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)

# Load the package
library(AvoidAttract)
#>
#> Attaching package: 'AvoidAttract'
#> The following object is masked _by_ '.GlobalEnv':
#>
#>     KScams_dat
```

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      Binomial
#> 1    Wkansas_2019 Mammalia    Carnivora Mustelidae Taxidea    taxus Taxidea taxus
```

```
#> 2     Wkansas_2019 Mammalia Artiodactyla    Bovidae    Bison    bison    Bison bison
#> 3     Wkansas_2019 Mammalia Artiodactyla    Bovidae    Bison    bison    Bison bison
#> 4     Wkansas_2019 Mammalia Artiodactyla    Bovidae    Bison    bison    Bison bison
#> 5     Wkansas_2019 Mammalia Artiodactyla    Bovidae    Bison    bison    Bison bison
#> 6     Wkansas_2019 Mammalia Artiodactyla    Bovidae    Bison    bison    Bison bison
#>        Common_name Year Site       DateTime      Date      Time      Timezone Latitude
#> 1 American badger 2019    0 9/1/2019 5:30:38 9/1/2019 5:30:38 America/Chicago 37.24655
#> 2  American bison 2019    0 9/3/2019 2:20:50 9/3/2019 2:20:50 America/Chicago 37.24655
#> 3  American bison 2019    0 9/3/2019 2:21:32 9/3/2019 2:21:32 America/Chicago 37.24655
#> 4  American bison 2019    0 9/3/2019 2:22:09 9/3/2019 2:22:09 America/Chicago 37.24655
#> 5  American bison 2019    0 9/3/2019 2:25:44 9/3/2019 2:25:44 America/Chicago 37.24655
#> 6  American bison 2019    0 9/3/2019 2:26:45 9/3/2019 2:26:45 America/Chicago 37.24655
#>   Longitude SetVisitDate
#> 1 -99.98253    8/7/2019
#> 2 -99.98253    8/7/2019
#> 3 -99.98253    8/7/2019
#> 4 -99.98253    8/7/2019
#> 5 -99.98253    8/7/2019
#> 6 -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"        "Family"
#>  [5] "Genus"           "Species"      "Binomial"     "Common_name"
#>  [9] "Year"            "Site"         "DateTime"     "Date"
#> [13] "Time"            "Timezone"     "Latitude"     "Longitude"
#> [17] "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

```
#> 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
# 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)]


