bison  American bison 2019    0 9/3/2019 2:21:32 9/3/2019
#> 4   Bison bison  American bison 2019    0 9/3/2019 2:22:09 9/3/2019
#> 5   Bison bison  American bison 2019    0 9/3/2019 2:25:44 9/3/2019
#> 6   Bison bison  American bison 2019    0 9/3/2019 2:26:45 9/3/2019
#>      Time        Timezone Latitude Longitude SetVisitDate
#> 1 5:30:38 America/Chicago 37.24655 -99.98253     8/7/2019
#> 2 2:20:50 America/Chicago 37.24655 -99.98253     8/7/2019
#> 3 2:21:32 America/Chicago 37.24655 -99.98253     8/7/2019
#> 4 2:22:09 America/Chicago 37.24655 -99.98253     8/7/2019
#> 5 2:25:44 America/Chicago 37.24655 -99.98253     8/7/2019
#> 6 2:26:45 America/Chicago 37.24655 -99.98253     8/7/2019
```

Great! We can see that the data has detection's of species at certain sites with a specific date and time for
that observation. Let's see how many different species were found.

```
# Let's see what the column names are
names(KScams_dat)
#>  [1] "General_project" "Class"         "Order"
#>  [4] "Family"          "Genus"         "Species"
#>  [7] "Binomial"        "Common_name"   "Year"
#> [10] "Site"            "DateTime"      "Date"
#> [13] "Time"            "Timezone"      "Latitude"
#> [16] "Longitude"       "SetVisitDate"

# What were the unique species using the "Common_name" column
unique(KScams_dat$Common_name)
#>  [1] "American badger"           "American bison"
#>  [3] "Black-tailed jackrabbit"   "Coyote"
#>  [5] "Raccoon"                   "Norway rat"
#>  [7] "Striped Skunk"             "White-Tailed Deer"
#>  [9] "Bobcat"                    "Cat"
#> [11] "Eastern cottontail rabbit" "Mouse"
#> [13] "Virginia opossum"          "Ord's kangaroo rat"
#> [15] "Mule Deer"                 "Dog"
#> [17] "Swift Fox"                 "Pronghorn"
#> [19] "Long-tailed weasel"        "Thirteen-lined ground squirrel"
#> [21] "Black-tailed Prarie Dog"   "Elk"
#> [23] "Nine-banded armadillo"     "North American porcupine"
```

Looking to see how many observations of each species there are in the data set using the spp_sum function
from the package.

```
# spp_sum requires the data input and a name column and provides a frequency table of observations
spp_sum(KScams_dat, name_col = "Common_name")
#>                      Name Observations
#> 1          American badger         1674
#> 2           American bison           45
#> 3  Black-tailed jackrabbit         3423
#> 4  Black-tailed Prarie Dog          881
```

```
#> 5                         Bobcat        113
#> 6                            Cat         54
#> 7                         Coyote       3624
#> 8                            Dog         85
#> 9       Eastern cottontail rabbit      3635
#> 10                            Elk          2
#> 11           Long-tailed weasel          5
#> 12                          Mouse        706
#> 13                      Mule Deer       2440
#> 14          Nine-banded armadillo         18
#> 15        North American porcupine        32
#> 16                     Norway rat        659
#> 17             Ord's kangaroo rat        788
#> 18                      Pronghorn        130
#> 19                        Raccoon       3965
#> 20                  Striped Skunk       2455
#> 21                      Swift Fox        341
#> 22 Thirteen-lined ground squirrel         63
#> 23               Virginia opossum        204
#> 24              White-Tailed Deer       5884
```

That's a lot of observations! Let's take a look at a few of the species that had a lot of observations and their interactions with coyotes using the AAR function.

Avoidance-Attraction Ratios

```
# First we have to format the DateTime column from a character string to a date time
# This is an important step since the function won't know how to read the date and time
# Make sure to modify the format if you are using a different dataset!!!
KScams_dat$DateTime  <- as.POSIXct(KScams_dat$DateTime ,
                                   tryFormats = "%m/%d/%Y %H:%M:%OS")


# Let's look at some of these species!


# ---------------------------------------
#
#      Bobcats as predators
#
# ---------------------------------------


# Starting with the Black-tailed jackrabbit
jrabbit_bobcat <- AAR(data = KScams_dat,
                  speciesA = "Black-tailed jackrabbit", speciesB = "Bobcat",
                  species_col = "Common_name", datetime_col = "DateTime",
                  site_col ="Site", unitTime = "hours")


