

# Explore EWC - ALR

Notes:

- I've just plotted basic lines here, these are always `geom_smooth(method = glm)`

Things I'm not sure about:

In subsequent analyses, we estimated the predator-prey habitat domain spatially as the interaction between the predator and prey habitat domains

We don't actually *spatially* interact the predator and prey domains right? How could we do this? Correlation of rasters? Difference between predator - prey RSF values?

## Setup

```
pkgs <- c('data.table', 'ggplot2', 'patchwork')
p <- suppressPackageStartupMessages(lapply(
  pkgs,
  library,
  character.only = TRUE)
)
```

## Data

```
caribou <- readRDS('output/4-sociality/caribouNNA-ALR.Rds')
elk <- readRDS('output/4-sociality/elkNNA-ALR.Rds')

coordCols <- c('EASTING', 'NORTHING')
idCol <- 'id'

caribou[, species := 'caribou']
elk[, species := 'elk']

DT <- rbindlist(list(caribou, elk), fill = TRUE)
```

A note regarding differences between this and the sociality models R scripts: I've combined the caribou and elk data into a global DT. Downstream I've added `by = species` wherever necessary.

## Variables

### Scaled RSF

Shouldn't this scaling be seasonal?

```
DT[, z.avgpreyRSF := scale(avgpreyRSF, center = T, scale = T)]
DT[, z.avgpredatorRSF := scale(avgpredatorRSF, center = T, scale = T)]

# By species*seasonal
DT[, z.avgpreyRSFBy := scale(avgpreyRSF, center = T, scale = T), .(species, season)]
DT[, z.avgpredatorRSFBy := scale(avgpredatorRSF, center = T, scale = T), .(species, season)]
```

Isn't this the second time scaling is performed? We scaled the global RSFs, then rescaled within the sampled points?

In scripts NL-RSF.R and RMNP-RSF.R:

```
### Rescale RSFs ----
q <- 0.999

winterQ <- quantile(winterCrop, q)
winterCrop[winterCrop > winterQ] <- winterQ

winterScaled <-
  (winterCrop - (cellStats(winterCrop, min))) /
  (quantile(winterCrop, q) - (cellStats(winterCrop, min)))

springQ <- quantile(springCrop, q)
springCrop[springCrop > springQ] <- springQ

springScaled <-
  (springCrop - (cellStats(springCrop, min))) /
  (cellStats(springCrop, max) - (cellStats(springCrop, min)))
```

### Bin 500m

```
# Dyads within 500m
setnames(DT, 'distance', 'dyadDist')
DT[dyadDist >= 500, bin500m := TRUE]
DT[dyadDist < 500, bin500m := FALSE]
```

The DI approach, as in Cr, measures cohesiveness irrespective of proximity between corresponding movement vectors (Table 2). Thus, to justify DI analysis, the researcher is required to have some a priori expectation of cohesive movement, which, for example, can be based on proximity (defined by distance threshold  $dc$ ), a measure of static interaction (e.g. home range overlap) or simultaneous capture (e.g. familial groups). DI can then be set to 0 when these conditions are not met

Is there a value less than 500m, relevant for setting DI to 0? Is 500m relevant for both elk and caribou?

```
# Set DI to 0 if > 500m between dyads
DT[dyadDist >= 500, di0 := 0]
DT[dyadDist < 500, di0 := di]
```

## Drop duplicated dyads

```
# Drop duplicated dyads (won't be exactly half
#   the number of rows because not all NN are NN with each other)
DT <- unique(DT[!is.na(NN)], by = c('dyadID', 'timegroup'))
```

## Global DI

Seems to me that global DI should likely be calculated for the full dataset, before subsetting because it is relevant for dyads that are not observed within 500m often

```
DT[, globalDI := mean(di0), .(season, dyadID)]
DT[, globalDIAngle := mean(diAngle), .(season, dyadID)]
DT[, globalDIDist := mean(diDist), .(season, dyadID)]
```

