

Network Analysis with statnet for Individual, Organizational, and International Relations Applications

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Basic resources

R webpage: <http://www.r-project.org>
Helpful **R** tutorials: <http://cran.r-project.org/other-docs.html>
statnet webpage: <http://statnet.org>
statnet help: statnet_help@statnet.org
Workshop web site: <http://polnet2010.ncasd.org/>

Typographical conventions

Text in **Courier bold** represents code for you to type.

Text in **Courier regular** represents comments or **R** output.

All other text represents instructions and guidance.

SECTION 0. GETTING STARTED

** The instructions in Section 0 match those on the workshop web page (<http://polnet2010.ncasd.org/>). If you have already installed the required software, there is no need to do so again. **

0.1. Download and install the latest version of **R**

- a. Go to <http://cran.r-project.org/>, and select Mirrors from the left-hand menu.
- b. Select a location near you.
- c. From the "Download and Install **R**" section, select the link for your operating system.
- d. Follow the instructions on the relevant page.
- e. Note that you need to download only the base distribution, not the contributed packages.
- f. Once you've downloaded the installation file, follow the instructions for installation.

0.2. Download and attaching **statnet** and associated packages:

- a. Open **R**.
- b. Install the **statnet** installer. At the **R** cursor `>`, type:

```
install.packages("statnet")
```

- c. Now, and in the future, you can install/update **statnet** at any point using the installer that comes with **statnet**. Step (b) is only necessary the first time you wish to use **statnet** but does not need to be repeated each time. At the **R** cursor, type:

```
update.statnet()
```

Follow the directions; feel free to say no to any optional packages, although we recommend saying yes. The first choice provided is to install all the required and optional packages.

- d. Attach **statnet** to your **R** session by typing:

```
library(statnet)
```

0.3. Download and install supplemental packages:

- a. We recommend installing some additional, non-**statnet** packages that are employed in selected exercises; you do not have to install these packages to use **statnet** in general, but some specific functions (or other analyses shown here) do expect them. To do so, at the **R** cursor type:

```
install.packages(c("numDeriv", "yacca", "rgl"))
```

Note: **rgl** sometimes has problems installing on specific platforms. If you can't install it, don't worry -- you need it for 3D network visualization, but not for anything else. Consult the **R** web site for more information on these or other contributed packages.

0.4. Set a specific working directory for this tutorial if you wish.

- a. If you are using Windows, go to File > Change Dir and choose the directory.
- b. Otherwise, use the `setwd` directory command:

```
setwd("full.path.for.the.folder")
```

SECTION 1. A BRIEF R TUTORIAL

1.1. A few facts to remember about R

- R mostly runs through the command line or through batch files. However, one can perform basic file management through the menu in the Windows version.
- Everything in R is an object, including data, output, functions—everything.
- Objects that are created during a session are saved in the “global environment” by default, which is stored as a single file (“.RData”) in the working directory.
- R is case sensitive.
- R comes with a set of pre-loaded functions. Others can be added by downloading from the R project website. Downloaded packages to be used must be attached using the *library* command during any R session in which they are to be used.

```
install.packages("coda")      # install package from CRAN
library(coda)                 # attach installed package
```

1.2. Introduction to basic R syntax

```
a <- 3                        # assignment
a                             # evaluation
[1] 3

sqrt(a)                      # perform an operation
b <- sqrt(a)                 # perform operation and save
b

a == a                       # A is A?
a != b                       # A is not B

ls()                          # list objects in global environment
help(sqrt)                   # help w/ functions
?sqrt                        # same thing
help.start()                 # lots of help
help.search("sqrt")          # what am I looking for?
apropos("sqrt")              # it's on the tip of my tongue...

rm(a)                        # remove an object
```

1.3. Vectors and matrices in R

```
# Creating vectors using the concatenation operator
a <- c(1,3,5)                # create a vector by concatenation
a
a[2]                         # select the second element
b <- c("one","three","five") # also works with strings
b
b[2]
a <- c(a,a)                   # can apply recursively
a
a <- c(a,b)                   # mixing types - who will win?
a                             # there can be only one!

# Sequences and replication
a <- seq(from=1,to=5,by=1)    # from 1 to 5 the slow way
b <- 1:5                      # a shortcut!
a==b                          # all TRUE
rep(1,5)                      # a lot of 1s
rep(1:5,2)                    # repeat an entire sequence
```

```

rep(1:5,each=2)           # same, but element-wise
rep(1:5,times=5:1)        # can vary the count of each element

# Any and all (with vectors)
a <- 1:5                   # create a vector
a>2                       # some TRUE, some FALSE
any(a>2)                  # are any elements TRUE?
all(a>2)                  # are all elements TRUE?

# From vectors to matrices
a <- matrix(1:25, nr=5, nc=5) # create a matrix the "formal" way
a                           # select a matrix element (two dimensions)
a[1,2]                     # shortcut for ith row
a[1,]                      # show the equivalence
a[,2]                      # can also perform for columns
a[2:3,3:5]                # select submatrices
a[-1,]                    # nice trick: negative numbers omit cells!
a[-2,-2]                  # get rid of number two

b <- cbind(1:5,1:5)        # another way to create matrices
b                           # can perform with rows, too
d <- rbind(1:5,1:5)
d                           # no go: must have compatible dimensions!
cbind(b,d)                 # what were those dimensions, anyway?
dim(b)
dim(d)
NROW(b)
NCOL(b)
cbind(b,b)                # here's a better example

t(b)                       # can transpose b
cbind(t(b),d)              # now it works