# The AAR function outputs several results. Let's take a look at just the total summary.
print(jrabbit_bobcat$total_summary)
#>         T1         T2         T3         T4      T2/T1       T4/T3
#> 90.1629630 29.0488889 21.3262520 69.7442593  0.3221821  3.2703477


# Okay we can see that this outputs the mean values
```

```r
# for all interaction events and the interaction ratios

# The AAR function also returns a list of how many times those interactions occurred.
print(jrabbit_bobcat$event_count)
#>    T1    T2    T3    T4
#>    12     6 3139     6

# That's quite a few counts for each interaction.
# Lets save just the ratios to use later on.

# Saving only the T2/T1 and T4/T3 ratios
jrabbit_bobcat_ratios <- jrabbit_bobcat$total_summary[c(5,6)]

# Now the other species

# Black-tailed Prarie Dog
pdog_bobcat <- AAR(data = KScams_dat,
                   speciesA = "Black-tailed Prarie Dog", speciesB = "Bobcat",
                   species_col = "Common_name", datetime_col = "DateTime",
                   site_col ="Site", unitTime = "hours")
#> Warning in AAR(data = KScams_dat, speciesA = "Black-tailed Prarie Dog", :
#> No T2 interaction events occurred. Cannot calculate a mean for this
#> event.
#> Warning in AAR(data = KScams_dat, speciesA = "Black-tailed Prarie Dog", :
#> No T4 interaction events occurred. Cannot calculate a mean for this
#> event.
#> Warning in AAR(data = KScams_dat, speciesA = "Black-tailed Prarie Dog", :
#> Unable to calculate site summary Avoidance-Attraction Ratios due to lack
#> of event occurances.
#> Warning in AAR(data = KScams_dat, speciesA = "Black-tailed Prarie Dog", :
#> Unable to calculate total summary Avoidance-Attraction Ratios due to lack
#> of event occurances.

# Okay there weren't enough time events to calculate ratios.
# Let's take a closer look.
print(pdog_bobcat$event_count)
#>   T1   T2   T3   T4
#>    1    0  869    0

# There were no T2 or T4 events and only one T1 event for the prarie dog
# and bobcat interaction. Since we are trying to compare differences between
# predator species we won't look into prairie dog's interactions with
# coyote and swift fox.

# Eastern cottontail rabbit
crabbit_bobcat <- AAR(data = KScams_dat,
                      speciesA = "Eastern cottontail rabbit", speciesB = "Bobcat",
                      species_col = "Common_name", datetime_col = "DateTime",
                      site_col ="Site", unitTime = "hours")

crabbit_bobcat_ratios <- crabbit_bobcat$total_summary[c(5,6)]
```

```r
# White-tailed Deer
wtd_bobcat <- AAR(data = KScams_dat,
                  speciesA = "White-Tailed Deer", speciesB = "Bobcat",
                  species_col = "Common_name", datetime_col = "DateTime",
                  site_col ="Site", unitTime = "hours")


wtd_bobcat_ratios <- wtd_bobcat$total_summary[c(5,6)]



# ---------------------------------------
#
#        Coyote as predators
#
# ---------------------------------------


# Starting with the Black-tailed jackrabbit
jrabbit_coyote <- AAR(data = KScams_dat,
                      speciesA = "Black-tailed jackrabbit", speciesB = "Coyote",
                      species_col = "Common_name", datetime_col = "DateTime",
                      site_col ="Site", unitTime = "hours")

# Saving only the T2/T1 and T4/T3 ratios
jrabbit_coyote_ratios <- jrabbit_coyote$total_summary[c(5,6)]

# Eastern cottontail rabbit
crabbit_coyote  <- AAR(data = KScams_dat,
                       speciesA = "Eastern cottontail rabbit", speciesB = "Coyote",
                       species_col = "Common_name", datetime_col = "DateTime",
                       site_col ="Site", unitTime = "hours")

crabbit_coyote_ratios <- crabbit_coyote$total_summary[c(5,6)]



# White-tailed Deer
wtd_coyote <- AAR(data = KScams_dat,
                  speciesA = "White-Tailed Deer", speciesB = "Coyote",
                  species_col = "Common_name", datetime_col = "DateTime",
                  site_col ="Site", unitTime = "hours")


wtd_coyote_ratios <- wtd_coyote$total_summary[c(5,6)]



# ---------------------------------------
#
#        Swift fox as predators
#
# ---------------------------------------


# Starting with the Black-tailed jackrabbit
jrabbit_fox <- AAR(data = KScams_dat,
                   speciesA = "Black-tailed jackrabbit", speciesB = "Swift Fox",
```