# White-tailed Deer
```

4

```r
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",
```

```r
                    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.

```r
# Load libraries
# If needed install.packages("tidyverse")
library(tidyverse)
#> -- Attaching core tidyverse packages -------------------------------- tidyverse 2.0.0 --
#> v dplyr     1.1.4     v readr     2.1.4
#> v forcats   1.0.0     v stringr   1.5.1
#> v ggplot2   3.4.4     v tibble    3.2.1
#> v lubridate 1.9.3     v tidyr     1.3.0
#> v purrr     1.0.2
#> -- Conflicts --------------------------------------------- tidyverse_conflicts() --
#> x dplyr::filter() masks stats::filter()
#> x dplyr::lag()    masks stats::lag()
#> i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error

# 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"]))
```

```r
# 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")

# 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
```

```r
                    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
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")
```

```r
# 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")

# 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",
```
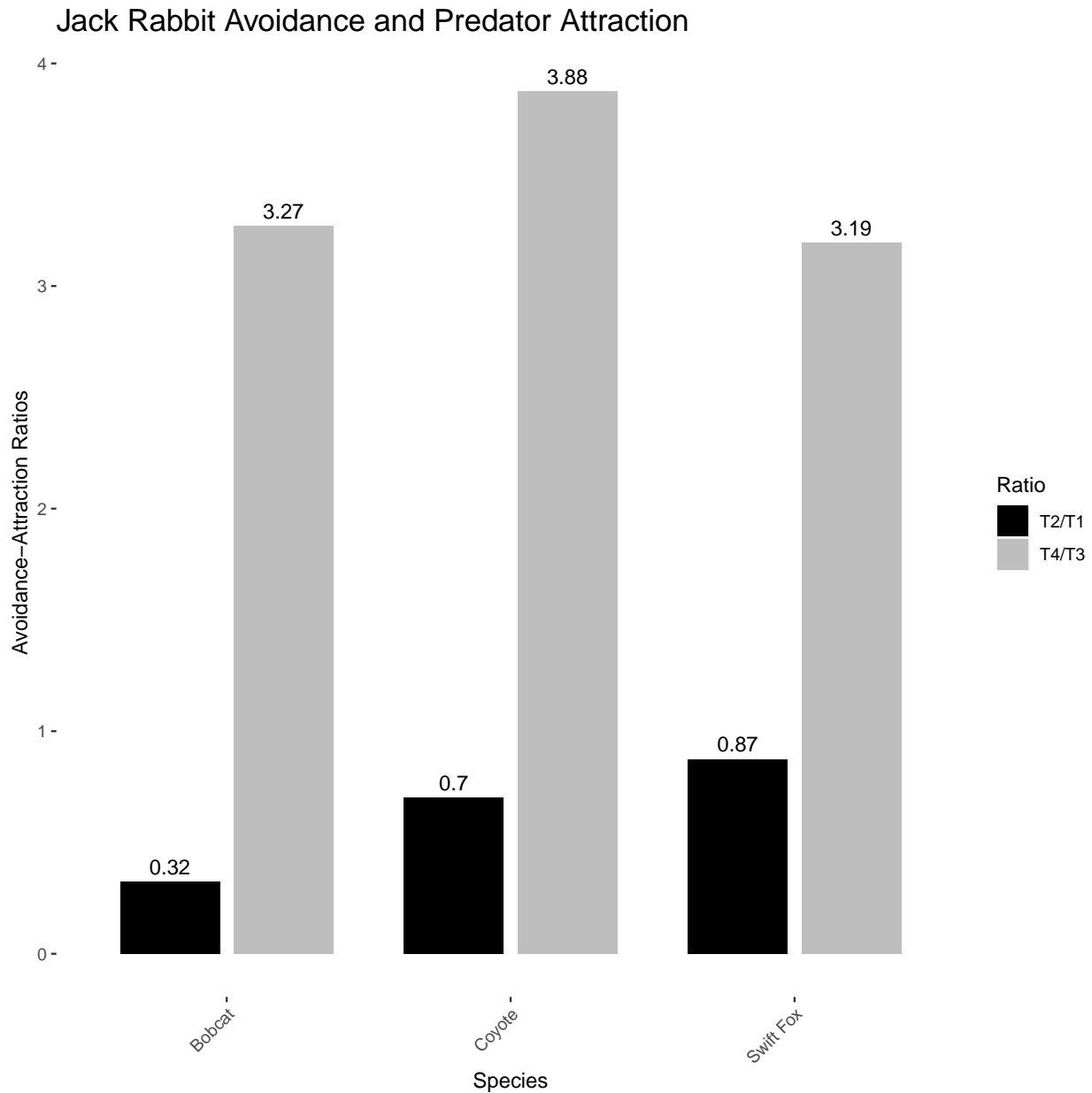
```
                title = "Jack Rabbit Avoidance and Predator Attraction") +
        theme(axis.text.x = element_text(angle = 45, hjust = 1),
              panel.background = element_rect(fill = "white"),
            plot.title = element_text(size = 16))
```

