Analysis of Drugnet network

CSS 692 – Final Presentation

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Objectives

- Identification of dominant people to reduce the spread of drugs and diseases
- Exploration of local network structures which forms the global pattern
- Comparison of observed network and simulated network

Introduction

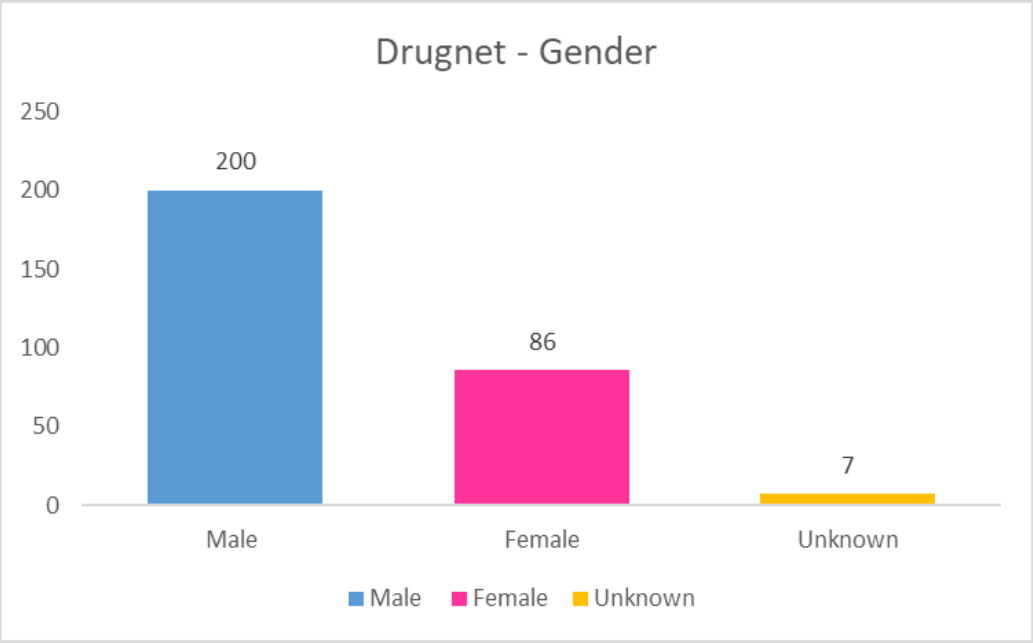
- Network represents the interaction of 293 people from Hartford, CT in the form of an adjacency matrix

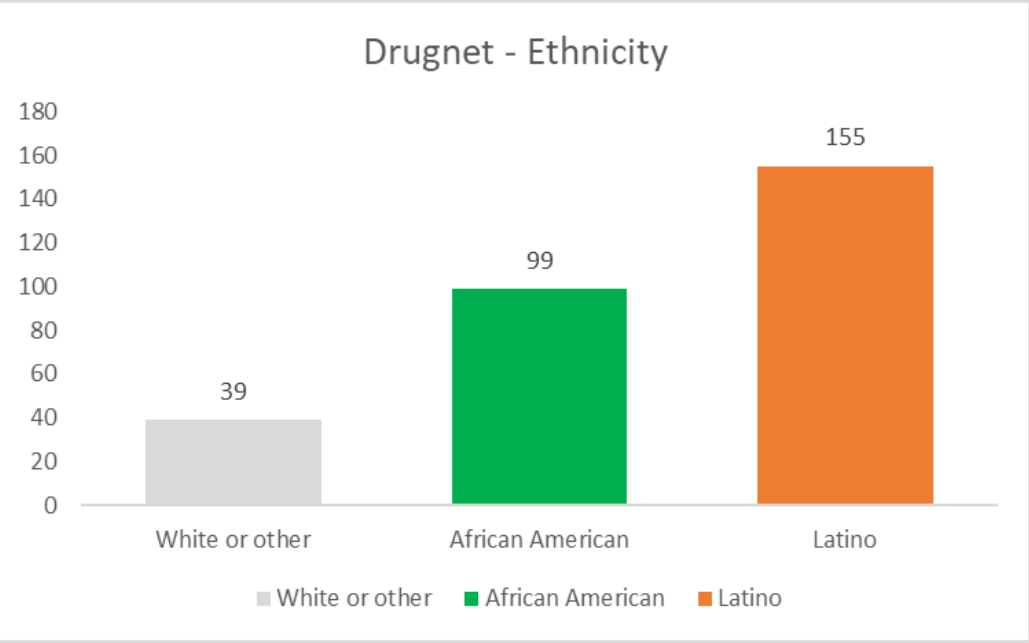
- The survey sample constructed through two methods
  - The majority (55%) was recruited through street outreach
  - The rest of the cohort was referred by the survey participants

- Eligibility criteria
  - At least 18 years of age
  - Reported active use of heroin, cocaine/crack or other injected illicit drug