```
                    species_col = "Common_name", datetime_col = "DateTime",
                    site_col ="Site", unitTime = "hours")

# Saving only the T2/T1 and T4/T3 ratios
jrabbit_fox_ratios <- jrabbit_fox$total_summary[c(5,6)]

# Eastern cottontail rabbit
crabbit_fox  <- AAR(data = KScams_dat,
                    speciesA = "Eastern cottontail rabbit", speciesB = "Swift Fox",
                    species_col = "Common_name", datetime_col = "DateTime",
                    site_col ="Site", unitTime = "hours")

crabbit_fox_ratios <- crabbit_fox$total_summary[c(5,6)]


# White-tailed Deer
wtd_fox <- AAR(data = KScams_dat,
               speciesA = "White-Tailed Deer", speciesB = "Swift Fox",
               species_col = "Common_name", datetime_col = "DateTime",
               site_col ="Site", unitTime = "hours")


wtd_fox_ratios <- wtd_fox$total_summary[c(5,6)]
```

Data Wrangling

Okay, we need to organize the ratios for each prey species into one dataframe for analysis.

```
# Load libraries
# If needed install.packages("tidyverse")
library(tidyverse)

# Combining jack rabbit ratio data
jrabbit_ratios <- t(data.frame(
                    # T2/T1 ratios
                    bobcat_T2_T1 = jrabbit_bobcat_ratios["T2/T1"],
                    coyote_T2_T1 = jrabbit_coyote_ratios["T2/T1"],
                    fox_T2_T1 = jrabbit_fox_ratios["T2/T1"],

                    # T4/T3 ratios
                    bobcat_T4_T3 = jrabbit_bobcat_ratios["T4/T3"],
                    coyote_T4_T3 = jrabbit_coyote_ratios["T4/T3"],
                    fox_T4_T3 = jrabbit_fox_ratios["T4/T3"]))


# Convert the matrix to a data frame
jrabbit_ratios <- as.data.frame(jrabbit_ratios)

# Change row names to a new column
jrabbit_ratios <- tibble::rownames_to_column(jrabbit_ratios, var = "RowName")

# We have to rename the columns to match the values correctly
colnames(jrabbit_ratios) <- c("Interaction", "Value")
```

```r
# Adding a ratio column
jrabbit_ratios$Ratio <- c("T2/T1", "T2/T1", "T2/T1",
                          "T4/T3", "T4/T3", "T4/T3")

# Checking to make sure the Ratios are named correctly with current interaction
# names
print(jrabbit_ratios)
#>     Interaction      Value Ratio
#> 1 bobcat_T2_T1 0.3221821 T2/T1
#> 2 coyote_T2_T1 0.7009002 T2/T1
#> 3    fox_T2_T1 0.8736247 T2/T1
#> 4 bobcat_T4_T3 3.2703477 T4/T3
#> 5 coyote_T4_T3 3.8752311 T4/T3
#> 6    fox_T4_T3 3.1943420 T4/T3

# Naming interactions by predator
jrabbit_ratios$Interaction <- c("Bobcat", "Coyote","Swift Fox",
                                "Bobcat", "Coyote", "Swift Fox")

# Checking to see if it looks correct
print(jrabbit_ratios)
#>   Interaction      Value Ratio
#> 1      Bobcat 0.3221821 T2/T1
#> 2      Coyote 0.7009002 T2/T1
#> 3   Swift Fox 0.8736247 T2/T1
#> 4      Bobcat 3.2703477 T4/T3
#> 5      Coyote 3.8752311 T4/T3
#> 6   Swift Fox 3.1943420 T4/T3

# It does, let's do the other prey species.

# Reshape data to long format ################
jrabbit_ratios_long <- tidyr::gather(jrabbit_ratios, key = "Interaction", value = "Value")



# Combining cottontail rabbit
crabbit_ratios <- t(data.frame(
                 # T2/T1 ratios
                 bobcate_T2_T1 = crabbit_bobcat_ratios["T2/T1"],
                 coyote_T2_T1 = crabbit_coyote_ratios["T2/T1"],
                 fox_T2_T1 = crabbit_fox_ratios["T2/T1"],

                 # Column for T4/T3 ratios
                 bobcate_T4_T3 = crabbit_bobcat_ratios["T4/T3"],
                 coyote_T4_T3 = crabbit_coyote_ratios["T4/T3"],
                 fox_T4_T3 = crabbit_fox_ratios["T4/T3"]))