Jack Rabbit Avoidance and Predator Attraction
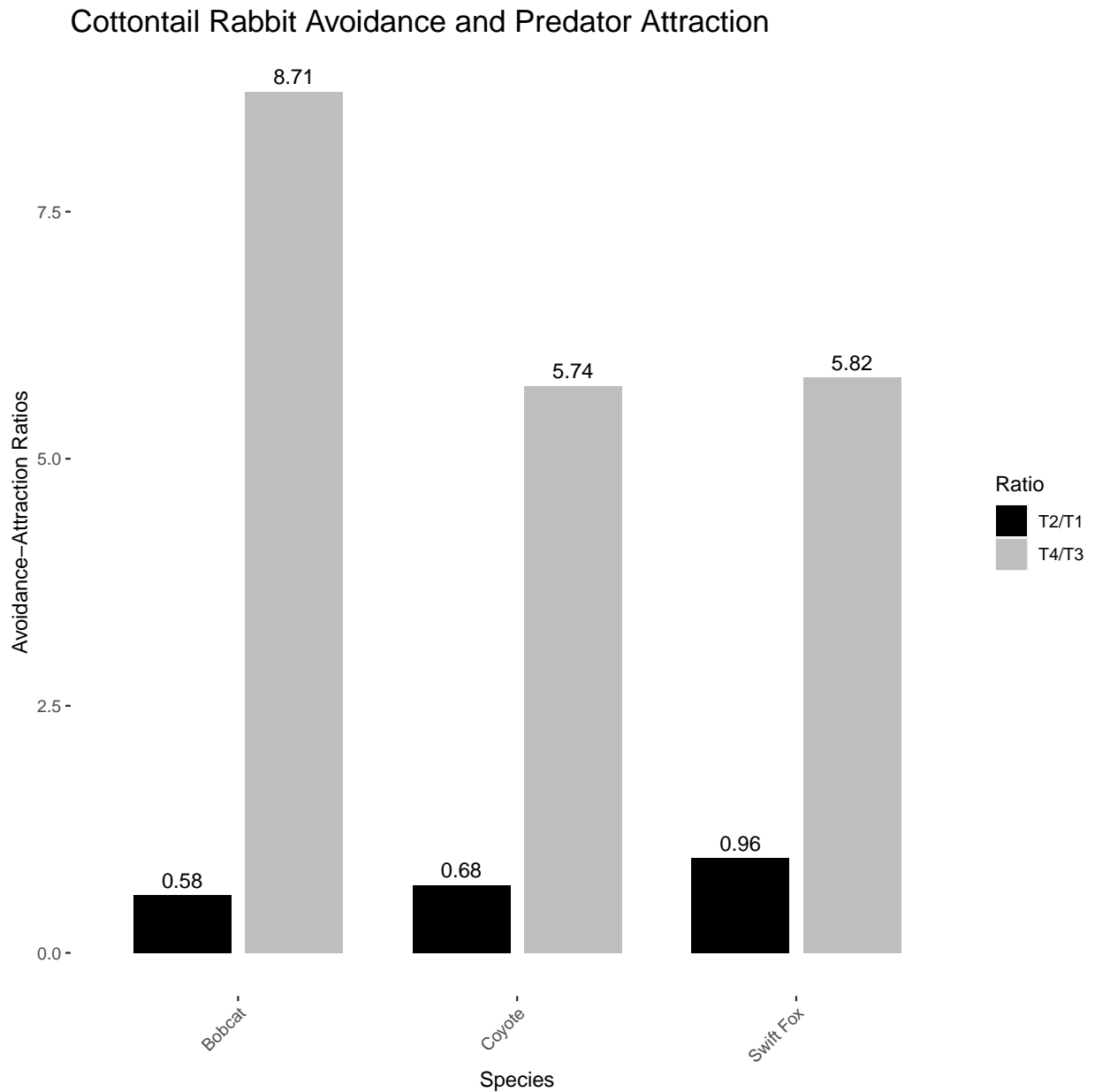


```
# Plotting Cottontail rabbit interactions
ggplot(crabbit_ratios, aes(x = Interaction, y = Value, fill = Ratio)) +
        geom_col(position = position_dodge(0.8), width = 0.7) +
        geom_text(aes(label = round(Value, 2)),
                position = position_dodge(0.8), vjust = -0.5, size = 4) +
        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



