

ERGM LAB: Exercises

Zack W Almquist (University of Minnesota)

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```
R> library(ergm)
R> library(sna)
R> library(coda)
```

Rural Arizona risk Networks

The Data

The data comes was aggregated by Martina Morris (University of Washington) and Richard Rothenberg (Emory University) and put online at ICPSR. The original data can be found [here](#). In this exercise we are going to investigate four networks derived from the *Rural Arizona risk networks* in Flagstaff, AZ. These networks were collected from May 1996 to Jan 1998 and originally had 95 respondents interviewed 5 times each. All participants are over 18 years old. This network was generated from random walk sampling strategy. **Warning** These networks are obviously from network sample and not *true* complete networks, but we are going to ignore that for this exercise and will treat them as complete.

- Name generator
 - Sex, needle, other (illicit) drug contact, social contact in last 6 months
 - Sampling strategy
 - * Six seeds chosen at random within same geographic area (Flagstaff) from persons presumed to be at elevated risk for HIV acquisition (through sex and/or drug behaviors)

Networks

Here, I have constructed 4 networks with attributes: race, ethnicity, sex, and age.

Load the data:

```
R> load("data/flagstaff_rural.rda")
```

Needle Network

```
R> flag_needle_net
```

Network attributes:

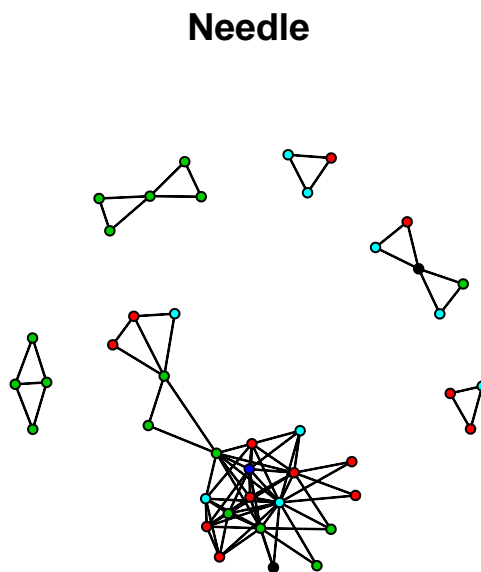
```
vertices = 42
directed = FALSE
hyper = FALSE
loops = FALSE
multiple = FALSE
bipartite = FALSE
total edges= 87
  missing edges= 0
  non-missing edges= 87
```

Vertex attribute names:

```
age ethn id race sex vertex.names
```

No edge attributes

```
R> plot(flag_needle_net, vertex.col = "race", main = "Needle")
```



Sexual Contact Network

```
R> flag_sex_net
```

Network attributes:

```
vertices = 167
directed = FALSE
hyper = FALSE
loops = FALSE
multiple = FALSE
bipartite = FALSE
total edges= 282
  missing edges= 0
```

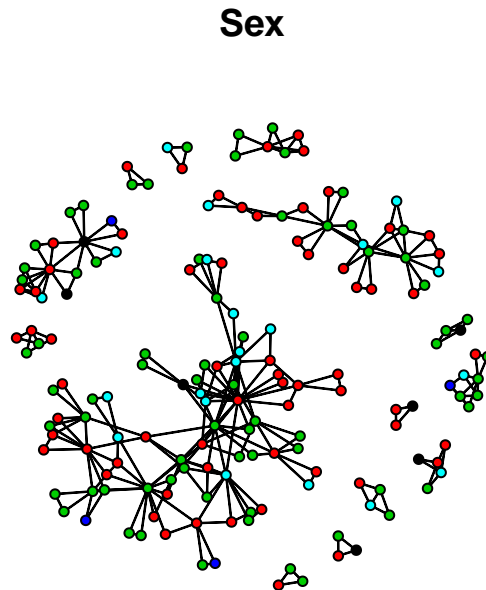
```
non-missing edges= 282
```

```
Vertex attribute names:
```

```
age ethn id race sex vertex.names
```

```
No edge attributes
```

```
R> plot(flag_sex_net, vertex.col = "race", main = "Sex")
```



Social Contact Network

```
R> flag_social_net
```

```
Network attributes:
```

```
vertices = 523  
directed = FALSE  
hyper = FALSE  
loops = FALSE  
multiple = FALSE  
bipartite = FALSE  
total edges= 2713  
  missing edges= 0  
  non-missing edges= 2713
```

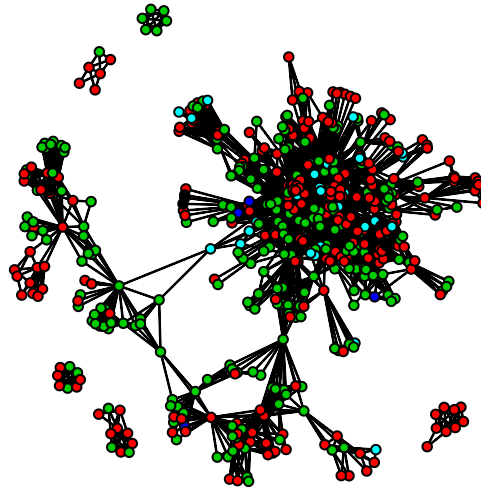
```
Vertex attribute names:
```

```
age ethn id race sex vertex.names
```

```
Edge attribute names not shown
```

```
R> plot(flag_social_net, vertex.col = "race", main = "Social")
```

Social



Drug Contact Network

```
R> flag_drug_net
```

Network attributes:

```
vertices = 352
directed = FALSE
hyper = FALSE
loops = FALSE
multiple = FALSE
bipartite = FALSE
total edges= 1626
  missing edges= 0
  non-missing edges= 1626
```

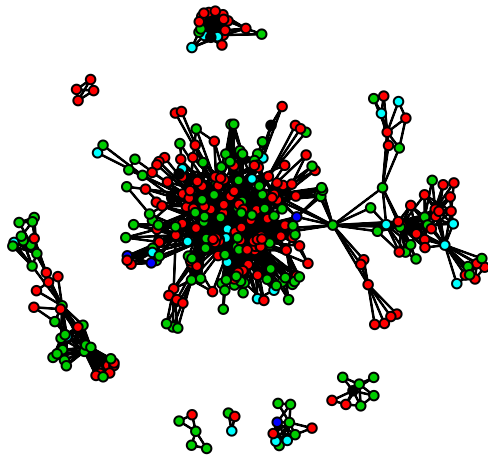
Vertex attribute names:

```
age ethn id race sex vertex.names
```

Edge attribute names not shown

```
R> plot(flag_drug_net, vertex.col = "race", main = "Drug")
```

Drug



Exercise

For each network explore the basic properties of the network (e.g., mixing matrix, density, etc.) and then attempt to develop a “good” ERG model for each network. After you have the best ERG model you can construct, use the tutorial to try to interpret the predicted probabilities and odds ratio of a given conditional tie. Further, attempt to explain what these results would mean substantively.