

## Lab 11: RSIENA Meta-Analysis for Multiple Networks

For this lab we will examine behavior and network co-evolution across multiple networks. We will use RSiena to test the diffusion of behaviors and evolution of ties in a longitudinal data set for multiple networks and combine the results into a single outcome.

Complete all tasks and answer all questions for full credit.

**NOTE:** This lab session uses the statistical program R. Before starting, you will need to open R and install the social network analysis packages in R which we will need for the exercises. The first step in R will be to change the directory (File->Change dir...). Set the directory to your folder in the shared drive.

### Dataset:

For this exercise, you will be working with the friendship data from a multiple schools in the Add Health study. The schools include 7<sup>th</sup> through 11<sup>th</sup> grade students. The dataset for the exercise consists of 4 school networks with 517 students who participated.

**Task 1.** Open the R program. Install the RSIENA and statnet packages.

```
setwd("PATHNAME FOR FOLDER")
install.packages('RSiena')
install.packages('statnet')
library(RSiena)
library(statnet)
```

**take a single class. evaluate: what are the structural and relationship attributes related to tie formation and behavioral attributes (tobacco use). selection of friends can be tied to behaviors. change of behavior might change my attitude my behavior. trying to understand the occurrence of behavior change and ties change simultaneously. Does this behavior carries over to multiple classrooms?**

**meta analytic review of research studies. Combined the findings to get an overall overview**

**Task 2.** The following code performs stochastic actor-based modeling, one at a time, on multiple school networks. Run the code in R.

```
friend.data.w1 <- as.matrix(read.table("class7.txt"))
friend.data.w2 <- as.matrix(read.table("class7_t2.txt"))
attr7<-read.table("attr7.txt",header=TRUE,stringsAsFactors=FALSE)
for (i in 1:nrow(attr7)) {if (attr7[i,48] > 98) {friend.data.w2[i,]=9}}
friend.data.w1[friend.data.w1 %in% c(6,9)] <- NA
friend.data.w2[friend.data.w2 %in% c(6,9)] <- NA
alcdrinkbeh<-cbind(attr7[,45],attr7[,48])
alcdrinkbeh[alcdrinkbeh %in% c(99)] <- NA
friendties <-
sienaNet(array(c(friend.data.w1,friend.data.w2),dim=c(nrow(attr7),nrow(attr7),2)))
```

```

alcdrinkbeh <- sienaNet(alcdrinkbeh,type="behavior")
ah_pvt <- coCovar(attr7[,36])
age <- coCovar(attr7[,38])
male <- coCovar(attr7[,40])
parentdrkfrq <- coCovar(attr7[,53])
tobacco <- coCovar(attr7[,56])
dataset.7 <-
sienaDataCreate(friendties,ah_pvt,age,male,parentdrkfrq,tobacco,alcdrinkbeh)
effects.7 <- getEffects(dataset.7)
effectsDocumentation(effects.7)

effects.7 <- includeEffects(effects.7,transTrip,type="eval")
effects.7 <- includeEffects(effects.7,cycle3,type="eval")
effects.7 <- includeEffects(effects.7,simX,type="eval",interaction1="age") #age
similarity
effects.7 <- includeEffects(effects.7,sameX,type="eval",interaction1="male") #same
gender
effects.7 <- includeEffects(effects.7,simX,type="eval",interaction1="ah_pvt")
#similar scholastic aptitude
effects.7 <- includeEffects(effects.7,simX,type="eval",interaction1="alcdrinkbeh")
#similar alcoholic use
effects.7 <-
includeEffects(effects.7,name="alcdrinkbeh",maxAlt,interaction1="friendties")
#average exposure
# effects.7 <-
includeEffects(effects.7,name="alcdrinkbeh",avRecAlt,interaction1="friendties")
#average exposure
effects.7 <-
includeEffects(effects.7,name="alcdrinkbeh",effFrom,type="eval",interaction1="age"
) #age effect
effects.7 <-
includeEffects(effects.7,name="alcdrinkbeh",effFrom,type="eval",interaction1="pare
ntdrkfrq") #parent drinking effect
effects.7 <-
includeEffects(effects.7,name="alcdrinkbeh",effFrom,type="eval",interaction1="toba
cco") #tobacco effect
effects.7 <-
includeEffects(effects.7,name="alcdrinkbeh",effFrom,type="eval",interaction1="ah_p
vt") #ah_pvt effect

modelall <- sienaModelCreate(useStdInits = FALSE, projname = 'AlcoholBehavior')

ans.7 <- siena07(modelall, data=dataset.7, effects=effects.7, batch=FALSE)
ans.7

friend.data.w1 <- as.matrix(read.table("class5809.txt"))
friend.data.w2 <- as.matrix(read.table("class5809_t2.txt"))
attr5809<-read.table("attr5809.txt",header=TRUE,stringsAsFactors=FALSE)
for (i in 1:nrow(attr5809)) {if (attr5809[i,48] > 98) {friend.data.w2[i,]=9}}
friend.data.w1[friend.data.w1 %in% c(6,9)] <- NA