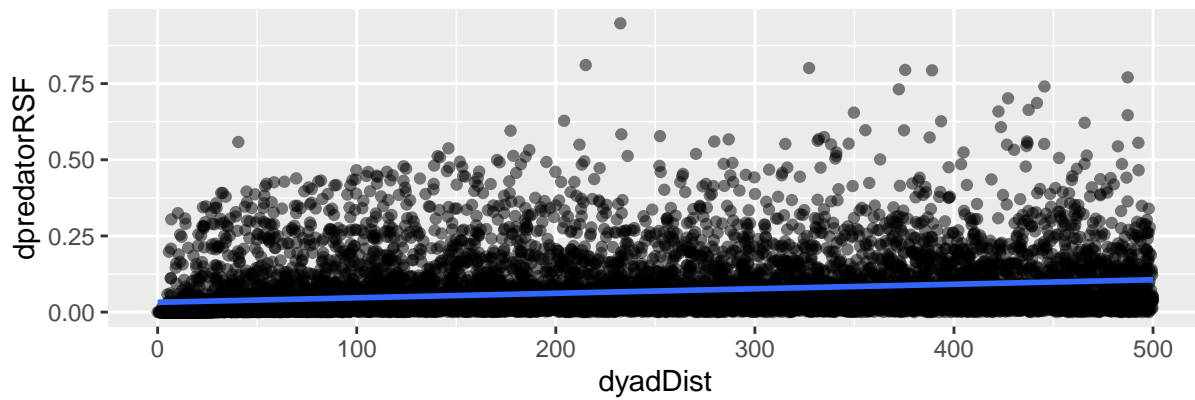
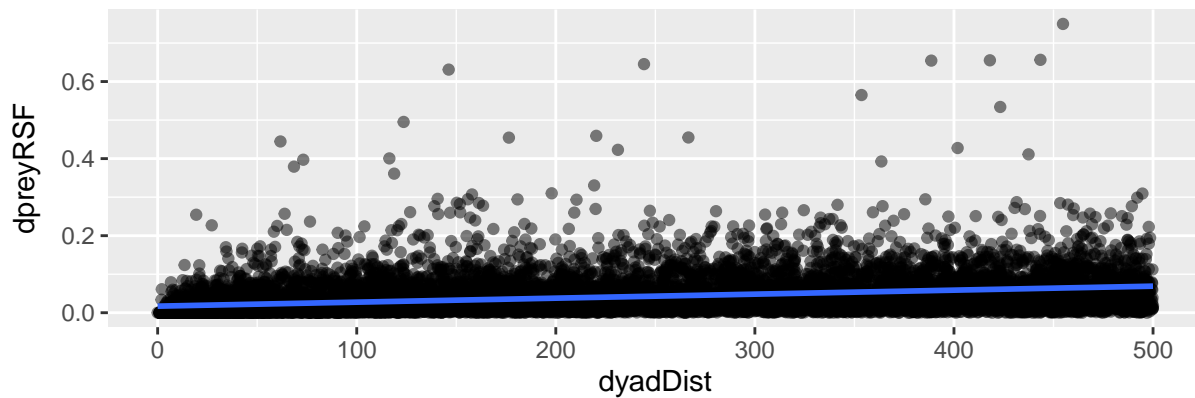
## Subset

```
DTsoc <- DT[dyadDist < 500]
```

