

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  tarus Taxidea tarus
```

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

# 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 prairie 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

```

```

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")
options(tidyverse.quiet = TRUE)
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")

```

```

# 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

```

```

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 follow the 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.

```

# 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")

```

```

# 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

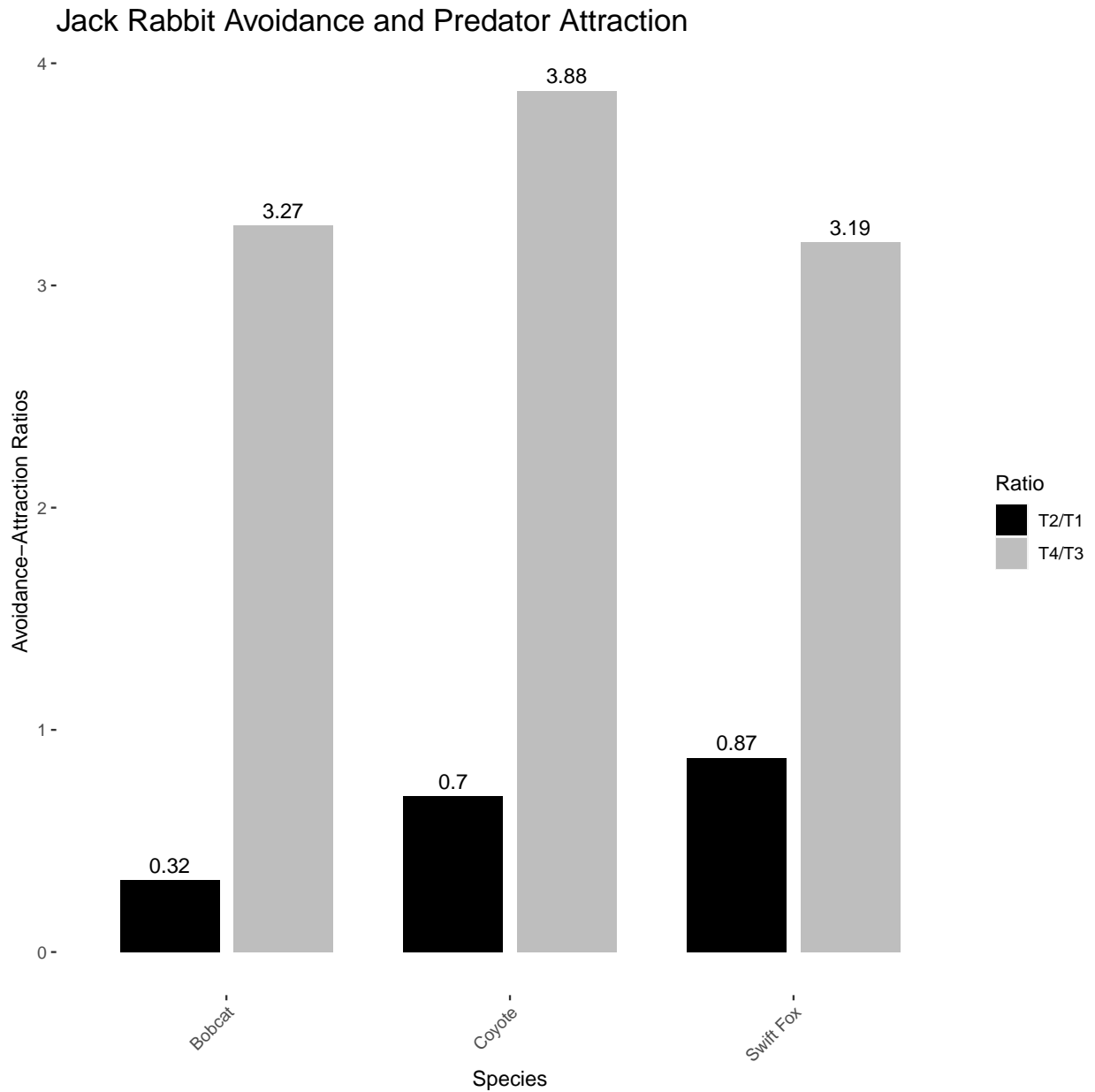
Let's plot both of the ratios and take a look.

```

# Let's plot the ratios with ggplot2
# If needed install.packages("ggplot2")
library(ggplot2, quiet = TRUE)

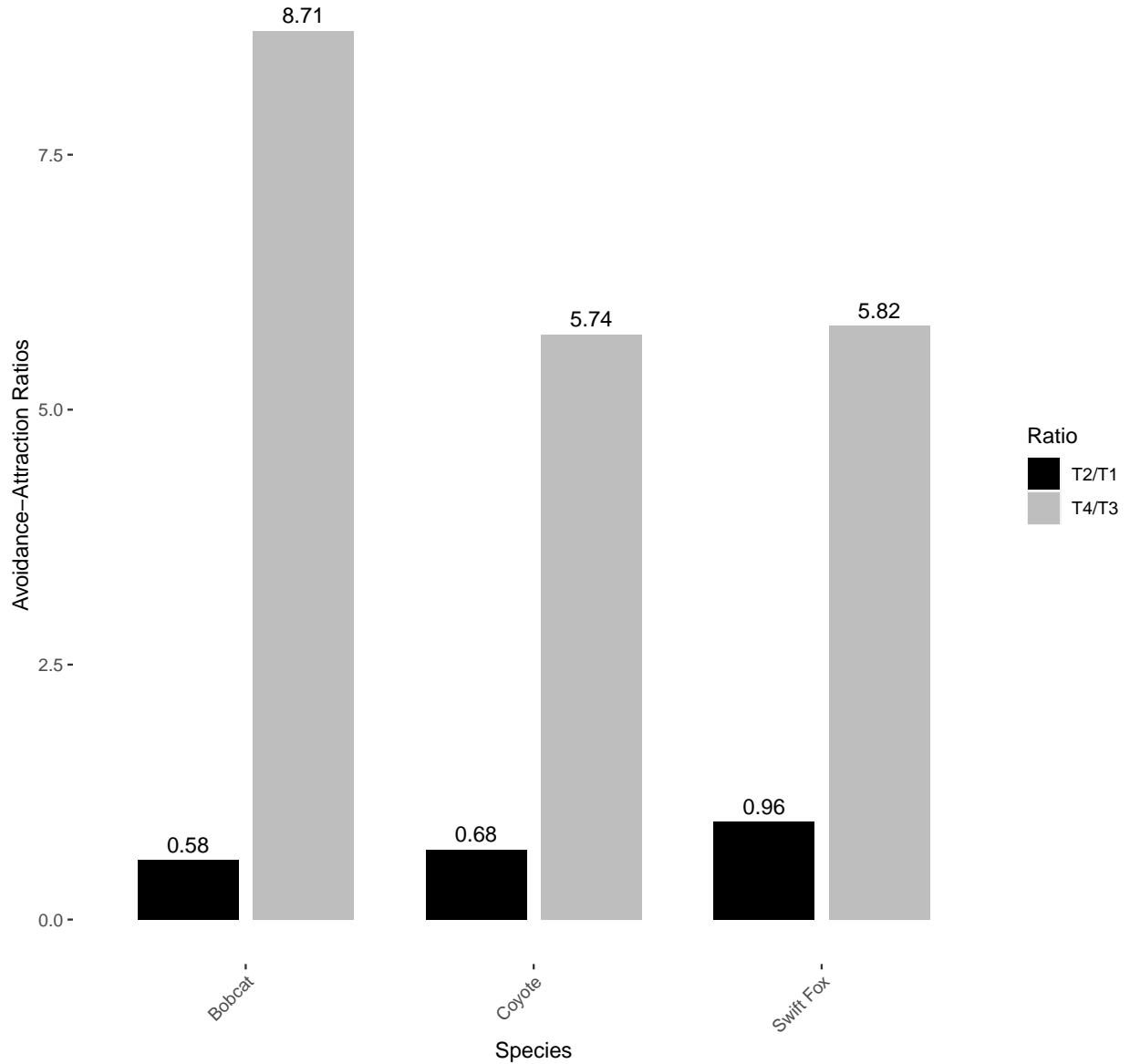
# Plotting Jack rabbit interactions
ggplot(jrabbit_ratios, aes(x = Interaction, y = Value, fill = Ratio)) +
  geom_col(position = position_dodge(0.8), width = 0.7) +
  geom_text(aes(label = round(Value, 2)),
            position = position_dodge(0.8), vjust = -0.5, size = 4) +
  scale_fill_manual(values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

