

# A social network analysis of a gonorrhea outbreak in Alberta, Canada

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12/07/2021



# Outline

- ▶ Background
- ▶ Methods
- ▶ Discussion
- ▶ Conclusion

## Background

- ▶ This dataset concerns a localised outbreak of *Neisseria gonorrhoeae* in an indigenous community located in Alberta, Canada.
- ▶ It was originally analyzed in a paper by Prithwish De, et al. (2004), in which they used measures of network centrality (e.g. information centrality) to determine the association between the risk of infection between members of the network and their position within the network itself.
- ▶ The data for the 2004 paper was sourced from an earlier 2001 study by the authors in which they formulated a plan to address the outbreak.
- ▶ The network consists of 89 individuals, both male and female, 17 of whom were found to be patrons of a local bar in the area.

# Background

- ▶ This work expands upon the original 2004 analysis by applying exponential random graph modeling (ERGM) to the network in order to quantify the effect of various attributes of the network (e.g. gender, bar attendance), as well as looking at other less common measures of network centrality to quantify the effect of an individuals' position in the network on the outbreak.

## Background

- ▶ Gonorrhea is a sexually transmitted disease/infection (STD/STI) which can be transmitted orally, vaginally or anally.
- ▶ Although it can have many serious side effects, it can also be symptomless, leading to individuals unknowingly infecting their partners.
- ▶ When untreated, it also makes HIV more susceptible to transmission, making gonorrhea itself a risk factor for the propagation of HIV.
- ▶ To this day, gonorrhea is the second most commonly reported STD in Canada.

## Background

- ▶ As of 2016, approximately 7% of Albertans identify as First Nations, compared to approximately 5% throughout all of Canada.
- ▶ First Nations peoples experience a disproportionate prevalence of STDs in their population relative to other groups in Canada.
- ▶ Cultural factors are acknowledged by Doherty, et al. (2001) as meaningful in the formation of social networks, particularly sexual ones, and likewise cultural differences have prevented the osmosis of responsible sexual health practices in regions predominantly occupied by First Nations.

# Background

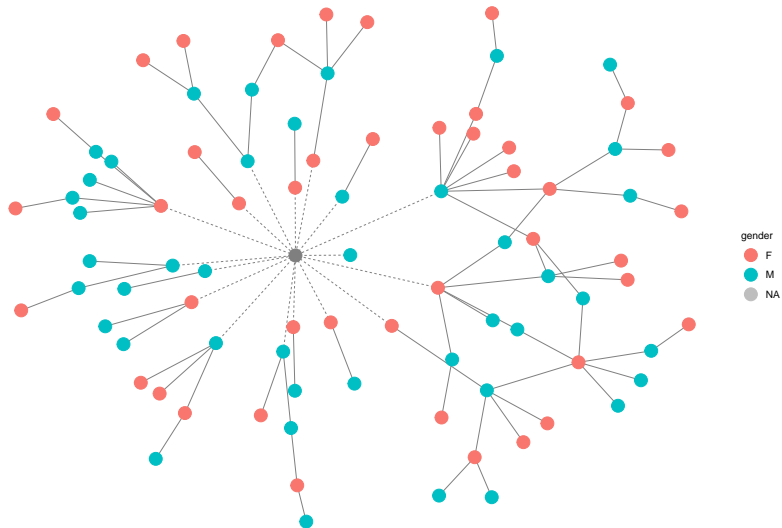
- ▶ Patients included in the 2001 study were asked for consent for their enrollment in the study.
- ▶ Questions about sexual risk factors and drug use were omitted from the survey after a high proportion of respondents opted not to answer it.
- ▶ Since STD clinical reports don't contain *complete* sexual contact information, the original index case could not be identified.
- ▶ It was found in 2001 that certain individuals acquired their respective infections from partners whom they met outside of their own local community.



# Background

- ▶ As is typical for data collection processes in which information is nominated by the ego, and especially in the sensitive case where sexual partnering is involved, there is bound to be some information missing from the data.
- ▶ e.g. Self-reported behavior from an ego may not necessarily reflect their practices in reality.
- ▶ The asymptomatic of some gonorrhea infections also implies that the network of disease transmission is potentially far greater than what is observed here.

