INTRODUCTION TO SOCIAL NETWORK ANALYSIS AND NETWORK SCIENCE METHODS

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James O'Malley, Ph.D.

Department of Biomedical Data Science

The Dartmouth Institute for Health Policy and Clinical Practice

Geisel School of Medicine at Dartmouth

Email: James.OMalley@Dartmouth.edu

Link to Materials Used in Workshop

- Github site with script and physician network data (just binary network) and physician attributes:
  - James Github site to access illustrative network data and code
  - README file
- Note that GRANDPA algorithm can be used to generate random networks for analysis.
  - Carly
  - Yifan
- Can generate a network that emulates a network whose actual relationship and attribute information is not able to be made public

Example network and data: Small physician clinic in the Boston area

- Relational data: QBS122_PhysPract.txt
- Node attribute data: nodecov.dat

- References:
  - Keating et al (2007)
  - O'Malley and Marsden (2008)

Segments of Code for 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: PhysDescriptClass.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(”QBS122_PhysPract.txt",sep="")
- nr <- sqrt(length(reldata)) #Number of physicians
- reldir <- matrix(reldata,ncol=nr,nrow=nr,byrow=T)

#Directed

- reldir <- ifelse(reldata>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")

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(paste(datdir,"nodecov.dat",sep=""))
- 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

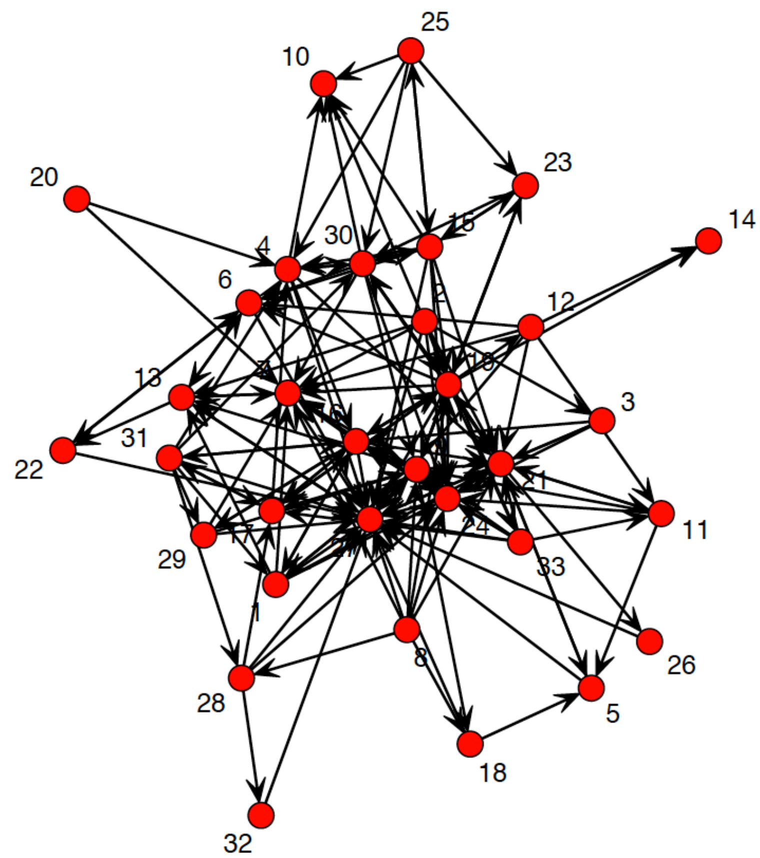
    R: install.packages(”sna”,”igraph”)

    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]))