```

1.4. Elementwise operations

```

# Most arithmetic operators are applied elementwise
a <- 1:5
a + 1                      # addition
a * 2                      # multiplication
a / 3                      # division
a - 4                      # subtraction
a ^ 5                      # you get the idea...

a + a                      # also works on pairs of vectors
a * a
a %% a                     # note, not elementwise!
a + 1:6                   # problem: need same length

a <- rbind(1:5,2:6)        # same principles apply to matrices
b <- rbind(3:7,4:8)
a + b
a / b

a %% t(b)                  # matrix multiplication

# Logical operators (generally) work like arithmetic ones
a > 0
a == b
a != b
!(a == b)
(a>2) | (b>4)
(a>2) & (b>4)
(a>2) || (b>4)             # beware the "double-pipe"!
(a>2) && (b>4)             # (and the "double-ampersand"!)

# Ditto for many other basic transformations
log(a)
exp(b)

```

```

sqrt(a+b)                                # note that we can nest statements!
log((sqrt(a+b)+a)*b)                     # as recursive as we wanna be

```

1.5 Lists, data frames, and arrays

```

# R has many other data types. One important type is the list.
a <- list(1:5)
a                                           # not an ordinary vector...
a <- list(1:5, letters[1:3])               # can we mix types and lengths?
a                                           # yes!
b <- matrix(1:3, 3, 3)
a <- list(1:5, letters[1:3], b)            # anything can be stuffed in here
a
a[[1]]                                     # retrieve the first item
a[[2]][3]                                 # the letter "c"
(a[[3]])[1, 3]                            # it's really just recursion again
a <- list(boo=1:4, hoo=5)                  # list elements are often named
names(a)                                  # get the element names
a[["boo"]]                                # ask for it by name
a$hoo                                     # use "$" to get what you want
a+3                                       # whoops - not a vector!
a[[1]]+3                                  # that works
a[[2]] <- a[[2]]*4                        # can also perform assignment
a$woo <- "glorp"                          # works with "$"
a[["foo"]] <- "shazam"                   # prolonging the magic
a

# Another useful generalization: the data frame
d <- data.frame(income=1:5, sane=c(T, T, T, T, F), name=LETTERS[1:5]) # Store multiple types
d
d[1, 2]                                  # acts a lot like a matrix!
d[, 1]*5
d[-1, ]
names(d)                                 # also acts like a list
d[[2]]
d$sane[3] <- FALSE
d
d[2, 3]                                  # hmm - our data got factorized!
d$name <- LETTERS[1:5]                   # eliminate evil factors by overwriting
d[2, 3]
d <- data.frame(income=1:5, sane=c(T, T, T, T, F), name=LETTERS[1:5], stringsAsFactors=FALSE)
d                                         # another way to fix it

d <- as.data.frame(cbind(1:5, 2:6))      # can create from matrices
d
is.data.frame(d)                         # how can we tell it's not a matrix?
is.matrix(d)                             # the truth comes out

# When two dimensions are not enough: arrays
a <- array(1:18, dim=c(2, 3, 3))         # now in 3D
a
a[1, 2, 3]                               # selection works like a matrix
a[1, 2, ]
a[1, , ]
a[-1, 2:3, 1:2]
a*5                                       # ditto for elementwise operations
a <- array(dim=c(2, 3, 2, 5, 6))         # can have any number of dimensions
dim(a)                                    # find out what we've allocated

```

1.6. Finding built-in data sets

```

# Many packages have built-in data for testing and educational purposes
data()                                    # list them all
data(package="base")                     # all base package
?USArrests                               # get help on a data set
data(USArrests)                          # load the data set

```

USArrests

view the object

1.7. Elementary visualization

```
# R's workhorse is the "plot" command
plot(USArrests$Murder,USArrests$UrbanPop)
plot(USArrests$Murder,USArrests$UrbanPop,log="xy")    # log-log scale
plot(USArrests$Murder,USArrests$Assault,xlab="Murder",ylab="Assault",main="My Plot")

# Can also add text
plot(USArrests$Murder,USArrests$Assault,xlab="Murder",ylab="Assault",main="My Plot",type="n")
text(USArrests$Murder,USArrests$Assault,rownames(USArrests))

# Histograms and boxplots are often helpful
hist(USArrests$Murder)
boxplot(USArrests)
```

1.8. Reading in data (and writing to disk)

We won't use them right now, but here are some useful commands:

?read.table	# a workhorse routine
?read.csv	# a specialized CSV version
?scan	# a more low-level variant
apropos("read")	# list various "read" commands
?load	# loads objects in native R format
?save	# saves objects in native R format
?write.table	# counterpart to read.table
apropos("write")	# various "write" functions

Remember that you can use the File menu to save your current global environment, change
working directory, exit, etc.