# Convert the matrix to a data frame
crabbit_ratios <- as.data.frame(crabbit_ratios)

# Change row names to a new column
```

```r
crabbit_ratios <- tibble::rownames_to_column(crabbit_ratios, var = "RowName")

# We have to rename the columns to match the values correctly
colnames(crabbit_ratios) <- c("Interaction", "Value")

# Adding a ratio column
crabbit_ratios$Ratio <- c("T2/T1", "T2/T1", "T2/T1",
                          "T4/T3", "T4/T3", "T4/T3")
# Naming interactions by predator
crabbit_ratios$Interaction <- c("Bobcat", "Coyote","Swift Fox",
                                "Bobcat", "Coyote", "Swift Fox")


# Combining cottontail rabbit
wtd_ratios <- t(data.frame(
                # T2/T1 ratios
                bobcate_T2_T1 = wtd_bobcat_ratios ["T2/T1"],
                coyote_T2_T1 = wtd_coyote_ratios["T2/T1"],
                fox_T2_T1 = wtd_fox_ratios["T2/T1"],

                # Column for T4/T3 ratios
                bobcate_T4_T3 = wtd_bobcat_ratios ["T4/T3"],
                coyote_T4_T3 = wtd_coyote_ratios["T4/T3"],
                fox_T4_T3 = wtd_fox_ratios["T4/T3"]))

# Convert the matrix to a data frame
wtd_ratios <- as.data.frame(wtd_ratios)

# Change row names to a new column
wtd_ratios <- tibble::rownames_to_column(wtd_ratios, var = "RowName")

# We have to rename the columns to match the values correctly
colnames(wtd_ratios) <- c("Interaction", "Value")

# Adding a ratio column
wtd_ratios$Ratio <- c("T2/T1", "T2/T1", "T2/T1",
                      "T4/T3", "T4/T3", "T4/T3")

# Naming interactions by predator
wtd_ratios$Interaction <- c("Bobcat", "Coyote","Swift Fox",
                            "Bobcat", "Coyote", "Swift Fox")
```

Statistical Analysis

Let's followthe analysis laid out by Parsons (2016) using a Wilcoxon test for each of our prey species and their interactions with the predator species and our prey species.

```r
# Jack rabbit
# Separate the data into two data frames for T2/T1 and T4/T3
jrabbit_t2t1 <- subset(jrabbit_ratios, Ratio == "T2/T1")
jrabbit_t4t3 <- subset(jrabbit_ratios, Ratio == "T4/T3")

# Run Wilcoxon pairwise tests for T2/T1
```

```
jrabbit_wilcox_t2t1 <- pairwise.wilcox.test(jrabbit_t2t1$Value,
                                            jrabbit_t2t1$Interaction,
                                            p.adjust.method = "bonferroni")

# Run Wilcoxon pairwise tests for T4/T3
jrabbit_wilcox_t4t3 <- pairwise.wilcox.test(jrabbit_t4t3$Value,
                                            jrabbit_t4t3$Interaction,
                                            p.adjust.method = "bonferroni")


# Print the results
print("Jack rabbit Wilcoxon Pairwise Test Results for T2/T1:")
#> [1] "Jack rabbit Wilcoxon Pairwise Test Results for T2/T1:"
print(jrabbit_wilcox_t2t1)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  jrabbit_t2t1$Value and jrabbit_t2t1$Interaction
#>
#>          Bobcat Coyote
#> Coyote   1      -
#> Swift Fox 1     1
#>
#> P value adjustment method: bonferroni

print("Jack rabbit Wilcoxon Pairwise Test Results for T4/T3:")
#> [1] "Jack rabbit Wilcoxon Pairwise Test Results for T4/T3:"
print(jrabbit_wilcox_t4t3)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  jrabbit_t4t3$Value and jrabbit_t4t3$Interaction
#>
#>          Bobcat Coyote
#> Coyote   1      -
#> Swift Fox 1     1
#>
#> P value adjustment method: bonferroni

# Cottontail rabbit

# Separate the data into two data frames for T2/T1 and T4/T3
crabbit_t2t1 <- subset(crabbit_ratios, Ratio == "T2/T1")
crabbit_t4t3 <- subset(crabbit_ratios, Ratio == "T4/T3")

# Run Wilcoxon pairwise tests for T2/T1
crabbit_wilcox_t2t1 <- pairwise.wilcox.test(crabbit_t2t1$Value,
                                    crabbit_t2t1$Interaction,
                                    p.adjust.method = "bonferroni")