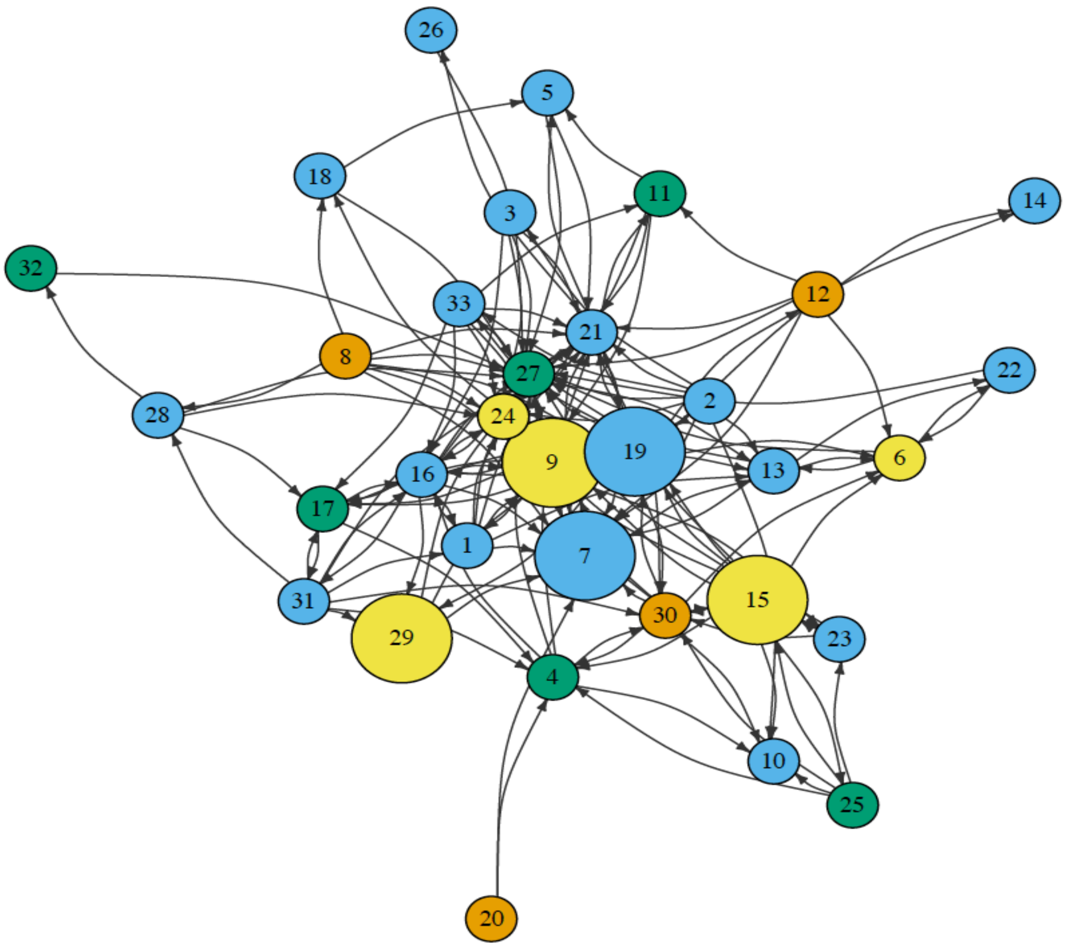
Make graph object from edgelist:

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

Plotting network in igraph

- 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)
- dev.copy2pdf(file=paste(outdir,"PhysNetNicePlot.pdf",sep=""), width=6, height=6) #to file

Visualization of network of physicians' professional relationships within a medical practice



Computing summary measures of networks in R

- Use SNA or igraph
  - Best to detach igraph if want to use SNA as igraph masks functions (has other functions by the same name)
  - 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")

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

Can't be 0!

