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 coyotes (*Canis latrans*) 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.

```
# Install the package
devtools::install_github("dpearcetamu/AvoidAttract", quiet = TRUE)

# Load the package
library(AvoidAttract)
```

Now that the package is installed and loaded, let's take a look at 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     Common_name
#> 1    Wkansas_2019 Mammalia    Carnivora Mustelidae Taxidea   taxus Taxidea taxus American badger
#> 2    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison   Bison bison  American bison
#> 3    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison   Bison bison  American bison
#> 4    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison   Bison bison  American bison
#> 5    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison   Bison bison  American bison
#> 6    Wkansas_2019 Mammalia Artiodactyla    Bovidae   Bison   bison   Bison bison  American bison
#>   Year Site         DateTime     Date     Time        Timezone Latitude Longitude SetVisitDate
#> 1 2019    0 9/1/2019 5:30:38 9/1/2019 5:30:38 America/Chicago 37.24655 -99.98253     8/7/2019
#> 2 2019    0 9/3/2019 2:20:50 9/3/2019 2:20:50 America/Chicago 37.24655 -99.98253     8/7/2019
#> 3 2019    0 9/3/2019 2:21:32 9/3/2019 2:21:32 America/Chicago 37.24655 -99.98253     8/7/2019
#> 4 2019    0 9/3/2019 2:22:09 9/3/2019 2:22:09 America/Chicago 37.24655 -99.98253     8/7/2019
#> 5 2019    0 9/3/2019 2:25:44 9/3/2019 2:25:44 America/Chicago 37.24655 -99.98253     8/7/2019
#> 6 2019    0 9/3/2019 2:26:45 9/3/2019 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.

```r
# Let's see what the column names are
names(KScams_dat)
#>  [1] "General_project" "Class"           "Order"           "Family"          "Genus"
#>  [6] "Species"         "Binomial"        "Common_name"     "Year"            "Site"
#> [11] "DateTime"        "Date"            "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.

```r
# 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.

```
# 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!

# Starting with the Black-tailed jackrabbit
jrabbit_AAR <- AAR(data = KScams_dat, speciesA = "Black-tailed jackrabbit", speciesB = "Coyote",
                   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_AAR$total_summary)
#>         T1         T2         T3         T4      T2/T1      T4/T3
#> 37.4752002 26.2663756 13.3018789 51.5478551  0.7009002  3.8752311

# Okay we can see that this outputs the mean values for all interaction events and the interaction rati

# The AAR function also returns a list of how many times those interactions occurred.
print(jrabbit_AAR$event_count)
#>   T1   T2   T3   T4
#>  498  230 2754  230

# 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_ratios <- jrabbit_AAR$total_summary[c(5,6)]

# Now the other species

# Black-tailed Prarie Dog
pdog_AAR <- AAR(data = KScams_dat, speciesA = "Black-tailed Prarie Dog", speciesB = "Coyote",
                species_col = "Common_name", datetime_col = "DateTime",
                site_col ="Site", unitTime = "hours")

pdog_ratios <- pdog_AAR$total_summary[c(5,6)]

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

crabbit_ratios <- crabbit_AAR$total_summary[c(5,6)]


# Mouse
mouse_AAR <- AAR(data = KScams_dat, speciesA = "Mouse", speciesB = "Coyote",
                 species_col = "Common_name", datetime_col = "DateTime",
                 site_col ="Site", unitTime = "hours")
```

```
mouse_ratios <- mouse_AAR$total_summary[c(5,6)]

# Norway rat
rat_AAR <- AAR(data = KScams_dat, speciesA = "Norway rat", speciesB = "Coyote",
               species_col = "Common_name", datetime_col = "DateTime",
               site_col ="Site", unitTime = "hours")

rat_ratios <- rat_AAR$total_summary[c(5,6)]

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


wtd_ratios <- wtd_AAR$total_summary[c(5,6)]
```