```



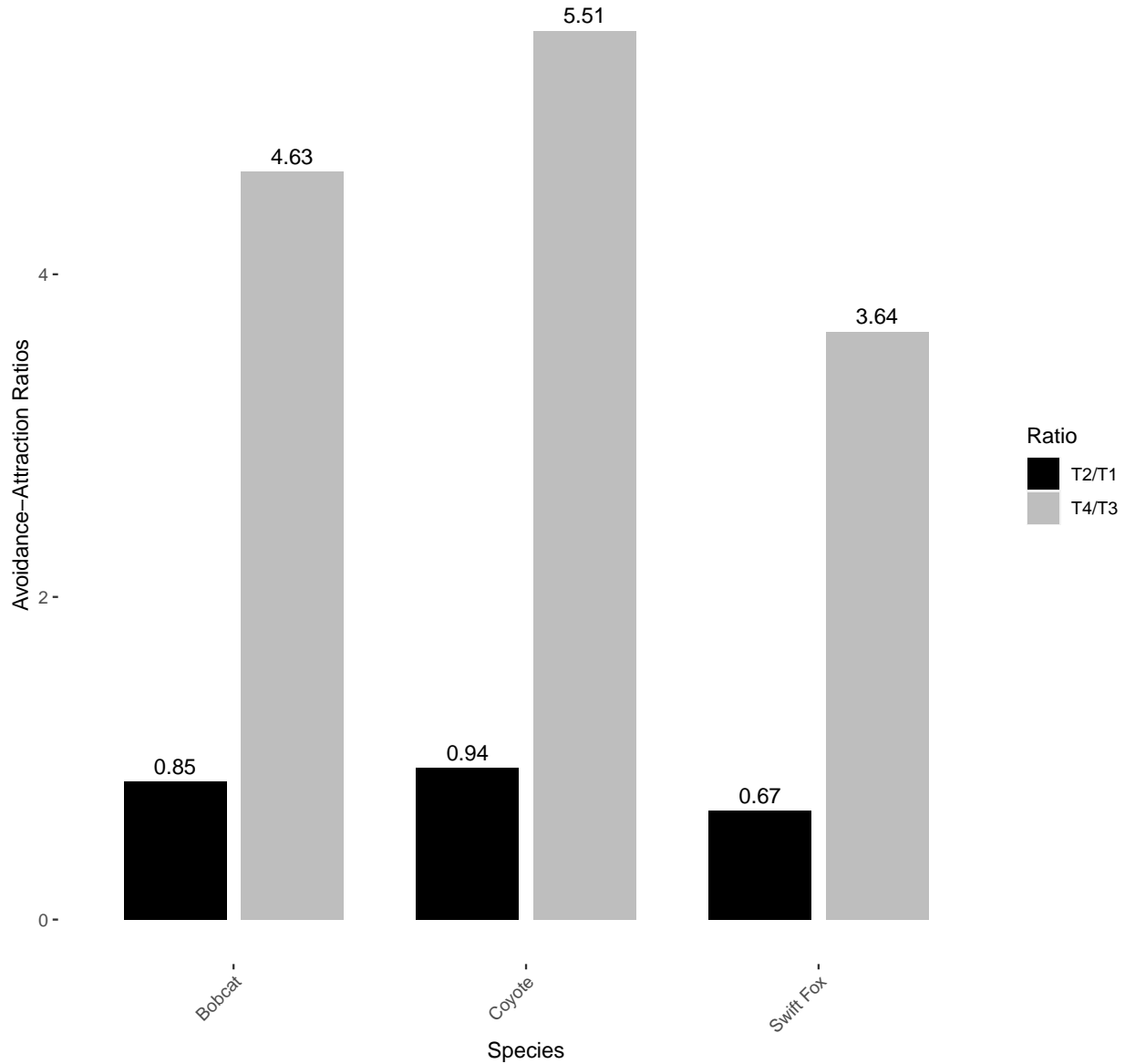
```
# Plotting Cottontail rabbit interactions
ggplot(crabbit_ratios, aes(x = Interaction, y = Value, fill = Ratio)) +
  geom_col(position = position_dodge(0.8), width = 0.7) +
  geom_text(aes(label = round(Value, 2)),
            position = position_dodge(0.8), vjust = -0.5, size = 4) +
  scale_fill_manual(values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

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```
# 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>