# Run Wilcoxon pairwise tests for T4/T3
crabbit_wilcox_t4t3 <- pairwise.wilcox.test(crabbit_t4t3$Value,
                                    crabbit_t4t3$Interaction,
                                    p.adjust.method = "bonferroni")
```

```r
# Print the results
print("Cottontail rabbit Wilcoxon Pairwise Test Results for T2/T1:")
#> [1] "Cottontail rabbit Wilcoxon Pairwise Test Results for T2/T1:"
print(crabbit_wilcox_t2t1)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  crabbit_t2t1$Value and crabbit_t2t1$Interaction
#>
#>          Bobcat Coyote
#> Coyote    1      -
#> Swift Fox 1      1
#>
#> P value adjustment method: bonferroni


print("Cottontail rabbit Wilcoxon Pairwise Test Results for T4/T3:")
#> [1] "Cottontail rabbit Wilcoxon Pairwise Test Results for T4/T3:"
print(crabbit_wilcox_t4t3)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  crabbit_t4t3$Value and crabbit_t4t3$Interaction
#>
#>          Bobcat Coyote
#> Coyote    1      -
#> Swift Fox 1      1
#>
#> P value adjustment method: bonferroni


# White-tailed Deer

# Separate the data into two data frames for T2/T1 and T4/T3
wtd_t2t1 <- subset(wtd_ratios, Ratio == "T2/T1")
wtd_t4t3 <- subset(wtd_ratios, Ratio == "T4/T3")

# Run Wilcoxon pairwise tests for T2/T1
wilcox_t2t1 <- pairwise.wilcox.test(wtd_t2t1$Value,
                                    wtd_t2t1$Interaction,
                                    p.adjust.method = "bonferroni")

# Run Wilcoxon pairwise tests for T4/T3
wilcox_t4t3 <- pairwise.wilcox.test(wtd_t4t3$Value,
                                    wtd_t4t3$Interaction,
                                    p.adjust.method = "bonferroni")

# Print the results
print("White-tailed Deer Wilcoxon Pairwise Test Results for T2/T1:")
#> [1] "White-tailed Deer Wilcoxon Pairwise Test Results for T2/T1:"
print(wilcox_t2t1)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  wtd_t2t1$Value and wtd_t2t1$Interaction
```

```
#>
#>           Bobcat Coyote
#> Coyote    1      -
#> Swift Fox 1      1
#>
#> P value adjustment method: bonferroni