## Plots

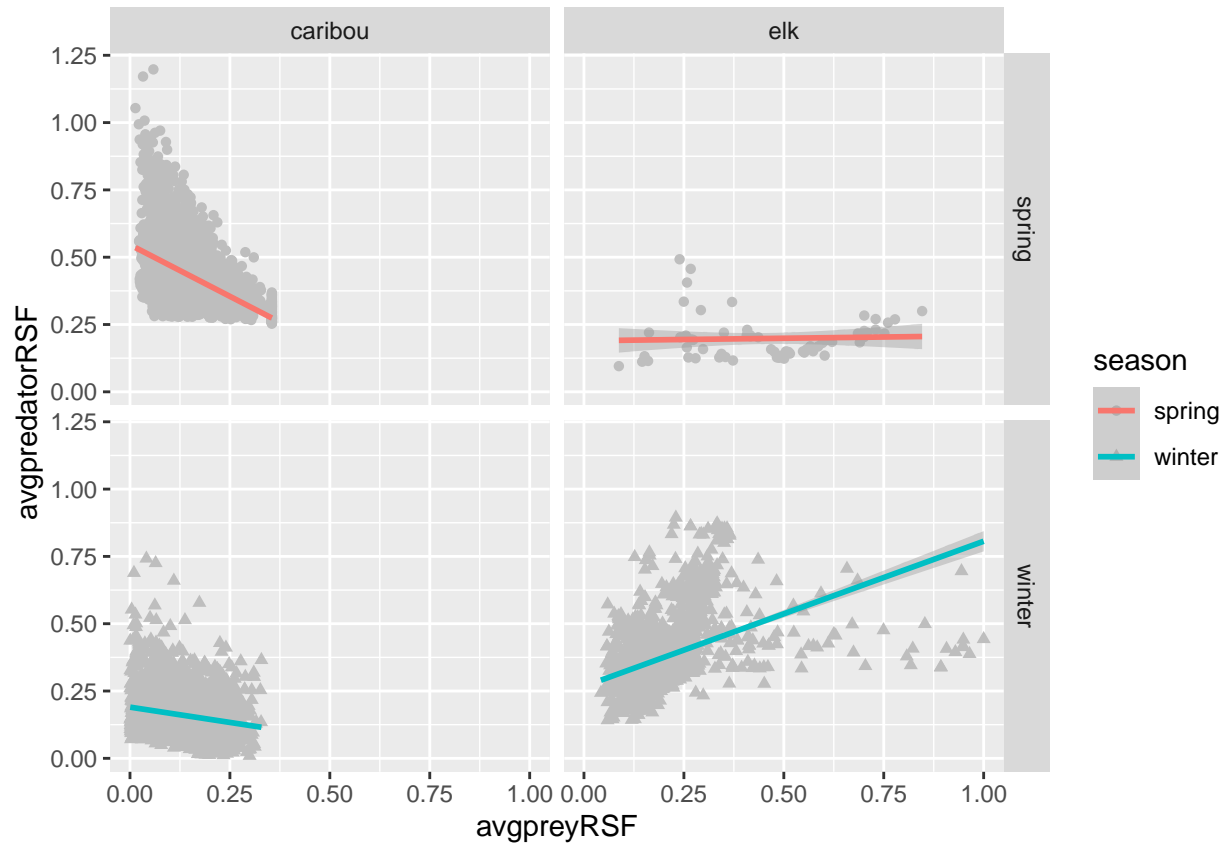
Relationship between difference in RSF and distance within dyad

```
# Dist vs diff in RSF  
g1 <- ggplot(DTsoc, aes(dyadDist, dpreyRSF)) +  
  geom_point(color = 'black', alpha = 0.5) +  
  geom_smooth(method = glm)  
  
g2 <- ggplot(DTsoc, aes(dyadDist, dpredatorRSF)) +  
  geom_point(color = 'black', alpha = 0.5) +  
  geom_smooth(method = glm)  
  
g1 / g2
```



Relationship between average predator RSF and average prey RSF

```
### Plots ----
ggplot(DTsoc, aes(avgpreyRSF, avgpredatorRSF, color = season)) +
  geom_point(color = 'grey', aes(shape = season)) +
  facet_grid(season ~ species) +
  geom_smooth(method = glm)
```



