NME 2021

Network Modeling for Epidemics

# DAY 3:

# PRACTICE WITH EGOCENTRIC DATA AND TARGET STATISTICS

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# Note

- Newly developed package *ergm.ego* can do much of the following for you
- Still worth understanding the nature of what is going on mechanically
- Definitely worth understanding how different assumptions lead to different values of statistics

# Practice

- You have a sample of 20 heterosexuals
- They live in two communities
- You have extracted their partnerships on the day of the interview
- You want to simulate an artificial population of size 2,000
- You want to include in your model mixing by community as well as sex-specific degree distributions
- You notice that nobody has more than two ongoing ties
- Relationships average 60 time steps
- How do you set up your network? What model terms and target stats will you specify?

# Egocentric data

**Ongoing partnerships by sex and community of ego and alters**

| Ego | Partner 1 | Partner 2 |
|---|---|---|
| F1 | M1 | |
| F1 | | |
| F1 | M1 | M1 |
| F1 | M1 | |
| F2 | M2 | |
| F2 | M1 | |
| F2 | M2 | |
| F2 | | |
| F2 | | |
| F2 | M1 | |

| Ego | Partner 1 | Partner 2 |
|---|---|---|
| M1 | F1 | F1 |
| M1 | | |
| M1 | | |
| M1 | F2 | |
| M2 | F2 | |
| M2 | | |
| M2 | F2 | F1 |
| M2 | F1 | |
| M2 | F2 | F2 |
| M2 | | |

# Set up network

- Note: you got lucky!
  - Sample has same # of males and females, and same community breakdown for each
  - Just need to scale up to 2,000

```
library(EpiModel)
mynet <- network_initialize(2000)

sex <- c(rep(1, 1000), rep(2, 1000))
mynet <- set_vertex_attribute(mynet, 'group', sex)

cmty <- c(rep(1,400), rep(2,600), rep(1,400), rep(2,600))
mynet <- set_vertex_attribute(mynet, 'cmty', cmty)
```

# Establish terms and target stats

- Term for overall relational effect
  - `~edges`
  - Have to reconcile that male mean deg = 0.9 and female mean deg = 0.8, and sex ratio in sample is equal
  - Could:
    1. assume a different sex ratio in population
    2. assume males are over-reporting (or sample is biased towards more active males)
    3. assume females are under-reporting (or sample is biased towards less active females)
  - We'll assume some of 2&3
  - Target stat = 850 = (2000 * 0.85 / 2)

# Establish terms and target stats

- Mean degree by community
  - Mean deg for community 1 = 7/8 = 0.875
  - Mean deg for community 2 =  10/12 = 0.833
  - Worth modeling this difference?
  - Could put in a nodefactor term into the ergm and see whether it is significant
  - Foreshadowing: it's not, so we'll just ignore

- Mixing by community:
  - Proportion of ties that are within community = 12/17 = 0.706
  - Term: `~nodematch('cmty')`
  - Target stat = 0.706*850 = 600

# Establish terms and target stats

- Let's first add a constraint that nobody has >2 partnerships at a time
  - term = `degrange(from=3)`
  - target stat = 0
- Then add degree terms = `~degree(1, by='group')`
- Why only 1 term per sex?
  - Target stats gets very tricky, since the mean degree was not the same by sex
  - How to adjust degree distribution for each sex to match the new degree distribution?
  - You **must** make assumptions
  - Observed degree dist =

| Deg | F | M |
|---|---|---|
| 0 | 0.30 | 0.40 |
| 1 | 0.60 | 0.30 |
| 2 | 0.10 | 0.30 |
| Mean deg | 0.80 | 0.90 |

Let's assume that all of the movement is between 1&2

| Deg | F | M |
|---|---|---|
| 0 | 0.30 | 0.40 |
| 1 | 0.55 | 0.35 |
| 2 | 0.15 | 0.25 |
| Mean deg | 0.85 | 0.85 |

  - target stats = c(550, 350) = c(0.55*1000, 0.35*1000)