```

```

friend.data.w2[friend.data.w2 %in% c(6,9)] <- NA
alcdrinkbeh<-cbind(attr5809[,45],attr5809[,48])
alcdrinkbeh[alcdrinkbeh %in% c(99)] <- NA
friendties <-
sienaNet(array(c(friend.data.w1,friend.data.w2),dim=c(nrow(attr5809),nrow(attr5809
),2)))
alcdrinkbeh <- sienaNet(alcdrinkbeh,type="behavior")
ah_pvt <- coCovar(attr5809[,36])
age <- coCovar(attr5809[,38])
male <- coCovar(attr5809[,40])
parentdrkfrq <- coCovar(attr5809[,53])
tobacco <- coCovar(attr5809[,56])
dataset.5809 <-
sienaDataCreate(friendties,ah_pvt,age,male,parentdrkfrq,tobacco,alcdrinkbeh)
effects.5809 <- getEffects(dataset.5809)

effects.5809 <- includeEffects(effects.5809,transTrip,type="eval")
effects.5809 <- includeEffects(effects.5809,cycle3,type="eval")
effects.5809 <- includeEffects(effects.5809,simX,type="eval",interaction1="age")
#age similarity
effects.5809 <- includeEffects(effects.5809,sameX,type="eval",interaction1="male")
#same gender
effects.5809 <- includeEffects(effects.5809,simX,type="eval",interaction1="ah_pvt")
#similar scholastic aptitude
effects.5809 <-
includeEffects(effects.5809,simX,type="eval",interaction1="alcdrinkbeh") #similar
alcoholic use
effects.5809 <-
includeEffects(effects.5809,name="alcdrinkbeh",maxAlt,interaction1="friendties")
#average exposure
# effects.5809 <-
includeEffects(effects.5809,name="alcdrinkbeh",avRecAlt,interaction1="friendties")
#average exposure
effects.5809 <-
includeEffects(effects.5809,name="alcdrinkbeh",effFrom,type="eval",interaction1="a
ge") #age effect
effects.5809 <-
includeEffects(effects.5809,name="alcdrinkbeh",effFrom,type="eval",interaction1="p
arentdrkfrq") #parent drinking effect
effects.5809 <-
includeEffects(effects.5809,name="alcdrinkbeh",effFrom,type="eval",interaction1="t
obacco") #tobacco effect
effects.5809 <-
includeEffects(effects.5809,name="alcdrinkbeh",effFrom,type="eval",interaction1="a
h_pvt") #ah_pvt effect

modelall <- sienaModelCreate(useStdInits = FALSE, projname = 'AlcoholBehavior')

ans.5809 <- siena07(modelall, data=dataset.5809, effects=effects.5809,
batch=FALSE)