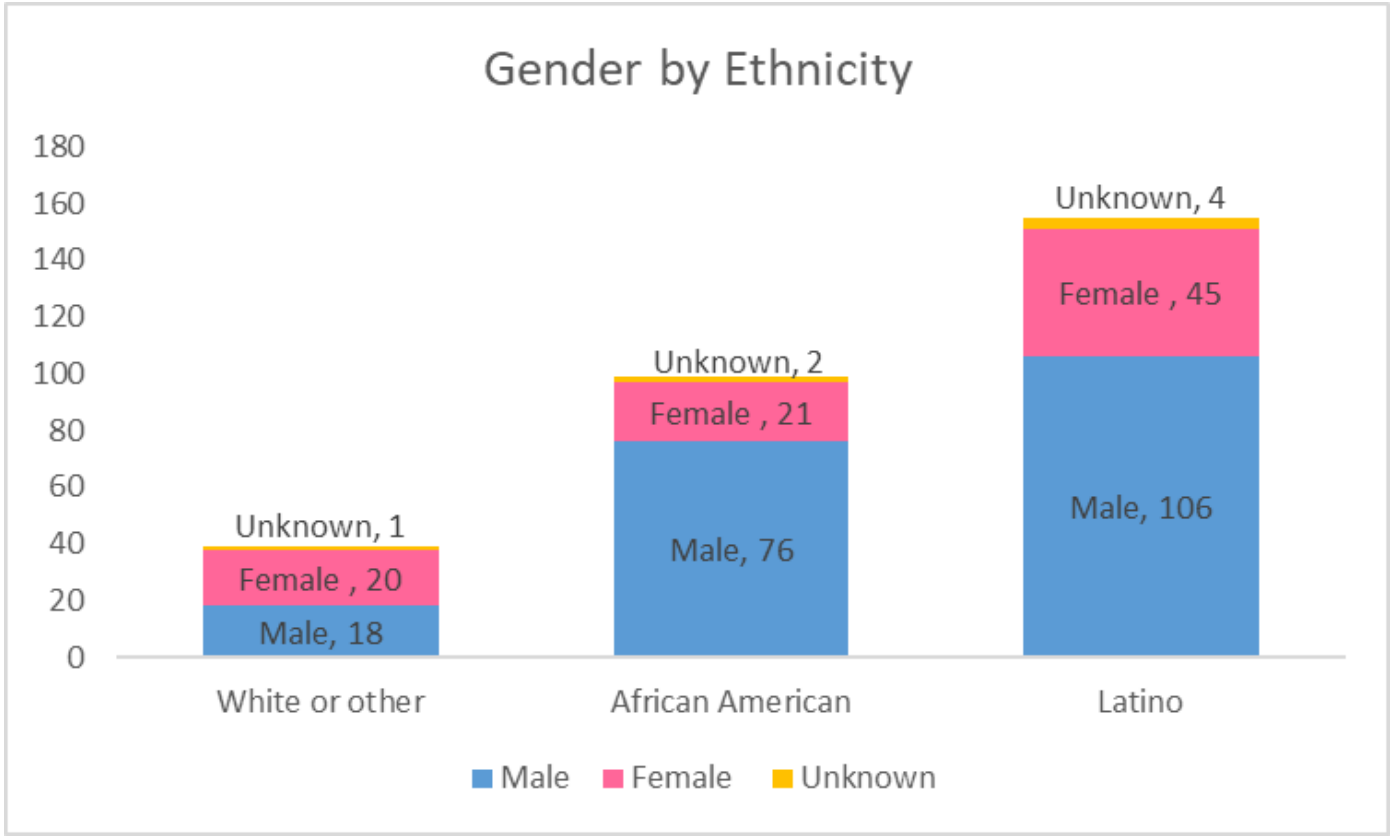
Network attributes

- Network has information about two attributes – Gender and Ethnicity

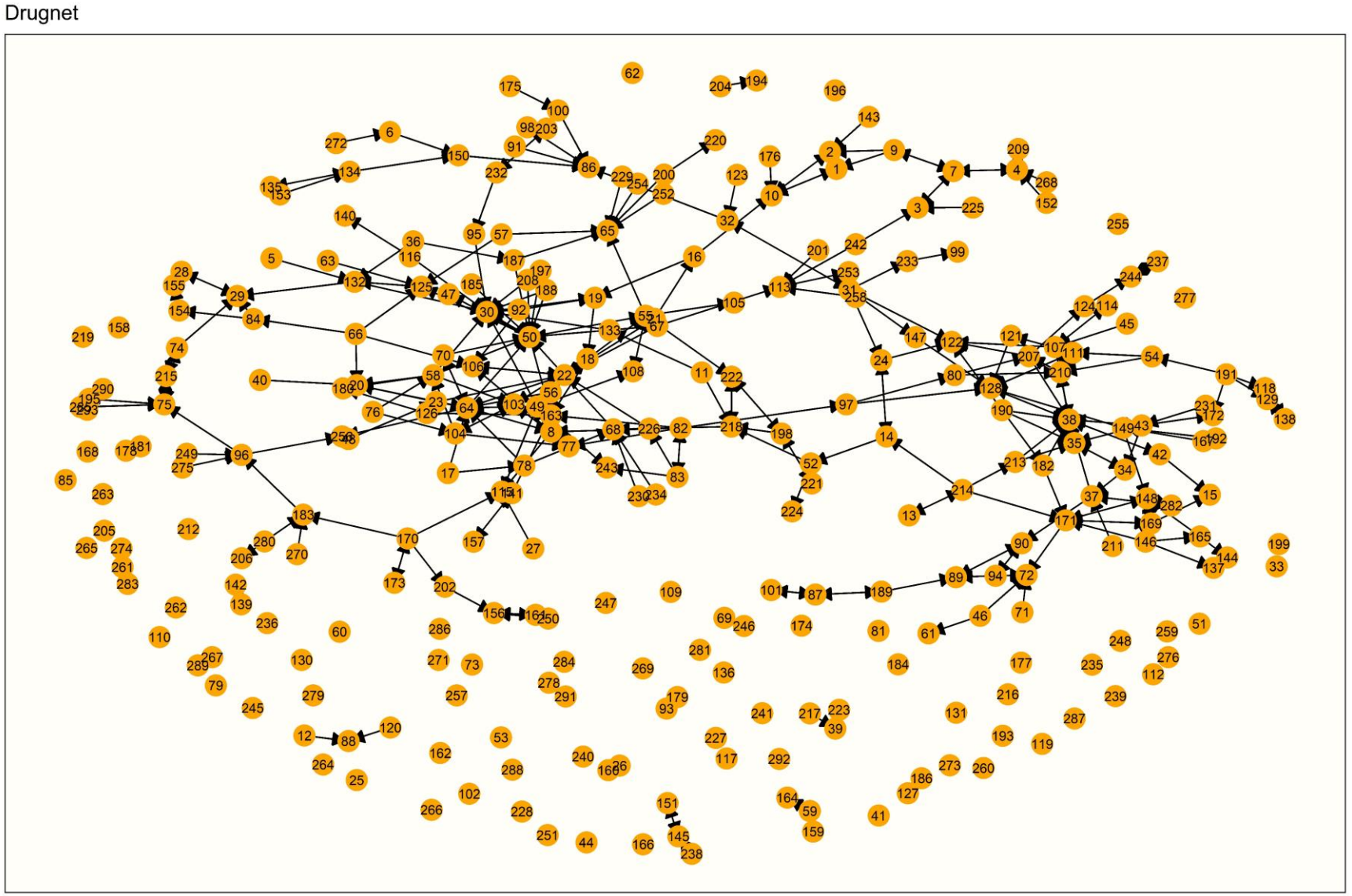




Network attributes

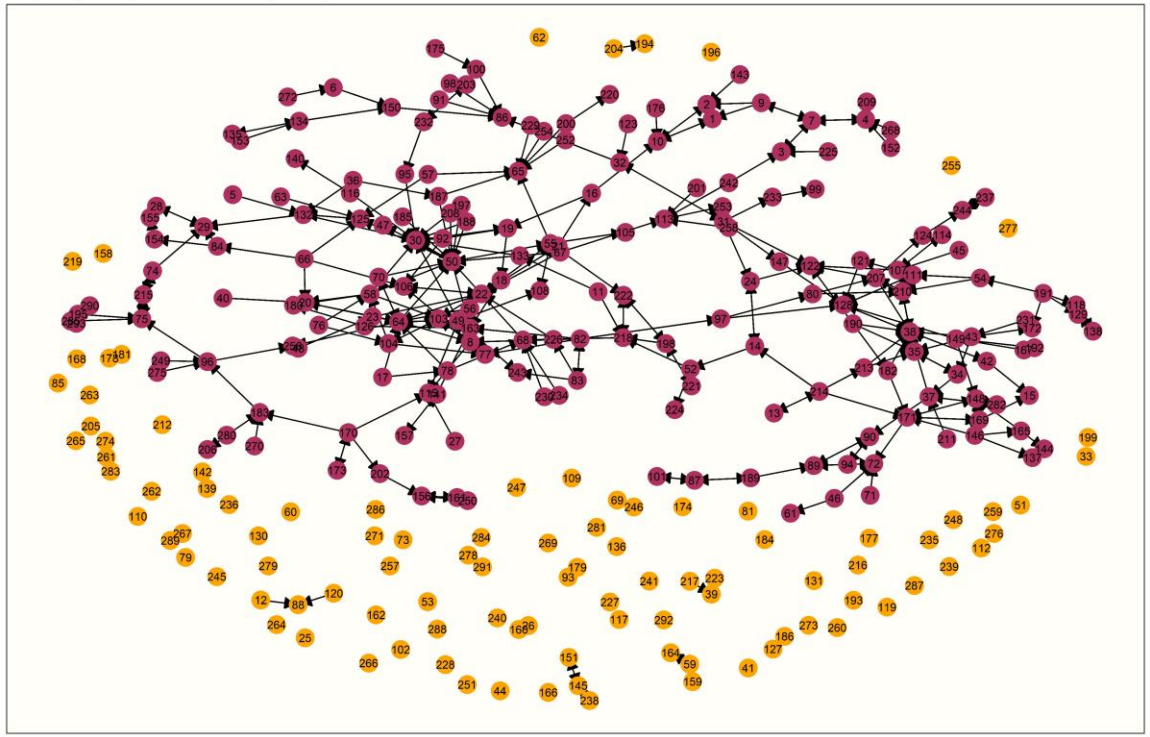


Network structure

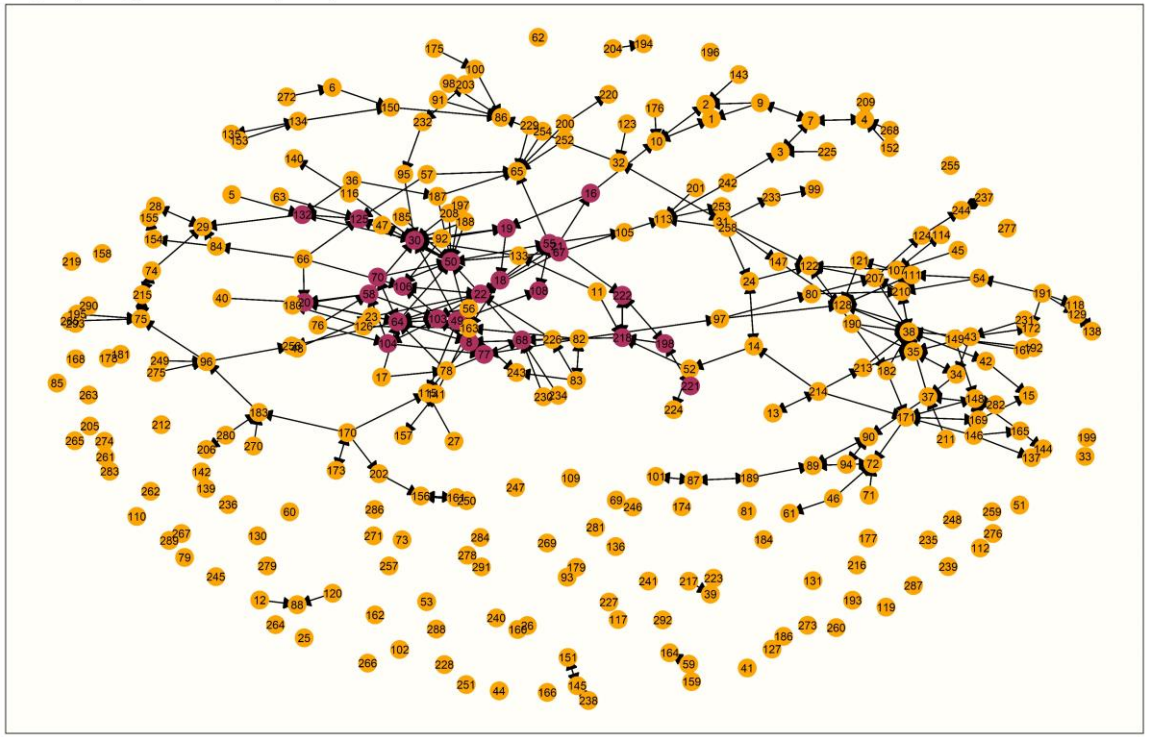


Network structure

Drugnet (Weakly Connected Component)



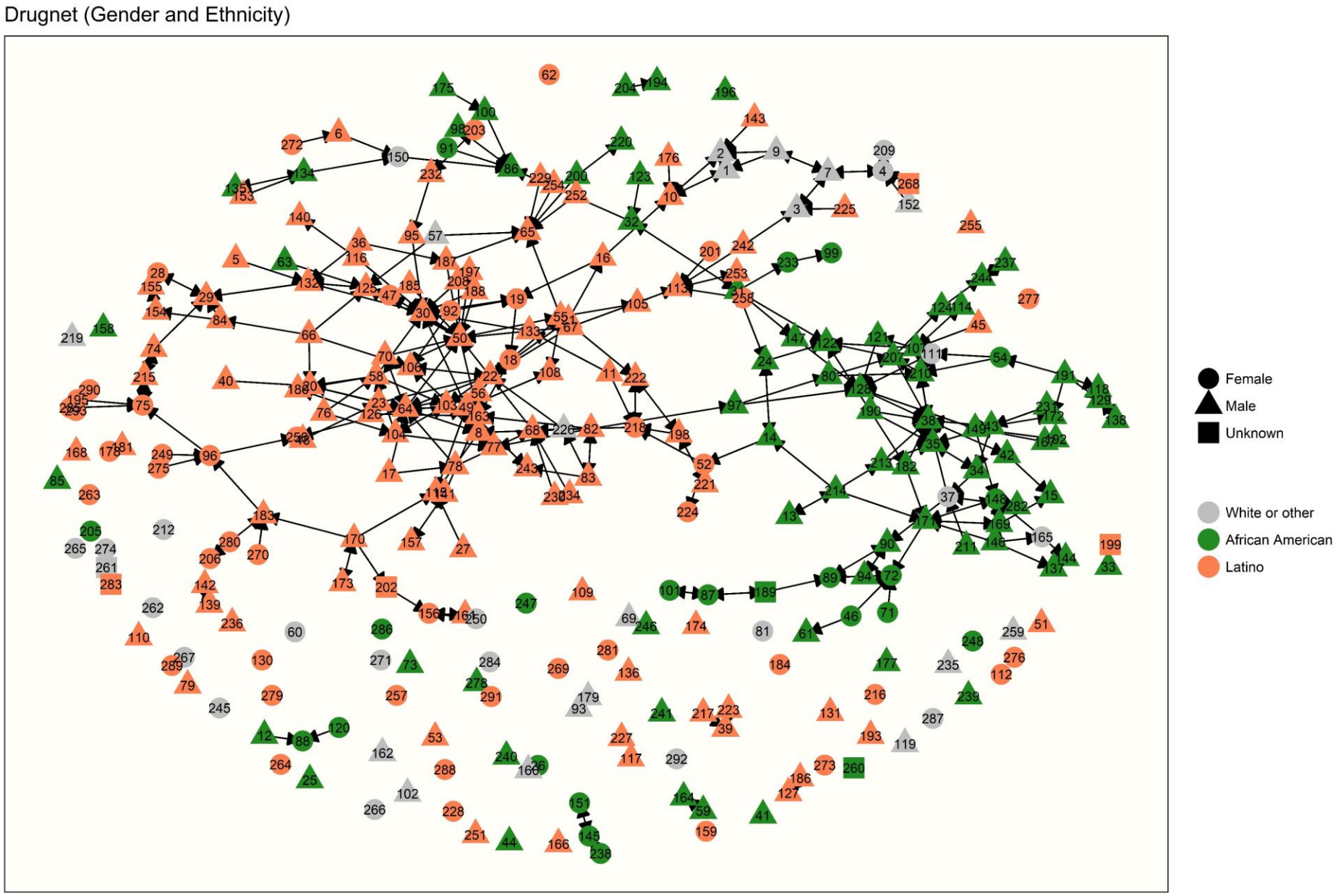
Drugnet (Strongly Connected Component)



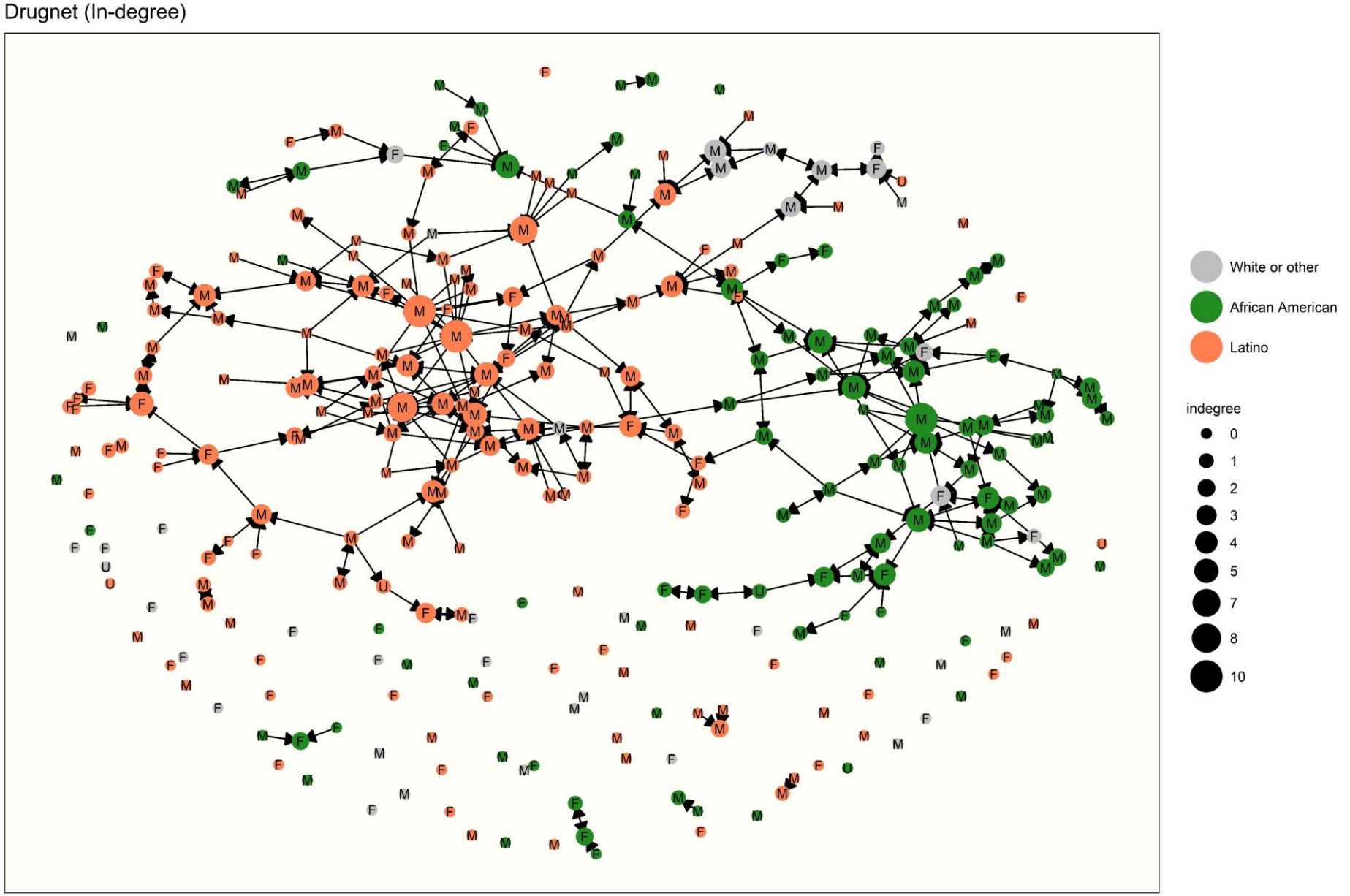
- Weakly connected component
  - Number of nodes – 193
  - Gender -> Male – 143 and Female – 43
  - Ethnicity -> White or other - 15
    African American - 69
    Latino - 109

- Strongly connected component
  - Number of nodes – 27
  - Gender -> Male – 24 and Female – 3
  - Ethnicity -> Latino - 27

Network structure - Gender and Ethnicity



In-degree centrality



In-degree centrality

In-degree	Node id	Gender	Ethnicity
10	30	Male	Latino
	38	Male	African American
	50	Male	Latino
8	64	Male	Latino
7	65	Male	Latino
5	22	Male	Latino
	75	Female	Latino
	87	Male	African American
	124	Male	African American
	130	Male	African American
	165	Male	Latino
	173	Male	African American

ERGMs

- ERGMs help us to understand about local processes and their interaction to form global network patterns

- In ERGM we include a parameter for each configuration and we estimate the value of the parameter that best matches the observed network

- These coefficients are estimated using MCMC (Markov Chain Monte Carlo) technique

ERGMs

- Three different models were built
  - Erdos-Renyi model (p_0 model) -> Edges
  - Holland and Leinhardt's p1 model -> Edges, Mutuality, Sender's effect & Receiver's effect
  - Created a model by selecting attributes based on Morris et al. (2008)

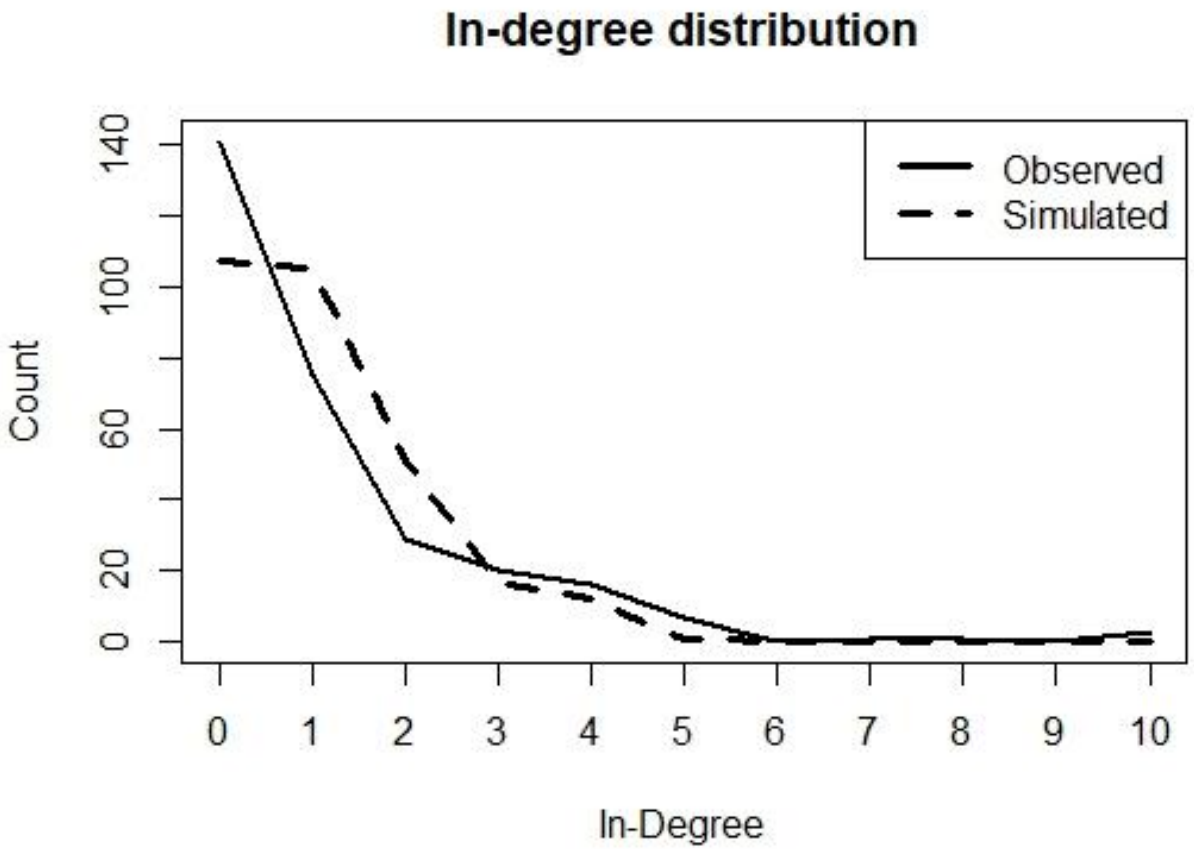
Erdos-Renyi model (p_0 model)

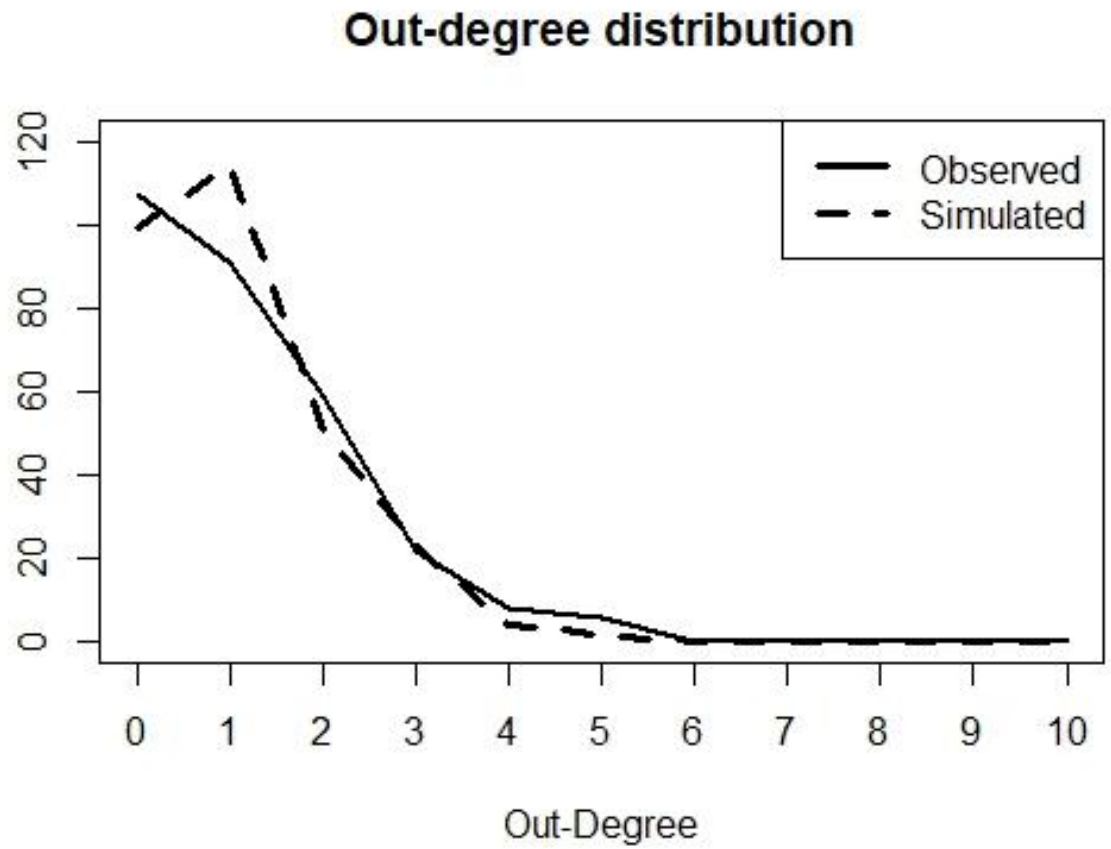
Console Terminal ×

C:/Users/ajask/Downloads/Social Network Analysis/Drugnet CSV/

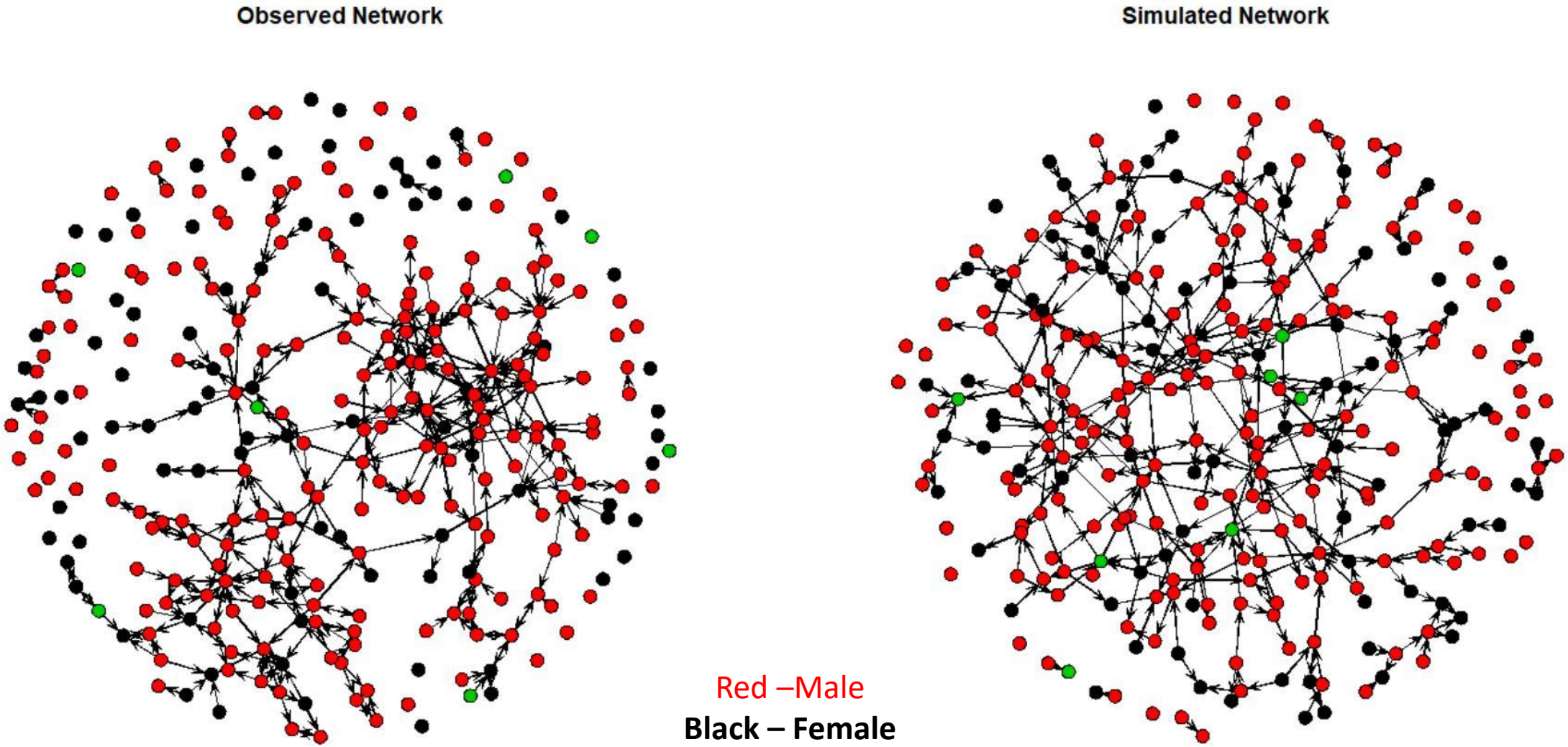
```
> m1 = ergm(net ~ edges)
Evaluating log-likelihood at the estimate.
> summary(m1)

==========================
Summary of model fit
==========================

Formula:   net ~ edges

Iterations:  8 out of 20

Monte Carlo MLE Results:
      Estimate Std. Error MCMC % p-value
edges -5.53290    0.05458      0  <1e-04 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

     Null Deviance: 118606  on 85556  degrees of freedom
 Residual Deviance:   4405  on 85555  degrees of freedom

AIC: 4407    BIC: 4416    (Smaller is better.)
>
```

Erdos-Renyi model (p_0 model)





Erdos-Renyi model (p_0 model)



Red –Male

Black – Female

Green - Unknown

Model based on selected attributes

- Model was built by selecting statistically relevant attributes from the list provided by Morris et al. (2008)

- Selected attributes

Attribute	Explanation
Edges	Edges in the network
Mutual	Mutuality
Asymmetric	Asymmetric dyads
Nodefactor	Main effect of a factor attribute
Nodematch	Interaction term - homophily
Simmelianties	Ties in Simmelian triads
Isolates	Isolates in the network

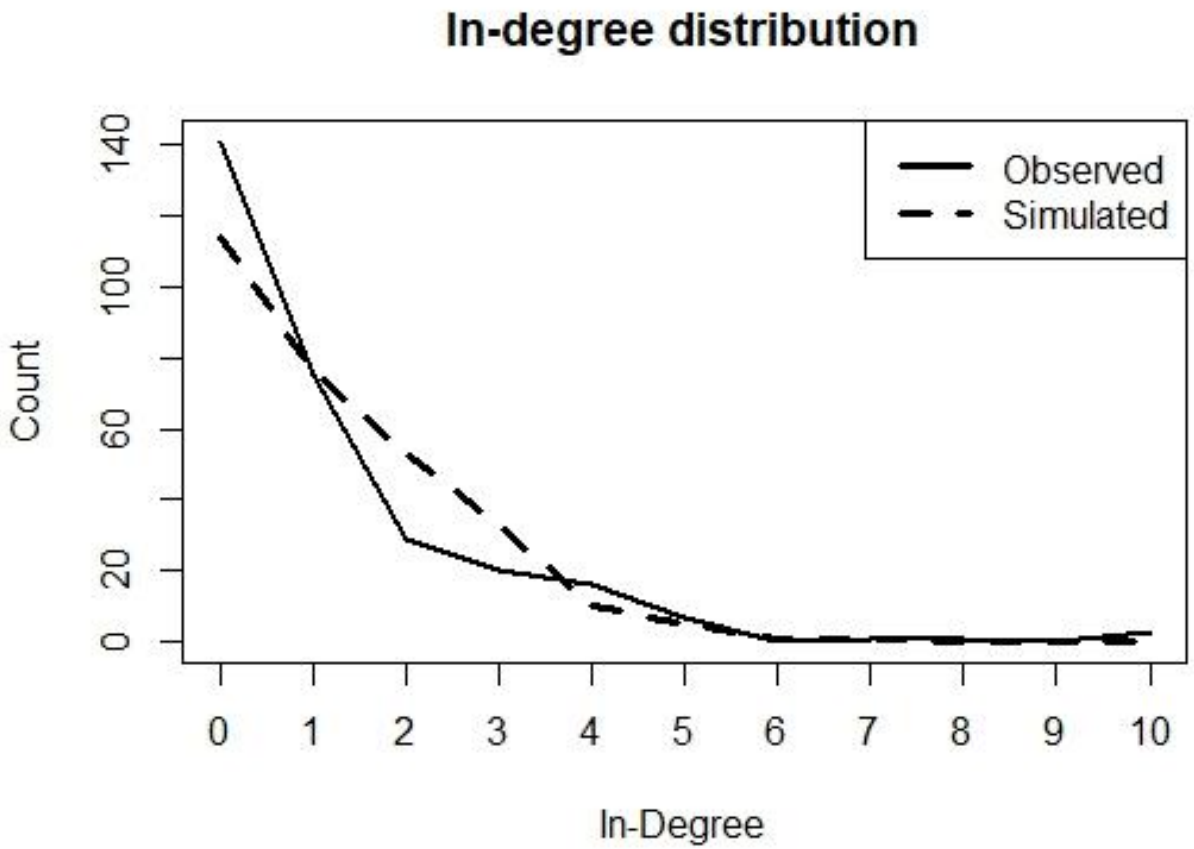
Model based on selected attributes

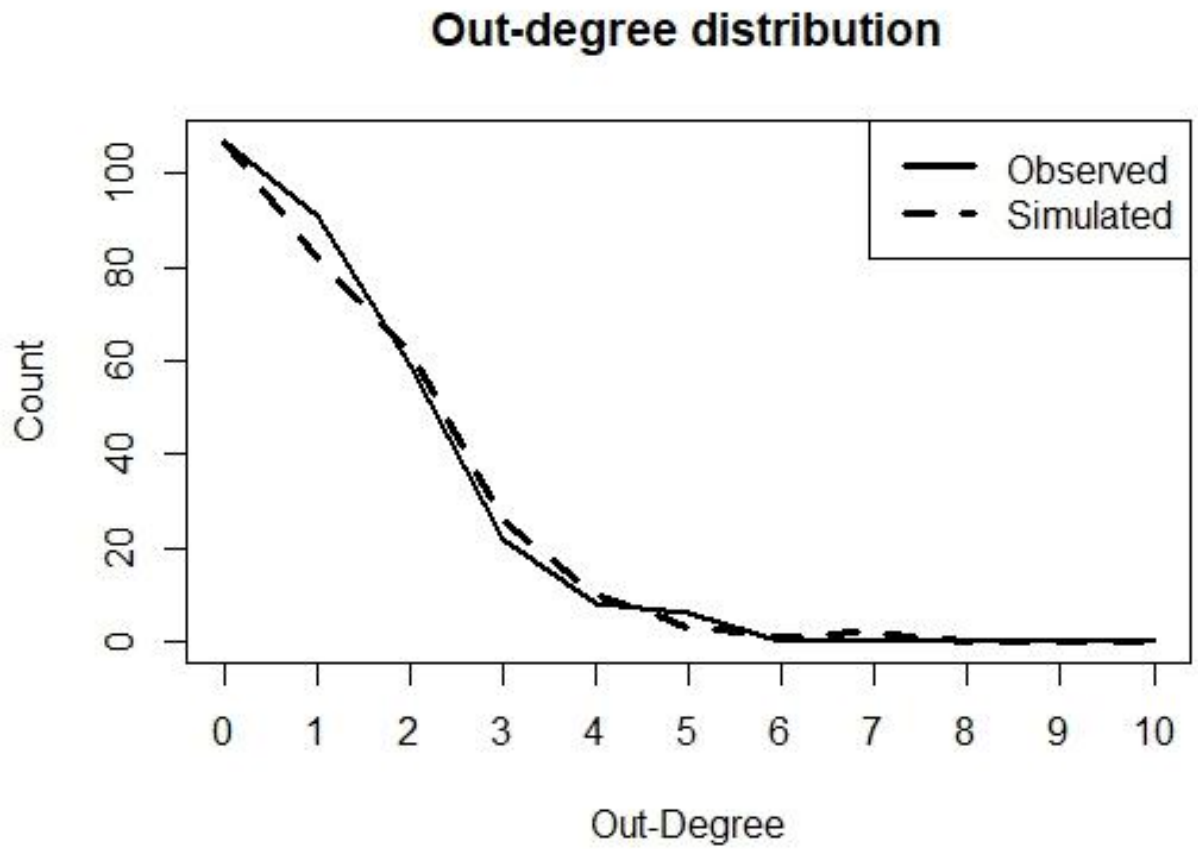
Console Terminal

C:/Users/ajask/Downloads/Social Network Analysis/Drugnet CSV/

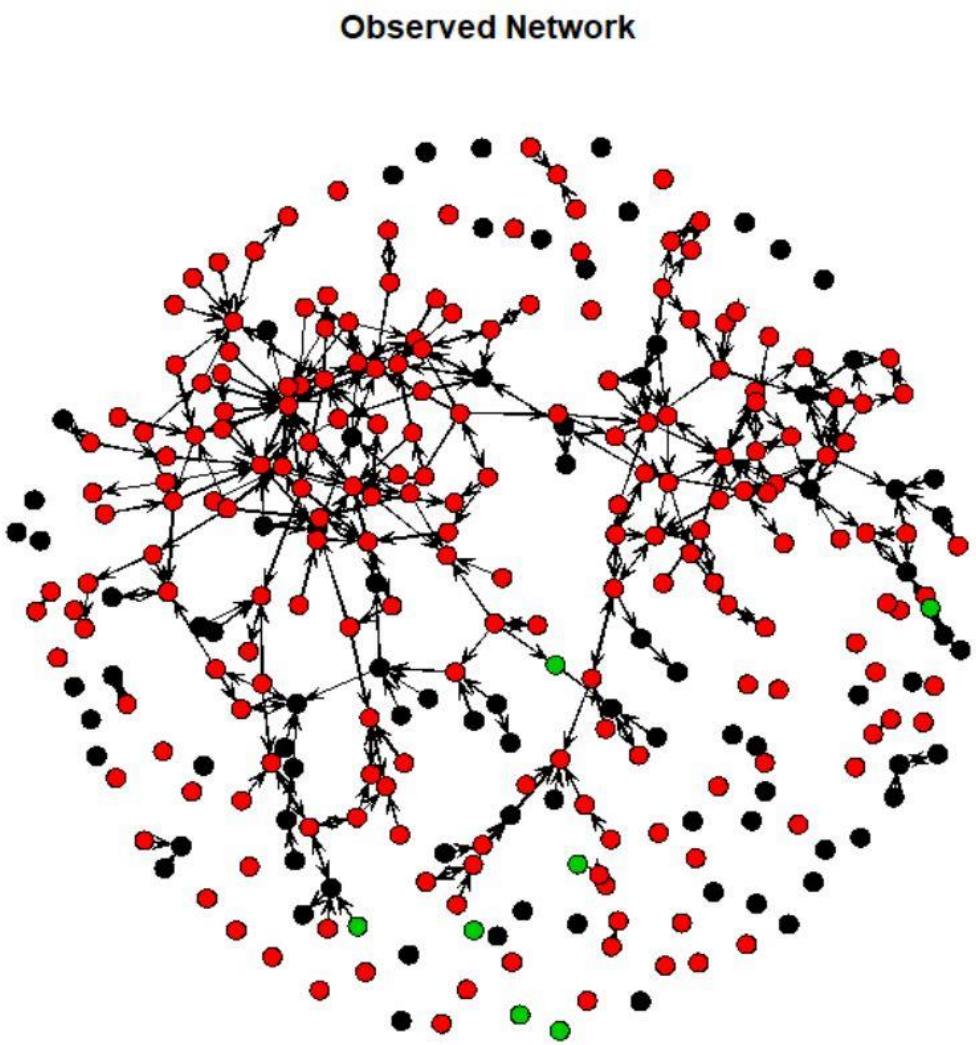
```
==========================
Summary of model fit
==========================

Formula:   net ~ edges + mutual + asymmetric("Gender", diff = FALSE) + asymmetric("Ethnicity",
    diff = FALSE) + nodematch("Ethnicity", diff = F) + nodefactor("Ethnicity") +
    simmelianties + isolates

Iterations:  9 out of 20

Monte Carlo MLE Results:
                           Estimate Std. Error MCMC %  p-value
edges                     -7.61993    0.24080      0  < 1e-04 ***
mutual                     7.01078    0.69272      0  < 1e-04 ***
asymmetric.Gender          0.94728    0.15397      0  < 1e-04 ***
asymmetric.Ethnicity       0.91375    0.34107      0 0.007385 **
nodematch.Ethnicity        1.49435    0.26764      1  < 1e-04 ***
nodefactor.Ethnicity.Latino -0.15842    0.03996      0  < 1e-04 ***
nodefactor.Ethnicity.White   0.19171    0.06642      0 0.003896 **
simmelianties              0.70382    0.18589      5 0.000153 ***
isolates                   1.20703    0.18657      0  < 1e-04 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

     Null Deviance: 118606  on 85556  degrees of freedom
 Residual Deviance:   3615  on 85547  degrees of freedom

AIC: 3633    BIC: 3717    (Smaller is better.)
> |
```

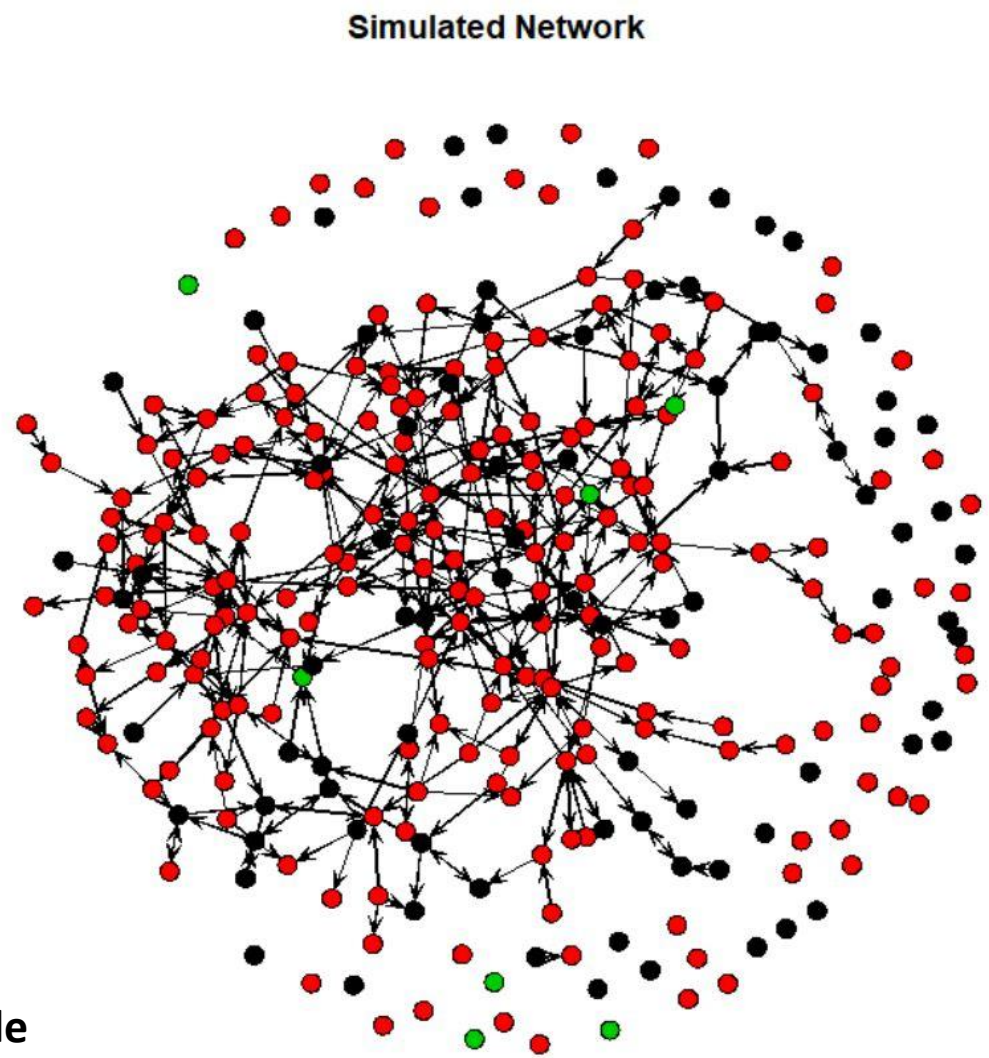
Model based on selected attributes





Model based on selected attributes





Red –Male

Black – Female

Green - Unknown

Conclusion

- The network is male-dominated and a high percentage of participants belongs from Latino ethnicity
- In-degree centrality is used to find important nodes and 12 nodes were selected to create the awareness about drugs as well as diseases
- Edges, mutuality, asymmetric dyads, isolates, homophily and ties in simmelian triads are the important local structures which represent some part of the global pattern in the network

References

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