

ProblemSet2_2

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a.

First, I stored the dataset interactions in `interac`, focal_names in `focaln`, all_names in `alln`.

```
## Store the datasets in variables
library(readr)
library(dplyr)
library(tidyr)
library(Hmisc)
library(ggplot2)
setwd('E:\\UM academy\\stat 506\\ProblemSet2')
interac=read_delim('./Stats506_F17_ps2_interactions.csv', delim=',',col_names=TRUE)
focaln=read_delim('./Stats506_F17_ps2_focal_names.csv', delim=',',col_names=F)
alln=read_delim('./Stats506_F17_ps2_all_names.csv', delim=',',col_names=F)
```

Then reformat the data as the data-frame `rmat` with one row per interaction type for each focal individual in the first column.

```
## Reformat the data as the data-frame rmat
separate_rows(interac,toward,sep = ',') %>%
  mutate(newtoward=capitalize(tolower(gsub("([ ?])", "",toward)))) %>%
  select(-toward) %>%
  rename(toward=newtoward) %>%
  filter(toward %in% alln$X1) %>%
  group_by(focal,behavior_cat,toward) %>%
  mutate(n()) %>%
  group_by(focal,behavior_cat,toward) %>%
  filter(row_number()==1) %>%
  spread(toward,`n()`)>rmat
rmat[is.na(rmat)]=0
```

b.

For each interaction type, use `dist()` function to compute pair-wise canberra distances measuring the similarity between pairs of focal animals.

```
## Compute pair-wise canberra distances
unique(rmat$behavior_cat)

## [1] "aggression" "approach" "carry" "groom" "mate"
## [6] "play" "share"

cdist=function(t){
  filter(rmat, behavior_cat==t) %>%
    dist(method = "canberra")>dmat
  return(dmat)
}
ag.d=cdist("aggression")
ap.d=cdist("approach")
ca.d=cdist("carry")
gr.d=cdist("groom")
```

```
ma.d=cdist("mate")
pl.d=cdist("play")
sh.d=cdist("share")
```

c.

Use multidimensional scaling to find a two-dimensional embedding of the pairwise distances. Use the MDS coordinates to produce plots showing the relations among animals for each interaction type. Present these plots as a single figure faceted by interaction type.

```
## Produce plots showing the relations among animals for each interaction type
ag.mds=cmdscale(ag.d,k=2)
ap.mds=cmdscale(ap.d,k=2)
ca.mds=cmdscale(ca.d,k=2)
gr.mds=cmdscale(gr.d,k=2)
ma.mds=cmdscale(ma.d,k=2)
pl.mds=cmdscale(pl.d,k=2)
sh.mds=cmdscale(sh.d,k=2)
type=c(rep("aggression",20),rep("approach",20),rep("carry",20),
      rep("groom",20),rep("mate",20),rep("play",20),rep("share",20))
mds=round(rbind(ag.mds,ap.mds,ca.mds,gr.mds,ma.mds,pl.mds,sh.mds),2)
mds=as.data.frame(mds)
mds=cbind(mds,type)
colnames(mds)=c("coordinate1", "coordinate2","type")
ggplot(mds,aes(coordinate1,coordinate2))+geom_point()+facet_wrap(~type)
```

