Advanced Features of the ergm Package for Modeling Networks

Statnet Development Team

Contents

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Introduction to this workshop/tutorial.

This workshop and tutorial cover advanced topics in modeling network data with *Exponential family Random Graph Models* (ERGMs) using `statnet` software. It assumes a familiarity with the `ergm` package at least at the level of the introductory workshop entitled ERGMs using statnet. This online tutorial is also designed for self-study, with example code and self-contained data.

Some of the material in this workshop is drawn from a pair of recent articles by Krivitsky et al.: ergm 4: New features and ergm 4: Computational Improvements.

Prerequisites

This workshop assumes basic familiarity with **R**, experience with network concepts and data, familiarity with the ERGM modeling framework, and proficiency using the `ergm` package.

Software installation

Minimally, you will need to install the latest version of **R** (available here) and the `statnet` packages `ergm.multi` and `ggrepel`, which will in turn pull in the rest of the packages needed to run the code presented here.
The workshops are conducted using the free version of `Rstudio` (available here).

If you have not already downloaded the `statnet` packages for this workshop, the quickest way to install these (and the other most commonly used packages from the `statnet` suite), is to open an R session and type:

```
install.packages(c('ergm.multi', 'ggrepel'))
update.packages(ask=FALSE, checkBuilt=TRUE)
```

The first line above will install all three required packages, since both `ergm.multi` depends on both `ergm` and `network`. The second line ensures that any already-installed packages, including `ergm` and `network`, are updated to their latest versions.

Now load `ergm.multi`, which will also load `ergm` and others.

```
library(ergm.multi)
```

```
Loading required package: ergm
```

```
Loading required package: network
```

```

'network' 1.18.2 (2023-12-04), part of the Statnet Project
* 'news(package="network")' for changes since last version
* 'citation("network")' for citation information
* 'https://statnet.org' for help, support, and other information

'ergm' 4.6.0 (2023-12-17), part of the Statnet Project
* 'news(package="ergm")' for changes since last version
* 'citation("ergm")' for citation information
* 'https://statnet.org' for help, support, and other information
```

```
'ergm' 4 is a major update that introduces some backwards-incompatible
changes. Please type 'news(package="ergm")' for a list of major
changes.

'ergm.multi' 0.2.1 (2024-02-20), part of the Statnet Project
```

```
* 'news(package="ergm.multi")' for changes since last version
* 'citation("ergm.multi")' for citation information
* 'https://statnet.org' for help, support, and other information


Attaching package: 'ergm.multi'

The following object is masked from 'package:ergm':

    snctrl
```

You can check the version number with:

```
packageVersion("ergm")
```

```
[1] '4.6.0'
```

Throughout, we will set a random seed via `set.seed()` for commands in tutorial that require simulating random values. This is not necessary, but it ensures that you will get the same results as the online tutorial.

1. Brief review of ERGM modeling framework

The general form of an ERGM can be written as

$$P(\mathbf{Y} = \mathbf{y}) = \frac{\exp(\boldsymbol{\theta}^\top \mathbf{g}(\mathbf{y}))}{k(\boldsymbol{\theta})},$$

where

- $\mathbf{Y}$ is the random variable for the state of the network (with realization $\mathbf{y}$),
- $\mathbf{g}(\mathbf{y})$ is a p-dimensional vector of model statistics for network $\mathbf{y}$,
- $\boldsymbol{\theta}$ is the p-dimensional vector of coefficients for those statistics, and
- $k(\boldsymbol{\theta})$ represents the quantity in the numerator summed over all possible networks (typically constrained to be all networks with the same node set as $\mathbf{y}$).

In particular, the model implies that the probability attached to a network y only depends on the network via the vector of statistics $g(y)$. Among other things, this means that maximum likelihood estimation may be carried out even if we don't observe the network itself, as long as we know the observed value of $g(y)$. We will see an example of this procedure in Section 2 of this tutorial.

The model statistics $\mathbf{g}(\mathbf{y})$: ERGM terms

The statistics $\mathbf{g}(\mathbf{y})$ can be thought of as the "covariates" in the model. In the network modeling context, these represent network features like density, homophily, triads, etc. In one sense, they are like covariates you might use in other statistical models. But they are different in one important respect: these $\mathbf{g}(\mathbf{y})$ statistics are functions of the network itself—each is defined by the frequency of a specific configuration of dyads observed in the network—so they are not measured by a question you include in a survey (e.g., the income of a node), but instead need to be computed on the specific network you have, after you have collected the data.

As a result, every term in an ERGM must have an associated algorithm for computing its value for your network. The `ergm` package in `statnet` includes about 150 term-computing algorithms. You can get an up-to-date list of all available terms, and the syntax for using them, by typing `?ergmTerm`. When using RStudio, it is possible to press the tab key after starting a line with `?ergm` to view the wide range of possible help options beginning with the letters `ergm`.

To obtain help for a specific term, use either `help("[name]-ergmTerm")` or the shorthand version `ergmTerm?[name]`, where `[name]` is the name of the term.

One key categorization of model terms is worth keeping in mind: terms are either *dyad independent* or *dyad dependent*. Dyad *independent* terms (like nodal homophily terms) imply no dependence between dyads—the presence or absence of a tie may depend on nodal attributes, but not on the state of other ties. Dyad *dependent* terms (like degree terms, or triad terms), by contrast, imply dependence between dyads. Dyad dependent terms have very different effects, and much of what is different about network models comes from these terms. They introduce complex cascading effects that can often lead to counter-intuitive and highly non-linear outcomes. In addition, a model with at least one dyad dependent term requires a different estimation algorithm, so when we use these terms below you will see some different components in the output.

ERGM probabilities at the tie level

The ERGM expression for the probability of the entire graph shown above can be re-expressed in terms of the conditional log-odds (that is, the logit of the conditional probability) of a single tie between two actors:

$$\text{logit}\, P(Y_{ij} = 1 | \mathbf{y}^c_{ij}) = \boldsymbol{\theta}^\top \boldsymbol{\delta}_{ij}(\mathbf{y}),$$

where

- Y_{ij} is the random variable for the state of the actor pair i, j (with realization y_{ij}), and
- $\mathbf{y}^c_{ij}$ signifies the complement of y_{ij}, i.e. the entire network $\mathbf{y}$ *except for* y_{ij}.
- $\boldsymbol{\delta}_{ij}(\mathbf{y})$ is a vector of the "change statistics" for each model term. The change statistic records how the $\mathbf{g}(\mathbf{y})$ term changes if the y_{ij} tie is toggled from off to on while fixing the rest of the network. So

$$\boldsymbol{\delta}_{ij}(\mathbf{y}) = g(\mathbf{y}^+_{ij}) - g(\mathbf{y}^-_{ij}),$$

where

- $\mathbf{y}^+_{ij}$ is defined as $\mathbf{y}^c_{ij}$ along with y_{ij} set to 1, and
- $\mathbf{y}^-_{ij}$ is defined as $\mathbf{y}^c_{ij}$ along with y_{ij} set to 0.

So $\boldsymbol{\delta}_{ij}(\mathbf{y})$ equals the value of $\mathbf{g}(\mathbf{y})$ when $y_{ij} = 1$ minus the value of $\mathbf{g}(\mathbf{y})$ when $y_{ij} = 0$, but all other dyads are as in $\mathbf{y}$. When this vector of change statistics is multiplied by the vector of coefficients $\boldsymbol{\theta}$, the equation above shows that this dot product is the log-odds of the tie between i and j, conditional on all other dyads remaining the same.

In other words, for an individual statistic, its change value for Y_{ij} times its corresponding coefficient can be interpreted as that term's contribution to the log-odds of that tie, conditional on all other dyads remaining the same.

2. Sample space constraints

Many applications take the sample space $\mathcal{Y}$ to be the power set $2^{\mathbb{Y}}$ of (possibly a subset of) all potential relationships. Yet it is sometimes desirable to restrict the sample space by placing constraints on which relationships (i, j) are allowed in $\mathbb{Y}$ and further which networks $\mathbf{y} \in 2^{\mathbb{Y}}$ are allowed in $\mathcal{Y}$.

For example, a bipartite network allows only edges connecting nodes from one subset, or mode, to nodes from its complement. Alternatively, we may wish to allow edges only *within* subsets of the node set, a situation often called a block-diagonal constraint. As still another, some applications impose a cap on the degree of any node, which constrains the sample space to include only those networks in which every node has a permitted degree.

Correct statistical inference for ERGMs depends on correctly incorporating constraints into the fitting process. They are specified using the `constraints` argument, a one-sided formula whose terms specify the constraints on the sample space.

For example, suppose we wish to constrain the sample space to only those networks with a particular edge density. To accomplish this, `constraints = ~ edges` specifies $\mathcal{Y}^{\text{edges}}(\mathbf{y}) = \{\mathbf{y}' \in \mathcal{Y} : |\mathbf{y}'| = |\mathbf{y}|\}$, where $\mathbf{y}$

is the observed network specified on the left-hand side. Here is a simple example in which we generate a random network according to a fitted ERGM and conditional on fixing the number of edges:

```
data("faux.mesa.high")
fmh.fit <- ergm(faux.mesa.high ~ edges + nodematch("Grade"))
newnw <- simulate(fmh.fit, constraints = ~edges, nsim = 10)
rbind(faux.mesa.high = summary(faux.mesa.high ~ edges),
      newnw = summary(newnw ~ edges))
```

```
                edges
faux.mesa.high    203
                  203
                  203
                  203
                  203
                  203
                  203
                  203
                  203
                  203
                  203
                  203
```

The number of edges in the randomly-simulated `newnw` above will always be the same as in `faux.mesa.high` due to the constraint.

A full list of currently implemented constraints is obtained via `?ergmConstraint`, and a specific constraint called `[name]` can be looked up with `help("[name]-ergmConstraint")` or `ergmConstraint?[name]`. The handling of various constraints by MCMC proposals in the `ergm` package is addressed in Krivitsky et al (2022b).

Dyad-independent constraints via the Dyads operator

Dyad-independent constraints, which affect $\mathcal{Y}$ only through $\mathbb{Y}$ and do not induce stochastic dependencies among the dyad states, may be combined arbitrarily because they do not require special Metropolis–Hastings proposal algorithms for efficient sampling.

In the remainder of this section, we illustrate some of `ergm`'s constraints using a dataset due to Coleman (1964). These data are self-reported friendship ties among 73 boys measured at two time points during the 1957–1958 academic year. They are included as a $2 \times 73 \times 73$ array and documented in the `sna` package.

Here, we use the Coleman data to create a `network` object with 2×73 nodes:

```
library("sna")
data("coleman")
cole <- matrix(0, 2 * 73, 2 * 73)
# Upper left block:
cole[1 : 73, 1 : 73] <- coleman[1, , ]
# Lower right block:
cole[73 + (1 : 73), 73 + (1 : 73) ] <- coleman[2, , ]
coleNW <- network(cole)
coleNW %v% "Semester" <- rep(c("Fall", "Spring"), each = 73)
coleNW
```

```
 Network attributes:
  vertices = 146
  directed = TRUE
  hyper = FALSE
  loops = FALSE
```

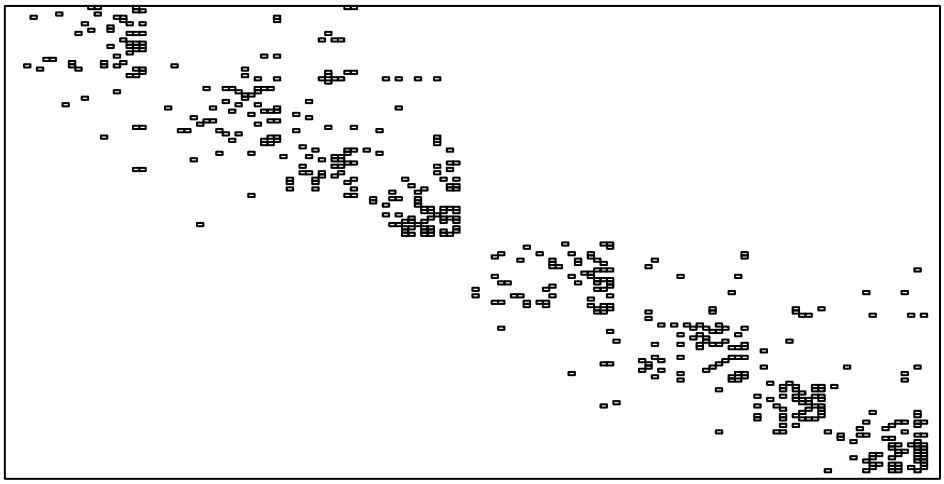
```
  multiple = FALSE
  bipartite = FALSE
  total edges= 506
    missing edges= 0
    non-missing edges= 506

 Vertex attribute names:
    Semester vertex.names

No edge attributes
```

By construction, the `coleNW` network includes the Fall 1957 semester data and the Spring 1958 data as the upper left 73×73 and lower right 73×73 blocks, respectively. To see this structure, we create a simple function to plot an binary adjacency matrix so that the zeros and ones are different colors:

```
BinaryMatrixPlot <- function(x) {
  n <- dim(x)[1]
  plot(0:n, 0:n, type="n", xaxt="n", yaxt="n", xlab="", ylab="", bty="n", ylim=c(n,0))
  therows <- row(x)[x>0]
  thecols <- col(x)[x>0]
  rect(thecols-1, therows-1, thecols, therows)
  rect(0,0,n,n)
}
```

Now we can visualize the constrained structure of the `coleNW` network, where the upper left corner depicts the relationships measured in the fall and the lower right corner depicts the spring relationships. Relationships are impossible in the upper right and lower left, a fact we must take into account when calculating statistical estimates.

```
BinaryMatrixPlot(as.matrix(coleNW))
```



The `Dyads(fix=NULL, vary=NULL)` operator takes one or two `ergm` formulas that may contain only dyad-independent terms. For the terms in the `fix=` formula, dyads that affect the network statistic (i.e., have nonzero change statistic) for *any* the terms will be fixed at their current values. For the terms in the `vary=` formula, only those that change *at least one* of the terms will be allowed to vary, and all others will be fixed. A formula passed without an argument name will default to `fix=`, for consistency with other constraints' semantics.

The key to our treatment of the `coleNW` network using the `Dyads` operator is the `Semester` vertex attribute:

```
table(coleNW %v% "Semester")
```

```
  Fall Spring
    73     73
```

In particular, the `nodematch("Semester")` term has a change statistic equal to one for exactly those dyads representing boys measured during the same semester, and this change statistic is zero otherwise. Therefore, in our 146-node directed network there are 146×145, or 21,170, total dyads, of which $2 \times 73 \times 72$, or 10,512, have nonzero change statistics for `nodematch("Semester")`.

We can easily see exactly how many total edges there are and verify that they all match on the "Semester" variable:

```
summary(coleNW ~ edges + nodematch("Semester"))
```

```
              edges nodematch.Semester
                506                 506
```

Another way to verify that no edges exist between Fall semester and Spring semester nodes uses the `mm` (for mixingmatrix) term:

```
summary(coleNW ~ mm("Semester", levels2 = TRUE))
```

```
    mm[Semester=Fall,Semester=Fall]   mm[Semester=Spring,Semester=Fall]
                                243                                   0
  mm[Semester=Fall,Semester=Spring] mm[Semester=Spring,Semester=Spring]
                                  0                                 263
```

If we ignore the constraints entirely, the `edges` coefficient is the log-odds, or logit, of 506 / 21170:

```
logit <- function (p) log(p / (1-p))
cbind(logit(506 / 21170),
  coef(ergm(coleNW ~ edges)))
```

```
           [,1]      [,2]
edges -3.709612 -3.709612
```

Next, we use the `Dyads` constraint allowing only those dyads with nonzero change statistics for `nodematch("Semester")` to vary, and verify that we now obtain the log-odds of 506 / 10512:

```
cbind(logit(506 / 10512),
  coef(ergm(coleNW ~ edges,
    constraints = ~ Dyads(vary = ~ nodematch("Semester")))))
```

```
           [,1]      [,2]
edges -2.984404 -2.984404
```

A significant limitation of this particular constraint is that its initialization requires testing every possible dyad and therefore takes up time and memory in proportion to the square of the number of nodes.

Constraints via blocks

We may reproduce the example above using the `blocks` operator, which constrains changes to any dyads that involve certain pairs of categories defined by a particular nodal covariate. First, consider the full complement of statistics produced by the `nodemix` model term:

```
summary(coleNW ~ nodemix("Semester",
                  levels = TRUE, levels2 = TRUE))
```

```
   mix.Semester.Fall.Fall   mix.Semester.Spring.Fall
                      243                         0
 mix.Semester.Fall.Spring mix.Semester.Spring.Spring
                        0                       263
```

The `levels = TRUE` argument ensures that nodemix considers every value of `"group"` in constructing a mixing matrix of possible dyad combinations. The `levels2 = TRUE` argument ensures that, from the full complement of such possible combinations, every one is included as a statistic. By default, `levels = TRUE` whereas `levels2 = -1`, since we frequently want to exclude at least one possible mixing combination to avoid collinearity in a model that also includes the `edges` term.

We may now use `levels2` in conjunction with `blocks` to select exactly which of the `nodemix` combinations should be constrained as fixed, namely, the second and third statistics from the full mixing matrix:

```
# This coefficient estimate should match the example above
coef(ergm(coleNW ~ edges,
    constraints = ~ blocks("Semester", levels2 = c(2, 3))))
```

```
    edges
-2.984404
```

Additional examples using `levels2`, among other nodal attribute features, are contained in the `nodal_attributes` vignette within the `ergm` package.

3. Tuning ERGM estimation

Recent versions of `ergm` allow for more control over various aspects of the ERGM fitting process, such as the Metropolis-Hastings proposal distribution and various algorithmic control parameters. Here, we illustrate some of these features using an example from Section 5 of Krivitsky et al (2022) in which we estimate the parameters of an ergm for a hypothetical network on 50,000 nodes.

Our network will be based on the `cohab` dataset in the `ergm` package, which consists of three **R** objects, none of them a network object. These objects are based on aggregated statistics from the National Survey of Family Growth (NSFG).

- `cohab_PopWts`: A set of NSFG demographic attributes—sex, age, and race/ethnicity/immigration status—along with weights that have been adjusted to match the demographics of King County in Washington State.
- `cohab_TargetStats`: A vector of expected statistics for a 15-term ERGM applied to a network of 50,000 nodes, with in which a tie represents a heterosexual cohabition relationship between two nodes.
- `cohab_MixMat`: A Mixing matrix on the 'race' variable, giving the number of cohabiting male-female pairs of each possible combination of 'race' values. The five values of this variable, which captures some aspects of race/ethnicity/immigration status, are Black, Black immigrant, Hispanic, Hispanic immigrant, and White. The 5×5 mixing matrix is, like `cohab_PopWts`, based on NSFG data reweighted to match King County demographics.

Additional information about the `cohab` dataset is available by typing `help(cohab)`.

The column names of `cohab_PopWts` tell us which nodal attributes we need to set for our 50,000-node network:

```
data("cohab")
names(cohab_PopWts)
```

```
[1] "weight"       "age"          "race"         "sex"          "sex.ident"
[6] "othr.net.deg" "agesq"        "sqrt.age.adj"
```

The first column of `cohab_PopWts` is the set of weights, proportional to the probabilities we will use to construct our random set of 50,000 nodes so that it matches the demographics of King County. The value

of `agesq` is simply the square of `age`, and `sqrt.age.adj` is the square root of `age` with a small upward adjustment for females.