SECTION 2: NETWORK OBJECTS: IMPORT, EXPLORATION, MANIPULATION

2.1 Built-in Datasets

```
data(package="network")      # List available datasets in network
library(network)             # Make sure that network is loaded
data(flo)                    # Load a built-in data set; see ?flo for more
flo                           # Examine the flo adjacency matrix

#For more information....
?data
?flo
```

2.2 Importing Relational Data

```
# Be sure to be in the directory where you stored the data for the workshop
dir()                         # Check what's in the working directory
#chwd("My File Location")    # Use if you need to change the working directory

#Read an adjacency matrix
floadj <- read.table("floadj.txt",header=TRUE)
floadj                        # Examine the matrix

#Read a Pajek file
flopaj <- read.paj("flo.paj")

names(flopaj)                 # This is a project file, with networks and other data
names(flopaj$networks)       # See which networks are in the file
nflo2 <- flopaj$networks[[1]] # Extract the marriage data
nflo2                         # Examine the network object

#For more information....
?names
?read.paj
?read.table
```

2.3 Creating network Objects

```
nflo <- network(flo, directed=FALSE) # Create a network object based on flo
nflo                                # Get a quick description of the data
nempty <- network.initialize(5)      # Create an empty graph with 5 vertices
nempty                              # Compare with nflo

#For more information....
?network
?as.network.matrix
```

2.4 Description and Visualization

```
summary(nflo)                  # Get an overall summary
print(nflo)                    # Simple print method
network.dyadcount(nflo)        # How many dyads in nflo?
network.edgcount(nflo)         # How many edges are present?
network.size(nflo)             # How large is the network?
as.sociomatrix(nflo)           # Show it as a sociomatrix
nflo[,]                        # Another way to do it

plot(nflo,displaylabels=T,boxed.labels=F) # Plot with names
plot(nflo,displaylabels=T,mode="circle")  # A less useful layout....
library(sna)                   # Load the sna library
gplot(nflo)                    # Requires sna

#For more information
?summary.network
```

```
?network.dyadcount
?network.edgecount
?as.sociomatrix
?as.matrix.network
?is.directed
?plot.network
```

2.5 Working With Edges

```
#Adding edges
g <- network.initialize(5)
g[1,2] <- 1
g[2,] <- 1
g
m <- matrix(0, nrow=5, ncol=5)
m[3,4:5] <- 1
g[m>0] <- 1
g

#Delete edges
g[3,5] <- 0
g
g[,] <- 0
g

#Testing adjacency
nflo[9,3]
nflo[9,]
nflo[1:4,5:8]
nflo[-9,-9]

#Setting edge values
m <- matrix(1:16^2, nrow=16, ncol=16)
nflo %e% "boo" <- m

#Retrieving edge values
list.edge.attributes(nflo)
nflo %e% "boo"
as.sociomatrix(nflo, attrname="boo")

#For more information....
?network.extraction
?add.edge
?delete.edges
?delete.vertices
?get.edges
```

```
# Create an empty graph
# Add an edge from 1 to 2
# Add edges from 2 to everyone else
# Examine the result
# Create an adjacency matrix
# Add entries from 3 to 4 and 5
# Add more entries

# Remove the edge from 3 to 5
# It's gone!
# Remove all edges
# Now, an empty graph

# Medici to Barbadori?
# Entire Medici row
# Subsets are possible
# Negative numbers _exclude_ nodes

# Create a matrix of edge "values"
# Value the marriage ties

# See what's available
# Use the %e% operator
# Can also do it this way
```

2.6 Network and Vertex Attributes

```
#Add some attributes
nflo %v% "woo" <- letters[1:16]
nflo %n% "zoo" <- "R is TanFastic!"

#Listing attributes
list.vertex.attributes(nflo)
list.network.attributes(nflo)

#Retrieving attributes
nflo %v% "woo"
nflo %n% "zoo"

#For more information
?attribute.methods
```

```
# Letter the families
# A key network-level covariate

# List all vertex attributes
# List all network attributes

# Retrieve the vertex attribute
# Retrieve the network attribute
```


SECTION 3: CLASSICAL NETWORK ANALYSIS WITH SNA

3.1 Getting started

```
library(sna)           # Load the sna library
help.start()           # If not done already...walk through the various sna pages
library(help="sna")    # See also this for a list
load("polnet2010.Rdata") # Load supplemental workshop data

#For more information....
?help.start
?library
?sna
```

3.2 Network data in sna

```
# sna can handle network data in many forms.  For instance, the function gden calculates
# network density; we can use it on a network object, an adjacency matrix, a list of
# such matrices, etc.
data(flo)
flo           # Adjacency form
gden(flo)
nflo<-network(flo,directed=FALSE) # Network form
gden(nflo)
gden(list(flo,nflo))              # Lists of matrices/networks
aflo<-array(dim=c(2,NROW(flo),NROW(flo))) # Array form
aflo[1,,]<-flo
aflo[2,,]<-flo
gden(aflo)
gden(list(flo,aflo,nflo))        # Yet more lists

# sna also supports a special kind of matrix called an "sna edgelist."  These are three-
# column matrices, each row of which represents an edge (via its sender, recipient, and
# value, respectively).  sna edgelists have special attributes that indicate their
# size, vertex names (if any), and bipartite status (if applicable).
eflo<-as.edgelist.sna(flo)       # Coerce flo to an sna edgelist
eflo
attr(eflo,"n")                  # How many vertices are there?
attr(eflo,"vnames")             # Are there vertex names?
attr(eflo,"n")<-30              # Could add isolates....
as.sociomatrix.sna(eflo)        # Can transform back w/as.sociomatrix.sna

# sna edgelists can be handy with large data sets (as a simple alternative to network
# objects).  To make one, just add an "n" attribute to a valid three-column matrix!
mat<-cbind(rep(2,4),3:6,rep(1,4)) # Create edges from 2 to 3:6
attr(mat,"n")<-6                 # Set total number of vertices to 6
mat
gden(mat)                       # Can now pass to sna routines
as.sociomatrix.sna(mat)         # Can see in adjacency form

# For more information....
?as.edgelist.sna
?as.sociomatrix.sna
?attr
?sna
```