```
# 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
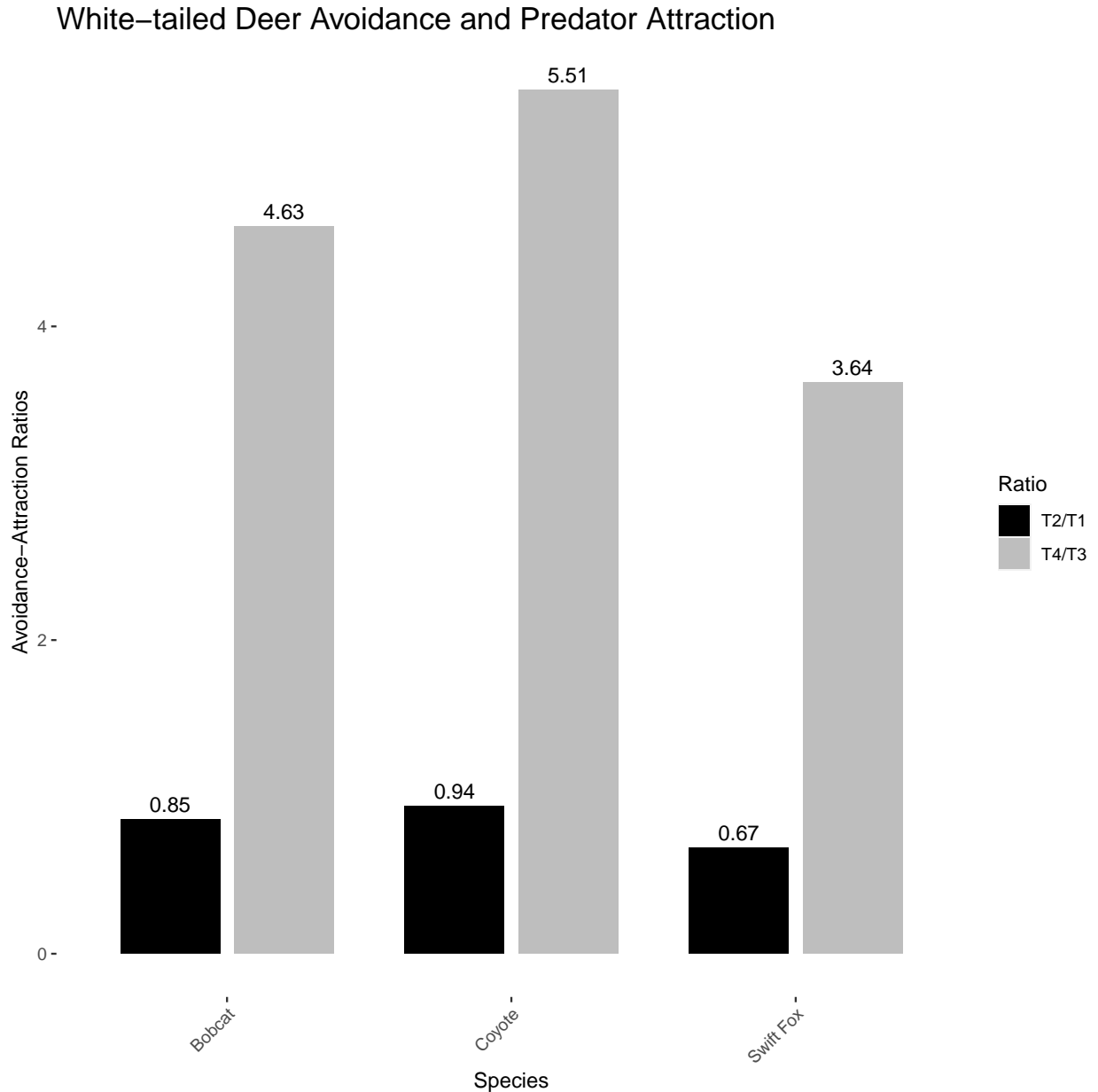
We can see from the plots that none of the T2/T1 values are >1. This suggests that none of the predator species are actively seeking out the prey species. But all of the T4/T3 values were >1 which suggests that the prey are avoiding the predator.

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