Letting `nw` denote our 50,000 network, the ERGM formula we wish to use is the same one used to generate the `cohab_TargetStats` object according to `?cohab`:

```
cohab.formula <-
  (nw ~ edges + nodefactor("sex.ident", levels = 3)
    + nodecov("age") + nodecov("agesq")
    + nodefactor("race", levels = -5)
    + nodefactor("othr.net.deg", levels = -1)
    + nodematch("race", diff = TRUE) + absdiff("sqrt.age.adj"))
```

Recall that we do not actually need to observe the `nw` network to fit an ERGM, although we do need the nodes in the network to be specified. Thus, our code first creates a network containing no edges in which the nodal attributes are selected according to the weights specified by `cohab_PopWts`.

```
set.seed(4321)
net_size <- 50000
nw <- network.initialize(net_size, directed = FALSE)
inds <- sample(seq_len(NROW(cohab_PopWts)),
               net_size, TRUE, cohab_PopWts$weight)
set.vertex.attribute(nw, names(cohab_PopWts)[-1],
                     cohab_PopWts[inds,-1])
```

In this network, a tie is by definition a heterosexual cohabitation relationship and we assume that no individual may have more than one such relationship. We wish to constrain the set of allowable networks according these assumptions, which we may accomplish using the `bd` (bounded degree) and `blocks` constraints: Thus, the following formula will be passed to the `ergm` function via the `constraints=` argument:

```
constraint.formula <-
  (~ bd(maxout = 1)
   + blocks(attr = ~sex, levels2 = diag(TRUE, 2)))
```

We may now fit the model. This takes a few minutes, so we'll start it and describe some of the control parameters as it runs:

```
set.seed(1234)
fit <- ergm(cohab.formula,
        target.stats = cohab_TargetStats,
        eval.loglik = FALSE,
        constraints = constraint.formula,
        control = snctrl(
          MCMC.prop = ~strat(attr = ~race, empirical = TRUE) + sparse,
          init.method = "MPLE",
          init.MPLE.samplesize = 5e7,
          MPLE.constraints.ignore = TRUE,
          MCMLE.effectiveSize = 64,
          SAN.nsteps = 5e7,
          SAN.prop=~strat(attr = ~race, pmat = cohab_MixMat) + sparse))
```

In RStudio, typing `?snctrl` shows all of the control arguments that may be used. The improvements to the fitting algorithm are not merely due to an expand list of control arguments; coding efficiencies too have resulted in quicker fitting. According to Krivitsky et al (2022), the example we just considered took anywhere from 1.3 hours to 22.64 hours to fit using `ergm` version 3.10, depending on the settings used.

Finally, we may examine the set of estimated coefficients.

```
coef(summary(fit))
```

```
                             Estimate   Std. Error MCMC %     z value
edges                       0.785277529 0.4839693005      0   1.6225772
nodefactor.sex.ident.msmf -1.509318824 0.2043290557      0  -7.3867068
nodecov.age               -0.401146744 0.0143411971      0 -27.9716360
nodecov.agesq              0.006836269 0.0002244601      0  30.4564931
nodefactor.race.B          1.398141315 0.1564859095      0   8.9346147
nodefactor.race.BI         1.303563897 0.1645346127      0   7.9227336
nodefactor.race.H          2.748098856 0.1416603826      0  19.3992054
nodefactor.race.HI         1.430449585 0.1051492120      0  13.6039972
nodefactor.othr.net.deg.1 -4.542462604 0.1292577459      0 -35.1426723
nodematch.race.B           3.258740036 0.2550856025      0  12.7750841
nodematch.race.BI          3.914819910 0.2603545458      0  15.0364953
nodematch.race.H           0.050088295 0.1998123726      0   0.2506766
nodematch.race.HI          2.883540053 0.1490205662      0  19.3499470
nodematch.race.W           3.003038059 0.1347766112      0  22.2815964
absdiff.sqrt.age.adj      -3.143347800 0.0571064224      0 -55.0436828
                             Pr(>|z|)
edges                       1.046798e-01
nodefactor.sex.ident.msmf  1.505100e-13
nodecov.age               3.597251e-172
nodecov.agesq             9.827730e-204
nodefactor.race.B          4.085994e-19
nodefactor.race.BI         2.323451e-15
nodefactor.race.H          7.837344e-84
nodefactor.race.HI         3.791330e-42
nodefactor.othr.net.deg.1 1.504186e-270
nodematch.race.B           2.259033e-37
nodematch.race.BI          4.233789e-51
nodematch.race.H           8.020641e-01
nodematch.race.HI          2.040520e-83
nodematch.race.W          5.573561e-110
absdiff.sqrt.age.adj       0.000000e+00
```

4. Term operators

`ergm` 4 introduces a new way to augment an `ergm` function call that we call a *term operator*, or simply *operator*. In mathematics, an operator is a function, like differentiation, that takes functions as its inputs; analogously, a term operator takes one or more ERGM formulas as input and transforms them by modifying their inputs and/or outputs.

Most `ergm` operators have the form `X(formula, ...)` where `X` is the name of the operator, typically capitalized, `formula` is a one-sided formula specifying the network statistics to be evaluated, and the remaining arguments control the transformation applied to the network before `formula` is evaluated and/or to the transformation applied to the network statistics obtained by evaluating `formula`. Operators are documented alongside other terms, accessible as `help("[name]-ergmTerm")` or `ergmTerm?[name]`

Filtering edges

The operator `F(formula, filter)` evaluates the terms in `formula` on a filtered network, with filtering specified by `filter`. Here, `filter` is the right-hand side of a formula that must contain one binary dyad-independent `ergm` term, having exactly one statistic with a dyadwise contribution of 0 for a 0-valued dyad.

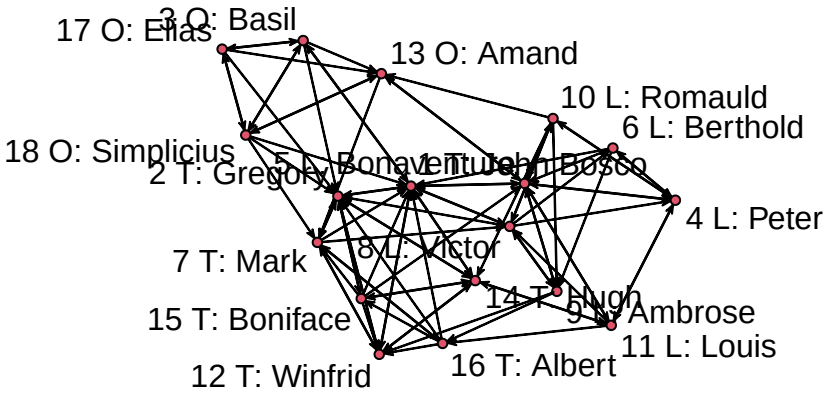
That is, the term must be expressible as

$$g(\mathbf{y}) = \sum_{(i,j)\in\mathbb{Y}} f_{i,j}(y_{i,j}), \tag{1}$$

where for all possible (i, j), $f_{i,j}(0) = 0$. One may verify that this condition implies that an ERGM containing the single term $g(\mathbf{y})$ has the property that the dyads $Y_{i,j}$ are jointly independent, which is why such a term is called "dyad-independent". Examples of such terms include `nodemix`, `nodematch`, `nodefactor`, `nodecov`, and `edgecov`. Then, `formula` will be evaluated on a network constructed by taking `y` and keeping only those edges for which $f_{i,j}(y_{i,j}) \neq 0$. This predicate can be modified slightly by very simple comparison or logical expressions in the `filter` formula. In particular, placing `!` in front of the term negates it (i.e., keep (i, j) only if $f_{i,j}(y_{i,j}) = 0$) and comparison operators (`==`, `<`, etc.) allow comparing $f_{i,j}(y_{i,j})$ to values other than 0.

Sampson's Monks can provide illustrative examples. `ergm` includes a version of these data reporting cumulative liking nominations over the three time periods Sampson asked a group of monks to identify those they liked. We may plot this directed, 18-node network, where in the labels we use "L", "O", or "T" to indicate Sampson's categorization of each monk as a Loyalist, Outcast, or Young Turk:

```
set.seed(123)
data("sampson")
lab <- paste0(1:18, " ", substr(samplike %v% "group", 1, 1),
              ": ", samplike %v% "vertex.names")
plot(samplike, displaylabels=TRUE, label = lab)
```



As an example of the `F` operator, the code below uses four different methods to summarize the number of ties between pairs of nodes in the `Turks` group:

```
summary(
  (samplike ~ nodematch("group", diff = TRUE, levels = "Turks")
    + F( ~ nodematch("group"), ~ nodefactor("group", levels = "Turks"))
    + F( ~ edges, ~ nodefactor("group", levels = "Turks") == 2)
    + F( ~ edges, ~ !nodefactor( ~ group != "Turks"))))
```

```
                                nodematch.group.Turks
                                                   30
F(nodefactor("group",levels="Turks"))~nodematch.group
                                                   30
       F(nodefactor("group",levels="Turks")==2)~edges
                                                   30
              F(!nodefactor(~group!="Turks"))~edges
                                                   30
```

Here, the third method works because this particular $f_{i,j}(y_{i,j})$ counts how many of the two nodes i and j are Turks, and so equals 2 if and only if both are; and the fourth method works because the new $f_{i,j}(y_{i,j})$ is 0 exactly when neither i nor j is a Turk.

It is also possible to filter on a quantitative variable. For instance, an alternative way to count the number of edges in `faux.mesa.high` that match on `"Grade"` is to report total edges after filtering by node pairs whose absolute difference on the `"Grade"` variable is less than 1:

```
cbind(summary(faux.mesa.high ~ nodematch("Grade")),
  summary(
    faux.mesa.high ~ F( ~ edges, ~ absdiff("Grade") < 1)))
```

```
                [,1] [,2]
nodematch.Grade  163  163
```

While `filter` must be dyad-independent, `formula` can have dyad-dependent terms as well. For instance, we may count the transitive triples—i.e., triples (i, j, k) where $y_{i,j} = y_{j,k} = y_{i,k} = 1$—in the `samplike` network, then perform the same count on the subnetwork consisting only of those edges connecting two monks not in attendance in the minor seminary of Cloisterville before coming to the monastery:

```
summary((samplike ~ ttriple
  + F( ~ ttriple, ~ nodefactor("cloisterville") == 0)))
```

```
                                    ttriple
                                        154
F(nodefactor("cloisterville")==0)~ttriple
                                         12
```

Treating directed networks as undirected

The operator `Symmetrize(formula, rule)` evaluates the terms in `formula` on an undirected network constructed by symmetrizing the underlying directed network according to `rule`. The possible values of `rule`, which match the terminology of the `symmetrize` function of the `sna` package, are (a) "weak", (b) "strong", (c) "upper", and (d) "lower". These four values result in an undirected tie between i and j, given any $i < j$, if and only if:

- weak: either $y_{i,j}$ or $y_{j,i}$ equals 1;
- strong: both $y_{i,j}$ and $y_{j,i}$ equal 1;
- upper: $y_{i,j} = 1$;
- lower: $y_{j,i} = 1$

For example, we can compute the number of node pairs $i < j$ with reciprocated edges, equivalent to mutuality:

```
summary((samplike ~ Symmetrize( ~ edges, "strong") + mutual))
```

```
Symmetrize(strong)~edges                   mutual
                     28                       28
```

We can also compute the number of node pairs in which at least one edge is present; adding this value to the number of mutually connected node pairs (so that the latter are counted twice each) yields the total number of directed edges:

```
summary((samplike ~ Symmetrize( ~ edges, "weak") + edges))
```

```
Symmetrize(weak)~edges                   edges
                    60                      88
```

Extracting subgraphs

The operator `S(formula, attrs)` evaluates the terms in `formula` on an induced subgraph constructed from vertices identified by `attrs`, a formula that can be one-sided or, to make the induced subgraph bipartite,

two-sided. For instance, suppose that we wish to model the density and mutuality dynamics within the group "Young Turks" as different from those of the rest of the network:

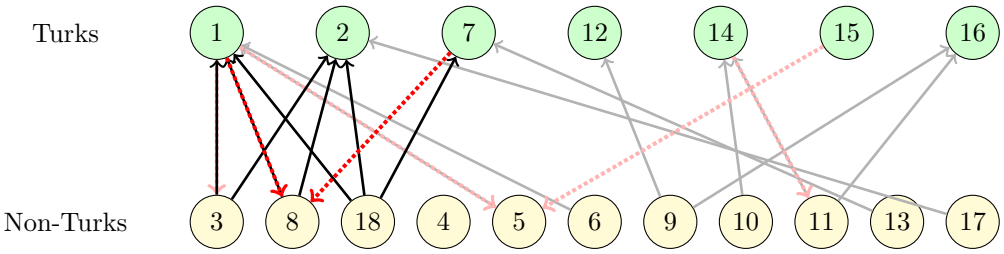
```
coef(summary(
  ergm(
    (samplike ~ edges + mutual
      + S( ~ edges + mutual, ~ (group == "Turks"))),
  control = snctrl(seed = 123))))
```

```
                            Estimate Std. Error MCMC %   z value     Pr(>|z|)
edges                      -2.007074  0.2377493      0 -8.441979 3.120095e-17
mutual                      2.351613  0.4996500      0  4.706519 2.519819e-06
S((group=="Turks"))~edges   2.812378  0.8650057      0  3.251282 1.148857e-03
S((group=="Turks"))~mutual -2.165222  1.1965294      0 -1.809585 7.036009e-02
```

Thus, the density within the group is statistically significantly higher, whereas the reciprocation within the group is lower, though not statistically significantly at the 5% level.

The `attrs` argument of the `S(formula, attrs)` operator either takes a value as explained in the `?nodal_attributes` online help or, to obtain a bipartite network, a two-sided formula with the left-hand side specifying the tails and the right-hand side specifying the heads.

As another example, consider the directed edges from non-Young Turks to Young Turks. Creating the induced subgraph from these edges results in a bipartite network, shown in the figure.



The emphasized edges in the figure are those involved in a 4-cycle. We can define the bipartite network, and count the 4-cycles in two ways: If only directed edges from non-Turks to Turks (black in the figure) are viewed as bipartite edges, there are three 4-cycles.

```
summary((samplike ~
  S( ~ cycle(4), (group != "Turks") ~ (group == "Turks"))))
```

```
S((group!="Turks"),(group=="Turks"))~cycle4
                                     3
```

If we also include edges from Turks to non-Turks (dotted red in the figure) via `Symmetrize` and the "weak" rule, we get two more.

```
summary(samplike
  ~ Symmetrize(
      ~ S( ~ cycle(4), (group != "Turks") ~ (group == "Turks")),
  "weak"))
```

```
Symmetrize(weak)~S((group!="Turks"),(group=="Turks"))~cycle4
                                                     5
```

The last example also illustrates that term operators may be nested arbitrarily.

Finally, we illustrate a common use case in which `Symmetrize` is used to analyze mutuality in a directed network as a function of a predictor. The `faux.dixon.high` dataset is a directed friendship network of

seventh through twelfth graders. Suppose we wish to check how strongly the tendency toward mutuality in friendships is affected by students' closeness in grade level.

```
data("faux.dixon.high")
FDHfit <- ergm(faux.dixon.high ~ edges + mutual + absdiff("grade")
               + Symmetrize( ~ absdiff("grade"), "strong"),
          control = snctrl(seed=321))
coef(summary(FDHfit) )
```

```
                                    Estimate Std. Error MCMC %    z value
edges                            -3.2468082 0.05110162      0 -63.536313
mutual                            3.2407587 0.12095858      0  26.792301
absdiff.grade                    -0.9145735 0.04309196      0 -21.223763
Symmetrize(strong)~absdiff.grade -0.4237874 0.18035755      0  -2.349707
                                        Pr(>|z|)
edges                            0.000000e+00
mutual                           3.972740e-158
absdiff.grade                    5.762326e-100
Symmetrize(strong)~absdiff.grade  1.878819e-02
```

After correcting for the overall network density, the propensity for friendships to be reciprocated, and the predictive effect of grade difference on friendship formation, the difference in grade level has a statistically significant negative effect on the tendency to form mutual friendships (p-value $= 0.019$).

Interaction effects

For binary ERGMs, interactions between dyad-independent `ergm` terms can be specified in a manner similar to `lm` and `glm` via the `:` and `*` operators.

Let us first consider the colon (`:`) operator. Generally, if term `A` creates p_A statistics and term `B` creates p_B statistics, then `A:B` will create $p_A \times p_B$ new statistics. If `A` and `B` are dyad-independent terms, expressed for $a = 1, \ldots, p_A$ and $b = 1, \ldots, p_B$ as

$$g_a(\mathbf{y}) = \sum_{(i,j)\in\mathbb{Y}} u^a_{i,j} y_{i,j} \text{ and } h_b(\mathbf{y}) = \sum_{(i,j)\in\mathbb{Y}} v^b_{i,j} y_{i,j}$$

for appropriate covariate matrices U^a and V^b, then the corresponding interaction term is

$$g_{a:b}(\mathbf{y}) = \sum_{(i,j)\in\mathbb{Y}} u^a_{i,j} v^b_{i,j} y_{i,j}. \tag{2}$$

As an example, consider the `Grade` and `Sex` effects, expressed as model terms via `nodefactor`, in the `faux.mesa.high` dataset:

```
summary(faux.mesa.high ~ nodefactor("Grade", levels = TRUE) : nodefactor("Sex"))
```

```
 nodefactor.Grade.7:nodefactor.Sex.M  nodefactor.Grade.8:nodefactor.Sex.M
                                  70                                   99
 nodefactor.Grade.9:nodefactor.Sex.M nodefactor.Grade.10:nodefactor.Sex.M
                                  63                                   46
nodefactor.Grade.11:nodefactor.Sex.M nodefactor.Grade.12:nodefactor.Sex.M
                                  38                                   26
```

In the call above, we deliberately include all `Grade`-factor levels via `levels=TRUE`, whereas we employ the default behavior of `nodefactor` for the `Sex` factor, which leaves out one level. Thus, the 6-level `Grade` factor and the 2-level `Sex` factor, with one level of the latter omitted, produce 6×1 interaction terms in this example.

The `*` operator, by contrast, produces all interactions in addition to the main effects or statistics. Therefore, in the scenario described above, `A*B` will add $p_A + p_B + p_A \times p_B$ statistics to the model. Below, we use the

default behavior of `nodefactor` on both the 6-level `Grade` factor and the 2-level `Sex` factor, together with an additional `edges` term, to produce a model with $1 + 5 + 1 + 5 \times 1$ terms:

```
m <- ergm(faux.mesa.high ~ edges + nodefactor("Grade") * nodefactor("Sex"))
print(summary(m), digits = 3)
```

```
Call:
ergm(formula = faux.mesa.high ~ edges + nodefactor("Grade") *
    nodefactor("Sex"))

Maximum Likelihood Results:

                                   Estimate Std. Error MCMC % z value
edges                                -3.028      0.173      0  -17.53
nodefactor.Grade.8                   -1.424      0.263      0   -5.41
nodefactor.Grade.9                   -1.166      0.229      0   -5.10
nodefactor.Grade.10                  -1.633      0.357      0   -4.58
nodefactor.Grade.11                  -0.328      0.237      0   -1.38
nodefactor.Grade.12                  -0.794      0.324      0   -2.45
nodefactor.Sex.M                     -1.764      0.240      0   -7.36
nodefactor.Grade.8:nodefactor.Sex.M   1.386      0.202      0    6.86
nodefactor.Grade.9:nodefactor.Sex.M   1.012      0.211      0    4.79
nodefactor.Grade.10:nodefactor.Sex.M  1.347      0.264      0    5.11
nodefactor.Grade.11:nodefactor.Sex.M  0.419      0.240      0    1.75
nodefactor.Grade.12:nodefactor.Sex.M  1.059      0.290      0    3.65
                                   Pr(>|z|)
edges                               < 1e-04 ***
nodefactor.Grade.8                  < 1e-04 ***
nodefactor.Grade.9                  < 1e-04 ***
nodefactor.Grade.10                 < 1e-04 ***
nodefactor.Grade.11                 0.16714
nodefactor.Grade.12                 0.01429 *
nodefactor.Sex.M                    < 1e-04 ***
nodefactor.Grade.8:nodefactor.Sex.M < 1e-04 ***
nodefactor.Grade.9:nodefactor.Sex.M < 1e-04 ***
nodefactor.Grade.10:nodefactor.Sex.M < 1e-04 ***
nodefactor.Grade.11:nodefactor.Sex.M 0.08074 .
nodefactor.Grade.12:nodefactor.Sex.M 0.00026 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 28987  on 20910  degrees of freedom
 Residual Deviance:  2189  on 20898  degrees of freedom

AIC: 2213  BIC: 2308  (Smaller is better. MC Std. Err. = 0)
```

Interactions involving dyad-dependent terms are not straightforward, so `ergm`'s default behavior if `:` or `*` is used with a dyad-dependent term is to return an error. This default behavior may be changed by setting the `interact.dependent` option; see `help("ergm-options")` for more details.