3.2 Network visualization with gplot

```
# Begin by plotting contiguity among nations in 1993 (from the Correlates of War project)
gplot(contig_1993)              # The default visualization
gplot(contig_1993, usearrows=FALSE) # Turn off arrows manually
gplot(contig_1993, gmode="graph") # Can also tell gplot the data is undirected

# We can add labels to the vertices - network.vertex.names reports them
gplot(contig_1993, gmode="graph",
```

```

label=network.vertex.names(contig_1993))

# This plot is too large/dense for the default settings to work. Let's refine them.
gplot(contig_1993, gmode="graph", label.cex=0.5, label.col=4,
      label=network.vertex.names(contig_1993))      # Shrink labels and recolor

# Here's an example of directed data - militarized interstate disputes (MIDs) for 1993
gplot(mids_1993, label.cex=0.5, label.col=4,
      label=network.vertex.names(mids_1993))      # Basic display, with labels

# All those isolates can get in the way - we can suppress them using displayisolates
gplot(mids_1993, displayisolates=FALSE, label.cex=0.5, label.col=4,
      label=network.vertex.names(mids_1993))

# The default layout algorithm is that of Fruchterman-Reingold (1991), can use others
gplot(mids_1993, displayisolates=FALSE, label.cex=0.5, label.col=4,
      label=network.vertex.names(mids_1993), mode="circle") # The infamous circle
gplot(mids_1993, displayisolates=FALSE, label.cex=0.5, label.col=4,
      label=network.vertex.names(mids_1993), mode="mds")      # MDS of position similarity

# When a layout is generated, the results can be saved for later reuse:
coords <- gplot(contig_1993)      # Capture the magic of the moment
coords      # Show the vertex coordinates

# Saved (or a priori) layouts can be used via the coord argument:
gplot(mids_1993, label.cex=0.5, label.col=4, coord=coords,
      label=network.vertex.names(mids_1993))      # Relive the magic

# When the default settings are insufficient, interactive mode allows for tweaking
coords <- gplot(contig_1993, interactive=TRUE) # Modify and save
gplot(contig_1993, coord=coords, gmode="graph") # Should reproduce the modified layout

# For more information....
?gplot
?gplot.layout

```

3.3 Three-dimensional visualization with gplot3d (requires the rgl package)

```

gplot3d(contig_1993, label=network.vertex.names(contig_1993)) # Experience the future!
# Other layouts are possible here, too:
gplot3d(contig_1993, label=network.vertex.names(contig_1993), mode="kamadakawai")

# For more information....
?gplot3d
?gplot3d.layout

```

3.4 Basic centrality indices: degree, betweenness, and closeness

```

# We begin with the simplest case: degree
degree(mids_1993)      # Default: total degree
ideg <- degree(mids_1993, cmode="indegree")      # Indegree for MIDs
odeg <- degree(mids_1993, cmode="outdegree")      # Outdegree for MIDs
all(degree(mids_1993) == ideg+odeg)      # In + out = total?

# Once centrality scores are computed, we can handle them using standard R methods:
plot(ideg, odeg, type="n", xlab="Incoming MIDs", ylab="Outgoing MIDs") # Plot ideg by odeg
abline(0, 1, lty=3)
text(jitter(ideg), jitter(odeg), network.vertex.names(contig_1993), cex=0.75, col=2)
# Plot simple histograms of the degree distribution:
par(mfrow=c(2,2))      # Set up a 2x2 display
hist(ideg, xlab="Indegree", main="Indegree Distribution", prob=TRUE)
hist(odeg, xlab="Outdegree", main="Outdegree Distribution", prob=TRUE)
hist(ideg+odeg, xlab="Total Degree", main="Total Degree Distribution", prob=TRUE)
par(mfrow=c(1,1))      # Restore display