print("White-tailed Deer Wilcoxon Pairwise Test Results for T4/T3:")
#> [1] "White-tailed Deer Wilcoxon Pairwise Test Results for T4/T3:"
print(wilcox_t4t3)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  wtd_t4t3$Value and wtd_t4t3$Interaction
#>
#>           Bobcat Coyote
#> Coyote    1      -
#> Swift Fox 1      1
#>
#> P value adjustment method: bonferroni
```

The results of the Wilcoxon test show that none of the ratios were statistically significant. But that doesn't mean that there isn't a response in attraction or avoidance, only that it wasn't statistically significant. We know that values >1 suggest nonrandom movement between the two species which suggests that there is an interaction. We also know that attraction of species B to species A would result in high T2/T1 ratios, but lower T4/T3 ratios. Avoidance of species A from species B would result in higher ratios of T4/T3.
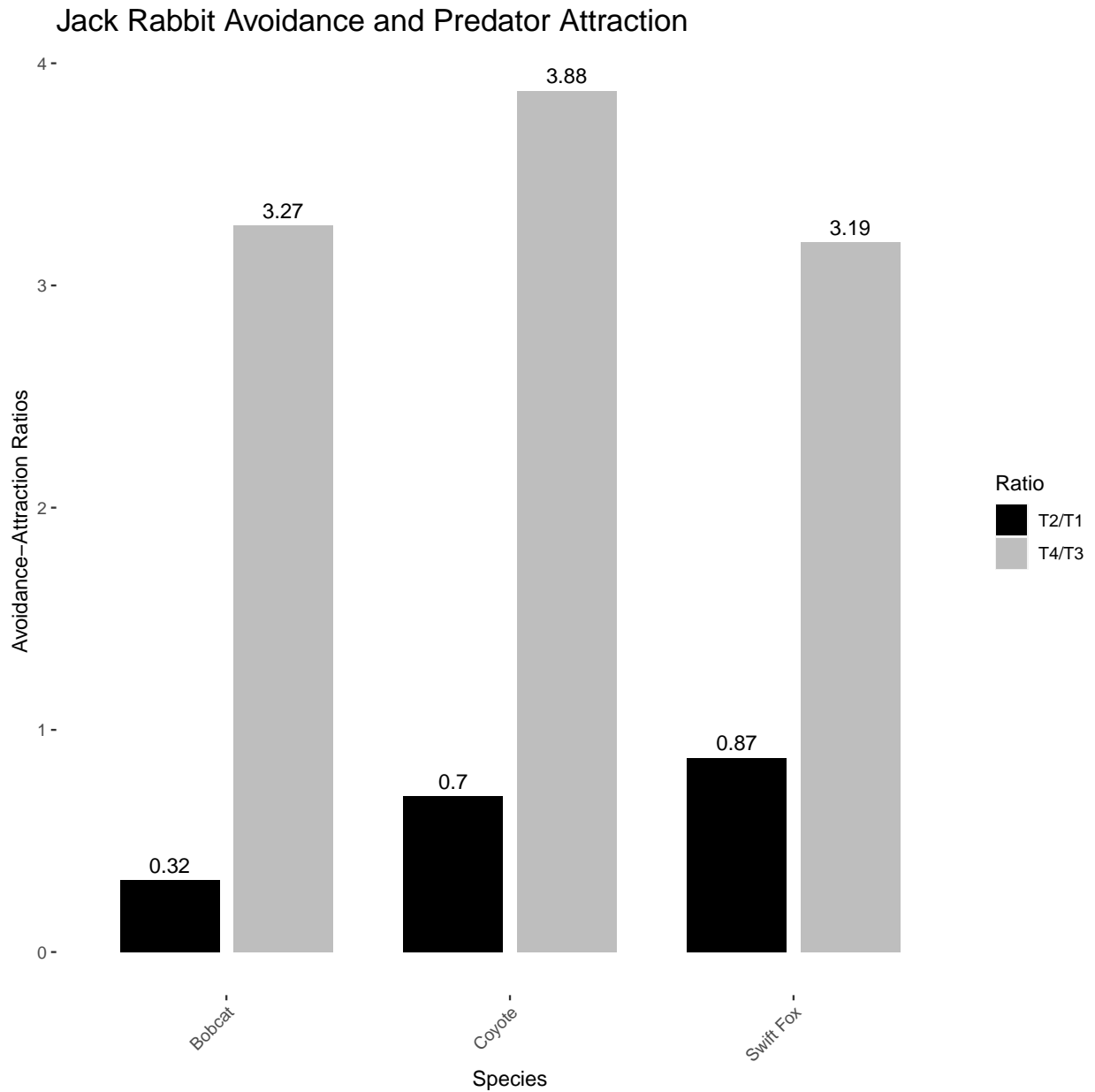
Plotting

Let's plot both of the ratios and take a look.

```
# Let's plot the ratios with ggplot2
# If needed install.packages("ggplot2")
library(ggplot2)