# Estimating and diagnosing

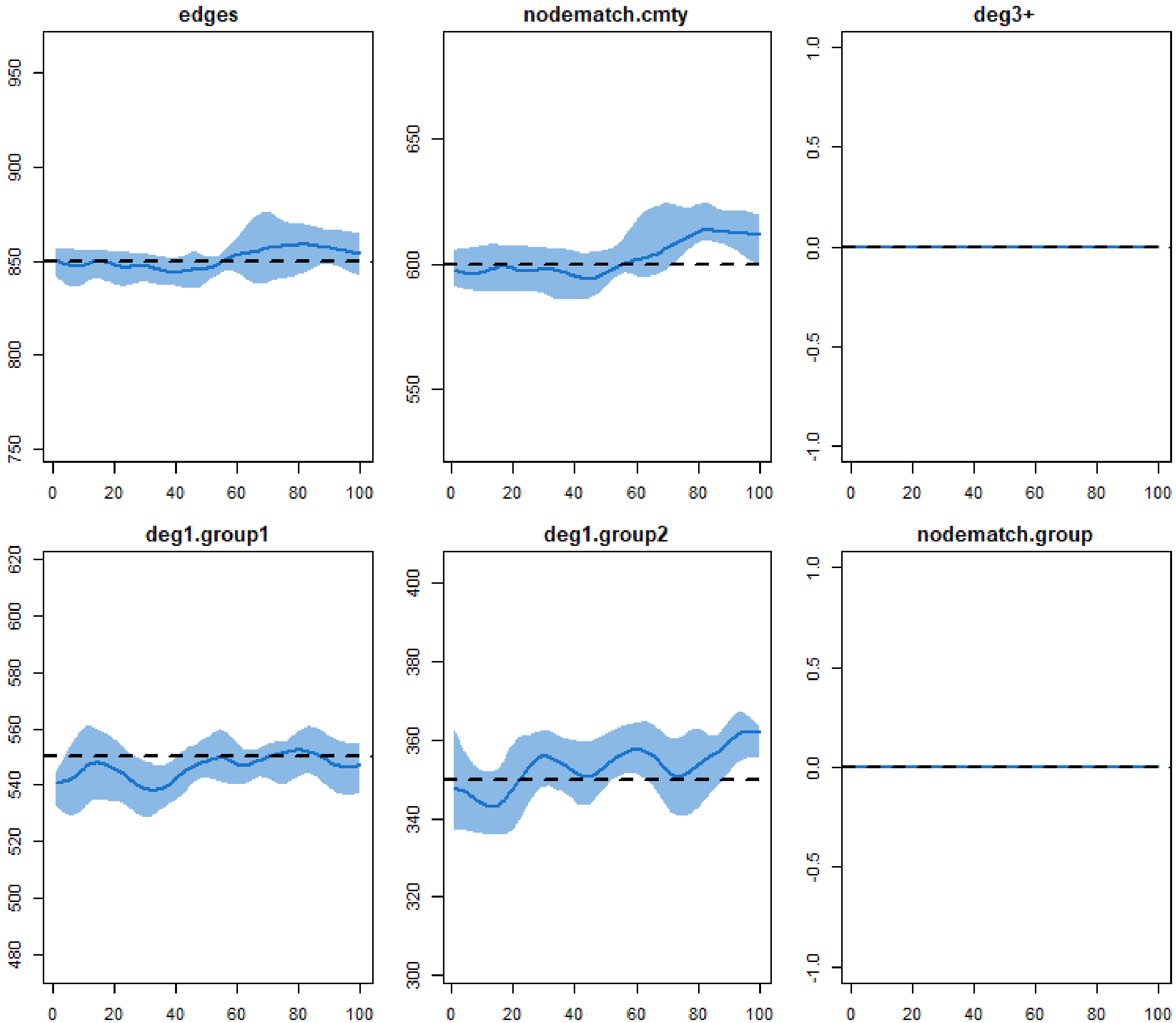
```
formation <- ~edges+nodematch('cmty')+degrange(from=3)+
                  degree(1, by='group') + nodematch('group', diff=FALSE)

target.stats <- c(850, 600, 0, 550, 350, 0)

myfit <- netest(mynet,
            formation=formation,
            target.stats = target.stats,
            coef.diss = dissolution_coefs(~offset(edges), 60))

mydx <- netdx(myfit, nsims=10, nsteps=100)
mydx
get_nwstats(mydx)
plot(mydx)
```

# Estimating and diagnosing



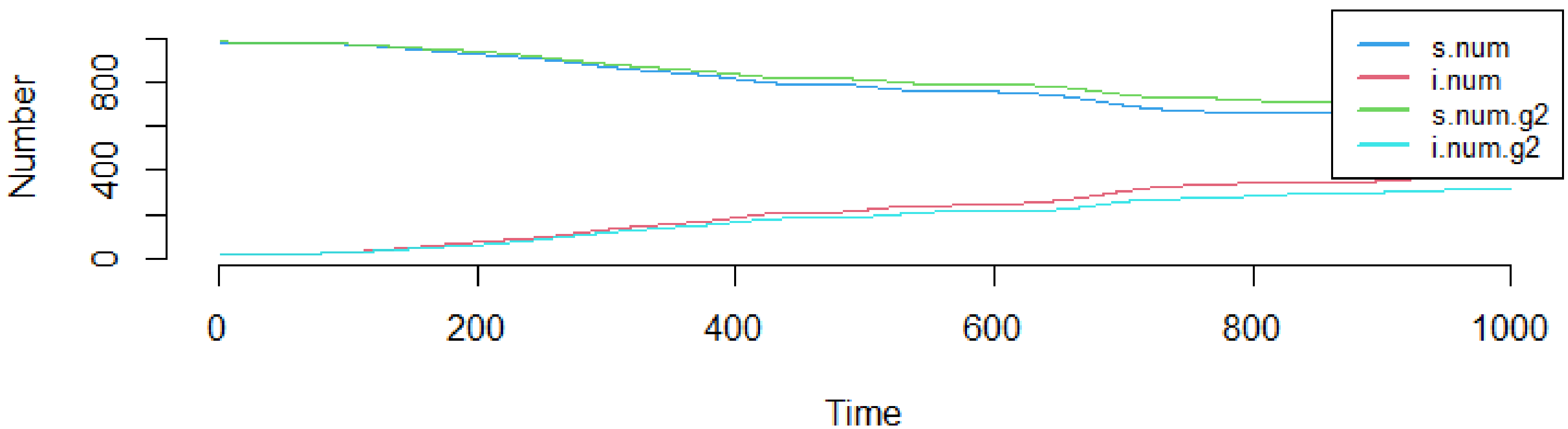
# Disease simulation

- Let's do a disease simulation on top of it just for fun!

```
mycontrol <- control.net("SIS", nsteps = 1000, nsims = 1,
          nwstats.formula = ~edges+nodematch('cmty') +
                    degree(0:5, by='group'), verbose = TRUE)
myinit <- init.net(i.num = 10, i.num.g2 = 10)
myparam <-param.net(inf.prob = 0.5, inf.prob.g2 = 0.5,
                     act.rate = 0.6,
                     rec.rate = 0.05, rec.rate.g2 = 0.05)

mySIS <- netsim(myfit, param = myparam, control = mycontrol,
                init = myinit)
plot(mySIS)
```

# Disease simulation



# Examining target stats

```
get_nwstats(mySIS)
plot(mySIS, type = "formation", sim.lines = TRUE)
```

# Examining target stats