```

```
# Centrality scores can also be used with other sna routines, e.g., gplot
gplot(mids_1993, vertex.cex=(ideg+odeg)^0.5/2, vertex.sides=50,
      label.cex=0.4, vertex.col=rgb(odeg/max(odeg),0,ideg/max(ideg)),
      label=network.vertex.names(mids_1993))

# Betweenness and closeness are also popular measures
bet <- betweenness(contig_1993, gmode="graph") # Geographic betweenness
bet
gplot(contig_1993, vertex.cex=sqrt(bet)/25, gmode="graph") # Use w/gplot
clo <- closeness(contig_1993) # Geographic closeness
clo # A large world after all?

# Can use sna routines to explore alternatives to the common measures....
closeness2 <- function(x){ # Create an alternate closeness function!
  geo <- 1/geodist(x)$gdist # Get the matrix of 1/geodesic distance
  diag(geo) <- 0 # Define self-ties as 0
  apply(geo, 1, sum) # Return sum(1/geodist) for each vertex
}
clo2 <- closeness2(contig_1993) # Use our new function on contiguity data
hist(clo2, xlab="Alt. Closeness", prob=TRUE) # Much better behaved!
cor(clo2, bet) # Correlate with betweenness
plot(clo2, bet) # Plot the bivariate relationship
all(clo2/185==closeness(contig_1993, cmode="suminvundir")) # Actually, we support this in sna!

#For more information....
?betweenness
?bonpow
?closeness
?degree
?evcent
?graphcent
?infocent
?prestige
?stresscent
```

3.5 From centrality to centralization

```
centralization(mids_1993, degree, cmode="indegree") # Do MIDs concentrate?
centralization(contig_1993, evcent) # Eigenvector centralization

#For more information....
?centralization
```

3.6 Elementary graph-level indices

```
gden(mids_1993) # Density
grecip(mids_1993) # Dyadic reciprocity
grecip(mids_1993, measure="edgewise") # Edgewise reciprocity
grecip(mids_1993, measure="edgewise.lrr") # Reciprocation LRR
gtrans(mids_1993) # Transitivity
log(gtrans(mids_1993)/gden(mids_1993)) # Transitive completion LLR

#For more information....
?gden
?grecip
?gtrans
?hierarchy
```

3.7 Subgraph census routines

```
dyad.census(mids_1993) # M,A,N counts
```

```

dyad.census(contig_1993) # No As in undirected graphs
triad.census(mids_1993) # Directed triad census
triad.census(contig_1993, mode="graph") # Undirected triad census
kpath.census(mids_1993, maxlen=6, tabulate.by.vertex=FALSE) # Count paths of length <=6
kcycle.census(mids_1993, maxlen=6, tabulate.by.vertex=FALSE) # Count cycles of length <=6
clique.census(mids_1993, tabulate.by.vertex=FALSE, enumerate=FALSE) # Find maximal cliques

#Can also look at more detailed tabulation/comembership for paths/cycles/cliques
kpath.census(mids_1993, maxlen=4) # Show tabulation by vertex
indirect <- kpath.census(mids_1993, maxlen=6, dyadic.tabulation="sum")$paths.bydyad
gplot(indirect, label.cex=0.4, vertex.cex=0.75, label=network.vertex.names(mids_1993))
# Plot indirect MIDs

#Component information can be obtained in various ways
components(mids_1993) # Strong component count
components(mids_1993, connected="weak") # Weak component count
cd <- component.dist(mids_1993, connected="weak") # Get weak components
cd
plot(1:length(cd$cdist), cd$cdist, xlab="Size", ylab="Frequency") # Component sizes
cl <- component.largest(mids_1993, connected="weak") # Who's in the largest component?
cl
gplot(mids_1993[cl,cl], boxed.lab=FALSE, label.cex=0.5, label.col=4,
      label=network.vertex.names(mids_1993)[cl]) # Plot the largest weak component

#Likewise, many routines exist for handling isolates
is.isolate(mids_1993, 3) # Is the third vertex (BHM) an isolate?
is.isolate(mids_1993, "BHM") # The peaceful islands?
is.isolate(mids_1993, "USA") # Perhaps less so....
isol <- isolates(mids_1993) # Get the entire list of isolates
isol
network.vertex.names(mids_1993)[isol] # Which countries are isolates?
gplot(mids_1993[-isol,-isol], label.cex=0.5, label.col=4,
      label=network.vertex.names(mids_1993)[-isol]) # Another way to remove isolates

#For more information....
?clique.census
?components
?component.dist
?dyad.census
?is.isolate
?isolates
?kcycle.census
?kpath.census
?triad.census

```

3.8 Elementary random graph generation

```

rgraph(10) # A uniform random digraph of order 10
rgraph(10, tp=3/9) # Homogeneous Bernoulli w/mean degree 3
rgraph(10, tp=3/9, mode="graph") # As above, but undirected
rgnm(1, 10, 20) # Uniform conditional on order, edges
rguman(1, 10, mut=0.5, asym=0.25, null=0.25) # Homogeneous multinomial on dyad census
rguman(1, 10, mut=0, asym=1, null=0) # An extreme case: random tournament
gplot3d(rgws(1,50,1,2,0)) # A Watts-Strogatz process - baseline
gplot3d(rgws(1,50,1,2,0.05)) # ...with rewiring probability 0.05
gplot3d(rgws(1,50,1,2,0.2)) # ...with rewiring probability 0.2

#For more information....
?rgbn
?rgmn
?rgraph
?rguman
?rgws

```

3.9 Basic connectivity/distance measurement, and cohesion

```
g <- rgraph(20, tp=3/19)           # Start with a random digraph
g
is.connected(g)                   # Is g strongly connected?
is.connected(g, connected="weak") # How about weakly connected?
geodist(g)                        # Get information on geodesics
reachability(g)                  # Return the reachability matrix
symmetrize(g)                    # Symmetrize g using the "or" rule
symmetrize(g, rule="strong")     # Symmetrize g using the "and" rule

#Several ways to get relatively cohesive groups
clique.census(g)                 # Maximal clique census
kcores(g)                       # k-cores (by degree)
bicomponent.dist(g)              # bicomponent properties
cutpoints(g)                     # find articulation points

#Showing cohesion information can aid visualization
gplot(contig_1993,vertex.col=2+cutpoints(contig_1993,mode="graph", # Show critical positions
  return.indicator=T))
kc<-kcores(contig_1993,cmode="indegree")                             # Show core nesting
gplot(contig_1993,vertex.col=rainbow(max(kc)+1)[kc+1])
gplot(contig_1993[kc>4,kc>4],vertex.col=rainbow(max(kc)+1)[kc[kc>4]+1]) # 5-core only

#For more information....
?bicomponent.dist
?cutpoints
?geodist
?kcores
?is.connected
?reachability
?symmetrize
```

3.10 Positional analysis

```
# Generate a structural equivalence clustering of the CoW alliance data
gplot(alliances_1993, gmode="graph", vertex.cex=0.5)           #An initial look...
ec <- equiv.clust(alliances_1993, mode="graph", plabels=network.vertex.names(alliances_1993))
ec                                                             # The clustering
plot(ec)                                                       # Plot the dendrogram
rect.hclust(ec$cluster, h=20)

# Use the clustering to form an SE blockmodel
bm <- blockmodel(alliances_1993, ec, h=20)
bm
#We can display the blockmodel in several ways....
plot.sociomatrix(alliances_1993[bm$order.vector,bm$order.vector], drawlab=FALSE)
bimage <- bm$block.model                                       # Extract the block image
bimage
bimage[is.nan(bimage)] <- 1
gplot(bimage, diag=TRUE, edge.lwd=bimage*5, vertex.cex=sqrt(table(bm$block.membership))/2,
  gmode="graph", vertex.sides=50, vertex.col=gray(1-diag(bimage))) # Positional relations
```

SECTION 4. NODE LEVEL INDICES, NETWORK COVARIATES, AND NETWORK REGRESSION

4.1 Getting Started

```
library(network)                #Load network if needed
data(emon)                      #Load Drabek et al. data

#Extract ties from the Cheyenne EMON communicating at least "every few hours"
g<-as.sociomatrix(emon[[1]],"Frequency")    #Need to get the frequency info
g<-symmetrize((g>0) & (g<4))                #Note the reverse coding!
```

4.2 Initial Analysis

```
#Get some potential covariates
drs<-emon[[1]]%v%"Decision.Rank.Score"      #Get decision rank (see man page)
crs<-emon[[1]]%v%"Command.Rank.Score"       #Get command rank

#Calculate some basic centrality measures
deg<-degree(g,gmode="graph")
bet<-betweenness(g,gmode="graph")
clo<-closeness(g,gmode="graph")

#Raw correlations
cor(cbind(deg,bet,clo),cbind(drs,crs))

#Classical tests (using asymptotic t distribution)
cor.test(deg,drs)
cor.test(bet,drs)
cor.test(clo,drs)
```

4.3 Testing correlations

```
#Permutation tests
perm.cor.test<-function(x,y,niter=5000){ #Define a simple test function
  c.obs<-cor(x,y,use="complete.obs")
  c.rep<-vector()
  for(i in 1:niter)
    c.rep[i]<-cor(x,sample(y),use="complete.obs")
  cat("Vector Permutation Test:\n\tObserved correlation: ",c.obs,"\tReplicate quantiles
(niter=",niter,")\n",sep="")
  cat("\t\tPr(rho>=obs):",mean(c.rep>=c.obs),"\n")
  cat("\t\tPr(rho<=obs):",mean(c.rep<=c.obs),"\n")
  cat("\t\tPr(|rho|>=|obs|):",mean(abs(c.rep)>=abs(c.obs)), "\n")
  invisible(list(obs=c.obs,rep=c.rep))
}
perm.cor.test(deg,drs)                #Non-parametric tests of correlation
perm.cor.test(bet,drs)
perm.cor.test(clo,drs)

#For more information....
?emon
?cor.test
?t.test
?sample
```

4.4 Using NLLs as regression covariates

```
pstaff<-emon[[1]]%v%"Paid.Staff" # Get more EMON covariates
vstaff<-emon[[1]]%v%"Volunteer.Staff"
govt<- (emon[[1]]%v%"Sponsorship")!="Private")

#Very simple model: decision rank is linear in size, degree, and govt status
mod<-lm(drs~deg+pstaff+vstaff+govt)
summary(mod)
anova(mod) #Some useful lm tools
AIC(mod)

#Try with alternative measures....
mod2<-lm(drs~bet+pstaff+vstaff+govt) #Betweenness
summary(mod2)
mod3<-lm(drs~clo+pstaff+vstaff+govt) #Closeness
summary(mod3)
AIC(mod,mod2,mod3) #Closeness wins!

#For more information....
?lm
?anova
?AIC
```