#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

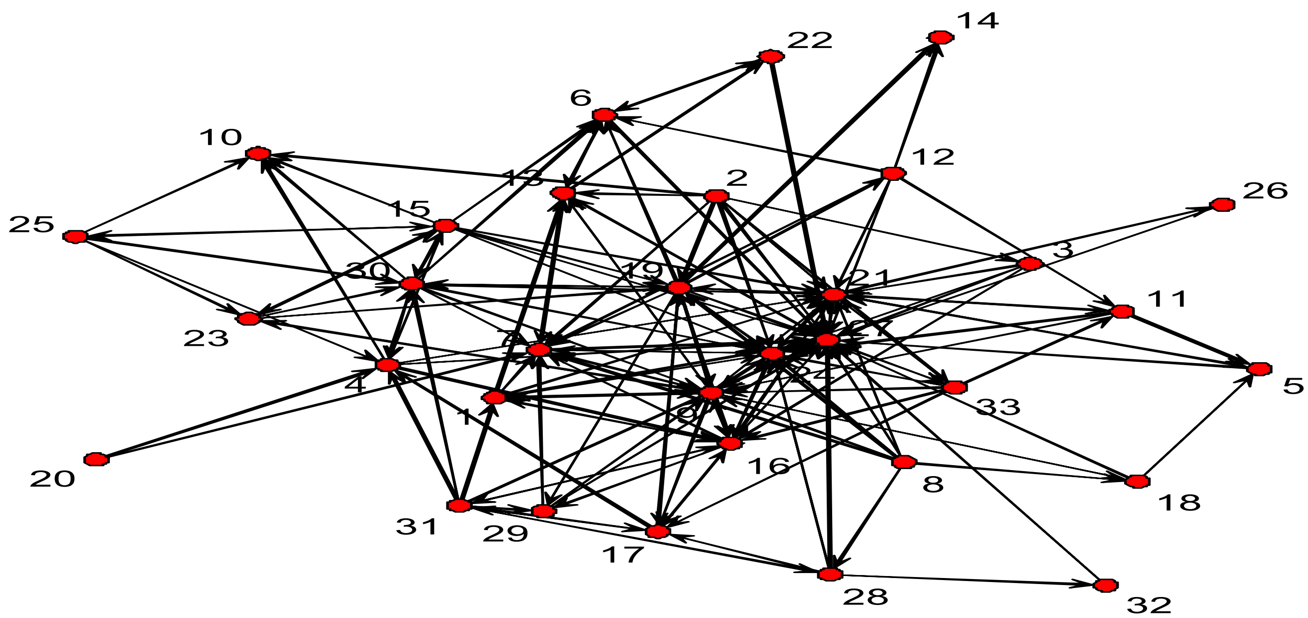
[33] 0.16081688

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
- R script: PhysNetClass.R

Example: Larger model (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?

Larger model cont.

- 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)

Ego (originator) covariate

Homophily covariate

- 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.)

Separate node-match (homophily) coefficients

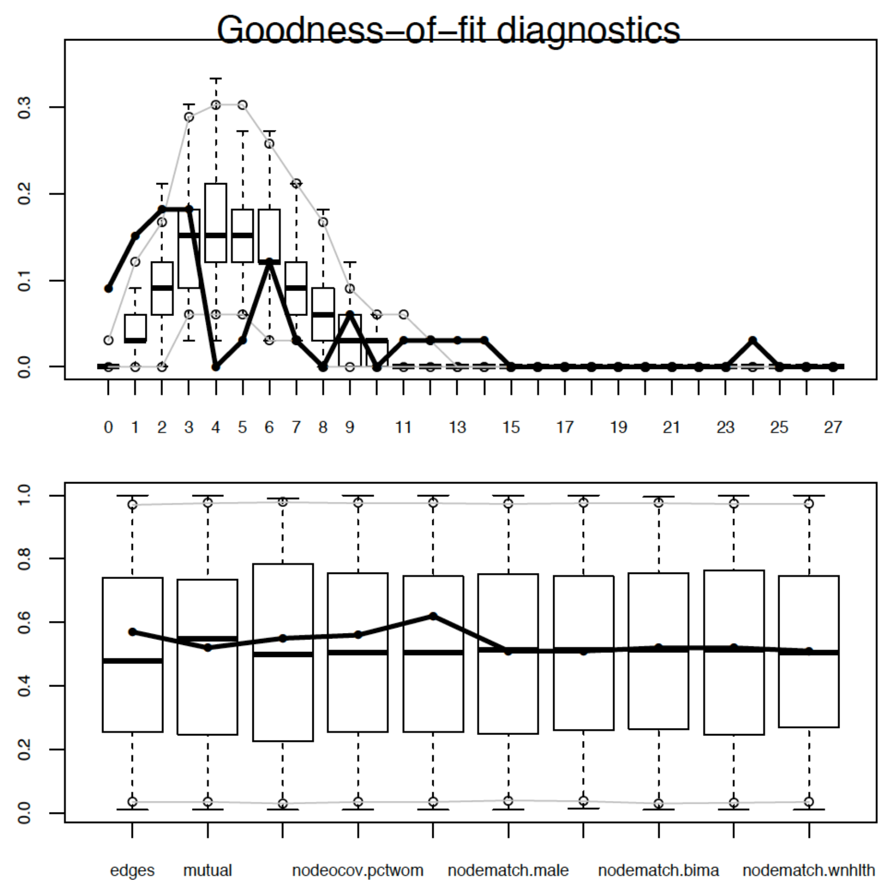
- model1f <- ergm(pnet~edges + mutual + nodeocov("whexpert") +nodeocov("pctwom") + nodeocov("numsess") + nodematch("male",diff=T) + nodematch("practice",diff=T))

Allows nodematch.male coefficient to vary by gender

- 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 ***

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)



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 *****

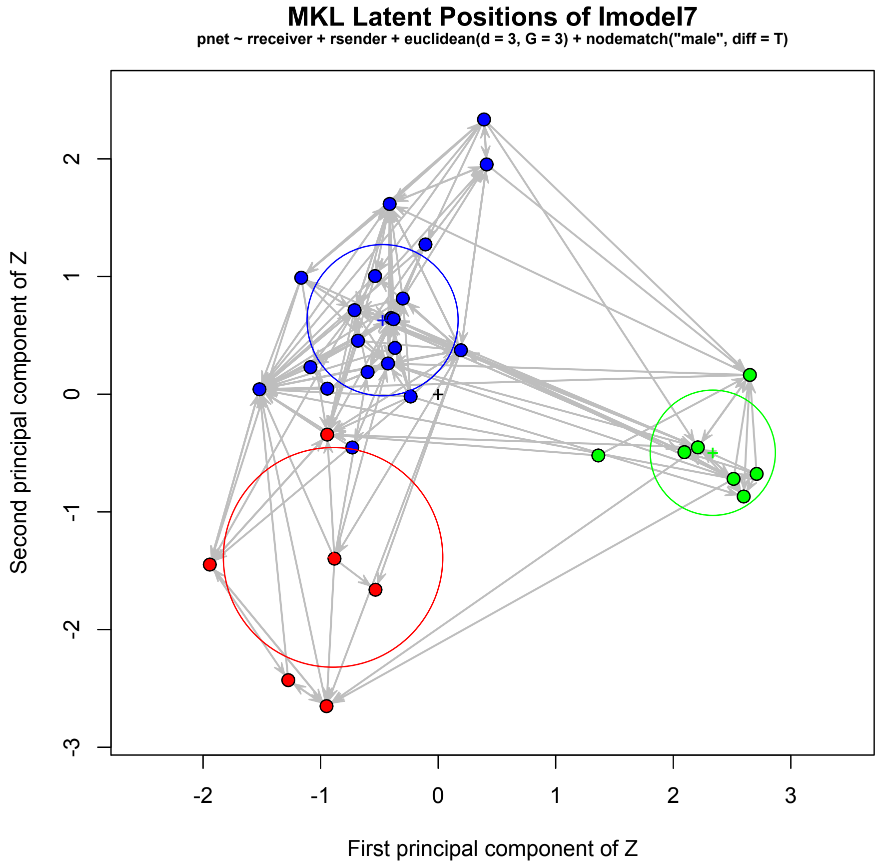
- **ERGM Formula: pnet ~ edges + nodematch("male", diff = F)**
-
- **Iterations: 5 out of 20**
-
- **Monte Carlo MLE Results:**
- **Estimate Std. Error MCMC % p-value**
- **edges -2.1552 0.1437 0 <1e-04 *****
- **nodematch.male 0.7898 0.1794 0 <1e-04 *****

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 (case 2) with $d = 3$ dimensions and 3 clusters (or groups)

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

Obvious application is to clusters actors into groups!



III. Statistical analyses of social influence or peer effects

- Use lnam 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

Autoregressive outcome model estimation in R

- reg.adj <- lm(sumhrt~x+hrtalt-1, data=regdata)
- lnam1.adj <- lnam(regdata$sumhrt,x,wtreldir)

Network autocorrelation model estimation in R

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

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