Relationship between average coyote, bear (and wolf for elk) RSF and average prey RSF

```
### Plots ----
g1 <- ggplot(DTsoc[species == 'caribou'], aes(avgpreyRSF, avgbearRSF, color = season)) +
  geom_point(color = 'grey', aes(shape = season)) +
  facet_grid(~ season) +
  geom_smooth(method = glm) +
  ggtitle('caribou')

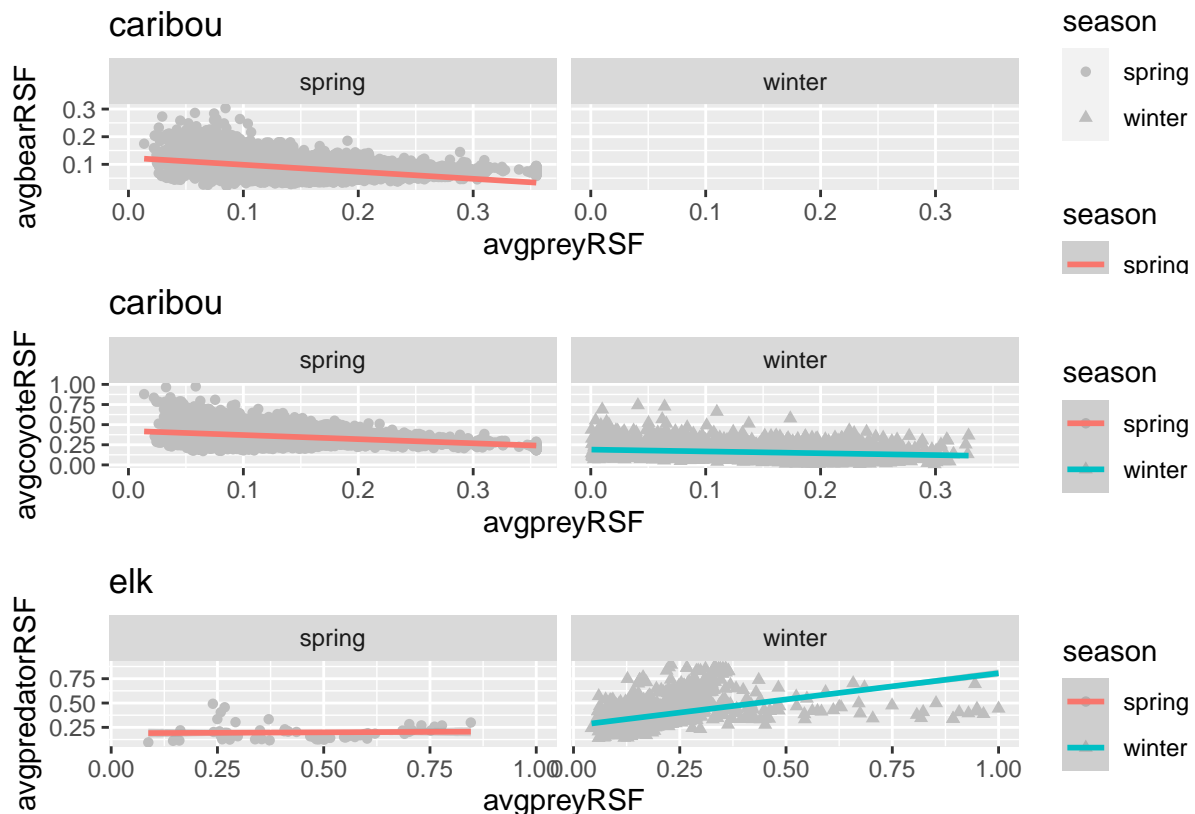
g2 <- ggplot(DTsoc[species == 'caribou'], aes(avgpreyRSF, avgcoyoteRSF, color = season)) +
  geom_point(color = 'grey', aes(shape = season)) +
  facet_grid(~ season) +
  geom_smooth(method = glm) +
  ggtitle('caribou')

g3 <- ggplot(DTsoc[species == 'elk'], aes(avgpreyRSF, avgpredatorRSF, color = season)) +
  geom_point(color = 'grey', aes(shape = season)) +
  facet_grid(~ season) +
  geom_smooth(method = glm) +
  ggtitle('elk')

g1 / g2 / g3
```

## Warning: Removed 4254 rows containing non-finite values (stat\_smooth).

## Warning: Removed 4254 rows containing missing values (geom\_point).



## Spatially explicit predator:prey domain

```
# Attempts at pred:prey domain  
DTsoc[, predpreyRSF := predatorRSF - preyRSF]  
DTsoc[, predpreyRSF.nn := predatorRSF.nn - preyRSF.nn]
```