4.5 Graph correlation and bivariate QAP

```
# Remember the Florentine families data
data(florentine)
plot(flobusiness) # Examine business ties
plot(flomarriage) # Examine marriage ties

# Could the two be related? Let's try a graph correlation
gcor(flobusiness,flomarriage)

# To test the correlation, we can use the qaptest routine
qt<-qaptest(list(flobusiness,flomarriage),gcor,g1=1,g2=2)
summary(qt) # Examine the results
plot(qt) # Plot the QAP distribution

# Testing against covariate effects
wealth<-sapply(flomarriage%v%"wealth",rep,network.size(flomarriage))
wealthdiff<-abs(outer(flomarriage%v%"wealth",flomarriage%v%"wealth",-"))
qt1<-qaptest(list(flomarriage,wealth),gcor,g1=1,g2=2)
qt2<-qaptest(list(flomarriage,wealthdiff),gcor,g1=1,g2=2)
summary(qt1) # Do wealthy families have more ties?
summary(qt2) # Is there a wealth difference effect?

# For more information....
?qaptest
?gcor
?outer
?sapply
?rep
```

4.6 Network regression

```
# We begin by preparing the response variable. We will use the Cheyenne
# EMON in valued form, but need to recode the frequency data
data(emon)
Y<-as.sociomatrix(emon[[1]], "Frequency") # Extract frequencies
Y[Y>0]<-5-Y[Y>0] # Now, higher -> more frequent

# Extract some vertex attributes
crk<-emon[[1]]%v%"Command.Rank.Score" # Command rank
spon<-emon[[1]]%v%"Sponsorship" # Type of organization
```

```

# Form some predictor matrices (X variables)
Xcr<-sapply(crk,rep,length(crk))
Xcr
Xsp<-outer(spon,spon,"!=")
Xsp

# Column effects for command rank
# Dyadic effect for type difference

# Fit the model (takes a while to perform QAP test)
cmfit<-netlm(Y,list(Xcr,Xsp))
summary(cmfit)
# Examine the results

# For more information....
?outer
?netlm

```

SECTION 5. GRAPH LEVEL INDICES AND CONDITIONAL UNIFORM GRAPH TESTS

5.1 Permutation tests for GLI/graph-level covariate association

```
# Here we consider the famous Sampson monastery data:
par(mfrow=c(4,3),mar=c(2,1,4,1))
for(i in 1:length(sampson))
  gplot(sampson[[i]],displaylabel=TRUE,boxed.label=FALSE,main=names(sampson)[i])
dev.off() # Only enter this when done

# Are positive relations more reciprocal (relative to density) than negative
# ones? Let's try a simple permutation test:
r4<-grecip(sampson,measure="edgewise.lrr")
ispos<-c(TRUE,FALSE,TRUE,FALSE,TRUE,TRUE,TRUE,FALSE,TRUE,FALSE)
obs<-sum(r4[ispos])-sum(r4[!ispos])
reps<-vector()
for(i in 1:1e4){
  temp<-sample(ispos)
  reps[i]<-sum(r4[temp])-sum(r4[!temp])
}
mean(reps>=obs) # Upper tail p-value
mean(abs(reps)>=abs(obs)) # Two-sided version
hist(reps)
abline(v=obs,col=2,lwd=3) # Visualize it

# We can look at transitivity as well. How does transitivity compare to density? (Log-odds
# method)
log(gtrans(sampson)/gden(sampson))

# Are positive relations more transitive (relative to density) than negative
# ones? Let's try another vector permutation test:
ltr<-log(gtrans(sampson)/gden(sampson))
obs<-sum(ltr[ispos])-sum(ltr[!ispos])
reps<-vector()
for(i in 1:1e4){
  temp<-sample(ispos)
  reps[i]<-sum(ltr[temp])-sum(ltr[!temp])
}
mean(reps>=obs) # Upper tail p-value
mean(abs(reps)>=abs(obs)) # Two-sided version
hist(reps)
abline(v=obs,col=2,lwd=3) # Visualize it
```

5.2 Comparing graphs via the triad census

```
# Let's get the triad census for each network
tc<-triad.census(sampson)
tc

# Cool trick: two-way correspondence analysis of graphs and their triad census
# scores (aka a "Faust diagram"). Networks here appear close to the triad
# types they contain at excess frequency (distances are chi-squared based;
# see references in ?corresp for more detail).
library(MASS) # Requires the MASS package
plot(corresp(tc,nf=2)) # Plot network/triad association

# What if this data were symmetric? We can symmetrize to illustrate.
tc<-triad.census(symmetrize(sampson),mode="graph") #Need to use mode="graph" here
rownames(tc)<-names(sampson)
plot(corresp(tc,nf=2)) # Plot undirected network/triad association

# For more information....
?gtrans
?triad.census
?corresp
?symmetrize
```

5.3 Simple univariate conditional uniform graph tests

```
# The cug.test function provides a simple interface for univariate CUG tests.
# Let's try testing some data on trade in complex manufactured goods to see if overall
# activity (density) is greater than would be expected from size alone.
cug.test(ctrade,gden)          # Call cug.test with the gden (density) function

# Is there more reciprocity than density would suggest? Let's see.
cug.test(ctrade,grecip,cmode="edges")    # Conditioning on edges, calling grecip

# Given biases in density and reciprocity, we might look to see if there is a
# bias in transitivity, too. This time, let's condition on all of the above.
cug.test(ctrade,gtrans,cmode="dyad")      # Conditioning on dyad census

# We are not limited to simple commands. Let's try indegree centralization:
ct<-cug.test(ctrade,centralization,cmode="dyad",FUN.arg=list(FUN=degree,
  cmode="indegree")) # Note that we here must pass not only arguments to
                        # cug.test, but also to centralization and degree!

ct                                     # Print the result
plot(ct)                             # Can also plot it!
```