# Plotting Jack rabbit interactions
ggplot(jrabbit_ratios, aes(x = Interaction, y = Value, fill = Ratio)) +
                  geom_col(position = position_dodge(0.8), width = 0.7) +
                  geom_text(aes(label = round(Value, 2)),
                            position = position_dodge(0.8), vjust = -0.5, size = 4) +
                  scale_fill_manual(values = c("black", "grey"), name = "Ratio") +
                  labs(x = "Species", y = "Avoidance-Attraction Ratios",
                       title = "Jack Rabbit Avoidance and Predator Attraction") +
                  theme(axis.text.x = element_text(angle = 45, hjust = 1),
                        panel.background = element_rect(fill = "white"),
                     plot.title = element_text(size = 16))
```
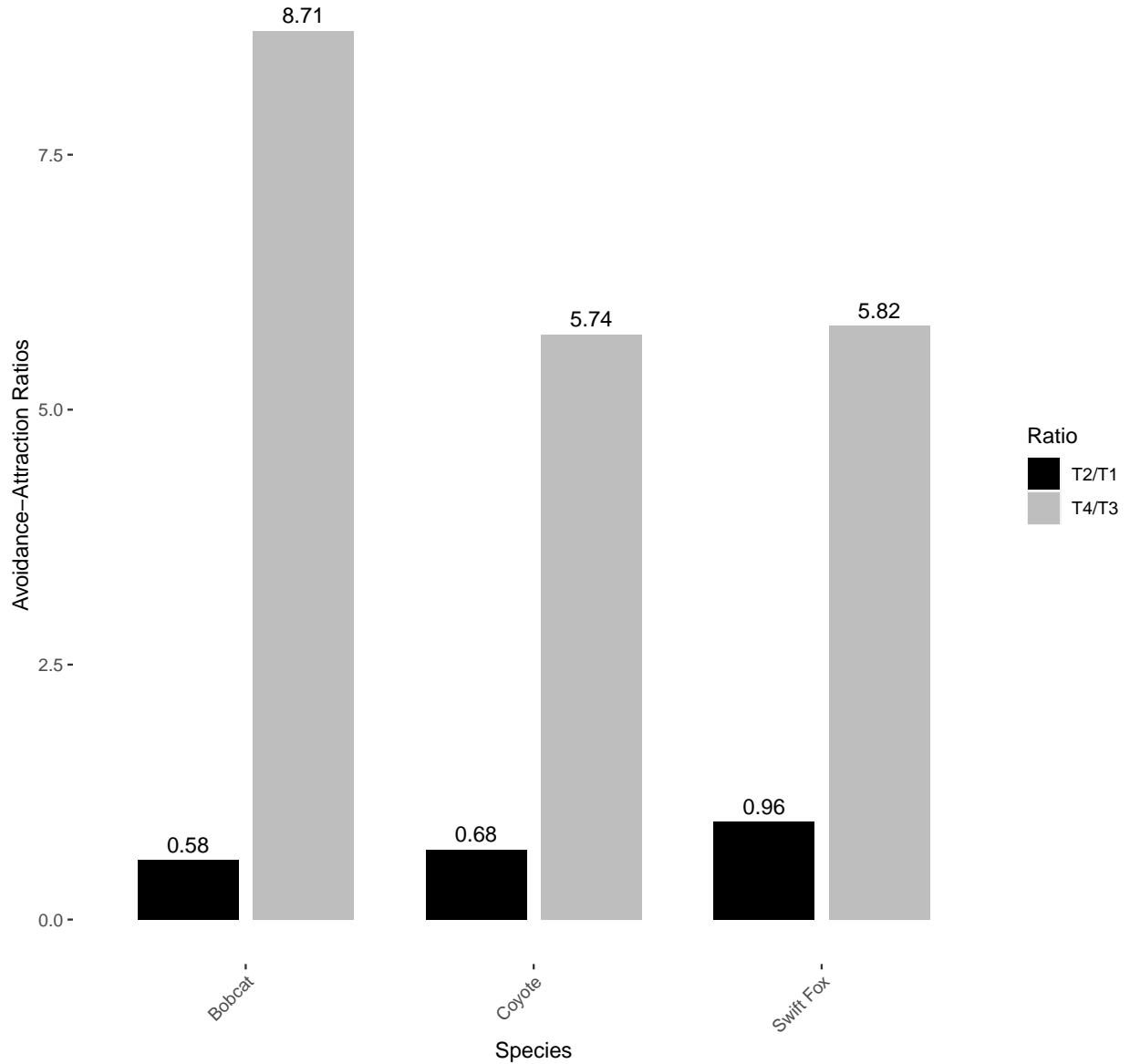
# Jack Rabbit Avoidance and Predator Attraction


```
# Plotting Cottontail rabbit interactions
ggplot(crabbit_ratios, aes(x = Interaction, y = Value, fill = Ratio)) +
        geom_col(position = position_dodge(0.8), width = 0.7) +
        geom_text(aes(label = round(Value, 2)),
                position = position_dodge(0.8), vjust = -0.5, size = 4) +
        scale_fill_manual(values = c("black", "grey"), name = "Ratio") +
        labs(x = "Species", y = "Avoidance-Attraction Ratios",
            title = "Cottontail Rabbit Avoidance and Predator Attraction") +
        theme(axis.text.x = element_text(angle = 45, hjust = 1),
            panel.background = element_rect(fill = "white"),
            plot.title = element_text(size = 16))
```

Cottontail Rabbit Avoidance and Predator Attraction