## The connected network with the bar as a node



## The connected network with the bar as a node

- ▶ There are 91 total edges in this network, with 17 of them being between the bar and individuals, leaving 74 of them to be between individuals.
- ▶ Of these 74, 67 (approx. 90.5%) of them are M-F edges, 6 of them are M-M, and 1 of them is F-F.
- ▶ Of these 74, 36 (approx. 48.6%) of them are between bar-attendees and non-attendees, and 38 (51.3%) are between non-attendees and other non-attendees only.
- ▶ Note that none of the bar attendees have ties to other bar attendees at all.

# Distribution of ties

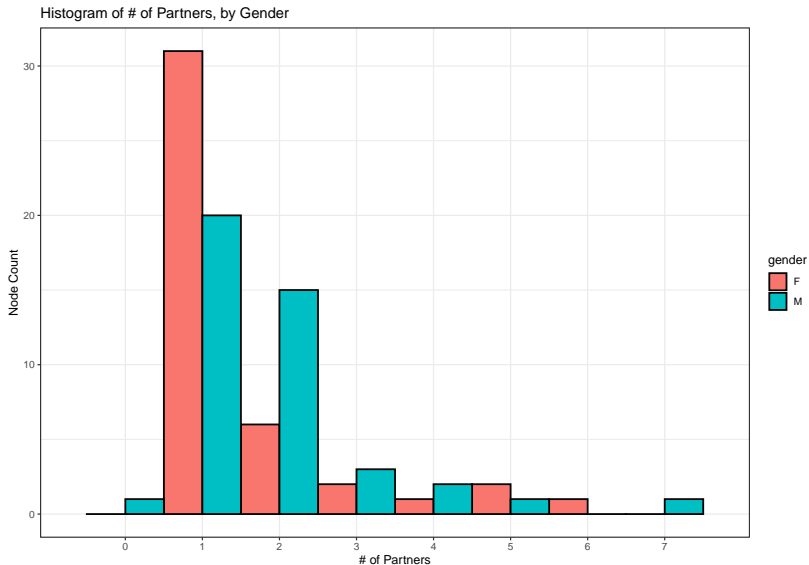


Figure 1: Histogram of partners, by gender.

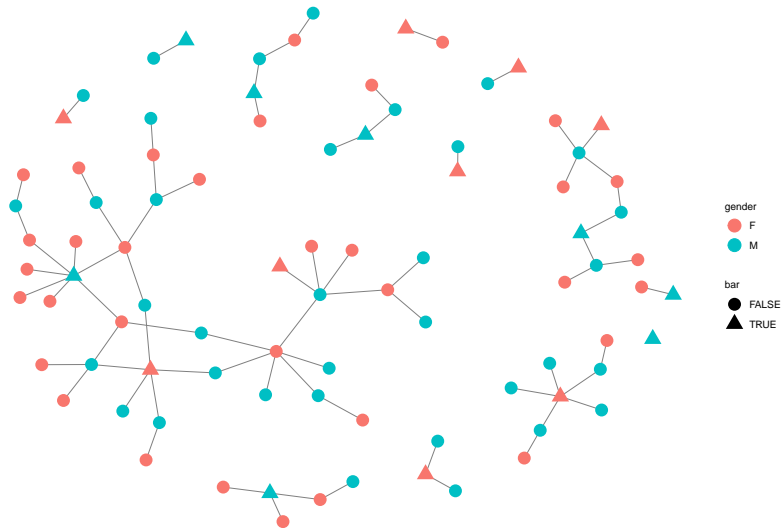
# Exponential Random Graph Model (ERGM)

- ▶ While measures such as network centrality and network density can provide us some information about the characteristics of a network, in the case of a sexual network in which ties have an explicitly social component to them, an ERGM which incorporates the attributes of actors within the network can be more informative.
- ▶ ERGMs model networks as a function of network statistics, by imagining the network as one instance of a set of possible, similar networks, i.e. the outcomes of a stochastic (random) process.

# Exponential Random Graph Model (ERGM)

- ▶ When modeling the ERGM for this network, the bar node was redacted so that the network could be a one-mode network, and instead attendance of the bar was assigned to the vertices as an attribute, as was gender. This model was saved as `gonnet_net_nobar` in R.

# The disconnected network



## The disconnected network

- ▶ There are about 9 or so subcomponents of this graph; notice that the largest among them has 3 bar attendees within it, 2 of whom have at least 5 ties to other individuals.
- ▶ Notice there is one isolate where a male node attended the bar but otherwise has no ties to any other node.
- ▶ There also a a series of smaller sub-components where there is only one edge between two nodes, one of whom is a bar attendee.
- ▶ Note the presence of a “6-cycle” in the largest subcomponent, in which 6 separate nodes are jointly connected through one another. This is the only such appearance of a k-cycle in the entire network.
- ▶ The largest subcomponent of the graph includes 38 of the 86 nodes in the network, or approximately 44% of all egos.