Since interactions are defined by multiplying change statistics dyadwise and then summing over all dyads, interactions of terms are not necessarily the same as terms derived from products. Here is an example using the undirected Florentine marriage dataset:

```
data("florentine")
summary(flomarriage ~ nodecov("wealth") : nodecov("wealth")
```

```
        + nodecov( ~ wealth ^ 2))
```

```
nodecov.wealth:nodecov.wealth             nodecov.wealth^2
                       284058                       187814
```

The reason the two statistics above are not the same is that `nodecov("wealth")` is expressed as

$$g(\mathbf{y}) = \sum_{(i,j)\in\mathbb{Y}} u_{i,j} y_{i,j}$$

by setting $u^a_{i,j} = \text{wealth}_i + \text{wealth}_j$. Thus, in the interaction term, each $y_{i,j}$ is multiplied by $(\text{wealth}_i + \text{wealth}_j)^2$, whereas in the `wealth ^ 2` term, each $y_{i,j}$ is multiplied by only $\text{wealth}_i^2 + \text{wealth}_j^2$.

Reparametrizing the model

The term operator `Sum(formulas, label)` allows arbitrary linear combinations of existing statistics to be added to the model. Suppose $\mathbf{g}_1(\mathbf{y}), \ldots, \mathbf{g}_K(\mathbf{y})$ is a set of K vector-valued network statistics, each corresponding to one or more `ergm` terms and of arbitrary dimension. Also suppose that $A_1, \ldots, A_K$ is a set of known constant matrices all having the same number of rows such that each matrix multiplication $A_k \mathbf{g}_k(\mathbf{y})$ is well-defined. Then it is now possible to define the statistic

$$\mathbf{g}_{\text{Sum}}(\mathbf{y}) = \sum_{k=1}^{K} A_k \mathbf{g}_k(\mathbf{y}).$$

The first argument to `Sum` is a formula or a list of K formulas, each representing a vector statistic. If a formula has a left-hand side, the left-hand side will be used to define the corresponding A_k matrix: If it is a scalar or a vector, A_k will be a diagonal matrix thus multiplying each element by its corresponding element; and if it is a matrix, A_k will be used directly. When no left-hand side is given, A_k is defined as 1. To simplify this function for some common cases, if the left-hand side is `"sum"` or `"mean"`, the sum (or mean) of the statistics in the formula is calculated.

As an example, consider a vector of statistics consisting of the numbers of friendship ties received by each subgroup of Sampson's monks:

```
summary(samplike ~ nodeifactor("group", levels = TRUE) )
```

```
   nodeifactor.group.Loyal nodeifactor.group.Outcasts
                        29                         13
   nodeifactor.group.Turks
                        46
```

We may create a single statistic equal to the friendship ties received by both groups of non-Outcasts by adding the first and third components of the `nodefactor` vector, either by left-multiplying by $\begin{bmatrix}1 & 0 & 1\end{bmatrix}$ or by deselecting the second component at the `nodeifactor` level and summing the remaining two:

```
summary(samplike ~
    Sum(cbind(1, 0, 1) ~ nodeifactor("group", levels = TRUE), "nf.L_T")
    + Sum("sum" ~ nodeifactor("group", levels = -2), "nf.L_T"))
```

```
Sum~nf.L_T Sum~nf.L_T
        75         75
```

Whereas the `Sum` operator calculates linear combinations of network statistics, the `Prod` operator calculates the products of their powers. As of this writing, it is implemented for nonnegative statistics only, by first applying the `Log` operator (which returns the natural logarithm, `log` in `R`, of the statistics passed to it), then the `Sum` operator, and finally the `Exp` operator (which returns the exponential function, `exp` in `R`). As a simple illustration, we may verify that the `Sum` and `Prod` operators do in fact produce network statistics as expected if we simply use each with a list of formulas having no left hand side:

```
summary(faux.dixon.high ~ edges + mutual
        + Sum(list( ~ edges, ~ mutual), "EdgesAndMutual")
        + Prod(list( ~ edges, ~ mutual), "EdgesAndMutual"))
```

```
                edges                mutual     Sum~EdgesAndMutual
                 1197                   219                   1416
Exp~Sum~EdgesAndMutual
                262143
```

The `For()` operator can be used to parametrize other terms. This operator evaluates the formula given to it substituting the specified loop counter variable with each element in a sequence. Provide:

1. An `ergm` formula in an unnamed argument containing placeholders to be substituted.
2. One or more named arguments in the form `<placeholder> = <sequence>`, indicating what to substitute:
   - vector or list
   - LHS formula or function evaluated on network

The following are equivalent ways to compute differential homophily:

```
data(sampson)
(groups <- sort(unique(samplike%v%"group"))) # Sorted list of groups.
```

```
[1] "Loyal"    "Outcasts" "Turks"
```

The "normal" way:

```
summary(samplike ~ nodematch("group", diff=TRUE))
```

```
   nodematch.group.Loyal nodematch.group.Outcasts    nodematch.group.Turks
                      23                       10                       30
```

One element at a time, specifying a list:

```
summary(samplike ~ For(~nodematch("group", levels=., diff=TRUE),
                       . = groups))
```

```
   nodematch.group.Loyal nodematch.group.Outcasts    nodematch.group.Turks
                      23                       10                       30
```

One element at a time, specifying a function that returns a list:

```
summary(samplike ~ For(~nodematch("group", levels=., diff=TRUE),
                       . = function(nw) sort(unique(nw%v%"group"))))
```

```
   nodematch.group.Loyal nodematch.group.Outcasts    nodematch.group.Turks
                      23                       10                       30
```

One element at a time, specifying a formula whose RHS expression returns a list:

```
summary(samplike ~ For(~nodematch("group", levels=., diff=TRUE),
                       . = ~sort(unique(.%v%"group"))))
```

```
   nodematch.group.Loyal nodematch.group.Outcasts    nodematch.group.Turks
                      23                       10                       30
```

Here, `absdiff()` is being computed for each combination of attribute and power, the "normal" way:

```
data(florentine)
summary(flomarriage ~ absdiff("wealth", pow=1) + absdiff("priorates", pow=1) +
```

```
                    absdiff("wealth", pow=2) + absdiff("priorates", pow=2) +
                    absdiff("wealth", pow=3) + absdiff("priorates", pow=3))
```

```
    absdiff.wealth  absdiff.priorates    absdiff2.wealth absdiff2.priorates
              1146                638              91570              26756
   absdiff3.wealth absdiff3.priorates
           8588334            1289504
```

and with a loop, with attribute (`a`) iterated within power (`.`):

```
summary(flomarriage ~ For(. = 1:3, a = c("wealth", "priorates"), ~absdiff(a, pow=.)))
```

```
    absdiff.wealth  absdiff.priorates    absdiff2.wealth absdiff2.priorates
              1146                638              91570              26756
   absdiff3.wealth absdiff3.priorates
           8588334            1289504
```

5. Modeling multiple networks

The `ergm.multi` package provides support for modeling multiple networks, as we illustrate in this section using datasets supplied in that package.

First, load the `ergm.multi` package along with some helper packages. You might need to use `install.packages` first if any of these is not yet installed:

```
library(ergm.multi)
library(dplyr)
library(purrr)
library(tibble)
```

Obtaining data

The list of networks studied by Goeyvaerts et al (2018) is included in this package:

```
data(Goeyvaerts)
length(Goeyvaerts)
```

```
[1] 318
```

An explanation of the networks, including a list of their network (`%n%`) and vertex (`%v%`) attributes, can be obtained via `?Goeyvaerts`. A total of 318 complete networks were collected, then two more excluded due to "nonstandard" family composition:

```
Goeyvaerts %>% discard(`%n%`, "included") %>% map(as_tibble, unit="vertices")
```

```
[[1]]
# A tibble: 4 x 5
  vertex.names   age gender na    role
         <int> <int> <chr>  <lgl> <chr>
1            1    32 F      FALSE Mother
2            2    48 F      FALSE Grandmother
3            3    32 M      FALSE Father
4            4    10 F      FALSE Child

[[2]]
# A tibble: 3 x 5
  vertex.names   age gender na    role
         <int> <int> <chr>  <lgl> <chr>
```

```
1            1    29 F      FALSE Mother
2            2    28 F      FALSE Mother
3            3     0 F      FALSE Child
```

To reproduce the analysis, exclude them as well:

```
G <- Goeyvaerts %>% keep(`%n%`, "included")
```

Data summaries

Obtain weekday indicator, network size, and density for each network, and summarize them as in Goeyvaerts et al (2018), Table 1:

```
G %>% map(~list(weekday = . %n% "weekday",
                n = network.size(.),
                d = network.density(.))) %>% bind_rows() %>%
  group_by(weekday, n = cut(n, c(1,2,3,4,5,9))) %>%
  summarize(nnets = n(), p1 = mean(d==1), m = mean(d)) %>% kable()
```

weekday	n	nnets	p1	m
FALSE	(1,2]	3	1.0000000	1.0000000
FALSE	(2,3]	19	0.7368421	0.8771930
FALSE	(3,4]	48	0.8541667	0.9618056
FALSE	(4,5]	18	0.7777778	0.9500000
FALSE	(5,9]	3	1.0000000	1.0000000
TRUE	(1,2]	9	1.0000000	1.0000000
TRUE	(2,3]	53	0.9056604	0.9622642
TRUE	(3,4]	111	0.7747748	0.9279279
TRUE	(4,5]	39	0.6410256	0.8974359
TRUE	(5,9]	13	0.4615385	0.8454212

Reproducing ERGM fits

We now reproduce the ERGM fits. First, we extract the weekday networks:

```
G.wd <- G %>% keep(`%n%`, "weekday")
length(G.wd)
```

```
[1] 225
```

Next, we specify the multi-network model using the `N(formula, lm)` operator. This operator will evaluate the `ergm` formula `formula` on each network, weighted by the predictors passed in the one-sided `lm` formula, which is interpreted the same way as that passed to the built-in `lm()` function, with its "`data`" being the table of network attributes.

Since different networks may have different compositions, to have a consistent model, we specify a consistent list of family roles.

```
roleset <- sort(unique(unlist(lapply(G.wd, `%v%`, "role"))))
```

We now construct the formula object, which will be passed directly to `ergm()`:

```
# Networks() function tells ergm() to model these networks jointly.
f.wd <- Networks(G.wd) ~
  # This N() operator adds three edge counts:
  N(~edges,
    ~ # one total for all networks  (intercept implicit as in lm),
```

```
    I(n<=3)+ # one total for only small households, and
    I(n>=5) # one total for only large households.
  ) +

# This N() construct evaluates each of its terms on each network,
# then sums each statistic over the networks:
N(
    # First, mixing statistics among household roles, including only
    # father-mother, father-child, and mother-child counts.
    # Since tail < head in an undirected network, in the
    # levels2 specification, it is important that tail levels (rows)
    # come before head levels (columns). In this case, since
    # "Child" < "Father" < "Mother" in alphabetical order, the
    # row= and col= categories must be sorted accordingly.
  ~mm("role", levels = I(roleset),
      levels2=~.%in%list(list(row="Father",col="Mother"),
                         list(row="Child",col="Father"),
                         list(row="Child",col="Mother"))) +
    # Second, the nodal covariate effect of age, but only for
    # edges between children.
    F(~nodecov("age"), ~nodematch("role", levels=I("Child"))) +
    # Third, 2-stars.
    kstar(2)
) +

# This N() adds one triangle count, totalled over all households
# with at least 6 members.
N(~triangles, ~I(n>=6))
```

See `ergmTerm?mm` for documentation on the `mm` term used above. Now, we can fit the model:

```
fit.wd <- ergm(f.wd)
```

```
summary(fit.wd)
```

```
Call:
ergm(formula = f.wd)

Monte Carlo Maximum Likelihood Results:

                                                    Estimate Std. Error
N(1)~edges                                           0.84277    0.53315
N(I(n <= 3)TRUE)~edges                               1.48525    0.43480
N(I(n >= 5)TRUE)~edges                              -0.80143    0.20811
N(1)~mm[role=Child,role=Father]                     -0.63765    0.48484
N(1)~mm[role=Child,role=Mother]                      0.13614    0.52994
N(1)~mm[role=Father,role=Mother]                     0.25377    0.58752
N(1)~F(nodematch("role",levels=I("Child")))~nodecov.age -0.07154    0.01695
N(1)~kstar2                                         -0.25767    0.21225
N(1)~triangle                                        2.05168    0.31374
N(I(n >= 6)TRUE)~triangle                           -0.28102    0.10850
                                                    MCMC % z value Pr(>|z|)
N(1)~edges                                                0   1.581 0.113936
N(I(n <= 3)TRUE)~edges                                    0   3.416 0.000636
N(I(n >= 5)TRUE)~edges                                    0  -3.851 0.000118
```

```
N(1)~mm[role=Child,role=Father]                                  0  -1.315 0.188450
N(1)~mm[role=Child,role=Mother]                                  0   0.257 0.797254
N(1)~mm[role=Father,role=Mother]                                 0   0.432 0.665792
N(1)~F(nodematch("role",levels=I("Child")))~nodecov.age          0  -4.220  < 1e-04
N(1)~kstar2                                                      0  -1.214 0.224754
N(1)~triangle                                                    0   6.539  < 1e-04
N(I(n >= 6)TRUE)~triangle                                        0  -2.590 0.009600

N(1)~edges
N(I(n <= 3)TRUE)~edges                                        ***
N(I(n >= 5)TRUE)~edges                                        ***
N(1)~mm[role=Child,role=Father]
N(1)~mm[role=Child,role=Mother]
N(1)~mm[role=Father,role=Mother]
N(1)~F(nodematch("role",levels=I("Child")))~nodecov.age       ***
N(1)~kstar2
N(1)~triangle                                                 ***
N(I(n >= 6)TRUE)~triangle                                     **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 1975  on 1425  degrees of freedom
 Residual Deviance:  611  on 1415  degrees of freedom

AIC: 631  BIC: 683.6  (Smaller is better. MC Std. Err. = 0.6565)
```

Similarly, we can extract the weekend network, and fit it to a smaller model. We only need one `N()` operator, since all statistics are applied to the same set of networks, namely, all of them.

```
G.we <- G %>% discard(`%n%`, "weekday")
fit.we <- ergm(Networks(G.we) ~
                 N(~edges +
                     mm("role", levels=I(roleset),
                        levels2=~.%in%list(list(row="Father",col="Mother"),
                                           list(row="Child",col="Father"),
                                           list(row="Child",col="Mother"))) +
                     F(~nodecov("age"), ~nodematch("role", levels=I("Child"))) +
                     kstar(2) +
                     triangles))
```

```
summary(fit.we)
```

```
Call:
ergm(formula = Networks(G.we) ~ N(~edges + mm("role", levels = I(roleset),
    levels2 = ~. %in% list(list(row = "Father", col = "Mother"),
        list(row = "Child", col = "Father"), list(row = "Child",
            col = "Mother"))) + F(~nodecov("age"), ~nodematch("role",
    levels = I("Child"))) + kstar(2) + triangles))

Monte Carlo Maximum Likelihood Results:

                                                 Estimate Std. Error
N(1)~edges                                         2.1574     1.4273
N(1)~mm[role=Child,role=Father]                   -1.1795     1.4697
N(1)~mm[role=Child,role=Mother]                    0.1391     1.5732
```

```
N(1)~mm[role=Father,role=Mother]                            -0.7507     1.5343
N(1)~F(nodematch("role",levels=I("Child")))~nodecov.age  -0.1765     0.0519
N(1)~kstar2                                                -0.8488     0.3592
N(1)~triangle                                               3.5582     0.7602
                                                          MCMC % z value Pr(>|z|)
N(1)~edges                                                     0   1.511 0.130662
N(1)~mm[role=Child,role=Father]                                0  -0.803 0.422257
N(1)~mm[role=Child,role=Mother]                                0   0.088 0.929571
N(1)~mm[role=Father,role=Mother]                               0  -0.489 0.624649
N(1)~F(nodematch("role",levels=I("Child")))~nodecov.age        0  -3.400 0.000674
N(1)~kstar2                                                    0  -2.363 0.018127
N(1)~triangle                                                  0   4.680  < 1e-04

N(1)~edges
N(1)~mm[role=Child,role=Father]
N(1)~mm[role=Child,role=Mother]
N(1)~mm[role=Father,role=Mother]
N(1)~F(nodematch("role",levels=I("Child")))~nodecov.age ***
N(1)~kstar2                                             *
N(1)~triangle                                           ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 802.7  on 579  degrees of freedom
 Residual Deviance: 133.2  on 572  degrees of freedom

AIC: 147.2  BIC: 177.8  (Smaller is better. MC Std. Err. = 0.7987)
```

Diagnostics

Perform diagnostic simulation (Krivitsky et al, 2022c), summarize the residuals, and make residuals vs. fitted and scale-location plots:

```
gof.wd <- gofN(fit.wd, GOF = ~ edges + kstar(2) + triangles)
```

```
Constructing simulation model(s).

Constructing GOF model.

Simulating unconstrained sample.

Collating the simulations.

Summarizing.
```

```
summary(gof.wd)
```

```
$`Observed/Imputed values`
     edges            kstar2         triangle
 Min.   : 1.000   Min.   : 0.00   Min.   : 0.000
 1st Qu.: 3.000   1st Qu.: 3.00   1st Qu.: 1.000
 Median : 6.000   Median :12.00   Median : 4.000
 Mean   : 5.778   Mean   :13.55   Mean   : 4.324
 3rd Qu.: 6.000   3rd Qu.:12.00   3rd Qu.: 4.000
 Max.   :18.000   Max.   :78.00   Max.   :23.000
                  NA's   :9       NA's   :9

$`Fitted values`
```

```
     edges            kstar2          triangle
 Min.   : 0.860   Min.   : 2.620   Min.   : 0.700
 1st Qu.: 2.950   1st Qu.: 7.622   1st Qu.: 2.348
 Median : 5.570   Median :10.610   Median : 3.390
 Mean   : 5.754   Mean   :13.409   Mean   : 4.277
 3rd Qu.: 5.840   3rd Qu.:11.473   3rd Qu.: 3.743
 Max.   :14.920   Max.   :59.360   Max.   :19.680
                  NA's   :9        NA's   :9

$`Pearson residuals`
     edges               kstar2           triangle
 Min.   :-5.498132   Min.   :-4.2209   Min.   :-4.20054
 1st Qu.: 0.215984   1st Qu.: 0.2233   1st Qu.: 0.19607
 Median : 0.364671   Median : 0.3825   Median : 0.39214
 Mean   : 0.000977   Mean   : 0.0052   Mean   : 0.01461
 3rd Qu.: 0.477977   3rd Qu.: 0.5123   3rd Qu.: 0.54272
 Max.   : 1.752754   Max.   : 2.0089   Max.   : 1.93910
                     NA's   :9         NA's   :9

$`Variance of Pearson residuals`
$`Variance of Pearson residuals`$edges
[1] 1.153315

$`Variance of Pearson residuals`$kstar2
[1] 1.091188

$`Variance of Pearson residuals`$triangle
[1] 1.028553


$`Std. dev. of Pearson residuals`
$`Std. dev. of Pearson residuals`$edges
[1] 1.073925

$`Std. dev. of Pearson residuals`$kstar2
[1] 1.044599

$`Std. dev. of Pearson residuals`$triangle
[1] 1.014176
```