```r
# Plotting White-tailed Deer interactions
ggplot(wtd_ratios, aes(x = Interaction, y = Value, fill = Ratio)) +
                geom_col(position = position_dodge(0.8), width = 0.7) +
                geom_text(aes(label = round(Value, 2)),
                        position = position_dodge(0.8), vjust = -0.5, size = 4) +
                scale_fill_manual(values = c("black", "grey"), name = "Ratio") +
                labs(x = "Species", y = "Avoidance-Attraction Ratios",
                    title = "White-tailed Deer Avoidance and Predator Attraction") +
                theme(axis.text.x = element_text(angle = 45, hjust = 1),
                    panel.background = element_rect(fill = "white"),
                    plot.title = element_text(size = 16))
```

White−tailed Deer Avoidance and Predator Attraction
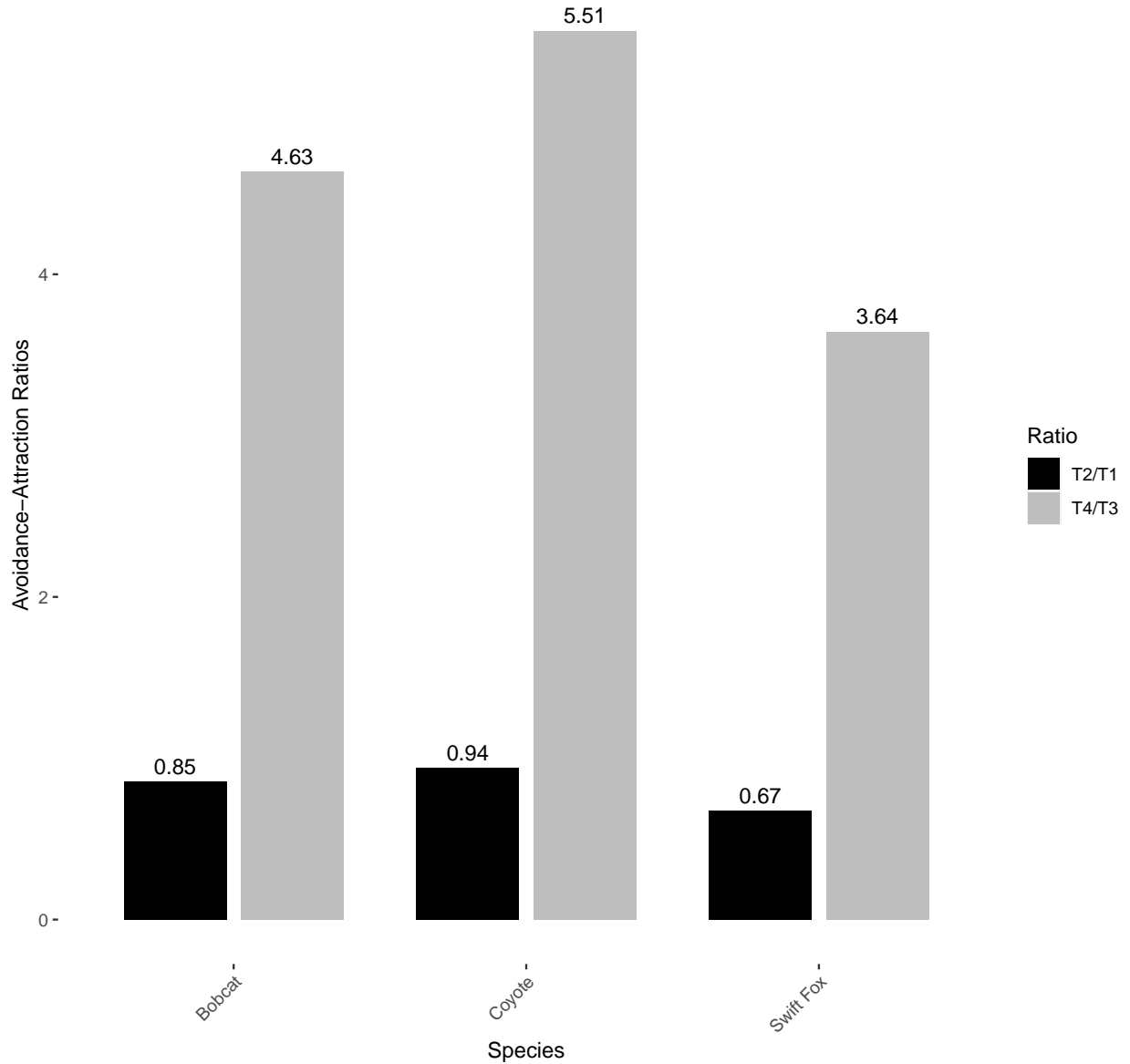
We can see from the plots that none of the T2/T1 values are >1. This suggests that none of the predator species are actively seeking out the prey species. But all of the T4/T3 values were >1 which suggests that the prey are avoiding the predator.

References:

Parsons, A. W., C. Bland, T. Forrester, M. C. Baker-Whatton, S. G. Schuttler, W. J. McShea, R. Costello, and R. Kays. 2016. The ecological impact of humans and dogs on wildlife in protected areas in eastern North America. Biological Conservation 203:75–88. URL: https://doi.org/10.1016/j.biocon.2016.09.001