 # EXAMPLE: weighted MDS using smacof package in R (run on Romney's kinship data)

```
install.packages("gtools")
install.packages("smacof")
library(gtools)
library(smacof)

# example: fitting weighted MDS model (indscal) in smacof

# problem: input to indscal / smacofIndDiff must be a list of proximity matrices (objects of type "dist")
# so we need to construct the input data set in this way

setwd("C:/Users/corter/Desktop/HUDM5124")
kinship <- read.delim("KINSHIP2_all.txt", sep=" ", header=TRUE)
kinship

# define one proximity matrix at a time:
kin1<-as.matrix(kinship[1:15,])
row.names(kin1) = colnames(kinship)
kin1
kin2<-as.matrix(kinship[16:30,])
row.names(kin2) = colnames(kinship)
kin2
kin3<-as.matrix(kinship[31:45,])
row.names(kin3) = colnames(kinship)
kin3
kin4<-as.matrix(kinship[46:60,])
row.names(kin4) = colnames(kinship)
kin4
kin5<-as.matrix(kinship[61:75,])
row.names(kin5) = colnames(kinship)
kin5
kin6<-as.matrix(kinship[76:90,])
row.names(kin6) = colnames(kinship)
kin6

# declare all prox matrices to be type "dist"
kin1<-as.dist(kin1)
kin2<-as.dist(kin2)
kin3<-as.dist(kin3)
kin4<-as.dist(kin4)
kin5<-as.dist(kin5)
kin6<-as.dist(kin6)

# now define input object "kinshipall" as a list of distance matrices:
kinshipall<-list(k1=kin1,k2=kin2,k3=kin3,k4=kin4,k5=kin5,k6=kin6)
kinshipall
```

```
# now fit the INDSCAL model to the data:
help(smacofIndDiff)

kin_ind<- indscal(kinshipall,type="interval",init="torgerson",verbose=TRUE)
# NOTE: can also specify "idioscal" model

# plot the group stimulus space
plot(kin_ind$gspace,asp=1,pch=' ')
text(kin_ind$gspace,colnames(kinship))

# print out subject weights space:
kin_ind$cweights
```

SELECTED R OUTPUT:

```
# subject weights space

> kin_ind$cweights
$k1
          D1        D2
D1 1.163557 0.0000000
D2 0.000000 0.8692691

$k2
           D1       D2
D1 0.9479076 0.000000
D2 0.0000000 1.079902

$k3
          D1       D2
D1 1.011088 0.000000
D2 0.000000 1.019042

$k4
          D1        D2
D1 1.053514 0.0000000
D2 0.000000 0.9699276

$k5
           D1       D2
D1 0.8169673 0.000000
D2 0.0000000 1.151791

$k6
           D1       D2
D1 0.8744749 0.000000
D2 0.0000000 1.118428
```

group stimulus space: