INTRODUCTION TO SOCIAL NETWORK ANALYSIS AND NETWORK SCIENCE METHODS

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Pre-workshop and during-workshop: Supplemental Materials Used in Workshop

- Github site with supplemental material, R scripts and data used in the illustrative examples presented in workshop:

https://github.com/kiwijomalley/ICHPS-Social-Network-Analysis-Workshop-2023

- GRANDPA algorithm
  - Use to generate random networks for analysis that approximates a base network
  - Very useful if data is confidential
  - Bobak CA, Zhao Y, Levy JJ, and O'Malley AJ. (2022). GRANDPA: GeneRAtive Network sampling using Degree and Property Augmentation applied to the analysis of partially confidential healthcare networks. doi.org/10.48550/arXiv.2211.15000
  - Presented in a conference poster by Carly Bobak on January 9, 2023

Running example network data: Small physician clinic in the Boston area

- Relational data (adjacency matrix form): ICHPS_PhysPractBin.txt

- Relational data (edgelist form): ICHPS_ClinEdgeList.txt

- Node attribute data: ICHPS_nodecov.dat

- References:
  - Keating, Ayanian, Cleary, and Marsden (2007)
  - O'Malley and Marsden (2008)

Segments of Code for the Three Key Problems

I.   Descriptive analyses involving networks

- Visualizing a network
- Descriptive features of networks

II.   Statistical analyses of social influence or peer effects

- Formation of weight matrix
- Cross-sectional cases

III.   Statistical analysis of relational data

- Exponential random graph models
- Latent-space models

I. Descriptive Analyses

- R script: WorkshopICHPS2023.R
  - Loads network
  - Forms directed and undirected binary-valued network objects
  - Makes plots of network
  - Computes summary measures of the network and of physicians' positions within the network

Loading Physician Practice Network

Adjacency matrix

- reldata <- scan("ICHPS_PhysPractBin.txt")
- nr <- sqrt(length(reldir)) #Number of physicians
- reldir <- matrix(reldir,ncol=nr,nrow=nr,byrow=T)

#Directed

- reldir <- ifelse(reldir>0,1,0) #Directed
  - Can use more stringent threshold (greater # conversations) to obtain sparser network by using threshold of 1

#Undirected

- relmut <- ifelse(reldir+t(reldir)>0,1,0) #Undirected
  - Use "And Rule" (threshold of >1) to obtain sparser network
- pnet <- network(reldir,directed=TRUE,matrixtype="adjacency")

Aside: Forming an edgelist from an adjacency matrix with IDs from 1 to nr

- idto <- seq(1,nr)
- edgelist=c()
- for (i in 1:nr) {
-    edge <- idto[(reldir[i,]==1)]
-    nc=length(edge)
-    edgelist=rbind(edgelist,cbind(rep(i,nc),edge))
- }
- edgelist <- data.frame(edgelist)
- names(edgelist) <- c("source","target")
- pnet <- network(reldir,directed=TRUE,matrixtype="edgelist")

More general loading of network data

- pnet <- network(yourdatafile,directed=TRUE,matrixtype="edgelist")

Use one of: adjacency, edgelist, incidence

Loading attribute data

\# Load attribute data

- covdata <- scan("ICHPS_nodecov.dat")
- covdata <- matrix(covdata,nrow=nr,byrow=T)
- colnames(covdata) <-
  c("id","male","whexpert","pctwom","numsess","practice",
  "sumhrt")

Software for descriptive analysis of network

- R is convenient
  - sna package contains many built-in features
  - igraph package

    R: install.packages("sna","igraph")

    R: library(sna)

    R: library(igraph

- Python
  - networkx package

Plotting network using SNA

- #Plot from adjacency matrix
- plot(pnet,mode="fruchtermanreingold",displaylabels=T)
 gplot(pnet,gmode="digraph",mode="fruchtermanreingold")
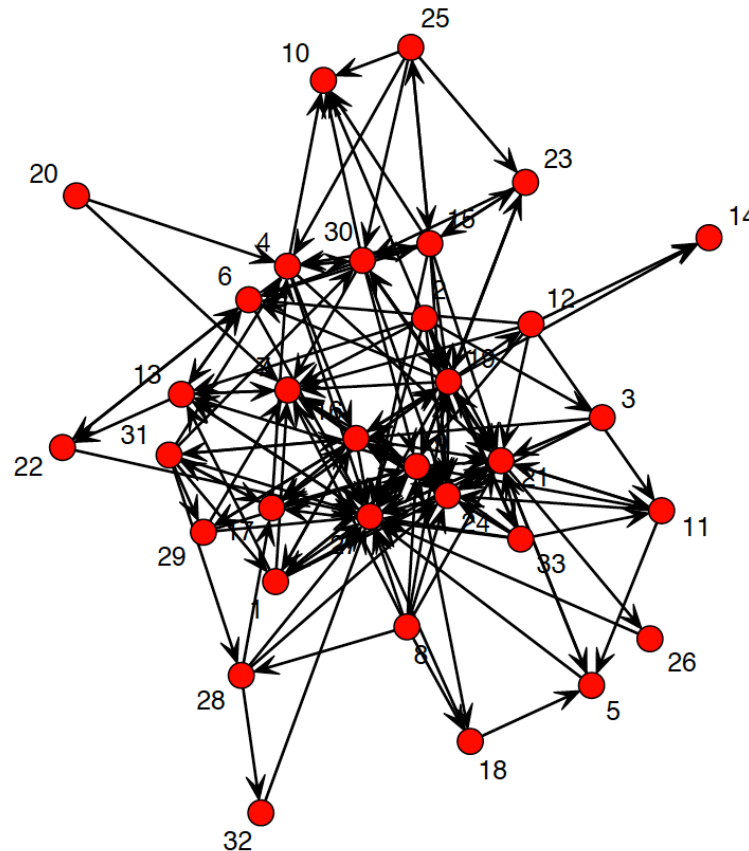
Using igraph

- Let edgelist be a N by 2 matrix in R with the network represented as an edgelist

- nodes <- unique(c(edgelist[,1],edgelist[,2]))

Make graph object from edgelist:

- gnet <- graph_from_data_frame(d=edgelist, vertices=nodes, directed=TRUE)

- print(gnet, e=TRUE, v=TRUE)

Plotting network using igraph in R

- V(gnet)$color <- covdata$practice
- V(gnet)$size <- 10*(covdata$whexpert+1)
- par(mar=c(0,0,0,0))
- plot(gnet,
-     vertex.color = V(gnet)$color, # Color of nodes
-     vertex.size = V(gnet)$size, # Size of nodes
-     vertex.label.color = "black", # change color of labels
-     vertex.label.cex = .75, # change size of labels to 75% of original size
-     edge.curved=.25, # add a 25% curve to the edges
-     edge.color="grey20", # change edge color to grey
-     edge.arrow.size=0.3)

Visualization of network of physicians' professional relationships within a medical practice
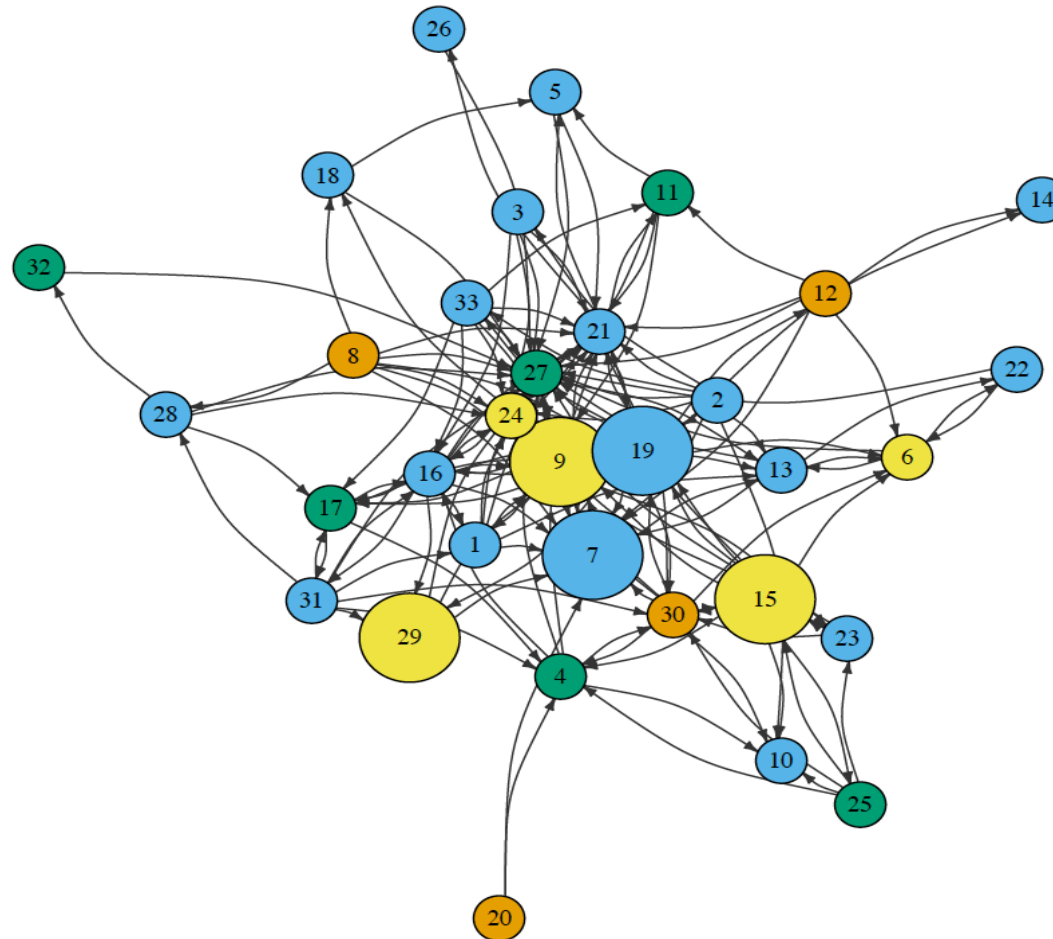
Computing summary measures of networks in R

- Use SNA or igraph
  - You might detach igraph if want to use SNA as igraph masks functions (some its functions have the same name as in SNA) or precede function name with package name (e.g., igraph::grecip)
  - detach("package:igraph", unload = TRUE)
- Dyad and Triad Census'
  - dyadc=dyad.census(reldir)
  - recip=grecip(reldir)
  - triadc_mut=triad.census(relmut,g="graph")
  - triadc_dir=triad.census(reldir,g="digraph")
  - trans=gtrans(reldir,mode="digraph")

Summary measures cont.

- Degree distributions
  - idegree=degree(reldir,cmode="indegree")
  - odegree=degree(reldir,cmode="outdegree")
  - central=centralization(reldir,degree)

- Centrality measures
  - closecent=closeness(reldir,gmode="digraph")
  - bcent=betweenness(reldir,gmode="digraph")
  - eigcent=evcent(reldir,gmode="digraph",use.eigen=FALSE)
  - powcent=bonpow(reldir,gmode="digraph")

Aside: Manual computation of eigenvector centrality

\# Column standardize as per Katz (1953): undirected network

- on=as.vector(rep(1,nrow(relmut)))
- rscale=as.vector(relmut %*% on)

Can't be 0!

- scnet=diag(rscale^(-1),nrow=length(cscale))
- srelmut=relmut %*% scnet #Row-stochastic adjacency mat
- seigcent=evcent(srelmut,gmode="digraph",use.eigen=FALSE)

\#manual

- sesys=eigen(srelmut,symmetric=TRUE) #First eigenvalue is 1
- seigcent2=abs(sesys$vector[,1]) #Same as seigcent

\# Differs from:

- eigcent = evcent(relmut,gmode="digraph",use.eigen=FALSE)

R Output

sesys$values

 [1] 1.00000000 0.58674579 -0.50090590 0.47303368 -0.43397276 0.42666878 -0.42491411 -0.39345582

 [9] 0.37479529 -0.37272600 0.34943660 -0.34833131 0.29465182 -0.29277386 -0.26530439 0.26150139

[17] -0.25725084 -0.25079539 -0.23908776 0.23292529 0.17182520 -0.15703102 -0.14330681 -0.12994348

[25] 0.12570645 -0.10902035 -0.10191533 0.09780081 0.06373494 -0.06033018 0.04989629 -0.04039014

[33] 0.01273312

> -sesys$vector[,1]

 [1] 0.14294834 0.16081688 0.08934271 0.17868542 0.07147417 0.12507980 0.23229105 0.14294834

 [9] 0.28589668 0.08934271 0.10721125 0.12507980 0.12507980 0.03573708 0.17868542 0.23229105

[17] 0.12507980 0.07147417 0.30376522 0.03573708 0.30376522 0.05360563 0.08934271 0.26802813

[25] 0.08934271 0.03573708 0.42884501 0.10721125 0.10721125 0.21442251 0.14294834 0.03573708

[33] 0.16081688

II. Statistical models involving comparative analysis of multiple networks

- Do social network characteristics correlate with other variables of interest?

- Often involves use of regression and hierarchical regression models

- Original data: Keating, Ayanian, Cleary, and Marsden (2007)

- R script: ICHPS2023models.R

Example plot and statistical analysis of network (O'Malley and Marsden, 2008)

- pnet <- network(physnetwork, directed=TRUE, matrixtype="adjacency",

  vertex.attr=nodecov,

  vertex.attrnames = c("male", "whexpert",

  "pctwom", "numsess", "practice", "bcma", "bima",
  "bpp", "wnhlth", "numcat", "pctcat"))

- plot(pnet,mode = "fruchtermanreingold", displaylabels=T)
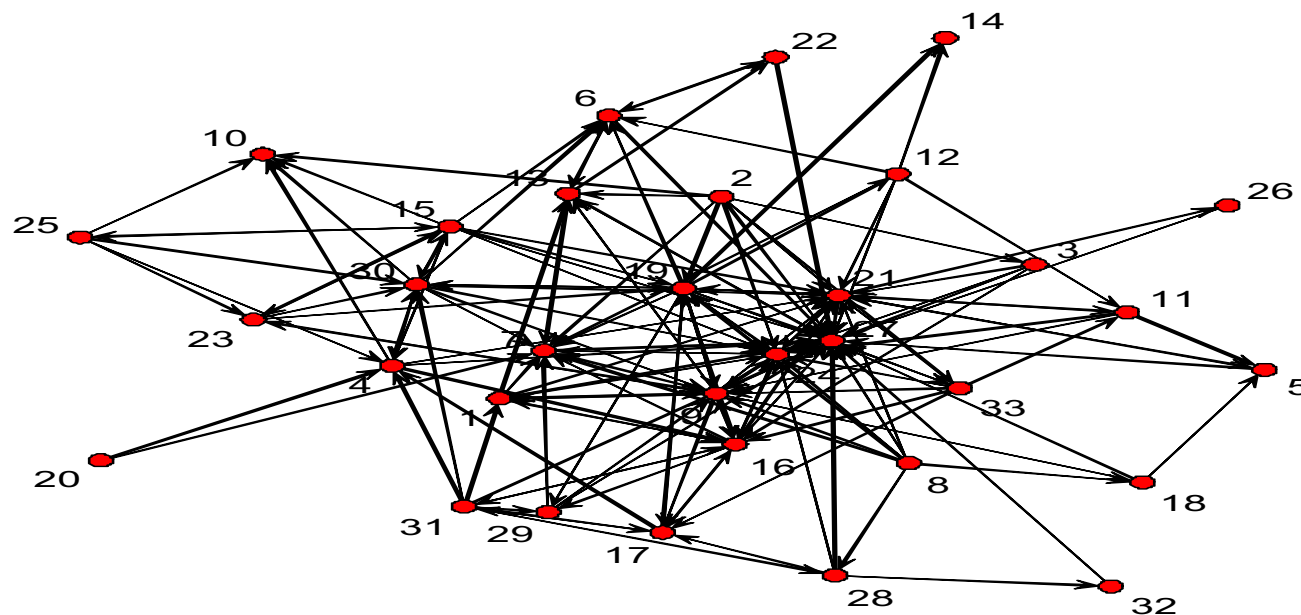
Simplest model

- model1a <- ergm(pnet~edges)
- Evaluating log-likelihood at the estimate.
- Formula: pnet ~ edges

- Iterations: 5 out of 20

- Monte Carlo MLE Results:
-       Estimate Std. Error MCMC % p-value
- edges -1.70084   0.08517   0 <1e-04 ***
- ---
- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

-       Null Deviance: 1463.9 on 1056 degrees of freedom
- Residual Deviance: 908.6 on 1055 degrees of freedom
-
- AIC: 910.6   BIC: 915.5   (Smaller is better.)

What is this the log-odds of?

Model used to estimate homophily effects

- Formula: pnet ~ edges + mutual + nodeocov("whexpert") + nodeocov("pctwom") +
- nodeocov("numsess") + nodematch("male", diff = F) + nodematch("bcma",
- diff = F) + nodematch("bima", diff = F) + nodematch("bpp",
- diff = F) + nodematch("wnhlth", diff = F)

- Monte Carlo MLE Results:
-             Estimate Std. Error MCMC % p-value
- edges   -4.560879 0.510615   0 < 1e-04 ***
- mutual   0.851292 0.293985   0 0.003862 **
- nodeocov.whexpert -0.391256   0.279232   0 0.161455
- nodeocov.pctwom -0.001583   0.004530   0 0.726830
- nodeocov.numsess   0.159686   0.039360   0 < 1e-04 ***
- nodematch.male   0.646502   0.181881   0 0.000396 ***
- nodematch.bcma   0.739658   0.278889   0 0.008119 **
- nodematch.bima   0.277871   0.199195   0 0.163321
- nodematch.bpp   1.396742   0.255284   0 < 1e-04 ***
- nodematch.wnhlth -0.046937   0.221694   0 0.832366
- ---
- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- AIC: 838.3   BIC: 887.9   (Smaller is better.)

Ego (originator) covariate

Homophily covariate

# Alternative model: Allow separate node-match (homophily) coefficients

- model1f <- ergm(pnet~edges + mutual + nodeocov("whexpert") +nodeocov("pctwom") + nodeocov("numsess") + nodematch("male",diff=T) + nodematch("practice",diff=T))

- Estimate Std. Error MCMC % p-value
- edges   -1.134295 0.417598   0 0.00671 **
- mutual   0.615252 0.316615   0 0.05226 .
- nodeocov.whexpert   -0.509118 0.293552   0 0.08315 .
- nodeocov.pctwom   -0.022326 0.005604   0 < 1e-04 ***
- nodeocov.numsess   -0.007532 0.045438   0 0.86837
- nodematch.male.0   1.534152 0.247805   0 < 1e-04 ***
- nodematch.male.1   -1.112795 0.420071   0 0.00819 **
- nodematch.practice.1 1.320874 0.849377   0 0.12022
- nodematch.practice.2 0.466084 0.215630   0 0.03088 *
- nodematch.practice.3 2.131637 0.423777   0 < 1e-04 ***
- nodematch.practice.4 1.981935 0.489350   0 < 1e-04 ***

Allows nodematch.male coefficient to vary by sex

Assessing Goodness of Fit with Respect to In-Degree Distribution

- model1e.gof <- gof(model1e~idegree,control=control.gof.ergm(nsim=100),verbose=T)

- plot(model1e.gof)

Goodness-of-fit diagnostics
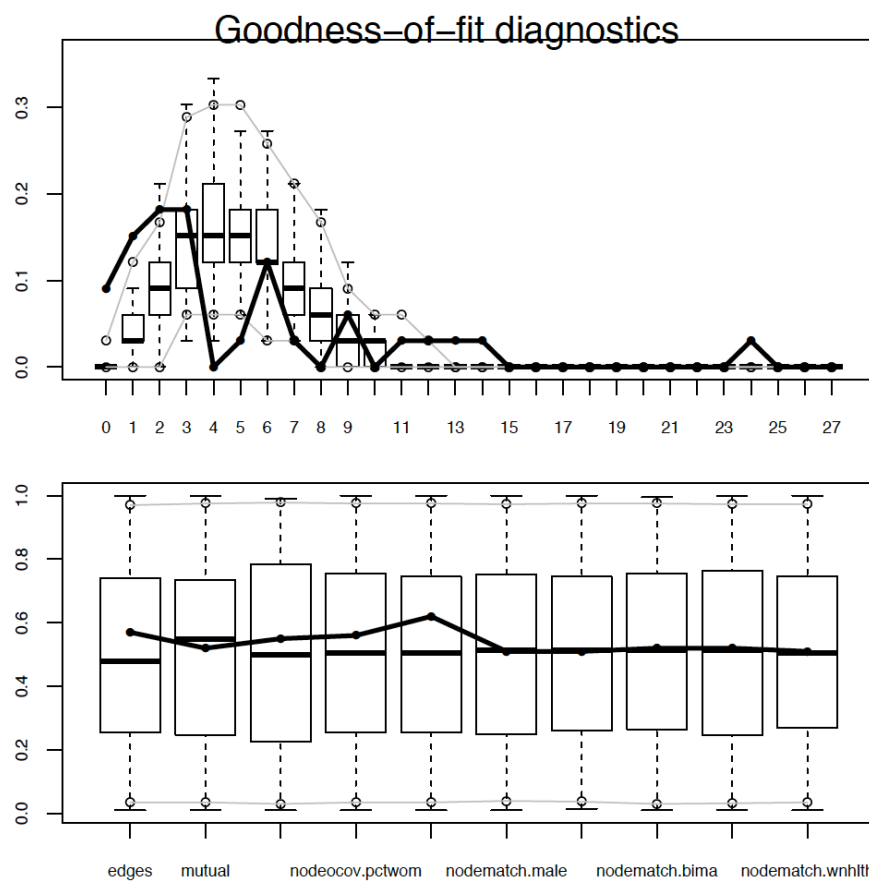
Estimating Latent-space models in R

- ergmm(formula, response = NULL, family = "Bernoulli", fam.par = NULL, control = control.ergmm(), user.start = list(), prior = ergmm.prior(), tofit = c("mcmc", "mkl", "mkl.mbc", "procrustes", "klswitch"), Z.ref = NULL, Z.K.ref = NULL, seed = NULL, verbose = FALSE)
  - "family" command allows different distributions in the exponential family (as for generalized linear models)
  - "prior" command gives some control over prior distributions for Bayesian analysis
  - "tofit" controls which elements of estimation are performed
- ?ergmm to get help and then terms.ergmm to get list of terms that are supported
  - Note that there are no mutual, triadic or higher-order network statistics are allowed in this model!

Equating Latentnet's ERGMM and Statnet's ERGM

- **ERGMM Formula:**   pnet ~ nodematch("male", diff = F)
- **Attribute: edges (included by default in ERGMM)**
- **Model:**   Bernoulli
- **MCMC sample of size 4000, draws are 10 iterations apart, after burnin of 10000 iterations.**
- **Covariate coefficients posterior means:**
-           **Estimate   2.5%   97.5% 2*min(Pr(>0),Pr(<0))**
- **(Intercept)   -2.15650 -2.44573 -1.8870   < 2.2e-16 ***
- **nodematch.male   0.78345   0.43672   1.1398   < 2.2e-16 ***

- **ERGM Formula:**   pnet ~ edges + nodematch("male", diff = F)
-
- **Iterations: 5 out of 20**
-
- **Monte Carlo MLE Results:**
-   **Estimate Std. Error MCMC % p-value**
- **edges   -2.1552   0.1437   0   <1e-04 ***
- **nodematch.male   0.7898   0.1794   0   <1e-04 ***

WARNING: Currently, the ERGMM procedure in R can only estimate models in which edges are conditionally independent. So cannot include network statistics involving mutual or triadic terms!

Euclidean distance with $d = 3$ dimensions and 3 clusters (or groups)

lmodel7 <- ergmm(pnet ~
rreceiver+rsender+euclidean(d=3,G=3)+nodematch("male",diff=T))

An application is to clusters actors into groups!

MKL Latent Positions of lmodel7
pnet ~ rreceiver + rsender + euclidean(d = 3, G = 3) + nodematch("male", diff = T)
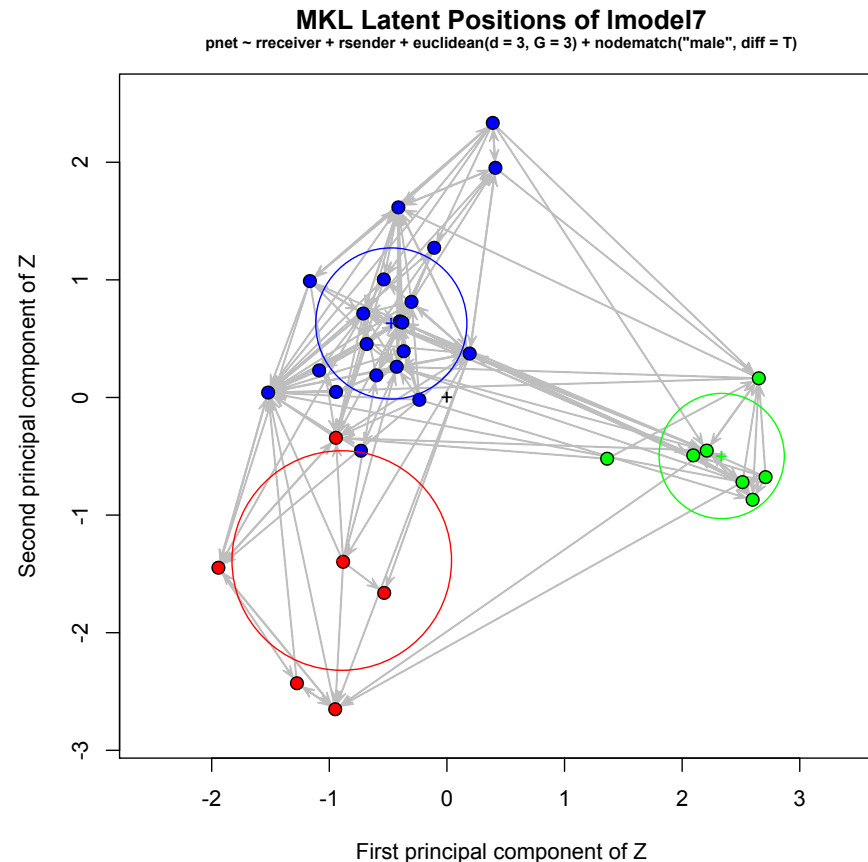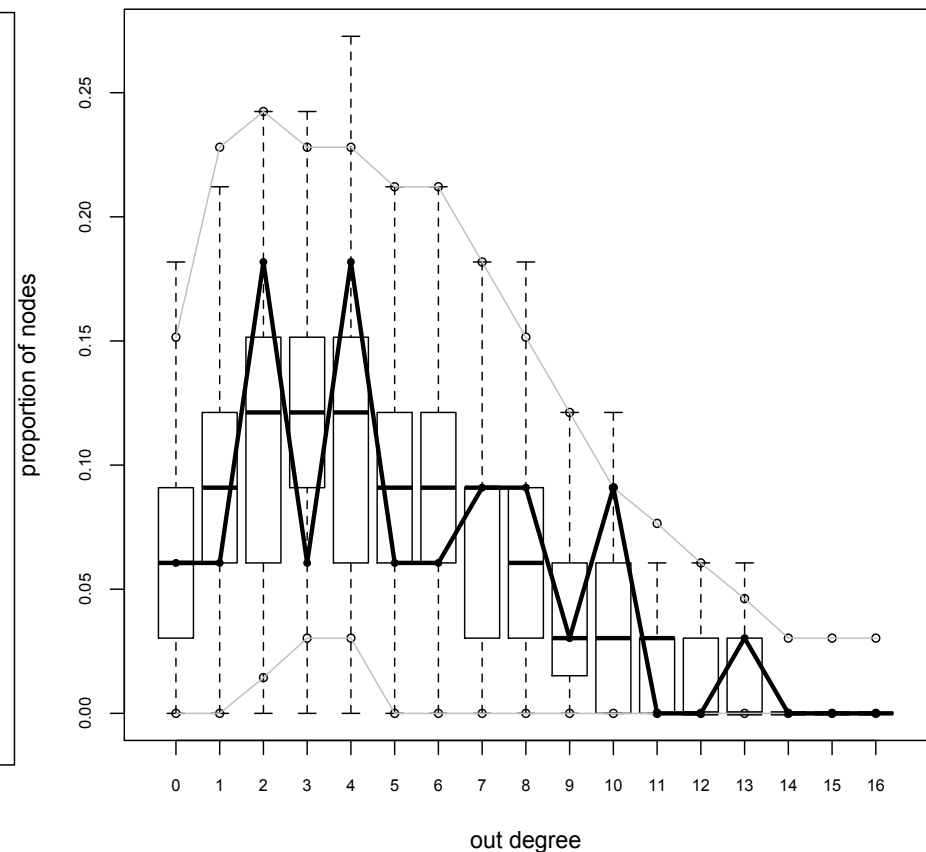
Assessment of Goodness of fit

- lmodel7i.gof <- gof(lmodel7,GOF=~idegree,control=ergmm.control(nsim=100),verbose=T)

- plot(lmodel7i.gof)

- lmodel7o.gof <- gof(lmodel7,GOF=~odegree,control=ergmm.control(nsim=100),verbose=T)

- plot(lmodel7o.gof)

Goodness of fit of degree distributions
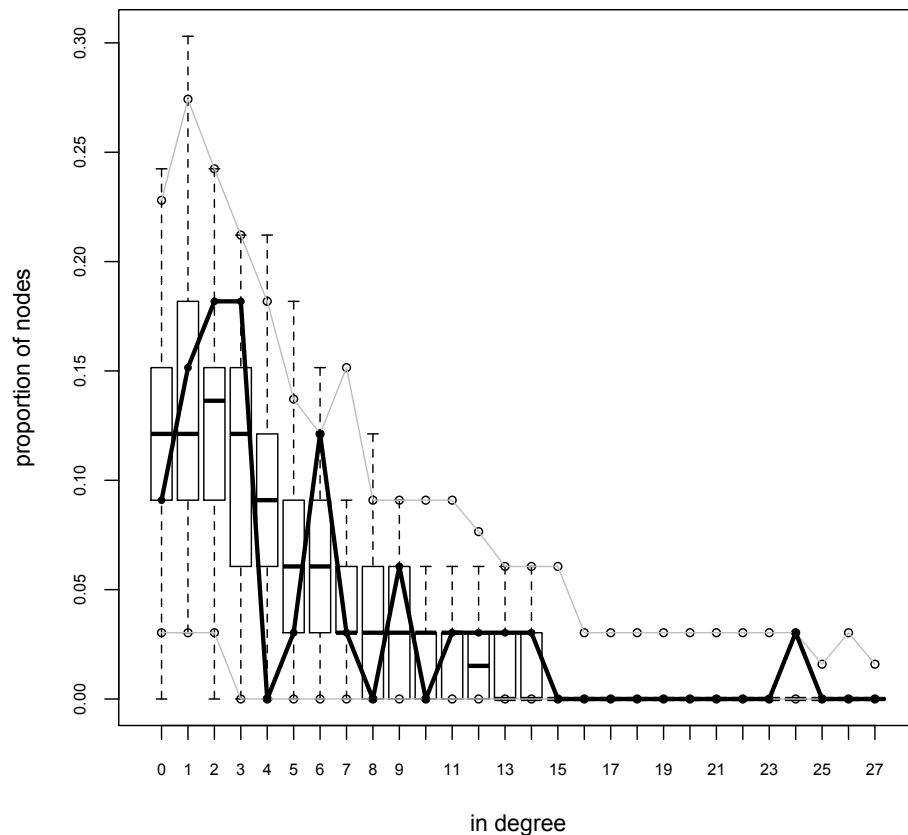## with Euclidean latent-space
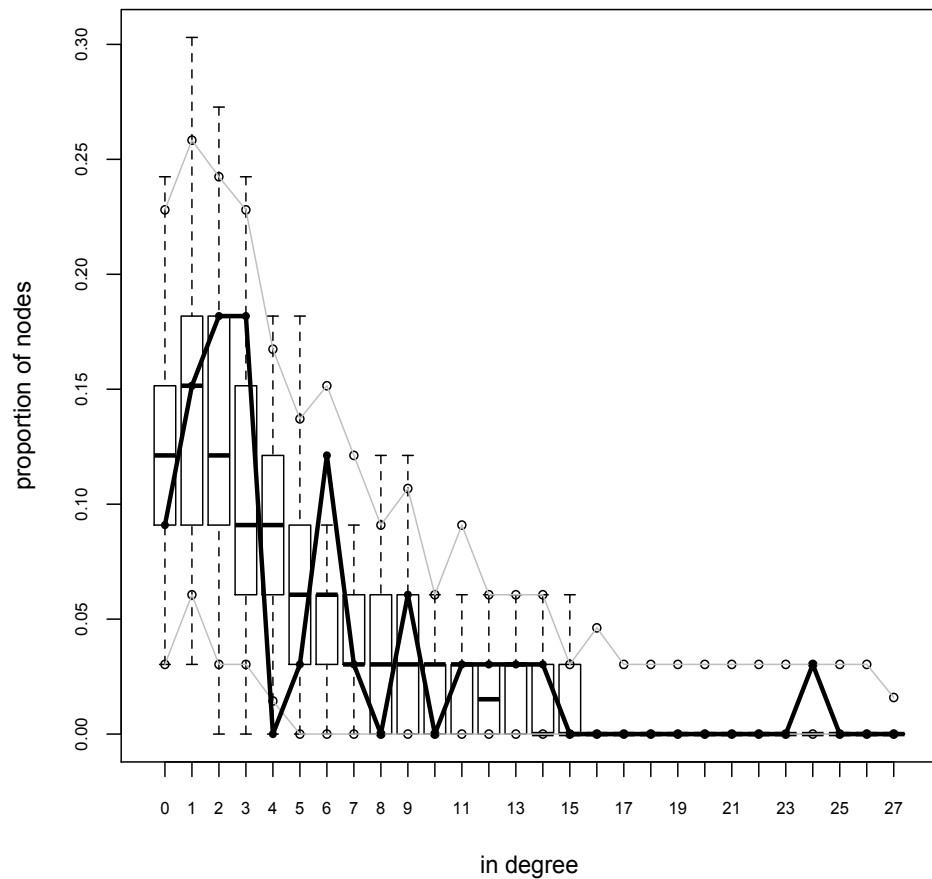
Goodness-of-fit diagnostics