# Model Selection

- ▶ When fitting the ERGM model, first we started with the simplest model that only models the number of edges (this would be akin to an intercept-only model in logistic regression). We then built several more models which only had one parameter, and then compared the Akaike Information Criteria (AIC) of the models to determine which among these model parameters were worth including.
- ▶ Among the model parameters fit were homophily (`nodematch`), heterophily (`nodemix`) and degree (`degree`).

# Akaike Information Criterion (AIC)

- ▶ The Akaike Information Criterion (AIC) is an estimator of out-of-sample prediction error.
- ▶ We use it as a means of model selection, where we generally opt to select the model with the lowest AIC.



$$AIC = -2 \ln(\mathcal{L}) + 2k$$

- ▶ Where  $L$  is the likelihood of the model, and  $k$  is the number of parameters.

# Model Selection

Table 1: Table of Akaike Information Criteria for each ERGM model

formula	aic
gonnet_net_nobar ~ edges	725.6599
gonnet_net_nobar ~ edges + nodematch("bar")	718.7543
gonnet_net_nobar ~ edges + degree(d = c(1:3))	681.9365
gonnet_net_nobar ~ edges + nodemix("gender")	669.8531
gonnet_net_nobar ~ edges + nodefactor("bar")	725.7581
gonnet_net_nobar ~ edges + nodemix("bar")	902.9734

# Likelihood Ratio Test

- ▶ A likelihood ratio test is a method to compare a full model to a nested model, where the nested model has some subset of the same parameters as the full model.
- ▶ When comparing a full model to a nested model, we can conduct a Likelihood Ratio Test, in which we take the ratio of the maximum likelihoods of both the full model and the nested model, in order to determine whether the nested model explains the data as well as the full model.

# Likelihood Ratio Test

- ▶  $\lambda = \frac{\mathcal{L}_s(\hat{\theta})}{\mathcal{L}_g(\hat{\theta})}$
- ▶  $\text{LRT} = -2 \ln \lambda$
- ▶ Where  $\mathcal{L}_s(\hat{\theta})$  is the maximized log-likelihood for the nested model, and  $\mathcal{L}_g$  is the maximized log-likelihood for the full model.

# Likelihood Ratio Test

- ▶  $H_0$ : The nested model fits the data as well as the full model. i.e. The nested model is preferred.
- ▶  $H_A$ : The nested model does not fit the data as well as the full model. i.e. The full model is preferred.
- ▶ We reject the null hypothesis  $H_0$  when the test statistic falls within the rejection region of a  $\chi^2$  distribution with degrees of freedom  $k$  where  $k$  is the difference in the number of parameters between the two models. Otherwise, we fail to reject  $H_0$ .