```

ans.5809

```
friend.data.w1 <- as.matrix(read.table("class8.txt"))
friend.data.w2 <- as.matrix(read.table("class8_t2.txt"))
attr8<-read.table("attr8.txt",header=TRUE,stringsAsFactors=FALSE)
for (i in 1:nrow(attr8)) {if (attr8[i,48] > 98) {friend.data.w2[i,]=9}}
friend.data.w1[friend.data.w1 %in% c(6,9)] <- NA
friend.data.w2[friend.data.w2 %in% c(6,9)] <- NA
alcdrinkbeh<-cbind(attr8[,45],attr8[,48])
alcdrinkbeh[alcdrinkbeh %in% c(99)] <- NA
friendties <-
sienaNet(array(c(friend.data.w1,friend.data.w2),dim=c(nrow(attr8),nrow(attr8),2)))
alcdrinkbeh <- sienaNet(alcdrinkbeh,type="behavior")
ah_pvt <- coCovar(attr8[,36])
age <- coCovar(attr8[,38])
male <- coCovar(attr8[,40])
parentdrkfrq <- coCovar(attr8[,53])
tobacco <- coCovar(attr8[,56])
dataset.8 <-
sienaDataCreate(friendties,ah_pvt,age,male,parentdrkfrq,tobacco,alcdrinkbeh)
effects.8 <- getEffects(dataset.8)

effects.8 <- includeEffects(effects.8,transTrip,type="eval")
effects.8 <- includeEffects(effects.8,cycle3,type="eval")
effects.8 <- includeEffects(effects.8,simX,type="eval",interaction1="age") #age
similarity
effects.8 <- includeEffects(effects.8,sameX,type="eval",interaction1="male") #same
gender
effects.8 <- includeEffects(effects.8,simX,type="eval",interaction1="ah_pvt")
#similar scholastic aptitude
effects.8 <- includeEffects(effects.8,simX,type="eval",interaction1="alcdrinkbeh")
#similar alcoholic use
effects.8 <-
includeEffects(effects.8,name="alcdrinkbeh",maxAlt,interaction1="friendties")
#average exposure
# effects.8 <-
includeEffects(effects.8,name="alcdrinkbeh",avRecAlt,interaction1="friendties")
#average exposure
effects.8 <-
includeEffects(effects.8,name="alcdrinkbeh",effFrom,type="eval",interaction1="age"
) #age effect
effects.8 <-
includeEffects(effects.8,name="alcdrinkbeh",effFrom,type="eval",interaction1="pare
ntdrkfrq") #parent drinking effect
effects.8 <-
includeEffects(effects.8,name="alcdrinkbeh",effFrom,type="eval",interaction1="toba
cco") #tobacco effect
effects.8 <-
includeEffects(effects.8,name="alcdrinkbeh",effFrom,type="eval",interaction1="ah_p
vt") #ah_pvt effect
```

```

modelall <- sienaModelCreate(useStdInits = FALSE, projname = 'AlcoholBehavior')

ans.8 <- siena07(modelall, data=dataset.8, effects=effects.8, batch=FALSE)
ans.8

friend.data.w1 <- as.matrix(read.table("class88.txt"))
friend.data.w2 <- as.matrix(read.table("class88_t2.txt"))
attr88<-read.table("attr88.txt",header=TRUE,stringsAsFactors=FALSE)
for (i in 1:nrow(attr88)) {if (attr88[i,48] > 98) {friend.data.w2[i,]=9}}
friend.data.w1[friend.data.w1 %in% c(6,9)] <- NA
friend.data.w2[friend.data.w2 %in% c(6,9)] <- NA
alcdrinkbeh<-cbind(attr88[,45],attr88[,48])
alcdrinkbeh[alcdrinkbeh %in% c(99)] <- NA
friendties <-
sienaNet(array(c(friend.data.w1,friend.data.w2),dim=c(nrow(attr88),nrow(attr88),2)))
alcdrinkbeh <- sienaNet(alcdrinkbeh,type="behavior")
ah_pvt <- coCovar(attr88[,36])
age <- coCovar(attr88[,38])
male <- coCovar(attr88[,40])
parentdrkfrq <- coCovar(attr88[,53])
tobacco <- coCovar(attr88[,56])
dataset.88 <-
sienaDataCreate(friendties,ah_pvt,age,male,parentdrkfrq,tobacco,alcdrinkbeh)
effects.88 <- getEffects(dataset.88)

effects.88 <- includeEffects(effects.88,transTrip,type="eval")
effects.88 <- includeEffects(effects.88,cycle3,type="eval")
effects.88 <- includeEffects(effects.88,simX,type="eval",interaction1="age") #age
similarity
effects.88 <- includeEffects(effects.88,sameX,type="eval",interaction1="male")
#same gender
effects.88 <- includeEffects(effects.88,simX,type="eval",interaction1="ah_pvt")
#similar scholastic aptitude
effects.88 <- includeEffects(effects.88,simX,type="eval",interaction1="alcdrinkbeh")
#similar alcoholic use
effects.88 <-
includeEffects(effects.88,name="alcdrinkbeh",maxAlt,interaction1="friendties")
#average exposure
# effects.88 <-
includeEffects(effects.88,name="alcdrinkbeh",avRecAlt,interaction1="friendties")
#average exposure
effects.88 <-
includeEffects(effects.88,name="alcdrinkbeh",effFrom,type="eval",interaction1="age
") #age effect
effects.88 <-
includeEffects(effects.88,name="alcdrinkbeh",effFrom,type="eval",interaction1="par
entdrkfrq") #parent drinking effect