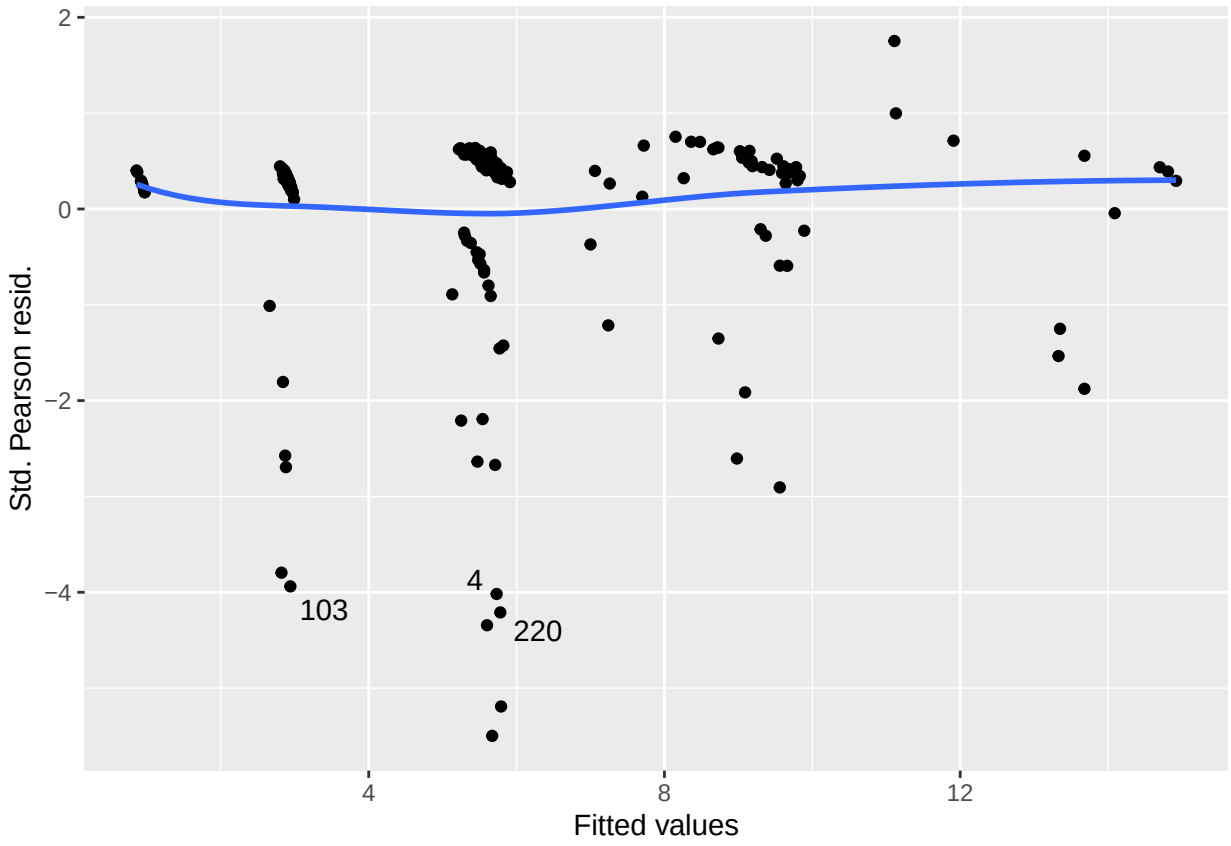
Variances of Pearson residuals substantially greater than 1 suggest unaccounted-for heterogeneity.

```
library(ggplot2)
autoplot(gof.wd)
```

```
Loading required namespace: ggrepel
```

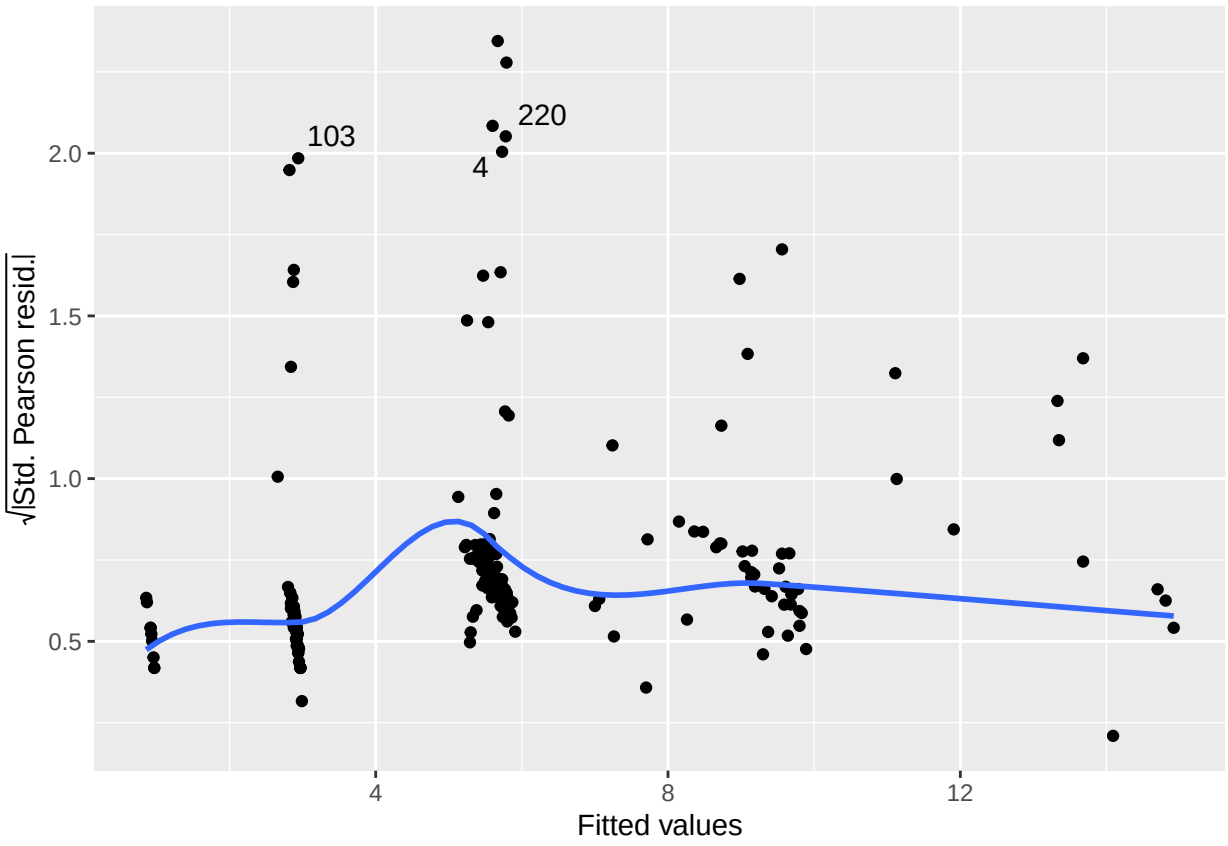
```
[[1]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```




```
[[2]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



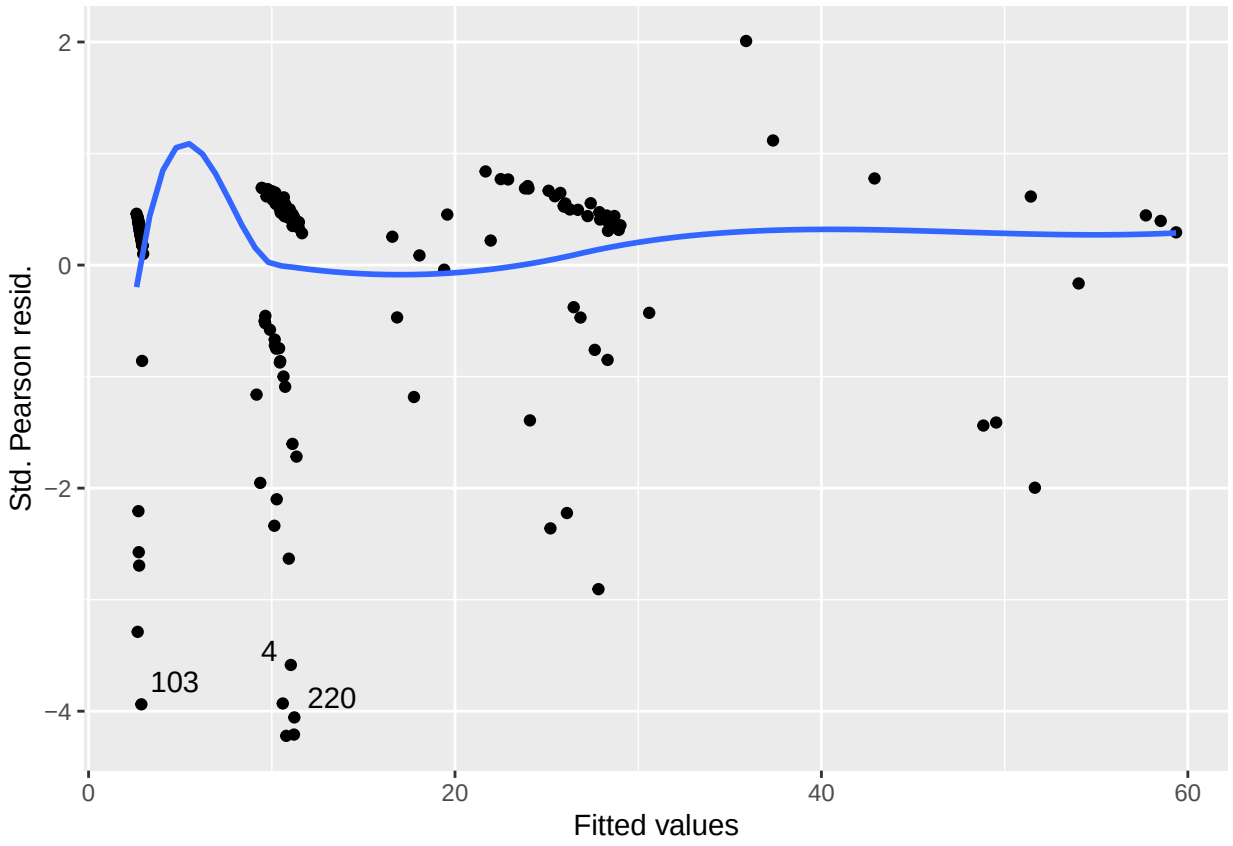

```
[[3]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```



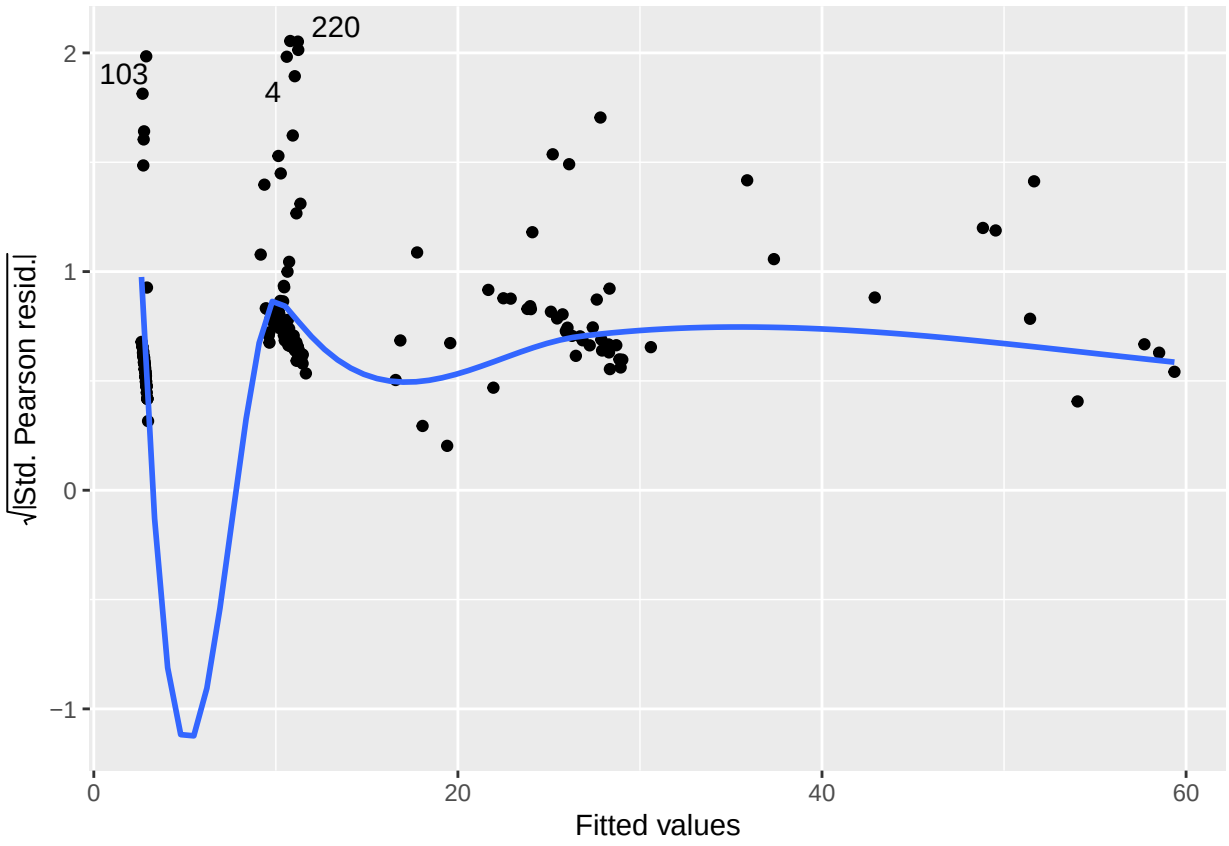

```
[[4]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

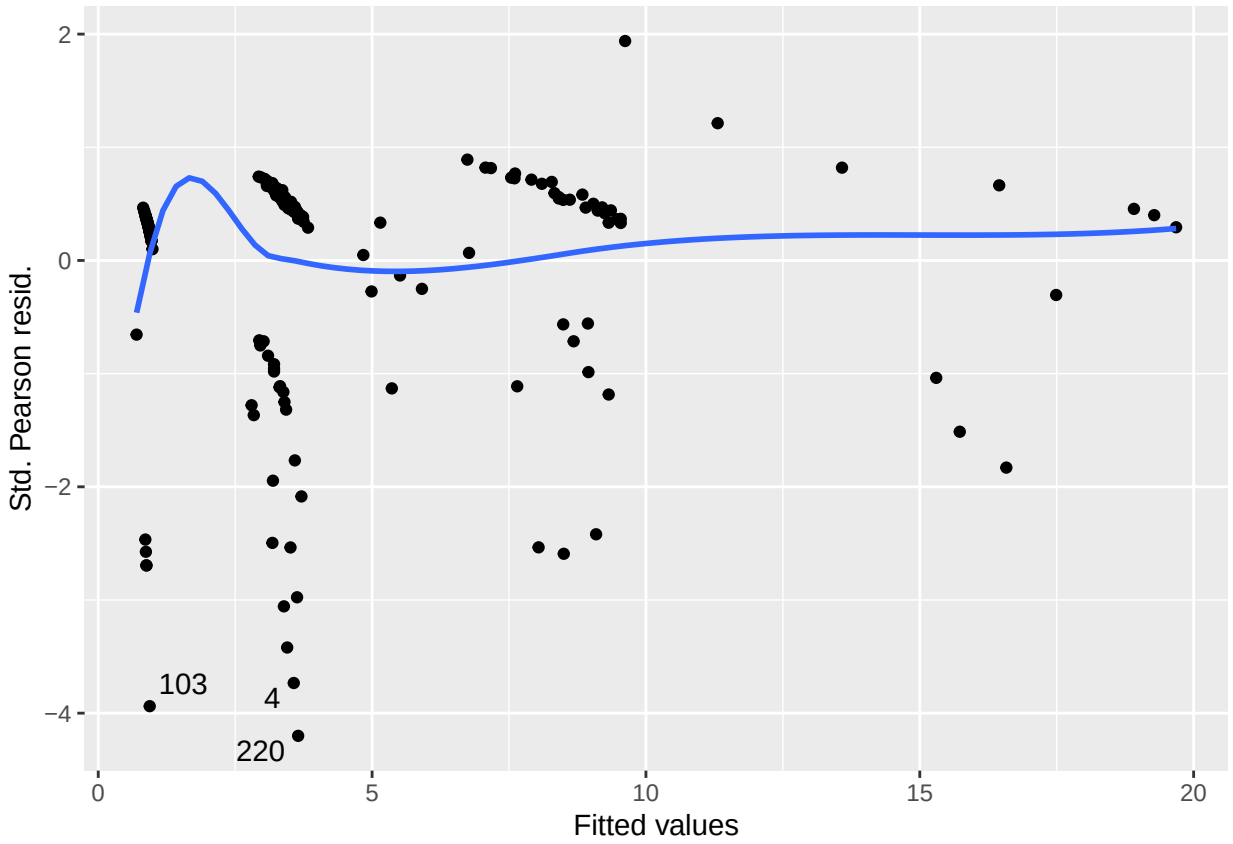
```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```




```
[[5]]

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'

Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).

Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).

Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```



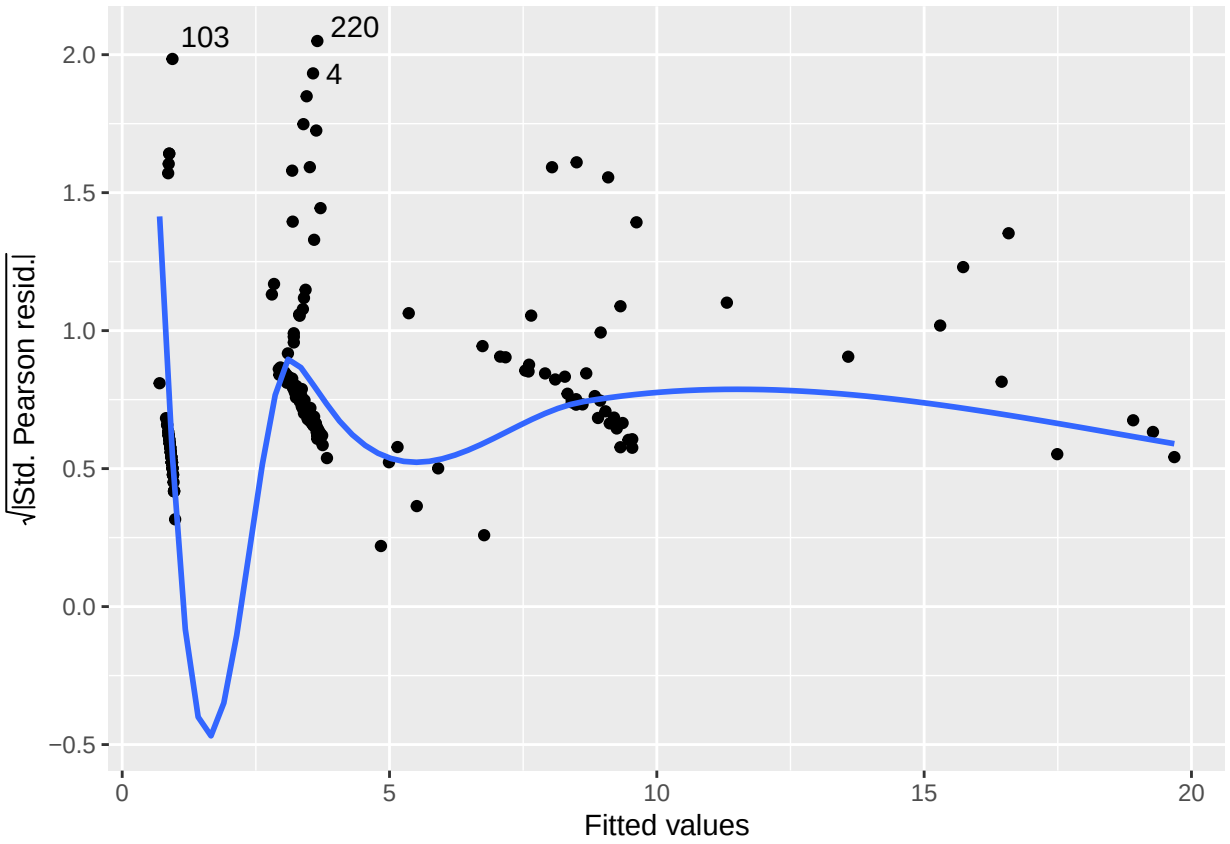

```
[[6]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```



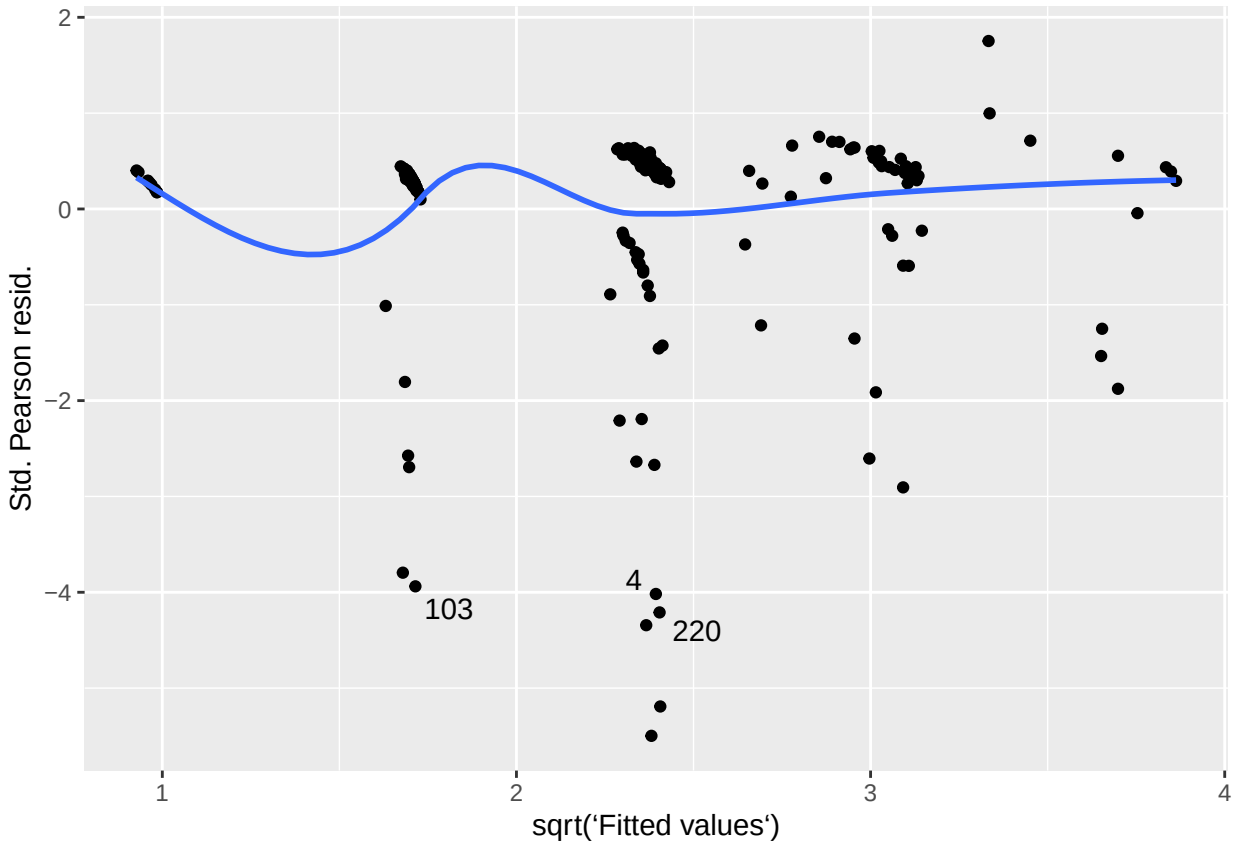
The plots don't look unreasonable.

Also make plots of residuals vs. square root of fitted and vs. network size:

```
autoplot(gof.wd, against=sqrt(.fitted))
```

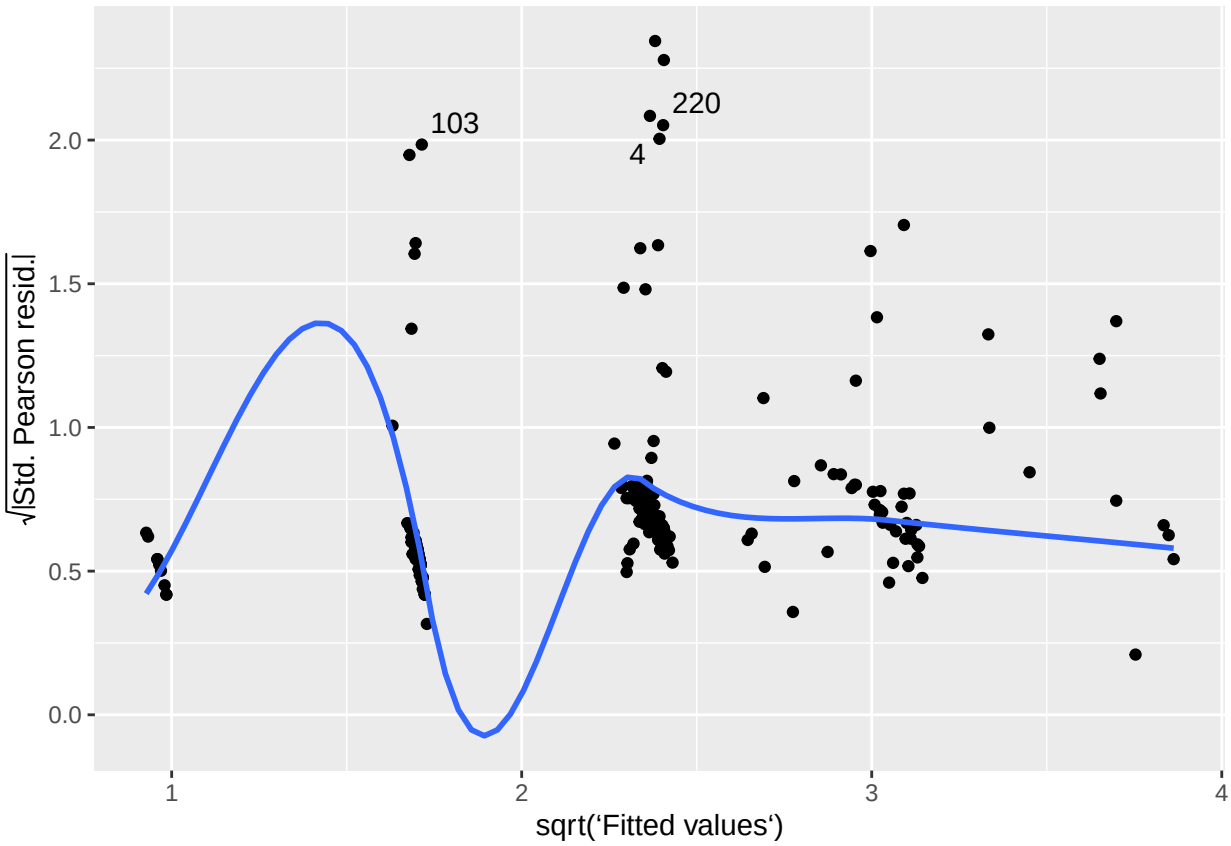
```
[[1]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```




```
[[2]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



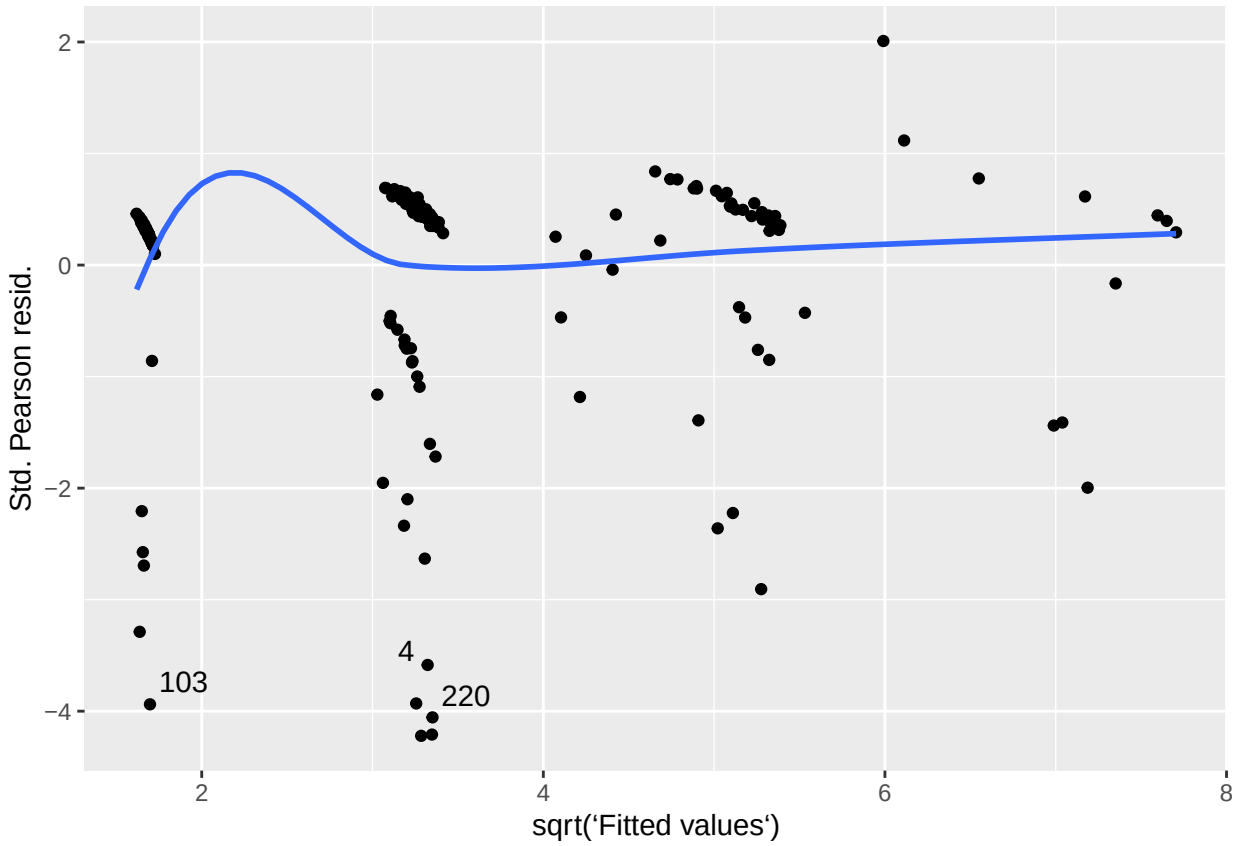

```
[[3]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```



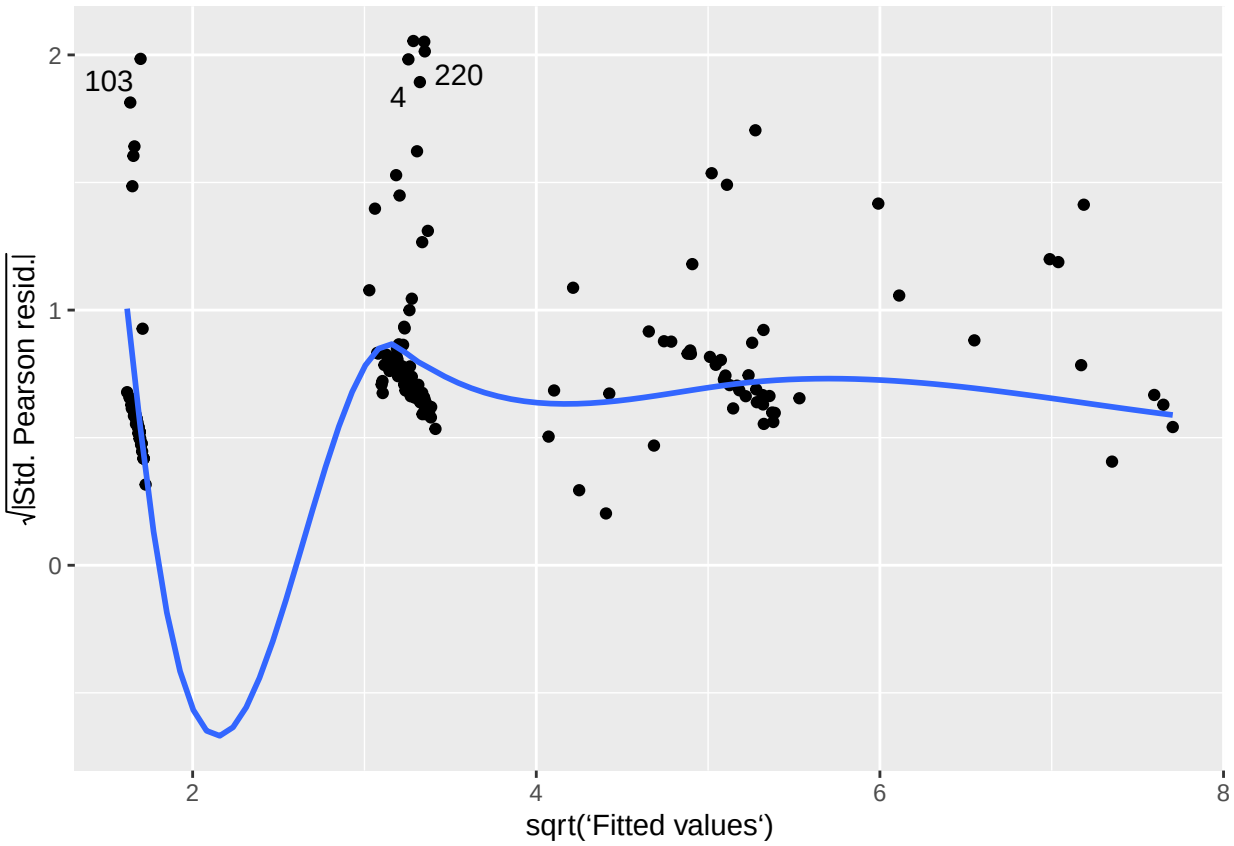

```
[[4]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

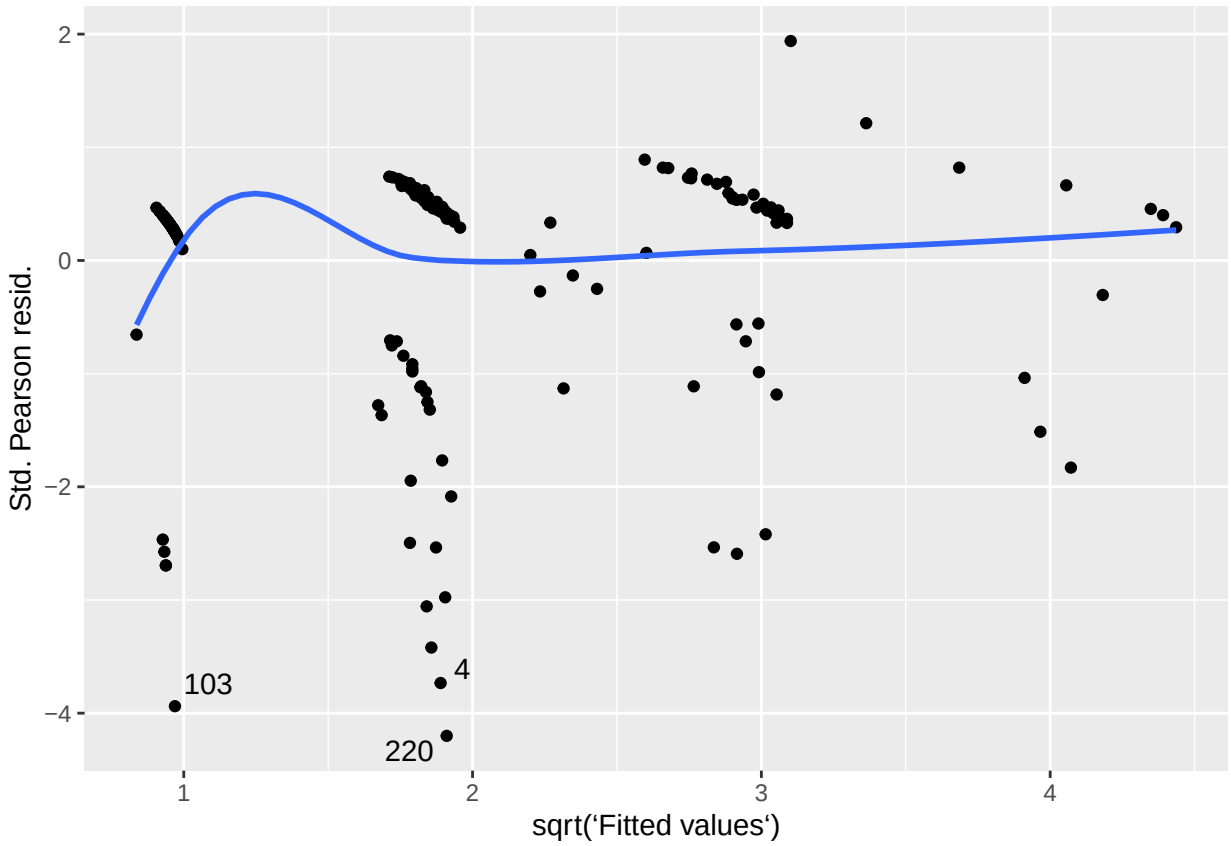
```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```




```
[[5]]

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'

Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).

Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).

Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```



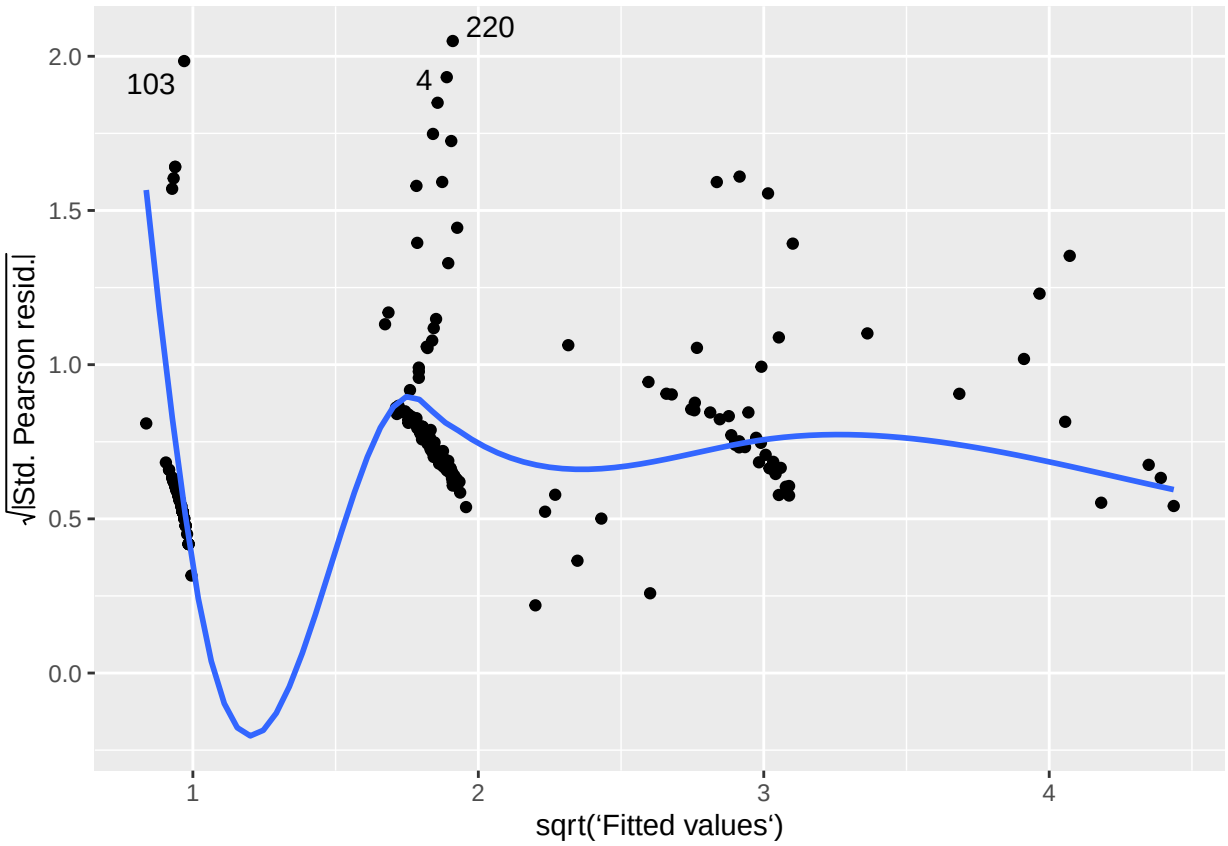

```
[[6]]
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_point()`).
```

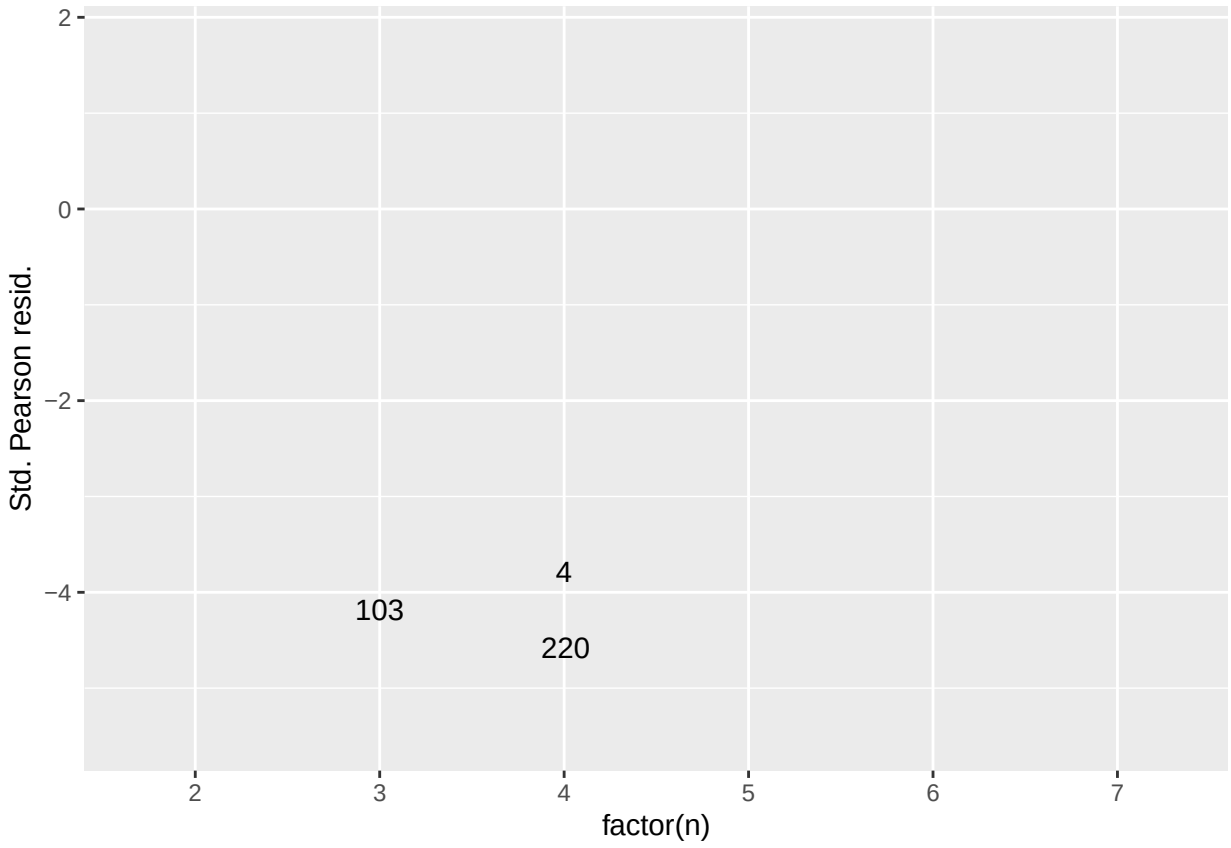
```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```




```
autoplot(gof.wd, against=factor(n))
```

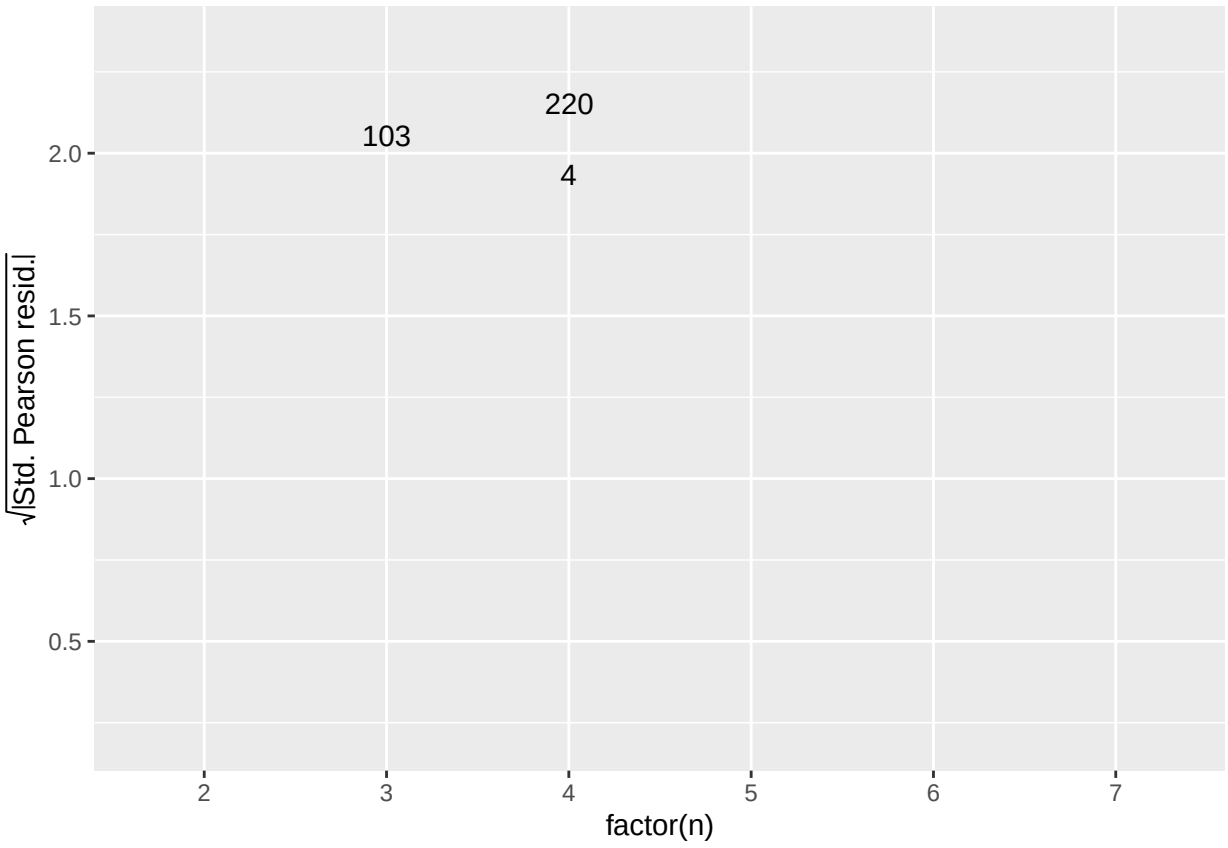
```
[[1]]
```

```
Warning: Computation failed in `stat_boxplot()`.
Caused by error in `loadNamespace()`:
! there is no package called 'quantreg'
```

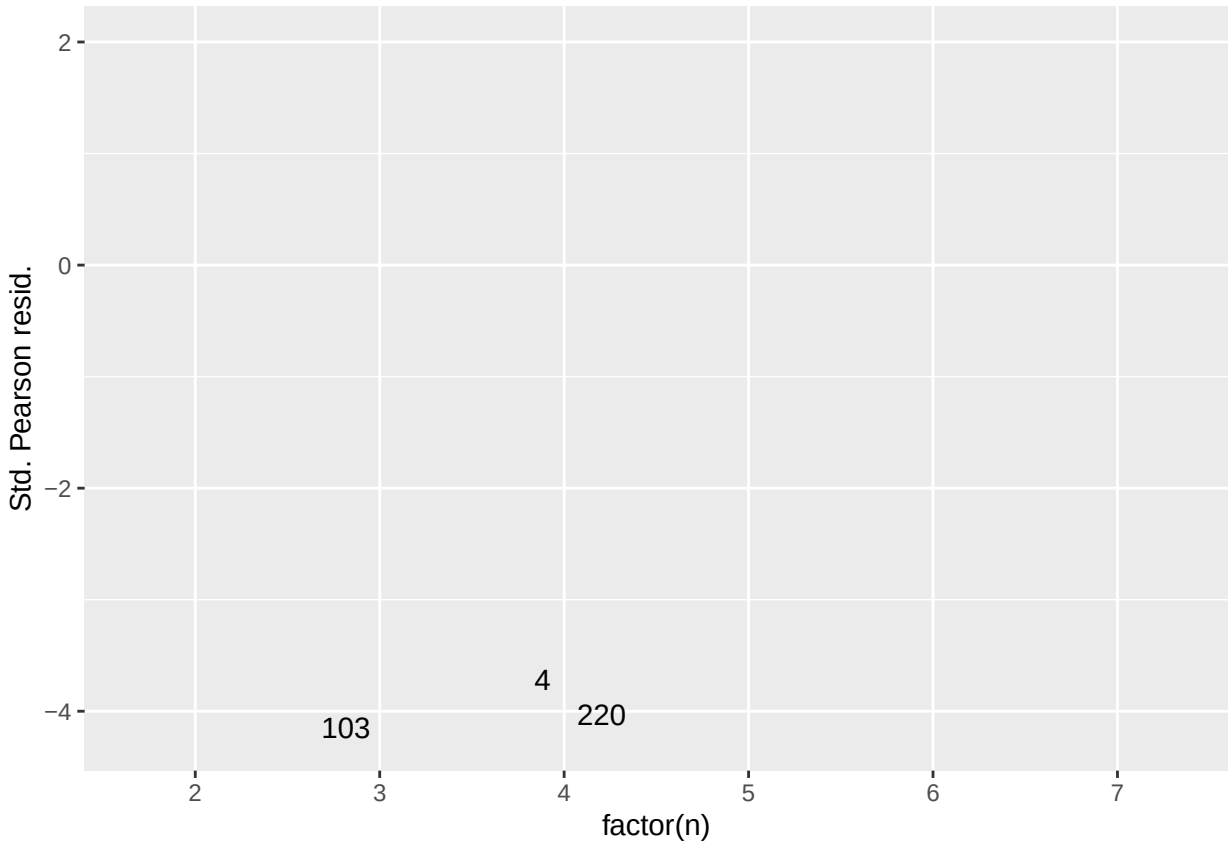



```
[[2]]
```

```
Warning: Computation failed in `stat_boxplot()`.
Caused by error in `loadNamespace()`:
! there is no package called 'quantreg'
```




```
[[3]]

Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_boxplot()`).

Warning: Computation failed in `stat_boxplot()`.
Caused by error in `loadNamespace()`:
! there is no package called 'quantreg'

Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```

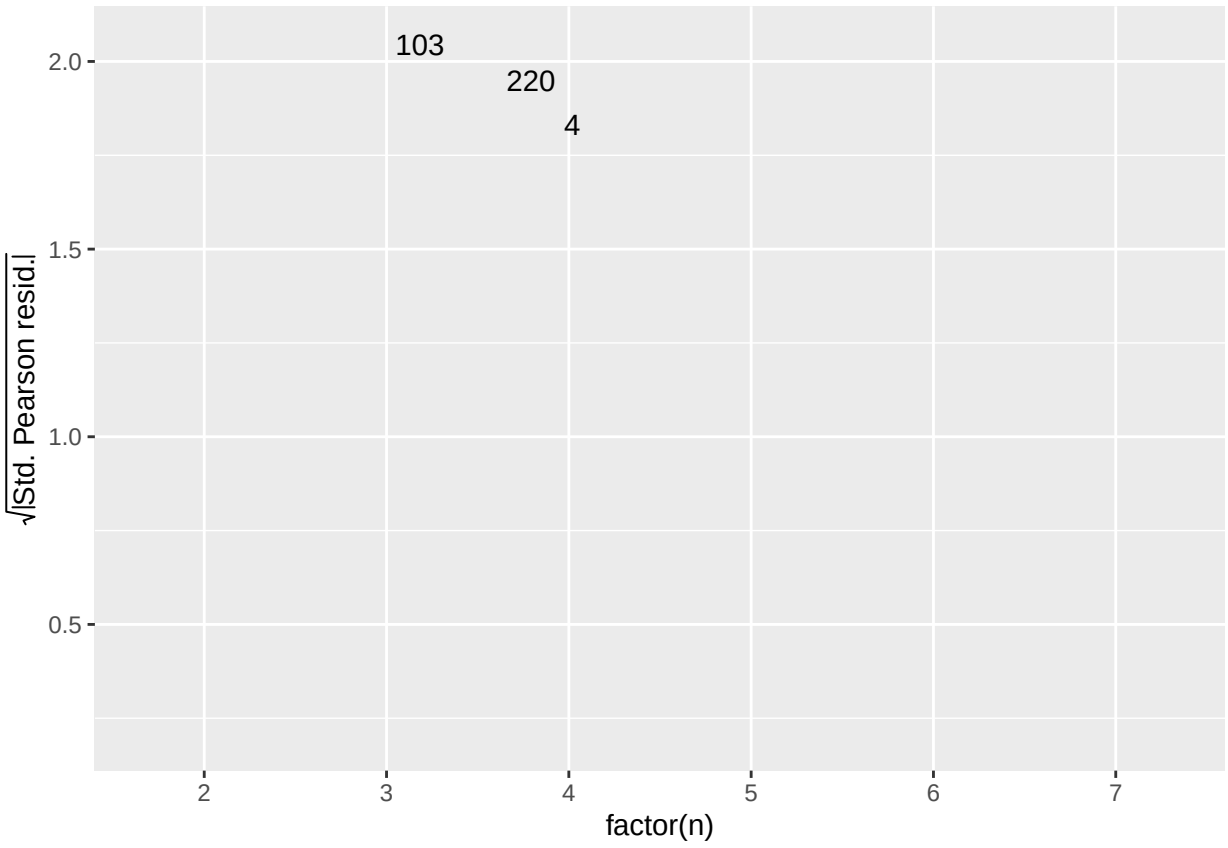



```
[[4]]
```

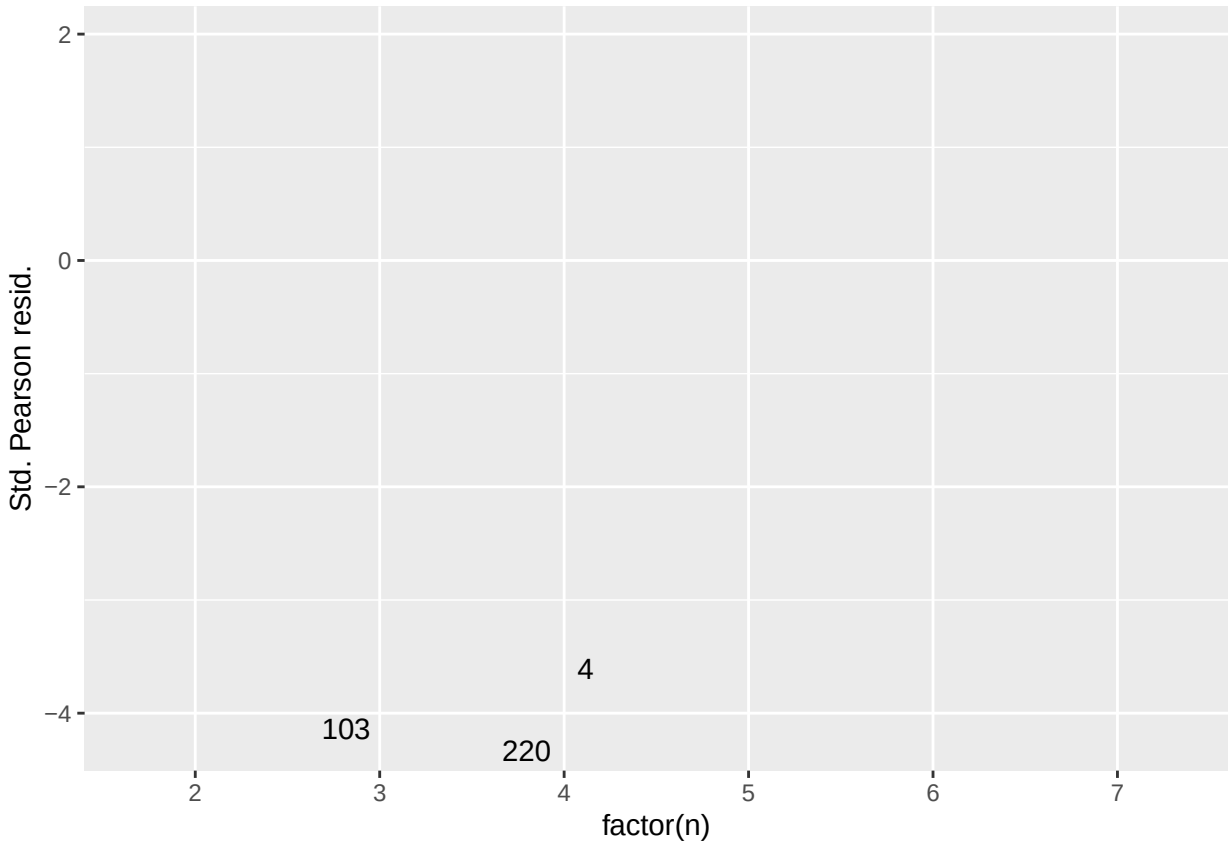
```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_boxplot()`).
```

```
Warning: Computation failed in `stat_boxplot()`.
Caused by error in `loadNamespace()`:
! there is no package called 'quantreg'
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```




```
[[5]]

Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_boxplot()`).

Warning: Computation failed in `stat_boxplot()`.
Caused by error in `loadNamespace()`:
! there is no package called 'quantreg'

Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```

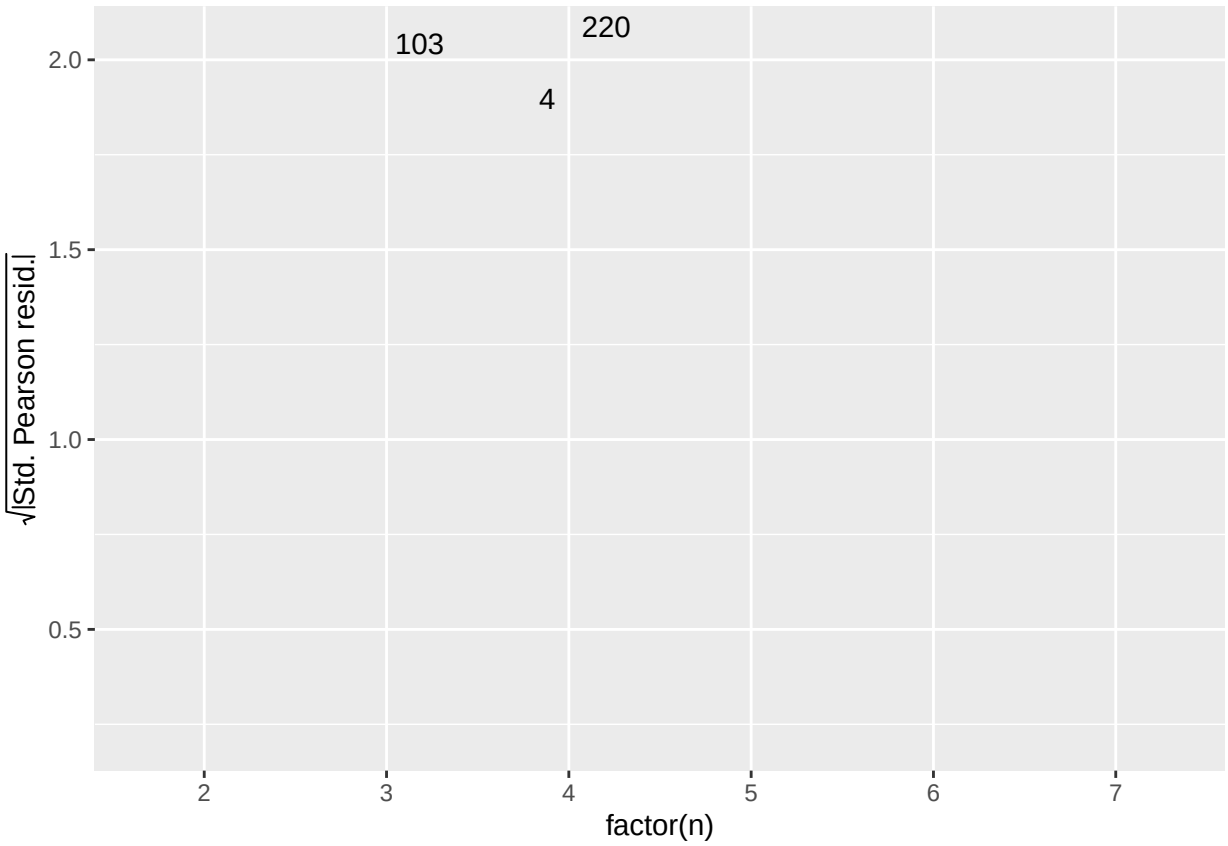



```
[[6]]
```

```
Warning: Removed 9 rows containing non-finite outside the scale range
(`stat_boxplot()`).
```

```
Warning: Computation failed in `stat_boxplot()`.
Caused by error in `loadNamespace()`:
! there is no package called 'quantreg'
```

```
Warning: Removed 9 rows containing missing values or values outside the scale
range (`geom_text_repel()`).
```



It looks like network-size effects are probably accounted for.

6. Estimation in the presence of missing data

It is quite common that network data are incomplete in various ways. The `ergm` package includes the capability to handle missing edge data, whereas other types of missingness such as missing nodal information are not addressed.

We illustrate using the `samplike` dataset used earlier. Consider a simple model with edges, mutuality (reciprocated dyads), transitive ties, and cyclical ties. For the sake of comparison, we first fit the model assuming no missing edge data. First, verify that `samplike` has no missing edges:

```
print(samplike)
```

```
 Network attributes:
  vertices = 18
  directed = TRUE
  hyper = FALSE
  loops = FALSE
  multiple = FALSE
  total edges= 88
    missing edges= 0
    non-missing edges= 88