Goodness of fit of degree distributions with Bilinear latent-space
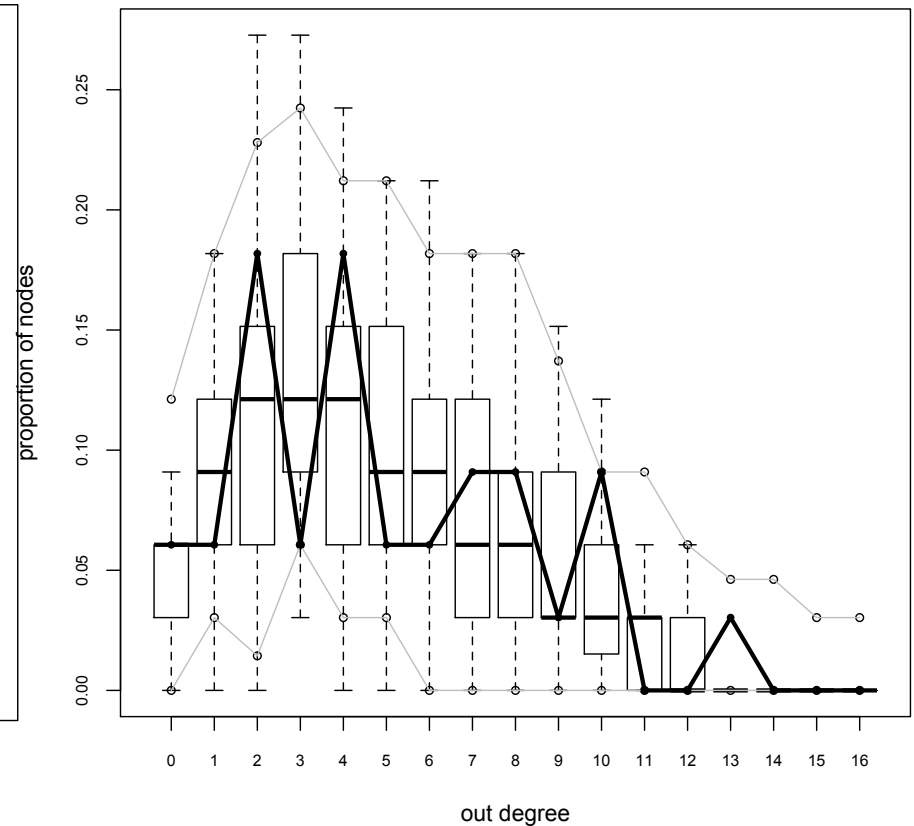

Goodness-of-fit diagnostics

Goodness-of-fit diagnostics

III. Statistical analyses of social influence or peer effects

- Use Inam function
  - Uses numerical approximation to second derivatives in Newton-family optimization routines
- Develop your own estimation routines
  - Use optim function for maximum likelihood inference
- Amenable to Bayesian inference

Data wrangling required to form peer actor outcome or attribute weighted average outcome

Data manipulation

- on <- as.vector(rep(1,nr))

- x <- as.matrix(cbind(on,regdata[,c("male", "pctwom","numalters")]))

Peer outcome predictor

- hrtalt <- wtreldir %*% as.vector(covdata$sumhrt)

- regdata <- data.frame(covdata,hrtalt=hrtalt,noalters=noalters,numalters=numalters)

Estimation of linear regression and autoregressive outcome models for cross-sectional network influence data in R using lnam function

Naïve regression model in R

- reg.adj <- lm(sumhrt~x+hrtalt-1, data=regdata)

Autoregressive outcome model estimation in R

- lnam1.adj <- lnam(regdata$sumhrt,x,wtreldir)

Network autocorrelation model estimation in R

- lnam2.adj <- lnam(regdata$sumhrt,x,NULL,wtreldir)

Results and Peer-effect Estimate Interpretation (assume isolates not influenced; set isoequal = 0 in R)

Term	Linear regression			Autoregressive outcome model		
	Estimate	SE	P-value	Estimate	SE	P-value
on	16.049	4.236	0.001	16.078	3.902	0.000
male	-0.327	2.492	0.897	-0.206	2.277	0.928
pctwom	-0.054	0.052	0.305	-0.052	0.047	0.275
numalters	-0.363	0.218	0.107	-0.353	0.199	0.077
hrtalt or rho1.1	0.299	0.195	0.136	0.277	0.171	0.106

Peer effect parameter under the autoregressive outcome model estimated by lnam

Estimation of network autocorrelation model in R and Interpretation of Peer-Effect Estimates

lnam2.adj <- lnam(regdata$sumhrt,x,NULL,wtreldir)

Term	Autoregressive outcome model			Network autocorrelation model		
	Estimate	SE	P-value	Estimate	SE	P-value
on	16.078	3.902	0.000	16.471	4.089	0.000
male	-0.206	2.277	0.928	1.324	2.159	0.540
pctwom	-0.052	0.047	0.275	-0.023	0.050	0.645
numalters	-0.353	0.199	0.077	-0.209	0.227	0.356
rho1.1 or rho2.1	0.277	0.171	0.106	0.026	0.445	0.953

lnam also accommodates models with both autoregressive outcome and network autocorrelation terms

Much larger SE

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