SECTION 6. MULTIVARIATE ANALYSIS OF GRAPH SETS

6.1 Distance based methods: clustering and scaling

```
# Start by calculating Hamming distances for the Sampson data
samphd<-hdist(sampson)
samphd

# Now, try an MDS solution
sampmds<-cmdscale(samphd)
sampmds
plot(sampmds,type="n") # Plot the results
text(sampmds,label=names(sampson))

# MDS suggests a three-cluster solution; let's try hclust
samphc<-hclust(as.dist(samphd))
plot(samphc,labels=names(sampson)) # Very clear solution
rect.hclust(samphc,k=3)

# Examine central graphs for each cluster
sampcg<-gclust.centralgraph(samphc,k=3,sampson)
par(mfrow=c(2,2))
gplot(sampcg[1,,],main="Positive CG")
gplot(sampcg[2,,],main="Negative CG")
gplot(sampcg[3,,],main="Liking CG")
par(mfrow=c(1,1))

# More fun - can plot stats by cluster!
gclust.boxstats(samphc,k=3,grecip(sampson,measure="edgewise.lrr"), names=c("Positive",
  "Negative","Liking"), main="Edgewise LRR Reciprocity by Relational Type")
gclust.boxstats(samphc,k=3,gtrans(sampson), names=c("Positive","Negative","Liking"),
  main="Transitivity by Relational Type")

# Can also plot stats by MDS
gdist.plotstats(samphd,cbind(grecip(sampson,measure="edgewise.lrr"),
  gtrans(sampson),centralization(sampson,degree,cmode="indegree")))
legend("bottom",legend=c("Reciprocity","Transitivity","Indegree Cent."),col=1:3,lty=1)

# For more information....
?hdist
?cmdscale
?hclust
?rect.hclust
?gclust.centralgraph
?gdist.plotstats
```

6.2 Network PCA

```
# To begin, let's get the graph correlation matrix for the Sampson nets

sampcor<-gcor(sampson)
sampcor

# Now, we compute the eigendecomposition (could also have used gcov above)
sampeig<-eigen(sampcor)

# Eigenvalues contain variance explained, to whit:
evals<-sampeig$value # Extract eigenvalues
evals/sum(evals) # Variance explained
# Show this as a scree plot
barplot(evals/sum(evals),names.arg=1:length(evals))

# Examine loadings (eigenvectors); looks like first 3 are key
load<-sampeig$vector[,1:3]
rownames(load)<-names(sampson)
load
```

```

# Can rotate using varimax
varimax(load)

# Try plotting the first two components
plot(load[,1:2],type="n",asp=1,xlab="PC 1",ylab="PC 2")
abline(h=0,v=0,lty=3)
arrows(0,0,load[,1],load[,2],col=2)          # Should be read angularly!
text(load[,1:2],label=names(sampson))

# Finally, extract scores
S1<-apply(sweep(as.sociomatrix.sna(sampson),1,load[,1],"*"),c(2,3),sum)
S2<-apply(sweep(as.sociomatrix.sna(sampson),1,load[,2],"*"),c(2,3),sum)
S3<-apply(sweep(as.sociomatrix.sna(sampson),1,load[,3],"*"),c(2,3),sum)

#Visualize a score graph (not too helpful in this case!)
coord<-gplot.layout.fruchtermanreingold(as.edgelist.sna(S1>0),NULL)
gplot(S1!=0,edge.col=sign(S1)+3,coord=coord)

# For more information....
?gcor
?gcov
?eigen
?varimax
?abline
?arrows
?sweep
?gplot.layout

```

6.3 Network CCA

```

# For this one, we're going to use the country trade data. Somewhat perversely,
# we're going to use yacca instead of netcancor (b/c this data set has
# missing data which netcancor doesn't handle, and b/c yacca currently has
# better visualizations).

```

```

library(yacca)          # You'll need to install this....

# Perform a canonical correlation analysis between relations and attribute
# differences
trade.cca<-cca(gvectorize(trade),gvectorize(tradediff),
               standardize.scores=FALSE)          # Turn off standardization b/c of NAs
summary(trade.cca)

# Visualize the output
plot(trade.cca)

# For more information
?netcancor
?yacca
?cca
?gvectorize

```

6.4 Studying Qualitative Dynamics with Network MDS

```

# Start by calculating Hamming distances for each of the two Johnson data sets

jp1d <- hdist(johnsonPolarY1)
jp2d <- hdist(johnsonPolarY2)

# Now try an MDS solution

jp1mds<-cmdscale(jp1d)
jp1mds
plot(jp1mds,type="l",lty=2)          # Plot the results
text(jp1mds,label=rownames(johnsonPolarY1),font=2)

```

```
jp2mds<-cmdscale(jp2d)
jp2mds
plot(jp2mds,type="l",lty=2) # Plot the results
text(jp2mds,label=rownames(johnsonPolarY2),font=2)
```