# Likelihood Ratio Test

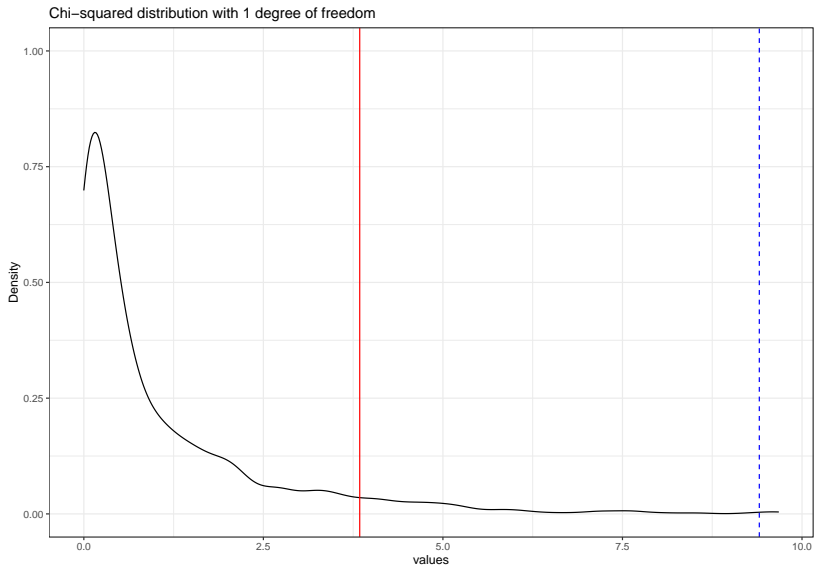
```
## Likelihood ratio test
##
## Model 1: gonnet_net_nobar ~ edges + degree(d = c(1:3)) + nodemix("gender") +
##   nodematch("bar")
## Model 2: gonnet_net_nobar ~ edges + degree(d = c(1:3)) + nodemix("gender")
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1    7 -302.05
## 2    6 -306.76 -1  9.4055   0.002163 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Likelihood Ratio Test

- ▶ The full model has 1 more parameter than the nested model, so we are comparing our LRT test statistic to a  $\chi^2$  distribution with 1 degree of freedom.
- ▶ The  $\chi^2$  test statistic for the likelihood ratio test had a p-value of  $\approx 0.002$ , which is less than our significance level  $\alpha = 0.05$ .
- ▶ Hence we have enough evidence to reject the null hypothesis and conclude that full model, which has the homophily attribute for bar attendance in addition to the heterophily attribute for gender and the degree attribute, is the preferred model.



# Likelihood Ratio Test



# Markov Chain Monte Carlo (MCMC)

- ▶ A Markov Chain is a stochastic process that goes from one state to another, with the future state  $X_{t+1}$  depending only on the current state  $X_t$  at time  $t$ .
- ▶  $\Pr(X_{t+1} = x | X_t = x_t)$
- ▶ A Monte Carlo process refers to a simulation that samples many random values from a posterior distribution of interest.
- ▶ Hence a Markov Chain Monte Carlo (MCMC) simulation is a simulation of a random process whose future value depends only on the current value.

# Metropolis-Hastings Algorithm

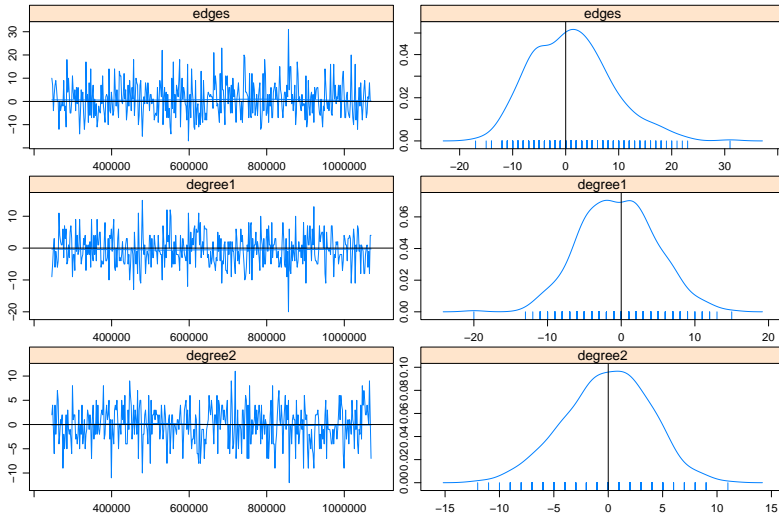
- ▶ A common MCMC algorithm is the Metropolis-Hastings algorithm, in which the process “randomly walks” starting from some  $\theta_0$ .
- ▶ To determine whether the process advances, a “candidate value”  $\theta$  is generated by sampling from the proposal distribution  $g(\theta|\theta_{s-1})$  at iteration  $s$ .
- ▶ We then derive the Metropolis-Hastings acceptance ratio  $\eta$ , which is a ratio of the estimated distribution at time  $\theta$  and at the proposed time  $\theta_n$ .
- ▶ We look at the smaller value between the acceptance ratio  $\eta$  and 1, which is designated as the acceptance probability  $\rho$ , i.e.  $\rho = \min(1, \eta)$
- ▶ We sample  $U \sim \text{Uni}(0, 1)$  to  $\rho$ . If  $U < \rho$  then we accept the candidate value such that  $\theta_s = \theta$
- ▶ Otherwise we repeat another iteration with  $\theta_s$  as before.

# MCMC Diagnostics

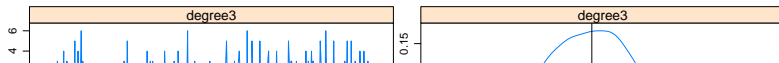
- ▶ When using MCMC chains our goal is for it to *converge*.
- ▶ We can diagnose this by looking at traceplots of the MCMC chain as well as the density curve.

# MCMC Diagnostics

Sample statistics



Sample statistics



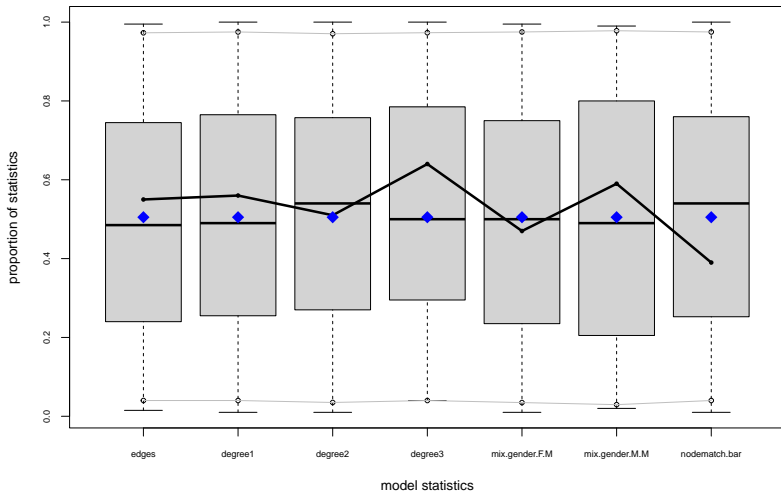
# Goodness of Fit