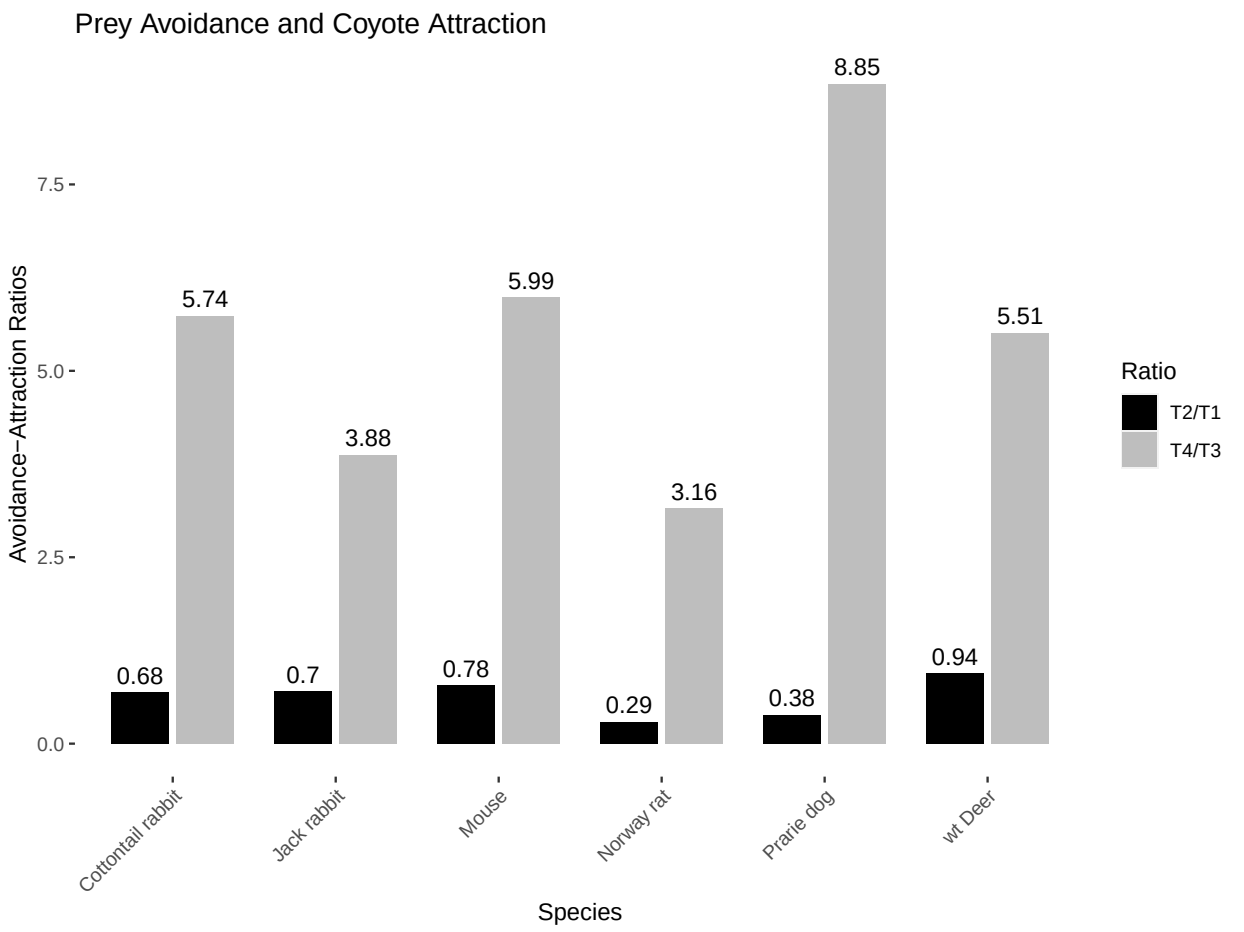
Okay, now lets combine all of the summaries into one dataframe.

```
# Combining ratio data
combined_ratios <- as.data.frame(rbind(Jack_rabbit = jrabbit_ratios,
                                       Prarie_dog = pdog_ratios,
                                       cottontail_rabbit = crabbit_ratios,
                                       Mouse = mouse_ratios,
                                       Norway_rat = rat_ratios,
                                       wt_Deer = wtd_ratios))

# Adding a column for species names
combined_ratios$Species  <- c("Jack rabbit", "Prarie dog",
                              "Cottontail rabbit", "Mouse", "Norway rat", "wt Deer")

# Future steps require that the data be in a long format.
# Let's convert the data from a wide format to long format.
combined_ratios_long <- tidyr::gather(combined_ratios, key = "Ratio",
                                      value = "Value", -Species)
# Take a quick look
print(combined_ratios)
#>                       T2/T1    T4/T3           Species
#> Jack_rabbit       0.7009002 3.875231       Jack rabbit
#> Prarie_dog        0.3845740 8.849047        Prarie dog
#> cottontail_rabbit 0.6845692 5.739222 Cottontail rabbit
#> Mouse             0.7841233 5.989303             Mouse
#> Norway_rat        0.2899148 3.156439        Norway rat
#> wt_Deer           0.9396498 5.508133           wt Deer
```

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

```
# Let's plot the ratios with ggplot2
library(ggplot2)

# Plotting
ggplot(combined_ratios_long, aes(x = Species, 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) +
  scale_fill_manual(values = c("black", "grey"), name = "Ratio") +
  labs(x = "Species", y = "Avoidance-Attraction Ratios",
       title = "Prey Avoidance and Coyote Attraction") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.background = element_rect(fill = "white"))
```



From Parsons (2016) we know that the T2/T1 (BA/AB) ratio could be influenced both by the avoidance of the species A and the attraction of species B and the T4/T3 ratio describes the avoidance of species A from species B. We also know that values >1 for T2/T1 or T4/T3 suggest nonrandom movement between the two species and attraction of species B to species A could also result in high T2/T1 ratios, but would result in lower ratios of T4/T3. We also know that lower T2/T1 ratios but higher T4/T3 ratios would suggest that species B isn't attracted to species A but species A is avoiding species B.

So, let's follow the analysis laid out by Parsons (2016) for coyote and our prey species.

```
# Perform pairwise Wilcoxon tests
wilcox_test_result <- pairwise.wilcox.test(
  combined_ratios_long$Value,
  combined_ratios_long$Species,
  p.adjust.method = "bonferroni"  # Adjust p-values for multiple comparisons
)
```

```r
# Print the results
print(wilcox_test_result)
#>
#>  Pairwise comparisons using Wilcoxon rank sum exact test
#>
#> data:  combined_ratios_long$Value and combined_ratios_long$Species
#>
#>             Cottontail rabbit Jack rabbit Mouse Norway rat Prarie dog
#> Jack rabbit 1                 -           -     -          -
#> Mouse       1                 1           -     -          -
#> Norway rat  1                 1           1     -          -
#> Prarie dog  1                 1           1     1          -
#> wt Deer     1                 1           1     1          1
#>
#> P value adjustment method: bonferroni
```

The results of the Wilcox test show that the ratios were not statistically significant. But that doesn't mean that there isn't a response in attraction or avoidance, only that it wasn't statistically significant and we know that values >1 suggest nonrandom movement between the two species.

This vignette shows how to implement the main functions in AvoidAttract to investigate species interactions using camera trapping data.

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