```

```

effects.88 <-
includeEffects(effects.88,name="alcdrinkbeh",effFrom,type="eval",interaction1="tobacco") #tobacco effect
effects.88 <-
includeEffects(effects.88,name="alcdrinkbeh",effFrom,type="eval",interaction1="ah_pvt") #ah_pvt effect

modelall <- sienaModelCreate(useStdInits = FALSE, projname = 'AlcoholBehavior')

ans.88 <- siena07(modelall, data=dataset.88, effects=effects.88, batch=FALSE)
ans.88

```

**Question 1: Which types of outcomes are likely to have more power in a co-evolution model: network selection effects or behavior influence effects? Explain why.**

network dynamics/selection has more power in a co-evolution model. in the selection, the sample size is squared. but in behavior, it is not. so we have a much larger sample for selection. In behavior, we only know about n individuals.

**Question 2: There are two ways in which co-evolution data from multiple schools could be analysed:**

- (1) By combining the data from all of the schools into a single network with the within school ties in block diagonals and ‘structural zero’ indicators for connections between students at different schools, since students from different schools cannot nominate each other as friends. Then conducting stochastic actor-based modeling on the single network.**
- (2) By analysing each of the schools independently using stochastic actor-based modeling. Then combining the parameter estimates for each of the effects across the different schools into global estimates using meta-analysis.**

**What are the advantages and disadvantages to each approach?**

- (1) adv: gives more statistical power, more ability to combine similar effects across the school  
limitation: if one of the schools is single-gender, we might get a degenerate model.
- (2) adv: heterogeneity between study results can be explained. So single-gendered issues might not be fatal like the previous one.

**Task 3.** The next set of code performs a meta-analysis of the results of the 4 individual models. Run the code.

```
meta <- siena08(ans.5809,ans.88,ans.7,ans.8)
summary(meta)
```

**Question 3:** Did all of the individual school models converge? What options do you have if there is poor convergence?

all of the schools converged pretty well. We can alter some features.

**Question 4.** What are the overall findings from the meta-analysis across schools? Which selection and influence effects are statistically significant across the 4 schools? How much variability is there in the parameter estimates across the 4 schools?

- > density is significantly smaller
- > significant contribution of reciprocity
- > three cycles: highly significant likelihood if two are connected then the third will close anyway (A->B, B-> C then C->A)
- > talcdrinkbeh period 1

**Question 5.** List other potential effects that you might be interested in testing in the model. How might these additional effects impact the selection or influence mechanisms?

I am interested in testing if centrality, localdensity, and prestige have impact on the model. Centrality and prestige might impact the ties and network selection of the model. Nodes with high centrality might attract others closer to those. I also want to test the impact of tobacco, cycling, sports, and hangout. These characteristics might change the behavior influence. Cycling might influence people to more cycling in wave2.

**Task 4.** Summary write-up. Write up a short description of your RSiena analysis of multiple networks. Suggest directions for future research.

The analysis shows that all four schools' models converge pretty well. The meta-analysis shows a significant effect of density, reciprocity, age similarity and three cycles on network dynamics. Also, talcdrinkbeh period 1 also has a significant effect on networks. From the meta-analysis, we can see that density, reciprocity, 3 cycle, and ah\_pvt similarity have significant effects on the relationship and behavior.