```
## Call:
## .f(formula = ..1)
##
## Monte Carlo Maximum Likelihood Results:
##
##           Estimate Std. Error MCMC % z value Pr(>|z|)
## edges          -5.1709    1.0264      0  -5.038 < 1e-04 ***
## degree1         2.8404    0.7129      0   3.984 < 1e-04 ***
## degree2         1.5528    0.5867      0   2.646 0.008134 **
## degree3         0.1393    0.6371      0   0.219 0.826926
## mix.gender.F.M   3.4620    0.9892      0   3.500 0.000465 ***
## mix.gender.M.M   1.7712    1.0855      0   1.632 0.102734
## nodematch.bar   -0.7419    0.2462      0  -3.013 0.002584 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance: 5066.9  on 3655  degrees of freedom
## Residual Deviance: 604.1  on 3648  degrees of freedom
##
## AIC: 618.1  BIC: 661.5  (Smaller is better. MC Std. Err. = 0.3362)

##           obs min  mean max MC p-value
## edges          74  60 74.69  92      1.00
## degree1         51  36 51.11  63      1.00
## degree2         21  10 20.57  32      1.00
## degree3          5   1  5.14  11      1.00
## mix.gender.F.M   67  53 67.25  81      0.94
## mix.gender.M.M    6   1  6.15  12      1.00
## nodematch.bar    38  28 36.98  49      0.78
```

# Plotting Goodness of Fit

Goodness-of-fit diagnostics



## Model Interpretation (Homophily)





## Discussion

- ▶ This work emphasizes the importance of

## Remaining Work

- ▶ Centrality measures e.g. eigenvector centrality, Katz centrality
- ▶ What other data is missing from this dataset that would help us answer more questions?
- ▶ Suggestions?

## References

De P, Singh AE, Wong T, et al. 2004. "Sexual network analysis of a gonorrhea outbreak." *Sexually Transmitted Infections* 80:280-285.

Carrington, P. and Scott, J., 2011. *The SAGE handbook of social network analysis*. 1st ed. Los Angeles [etc.]: SAGE Publications, pp.484-500.

Irene A. Doherty, Nancy S. Padian, Cameron Marlow, Sevgi O. Aral, Determinants and Consequences of Sexual Networks as They Affect the Spread of Sexually Transmitted Infections, The Journal of Infectious Diseases, Volume 191, Issue Supplement\_1, February 2005, Pages S42–S54, <https://doi.org/10.1086/425277>

Wasserman, S. and Faust, K., 1994. Social network analysis: methods and applications. Cambridge: Cambridge University Press.

DE, PRITHWISH MHSc; SINGH, AMEETA E. BMBS, MSc, FRCPC†; WONG, TOM MD, MPH, FRCPC; YACOUB, WADIEH MBBCh, MSc, FRCPC‡ Outbreak of *Neisseria gonorrhoeae* in Northern Alberta, Canada, Sexually Transmitted Diseases: June 2003 - Volume 30 - Issue 6 - p 497-501