 Vertex attribute names:
    cloisterville group vertex.names

 Edge attribute names:
```

```
    nominations
```

Now fit the model:

```
summary(full.fit <-
  ergm(samplike ~ edges + mutual + transitiveties + cyclicalties,
       eval.loglik = TRUE), control = snctrl(seed = 321))
```

```
Call:
ergm(formula = samplike ~ edges + mutual + transitiveties + cyclicalties,
    eval.loglik = TRUE)

Monte Carlo Maximum Likelihood Results:

               Estimate Std. Error MCMC % z value Pr(>|z|)
edges           -1.8942     0.3648      0  -5.192   <1e-04 ***
mutual           2.4790     0.4375      0   5.666   <1e-04 ***
transitiveties   0.5225     0.3076      0   1.699   0.0894 .
cyclicalties    -0.4546     0.2493      0  -1.823   0.0682 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 424.2  on 306  degrees of freedom
 Residual Deviance: 329.5  on 302  degrees of freedom

AIC: 337.5  BIC: 352.4  (Smaller is better. MC Std. Err. = 0.4547)
```

Next, suppose that Monk #1 (John Bosco) refused to respond during all three waves, rendering his replies missing:

```
samplike1 <- samplike
samplike1[1, ] <- NA
print(samplike1)
```

```
 Network attributes:
  vertices = 18
  directed = TRUE
  hyper = FALSE
  loops = FALSE
  multiple = FALSE
  total edges= 99
    missing edges= 17
    non-missing edges= 82

 Vertex attribute names:
    cloisterville group vertex.names

 Edge attribute names:
    nominations
```

If we pass this modified object to `ergm`, it will automatically calculate the MLE under the assumption that the monk's refusal is unrelated to his choice of relations, i.e., that the data are ignorably missing with respect to the specified model:

```
summary(m1.fit <-
  ergm(samplike1 ~ edges + mutual + transitiveties + cyclicalties,
       eval.loglik = TRUE), control = snctrl(seed = 321))
```

```
Call:
ergm(formula = samplike1 ~ edges + mutual + transitiveties +
    cyclicalties, eval.loglik = TRUE)

Monte Carlo Maximum Likelihood Results:

               Estimate Std. Error MCMC % z value Pr(>|z|)
edges           -2.0219     0.3918      0  -5.161   <1e-04 ***
mutual           2.4080     0.4734      0   5.087   <1e-04 ***
transitiveties   0.4585     0.4021      0   1.140    0.254
cyclicalties    -0.2777     0.3701      0  -0.750    0.453
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 400.6  on 289  degrees of freedom
 Residual Deviance: 313.7  on 285  degrees of freedom

AIC: 321.7  BIC: 336.4  (Smaller is better. MC Std. Err. = 0.6715)
```

The degrees of freedom associated with the missing data fit have decreased because unobserved dyads do not carry information.

For the theoretical grounding of the `ergm` package's algorithm for networks with missing edges, see Krivitsky et al (2022d), which is based on the framework developed by Handcock and Gile (2010). For more on the ignorability assumption for edge variables, see Handcock and Gile (2010).

The estimation approach above can be extended to other types of incomplete network observation. Karwa et al. (2017) applied it to fit arbitrary ERGMs to networks whose dyad values had been stochastically perturbed—ties added and removed at random, with known probabilities—in order to preserve privacy. Another use case is multiple imputation for networks with missing data, in which multiple random versions of the full network are constructed by randomly inserting values for unobserved dyads according to probabilities that are determined based on, say, some type of logistic regression model.

These mechanisms may be invoked by passing an `obs.constraints` formula, specifying how the network of interest was observed. Of particular interest are the following constraints:

`observed` restricts the proposal to changing only those dyads that are recorded as missing.

`egocentric(attr = NULL, direction = c("both", "out", "in") )` restricts the proposal to changing only those dyads that would not be observed in an egocentric sample. That is, dyads cannot be modified that are incident on vertices for which attribute specification `attr` has value `TRUE` or, if `attr` is `NULL`, the vertex attribute `"na"` has value `FALSE`. For directed networks, `direction=="out"` only preserves the out-dyads of those actors, and `direction=="in"` preserves their in-dyads.

`dyadnoise(p01, p10)` Unlike the others, this is a soft constraint to adjust the sampled distribution for dyad-level noise with known perturbation probabilities, which can arise in a variety of contexts. It is assumed that the observed LHS network is a noisy observation of some unobserved true network, with `p01` giving the dyadwise probability of erroneously observing a tie where the true network had a non-tie and `p10` giving the dyadwise probability of erroneously observing a nontie where the true network had a tie. `p01` and `p10` can be either both be scalars or both be adjacency matrices of the same dimension as that of the LHS network giving these probabilities.

We may use the `obs.constraints` argument to re-fit the model above:

```
samplike2 <- samplike
samplike2[1,] <- 0 # Careful!  Zeros are not the same as missing, but...
samplike2 %v% "refused" <-
  rep(c(TRUE,FALSE),c(1,17)) # This new nodal covariate labels who is missing
```

```
print(samplike2)
```

```
 Network attributes:
  vertices = 18
  directed = TRUE
  hyper = FALSE
  loops = FALSE
  multiple = FALSE
  total edges= 82
    missing edges= 0
    non-missing edges= 82

 Vertex attribute names:
    cloisterville group refused vertex.names

 Edge attribute names:
    nominations
```

```
summary(m2.fit <-
  ergm(samplike2 ~ edges + mutual + transitiveties + cyclicalties,
        obs.constraints = ~ egocentric( ~ !refused, "out"),
        control = snctrl(seed = 123) ) )
```

```
Call:
ergm(formula = samplike2 ~ edges + mutual + transitiveties +
    cyclicalties, obs.constraints = ~egocentric(~!refused, "out"),
    control = snctrl(seed = 123))

Monte Carlo Maximum Likelihood Results:

               Estimate Std. Error MCMC % z value Pr(>|z|)
edges           -2.0149     0.4104      0  -4.910   <1e-04 ***
mutual           2.4407     0.4792      0   5.093   <1e-04 ***
transitiveties   0.4519     0.4335      0   1.042    0.297
cyclicalties    -0.2832     0.3903      0  -0.726    0.468
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 400.6  on 289  degrees of freedom
 Residual Deviance: 314.0  on 285  degrees of freedom

AIC: 322  BIC: 336.6  (Smaller is better. MC Std. Err. = 0.5995)
```

Finally, the observational process can be included as a part of the network dataset using the `%ergmlhs%` operation. If we do this, we do not need to explicitly pass the `obs.constraints` argument to the `ergm` function:

```
samplike2 %ergmlhs% "obs.constraints" <- ~ egocentric( ~ !refused, "out")
summary(m3.fit <-
  ergm(samplike2 ~ edges + mutual + transitiveties + cyclicalties),
        control = snctrl(seed = 231) )
```

```
Call:
ergm(formula = samplike2 ~ edges + mutual + transitiveties +
    cyclicalties)
```

```
Monte Carlo Maximum Likelihood Results:

               Estimate Std. Error MCMC % z value Pr(>|z|)
edges           -2.0409     0.3773      0  -5.409   <1e-04 ***
mutual           2.4716     0.4719      0   5.238   <1e-04 ***
transitiveties   0.4148     0.4128      0   1.005    0.315
cyclicalties    -0.2314     0.3691      0  -0.627    0.531
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 400.6  on 289  degrees of freedom
 Residual Deviance: 313.1  on 285  degrees of freedom

AIC: 321.1  BIC: 335.8  (Smaller is better. MC Std. Err. = 0.6085)
```

7. Multilayer networks

Also known as multiplex, multirelational, or multivariate networks, in a multilayer network a pair of actors can have multiple simultaneous relations of different types. For example, in the famous Lazega lawyer, each pair of lawyers in the firm can have an advice relationship, a coworking relationship, a friendship relationship, or any combination thereof. Application of ERGMs to multilayer networks has a long history (e.g., Pattison and Wasserman 1999, Lazega and pattison 1999), and a number of R packages exist for analysing and estimating them.

`ergm.multi` implements the general approach of Krivitsky, Koehly, and Marcum (2020) for specifying multilayer ERGMs, including Layer Logic and the various cross-layer specifications. Its advantages include seamless integration with `ergm()`, number of layers limited only by computing power, ability to incorporate any ERGM effects into the framework, handling of networks that have both directed and undirected layers, and experimental multimode/multilevel support.

Preparing multilayer networks for analysis

To keep things simple (and fast), we will use the Florentine dataset included with `ergm`. It comprises two networks of relations among Florentine families, one of marriages, the other of business relations. Although the following examples only include two layers, `ergm.multi` supports an arbitrary number.

```
data(florentine)

# Method 1: list of networks
flo <- Layer(list(m = flomarriage, b = flobusiness))

# Method 2: networks as arguments
flo <- Layer(m = flomarriage, b = flobusiness)

# Method 3: edge attributes:
flo2 <- flomarriage | flobusiness # superset of all edges in any layer
# set attributes
flo2[,, names.eval="m"] <- as.matrix(flomarriage)
flo2[,, names.eval="b"] <- as.matrix(flobusiness)
flo2
```

```
 Network attributes:
  vertices = 16
  directed = FALSE
  hyper = FALSE
  loops = FALSE
```

```
  multiple = FALSE
  bipartite = FALSE
  total edges= 27
    missing edges= 0
    non-missing edges= 27

 Vertex attribute names:
    vertex.names

 Edge attribute names:
    b m
```

```
flo <- Layer(flo2, c("m","b"))

flo
```

```
 Combined 2 networks on '.LayerID'/'.LayerName':
  1: n = 16, directed = FALSE, bipartite = FALSE, loops = FALSE
  2: n = 16, directed = FALSE, bipartite = FALSE, loops = FALSE

 Network attributes:
  vertices = 32
  directed = FALSE
  hyper = FALSE
  loops = FALSE
  multiple = FALSE
  bipartite = FALSE
  ergm:
            Length Class   Mode
constraints 2      formula call
  total edges= 35
    missing edges= 0
    non-missing edges= 35

 Vertex attribute names:
    .bipartite .LayerID .LayerName .undirected vertex.names

 Edge attribute names:
    b m
```

`flo` is now a network with some additional metadata set.

Incidentally, we can extract the network defined by a particular edge attribute using the `network_view()` helper function:

```
all(as.matrix(network_view(flo2, "m")) == as.matrix(flomarriage))
```

```
[1] TRUE
```

We will also use the Lazega Lawyers data to illustrate available techniques. This dataset is included with the `ergm.multi` package:

```
data(Lazega)
Lazega
```

```
 Network attributes:
  vertices = 71
  directed = TRUE
```

```
 hyper = FALSE
 loops = FALSE
 multiple = FALSE
 bipartite = FALSE
 total edges= 1574
   missing edges= 0
   non-missing edges= 1574

Vertex attribute names:
   age gender office practice school seniority status vertex.names yrs_frm

Edge attribute names not shown
```

This network has a number of vertex attributes, including each lawyer's demographic information, status in the firm, and professional history. It also has three non-NA edge attributes,

```
list.edge.attributes(Lazega)
```

```
[1] "advice"     "coworker"   "friendship" "na"
```

```
head(Lazega %e%"advice")
```

```
[1] 1 1 1 1 1 0
```

```
head(Lazega %e%"coworker")
```

```
[1] 0 0 0 0 0 0
```

```
head(Lazega %e%"friendship")
```

```
[1] 0 0 0 0 0 1
```

each representing a type of relationship collected. Note that the edges of the network itself are a superset of all layers' edges:

```
all(Lazega %e%"advice" + Lazega %e%"coworker" + Lazega %e%"friendship" > 0)
```

```
[1] TRUE
```

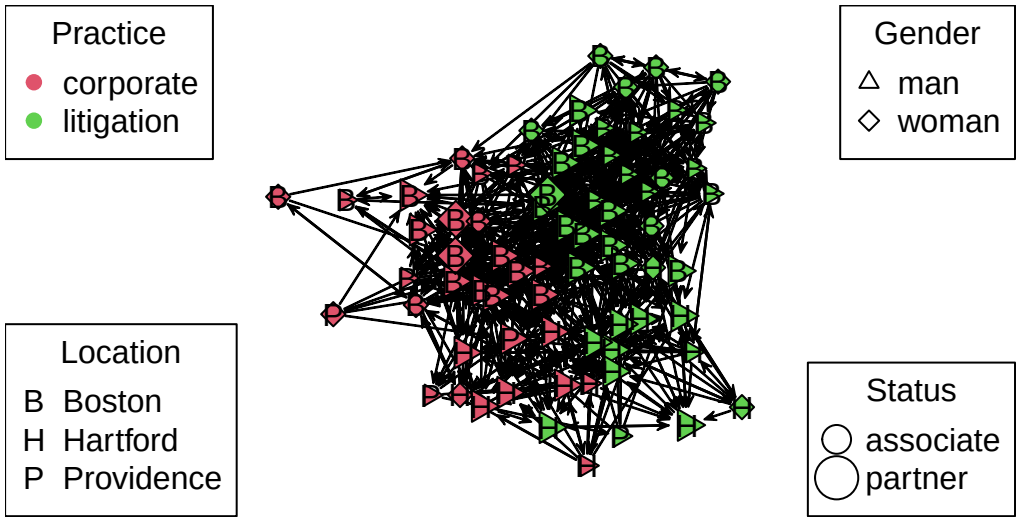
We can extract the individual layers using a helper function `network_view()`:

```
(L.a <- network_view(Lazega, "advice"))
```

```
Network attributes:
 vertices = 71
 directed = TRUE
 hyper = FALSE
 loops = FALSE
 multiple = FALSE
 bipartite = FALSE
 total edges= 892
   missing edges= 0
   non-missing edges= 892

Vertex attribute names:
   age gender office practice school seniority status vertex.names yrs_frm

Edge attribute names not shown
```

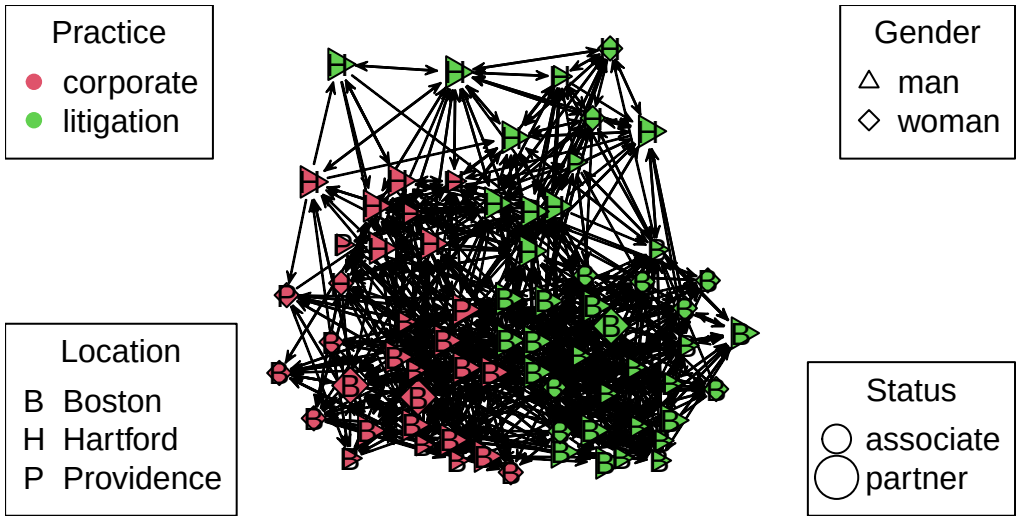
```
L.c <- network_view(Lazega, "coworker")
L.f <- network_view(Lazega, "friendship")
```

```
library(sna)
# Plot the advice network
coord <- gplot(L.a,
# Colour the vertex according to the practice.
      vertex.col=as.numeric(as.factor(Lazega%v%"practice"))+1,
# Size the vertex according the seniority (2 if associate, 3 if partner):
      vertex.cex=2+(Lazega%v%"status"=="partner"),
# # sides according to gender (2+1 for Female, 2+2 for Male):
     vertex.sides=as.numeric(as.factor(Lazega%v%"gender"))+2,
      displayisolates=FALSE)
text(coord, label=substr(Lazega%v%"office",1,1))
# Also, add a legend for colour, shape, plotting symbol, and letter:
legend("topleft",legend=levels(as.factor(Lazega%v%"practice")),
       col=2:3,pch=19, title="Practice")
legend("topright",legend=levels(as.factor(Lazega%v%"gender")),
       pch=c(2,5), title="Gender")
legend("bottomright",legend=levels(factor(Lazega%v%"status")),
       pt.cex=c(2,3), pch=1, title="Status")
legend("bottomleft",legend=levels(factor(Lazega%v%"office")),
       pch=substr(levels(factor(Lazega%v%"office")),1,1),title="Location")
```

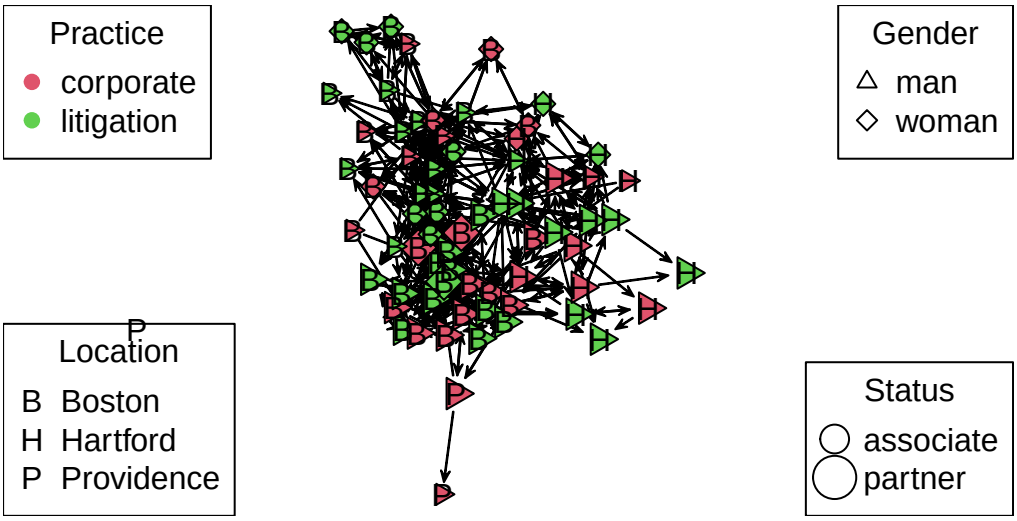



```
# Plot the coworker network
coord <- gplot(L.c,
# Colour the vertex according to the practice.
      vertex.col=as.numeric(as.factor(Lazega%v%"practice"))+1,
# Size the vertex according the seniority (2 if associate, 3 if partner):
      vertex.cex=2+(Lazega%v%"status"=="partner"),
# # sides according to gender (2+1 for Female, 2+2 for Male):
     vertex.sides=as.numeric(as.factor(Lazega%v%"gender"))+2,
      displayisolates=FALSE)
text(coord, label=substr(Lazega%v%"office",1,1))
# Also, add a legend for colour, shape, plotting symbol, and letter:
legend("topleft",legend=levels(as.factor(Lazega%v%"practice")),
       col=2:3,pch=19, title="Practice")
```

```
legend("topright",legend=levels(as.factor(Lazega%v%"gender")),
       pch=c(2,5), title="Gender")
legend("bottomright",legend=levels(factor(Lazega%v%"status")),
       pt.cex=c(2,3), pch=1, title="Status")
legend("bottomleft",legend=levels(factor(Lazega%v%"office")),
       pch=substr(levels(factor(Lazega%v%"office")),1,1),title="Location")
```




```
# Plot the friendship network
coord <- gplot(L.f,
# Colour the vertex according to the practice.
      vertex.col=as.numeric(as.factor(Lazega%v%"practice"))+1,
# Size the vertex according the seniority (2 if associate, 3 if partner):
      vertex.cex=2+(Lazega%v%"status"=="partner"),
# # sides according to gender (2+1 for Female, 2+2 for Male):
     vertex.sides=as.numeric(as.factor(Lazega%v%"gender"))+2,
      displayisolates=FALSE)
text(coord, label=substr(Lazega%v%"office",1,1))
# Also, add a legend for colour, shape, plotting symbol, and letter:
legend("topleft",legend=levels(as.factor(Lazega%v%"practice")),
       col=2:3,pch=19, title="Practice")
legend("topright",legend=levels(as.factor(Lazega%v%"gender")),
       pch=c(2,5), title="Gender")
legend("bottomright",legend=levels(factor(Lazega%v%"status")),
       pt.cex=c(2,3), pch=1, title="Status")
legend("bottomleft",legend=levels(factor(Lazega%v%"office")),
       pch=substr(levels(factor(Lazega%v%"office")),1,1),title="Location")
```



To model it, we need to tell `ergm` to interpret it as a multilayer network, which we do using the `Layer()` function (*not* an ERGM term). In this case, the most convenient way to do so is by referencing edge attributes:

```
LLazega <- Layer(Lazega, c("advice", "coworker", "friendship"))
```

However, an optionally named list of networks or networks as named arguments are also accepted. We will use it to shorten the layer names:

```
LLazega <- Layer(a=L.a, c=L.c, f=L.f)
```

More generally, `Layer()` will produce the "least common denominator" network: if any unipartite layers are present, bipartite layers will be coerced to unipartite (with some additional metadata to ensure that disallowed edges are never formed), and if any directed layers are present, all layers will be coerced to directed. It is possible to use `Symmetrize()` and `S()` (Subgraph) operators to evaluate undirected and bipartite effects on these layers.

Specifying models for multilayer networks

Given the `Layer()` construct on the LHS of an `ergm()` formula, we can use *layer-aware* terms on the RHS. By convention, layer-aware terms have capital `L` appended to them. For example, `mutualL` is a layer-aware generalization of `mutual`. These terms have one or more explicit (usually optional) layer specification arguments. By convention, an argument that requires one layer specification is named `L=` and one that requires a list of specifications (constructed by `list()` or just `c()` is named `Ls=`; and a specification of the form `~.` is a placeholder for all observed layers.

We can get a list of layer-aware terms currently visible to ERGM with

```
search.ergmTerms(keywords="layer-aware")
```

```
Found  10  matching ergm terms:
CMBL(Ls=~.) (binary)
    Conway--Maxwell-Binomial dependence among layers

ddspL(d, type="OTP", Ls.path=NULL, L.in_order=FALSE) (binary)
dspL(d, type="OTP", Ls.path=NULL, L.in_order=FALSE) (binary)
    Dyadwise shared partners on layers

despL(d, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary)
espL(d, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary)
    Edgewise shared partners on layers
```

```
dgwdspL(decay, fixed=FALSE, cutoff=30, type="OTP", Ls.path=NULL, L.in_order=FALSE) (binary)
gwdspL(decay, fixed=FALSE, cutoff=30, type="OTP", Ls.path=NULL, L.in_order=FALSE) (binary)
    Geometrically weighted dyadwise shared partner distribution on layers

dgwespL(decay, fixed=FALSE, cutoff=30, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary
gwespL(decay, fixed=FALSE, cutoff=30, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary)
    Geometrically weighted edgewise shared partner distribution on layers

dgwnspL(decay, fixed=FALSE, cutoff=30, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary
gwnspL(decay, fixed=FALSE, cutoff=30, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary)
    Geometrically weighted non-edgewise shared partner distribution on layers

dnspL(d, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary)
nspL(d, type="OTP", L.base=NULL, Ls.path=NULL, L.in_order=FALSE) (binary)
    Non-edgewise shared partners and paths on layers

L(formula, Ls=~.) (binary)
    Evaluation on layers

mutualL(same=NULL, diff=FALSE, by=NULL, keep=NULL, Ls=NULL) (binary)
    Mutuality

twostarL(Ls, type, distinct=TRUE) (binary)
    Multilayer two-star
```

Layer Logic But how do we specify layers?

Layer Logic is an approach to specifying layers, their transformations, and interactions between two or more layers by constructing *logical layers*, which are layers constructed by evaluating logical expressions on observed layers.

Each formula's right-hand side describes an observed layer *or* some "logical" layer, whose ties are a function of corresponding ties in observed layers. (Krivitsky et al. 2020)

The observed layers can be referenced either by name or by number (i.e., order in which they were passed to `Layer`). When referencing by number, enclose the number in quotation marks (e.g., `"1"`) or backticks (e.g., `` `1` ``).

Standard arithmetical, comparison, and logical operations can be used, as well as as some mathematical functions such as `abs()`, `round()`, and `sign()`. Standard operator precedence is followed applies, so use of parentheses is recommended to ensure the logical expression is what it looks like.

For example, if LHS is `Layer(A=nwA, B=nwB)`, both `` ~`2` `` and `~B` refer to `nwB`, while `A&!B` refers to a logical layer that has ties that are in `nwA` but not in `nwB`.

Transpose function `t()` applied to a directed layer will reverse the direction of all relations (transposing the sociomatrix). Unlike the others, it can only be used on an observed layer directly. For example, `` ~t(`1`)&t(`2`) `` is valid but `` ~t(`1`&`2`) `` is not.

At this time, logical expressions that produce complete graphs from empty graph inputs (e.g., `A==B` or `!A`) are not supported.

The `L(formula, Ls)` operator This is probably the most frequently used layer-aware term: it takes an arbitrary binary `ergm` formula and evaluates it on each observed or logical layer specified in `Ls`, and then adds up the results elementwise. A very common usage is to write `L(~[TERMS], ~.)` to fit an effect of `[TERMS]` homogeneous over all layers.

```
summary(LLazega~L(~edges, ~f))
```

```
L(f)~edges
       575
```

```
summary(L.f~edges)
```

```
edges
  575
```

```
summary(LLazega~L(~edges, c(~f, ~a)))
```

```
L((f,a))~edges
          1467
```

```
summary(L.f~edges) + summary(L.a~edges)
```

```
edges
 1467
```

```
summary(LLazega~L(~edges, ~.))
```

```
L(.)~edges
      2571
```

```
summary(L.f~edges) + summary(L.c~edges) + summary(L.a~edges)
```

```
edges
 2571
```

```
summary(LLazega~L(~edges, ~f|a))
```

```
L(f|a)~edges
        1109
```

```
summary((L.f|L.a)~edges)
```

```
edges
 1109
```

However, note that while the statistics are the same, the MLEs are different:

```
ergm(Layer(f=L.f, a=L.a)~L(~edges, ~f|a))
```

```
Call:
ergm(formula = Layer(f = L.f, a = L.a) ~ L(~edges, ~f | a))

Monte Carlo Maximum Likelihood Coefficients:
L(f|a)~edges
      -2.342
```

```
ergm((L.f|L.a)~edges)
```

```
Call:
ergm(formula = (L.f | L.a) ~ edges)

Maximum Likelihood Coefficients:
 edges
-1.247
```

This is because the sample space for the first one is all-possible two-layer networks, whereas the sample space for the second one is all possible one-layer networks. Thus, the normalizing constant is different.

Modelling association between layers

- `CMBL(Ls)`: ***Conway–Maxwell-binomial distribution*:** By "default", if m layers in `Ls` are homogeneous, the number of the layers with an edge should be Binomial(m, p) where p is the density of each layer. CMB replaces the "$\binom{m}{y_{i,j}}$" in the binomial density with "$\binom{m}{y_{i,j}}^{\theta_{CMB}}$": a positive coefficient implies positive dependence and a negative one induces negative dependence.

Is there an overall positive association between nominations?

```
summary(ergm(LLazega~L(~edges, ~.) + CMBL(~.)))
```

```
Call:
ergm(formula = LLazega ~ L(~edges, ~.) + CMBL(~.))

Monte Carlo Maximum Likelihood Results:

           Estimate Std. Error MCMC % z value Pr(>|z|)
L(.)~edges -0.82841    0.01878      0  -44.12   <1e-04 ***
CMBL(~.)    1.42167    0.03479      0   40.87   <1e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 20670  on 14910  degrees of freedom
 Residual Deviance: 12290  on 14908  degrees of freedom

AIC: 12294  BIC: 12309  (Smaller is better. MC Std. Err. = 3.847)
```

Yes!

What if we focus on giving advice rather than receiving?

```
summary(ergm(LLazega~L(~edges, c(~t(a),~c,~f)) + CMBL(c(~t(a),~c,~f))))
```

```
Call:
ergm(formula = LLazega ~ L(~edges, c(~t(a), ~c, ~f)) + CMBL(c(~t(a),
    ~c, ~f)))

Monte Carlo Maximum Likelihood Results:

                       Estimate Std. Error MCMC % z value Pr(>|z|)
L((t(a),c,f))~edges    -0.89666    0.02148      1  -41.75   <1e-04 ***
CMBL(list(~t(a),~c,~f))  1.21809    0.03489      0   34.91   <1e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 20670  on 14910  degrees of freedom
 Residual Deviance: 12732  on 14908  degrees of freedom

AIC: 12736  BIC: 12751  (Smaller is better. MC Std. Err. = 4.932)
```

Still yes.

Direct layer logic effects Consider a two-layer model for a dyad (i, j),

$$\Pr(Y_{i,j,A} = y_{i,j,A} \wedge Y_{i,j,B} = y_{i,j,B}) \propto \exp(\theta_1 y_{i,j,A} + \theta_2 y_{i,j,B} + \theta_3 y_{i,j,A\square B}),$$

for some logical operation $\square$.

What happens if we fix $y_{i,j,B}$ and look at the conditional probability of $\Pr(Y_{i,j,A} = 1)$?

- `a&b`: ***Conjunction***: $\text{logit}^{-1}(\theta_1 + \theta_3 y_{i,j,B})$, so $\theta_3 > 0 \implies$ presence of an edge in layer `b` will increase the probability of the edge in layer `a`.
- `xor(a,b)`: ***Mutual exclusivity***: $\text{logit}^{-1}(\theta_1 + \theta_3 (-1)^{y_{i,j,B}})$, so $\theta_3 > 0 \implies$ presence of an edge in layer `b` will decrease the probability of the edge in layer `a`.
- `a|b`: ***Substitutability***: $\text{logit}^{-1}(\theta_1 + \theta_3 (1 - y_{i,j,B}))$, so $\theta_3 > 0 \implies$ presence of an edge in layer `b` will undo a "default" increase in the probability of the edge in layer `a`.

```
summary(ergm(Layer(a=L.a,c=L.c)~L(~edges, ~a) + L(~edges, ~c) + L(~edges, ~a&c)))
```

```
Call:
ergm(formula = Layer(a = L.a, c = L.c) ~ L(~edges, ~a) + L(~edges,
    ~c) + L(~edges, ~a & c))

Monte Carlo Maximum Likelihood Results:

             Estimate Std. Error MCMC % z value Pr(>|z|)
L(a)~edges   -2.43931    0.05655      0  -43.14   <1e-04 ***
L(c)~edges   -1.92166    0.04613      0  -41.66   <1e-04 ***
L(a&c)~edges  2.54346    0.08299      0   30.65   <1e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 13780  on 9940  degrees of freedom
 Residual Deviance:  8951  on 9937  degrees of freedom

AIC: 8957  BIC: 8979  (Smaller is better. MC Std. Err. = 3.07)
```

```
summary(ergm(Layer(a=L.a,c=L.c)~L(~edges, ~a) + L(~edges, ~c) + L(~edges, ~xor(a,c))))
```

```
Call:
ergm(formula = Layer(a = L.a, c = L.c) ~ L(~edges, ~a) + L(~edges,
    ~c) + L(~edges, ~xor(a, c)))

Monte Carlo Maximum Likelihood Results:

                  Estimate Std. Error MCMC % z value Pr(>|z|)
L(a)~edges        -1.16375    0.04221      0  -27.57   <1e-04 ***
L(c)~edges        -0.64265    0.04132      0  -15.55   <1e-04 ***
L(xor(a,c))~edges -1.27716    0.04052      0  -31.52   <1e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 13780  on 9940  degrees of freedom
 Residual Deviance:  8951  on 9937  degrees of freedom

AIC: 8957  BIC: 8978  (Smaller is better. MC Std. Err. = 3.54)
```

```
summary(ergm(Layer(a=L.a,c=L.c)~L(~edges, ~a) + L(~edges, ~c) + L(~edges, ~a|c)))
```

```
Call:
ergm(formula = Layer(a = L.a, c = L.c) ~ L(~edges, ~a) + L(~edges,
    ~c) + L(~edges, ~a | c))
```

```
Monte Carlo Maximum Likelihood Results:

             Estimate Std. Error MCMC % z value Pr(>|z|)
L(a)~edges    0.11157    0.05773      0   1.933   0.0533 .
L(c)~edges    0.63421    0.06919      0   9.166   <1e-04 ***
L(a|c)~edges -2.55271    0.07640      0 -33.413   <1e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 13780  on 9940  degrees of freedom
 Residual Deviance:  8950  on 9937  degrees of freedom

AIC: 8956  BIC: 8978  (Smaller is better. MC Std. Err. = 2.848)
```

Cross-layer reciprocity

- `mutualL(Ls)`: ***Layer-aware mutuality*:** Given `Ls=c(~a, ~b)`, counts the number of ordered pairs (i, j) for which $y_{i,j,A} = 1 \wedge y_{j,i,B} = 1$.
- `L(~..., ~a&t(b))`: ***Reversal layer logic*:** Another way of expressing the above.

Net of within-layer density and mutuality and co-occurrence, does advice reciprocate coworking?

```
summary(ergm(Layer(a=L.a,c=L.c)~L(~edges + mutual, ~a) + L(~edges + mutual, ~c) +
               L(~edges, ~a&c) + mutualL(Ls=c(~a,~c))))
```

```
Call:
ergm(formula = Layer(a = L.a, c = L.c) ~ L(~edges + mutual, ~a) +
    L(~edges + mutual, ~c) + L(~edges, ~a & c) + mutualL(Ls = c(~a,
    ~c)))

Monte Carlo Maximum Likelihood Results:

              Estimate Std. Error MCMC % z value Pr(>|z|)
L(a)~edges    -2.55765    0.06282      0 -40.711   <1e-04 ***
L(a)~mutual    0.34352    0.15616      0   2.200   0.0278 *
L(c)~edges    -2.79888    0.06573      0 -42.584   <1e-04 ***
L(c)~mutual    2.54717    0.14507      0  17.558   <1e-04 ***
L(a&c)~edges   2.07234    0.10850      0  19.100   <1e-04 ***
L(a,c)~mutual  0.64414    0.12039      0   5.351   <1e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

     Null Deviance: 13780  on 9940  degrees of freedom
 Residual Deviance:  8116  on 9934  degrees of freedom

AIC: 8128  BIC: 8172  (Smaller is better. MC Std. Err. = 2.295)
```

It appears so.

Equivalently, we can write:

```
summary(ergm(Layer(a=L.a,c=L.c)~L(~edges + mutual, ~a) + L(~edges + mutual, ~c) +
               L(~edges, ~a&c) + L(~edges, ~a&t(c))))
```

Multilayer paths

- `twostarL(Ls, type, distinct)`: ***Cross-layer two-star or two-path*:** `Ls` is a list of two layers of interest (e.g., `list(~a,~b)`), and `type` is
  - `"any"` Undirected: instances where node i has an edge in layer `a` and an edge in layer `b`. (Whether these edges may be coincident depends on `distinct`.)
  - `"out"/"in"` Directed: instances where node i has out-edge/in-edge in `a` and out-edge/in-edge in `b`. (Whether these edges may be coincident depends on `distinct`.)
  - `"path"` Directed: instances where i has in-edge in `a` and an out-edge in `b`. (Whether these edges may be reciprocal depends on `distinct`.)

For illustration purposes, I will set `distinct=FALSE`. In your case, it should be driven by substantive or theoretical considerations.

```
summary(LLazega~twostarL(c(~c,~f), type="out", distinct=FALSE))
```

```
twostarL(c<>f)
         10563
```

```
# Equivalently...
sum(
  rowSums(as.matrix(L.c)) # Outdegree of each node in layer c
  *
  rowSums(as.matrix(L.f)) # Outdegree of each node in layer f
)
```

```
[1] 10563
```

```
summary(LLazega~twostarL(c(~c,~f), type="in", distinct=FALSE))
```

```
twostarL(c><f)
         10118
```

```
# Equivalently...
sum(
  colSums(as.matrix(L.c)) # Indegree of each node in layer c
  *
  colSums(as.matrix(L.f)) # Indegree of each node in layer f
)
```

```
[1] 10118
```

```
summary(LLazega~twostarL(c(~c,~f), type="path", distinct=FALSE))
```

```
twostarL(c>>f)
          9890
```

```
# Equivalently...
sum(
  colSums(as.matrix(L.c)) # Indegree of each node in layer c
  *
  rowSums(as.matrix(L.f)) # Outdegree of each node in layer f
)
```

```
[1] 9890
```

Multilayer triadic effects Triadic effects are generalized by `gwdspL`, `gwespL`, and `gwnspL` which take the standard arguments of `gw*sp` and `dgw*sp` effects, incluidng `type`, and, in addition, `L.base`, `Ls.path`, and `L.in_order`, specifying the layer of the base (for `gwespL` and `gwnspL`), the layer of the two-path, and whether, for the directed case, the order of the two-path matters.

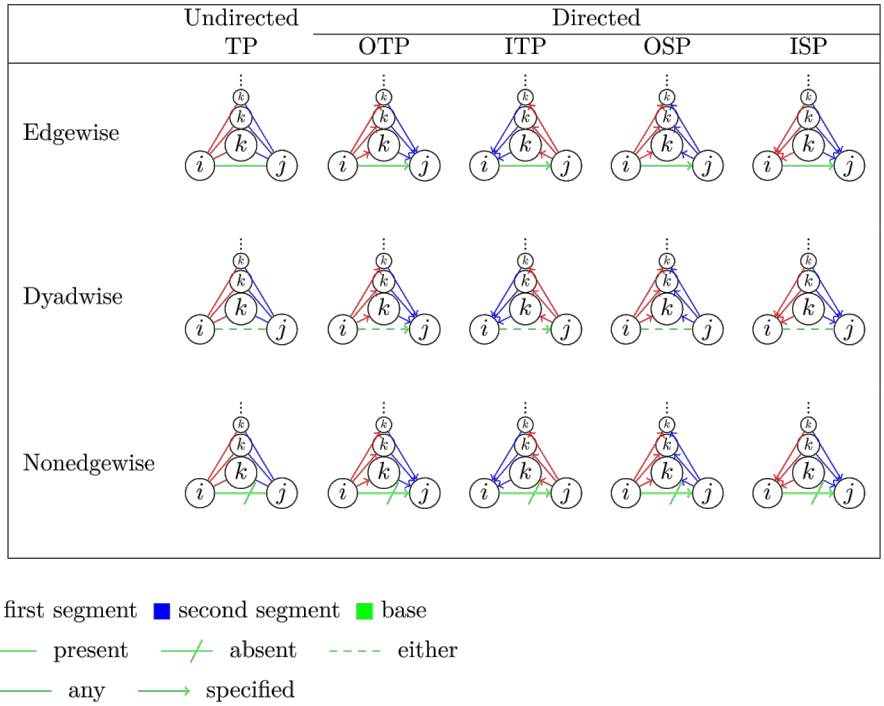


Figure 1: Taxonomy of cross-layer triadic structures. Reproduced from Krivitsky et al. (2020).

References

For a general orientation to the `statnet` packages, the best place to start is the special volume of the *Journal of Statistical Software* (JSS) devoted to `statnet`: https://www.jstatsoft.org/issue/view/v024. The nine papers in this volume cover a wide range of theoretical and practical topics related to ERGMs, and their implementation in `statnet`.

However, this volume was written in 2008. The `statnet` code base has evolved considerably since that time, and with the release of `ergm` version 4.0, the most current paper describing the capabilities of the `ergm` package is the following preprints:

Krivitsky, P. N., Hunter, D. R., Morris, M., and Klumb, C. (2023). ergm 4: New Features for Analyzing Exponential-Family Random Graph Models. *Journal of Statistical Software*, 105(6), 1–44. doi: 10.18637/jss.v105.i06

Krivitsky, P. N., David R. Hunter, Martina Morris, and Chad Klumb (2022b). ergm 4.0: Computational Improvements. arXiv: 2203.08198.

For social scientists, a good introductory application paper is:

Goodreau, S., J. Kitts and M. Morris (2009). Birds of a Feather, or Friend of a Friend? Using Statistical Network Analysis to Investigate Adolescent Social Networks. *Demography* 46(1): 103-125. doi: 10.1353/dem.0.0045

Goodness of Fit

Hunter, D. R., Goodreau, S. M., and Handcock, M. S. (2008).
Goodness of Fit for Social Network Models. *Journal of the American Statistical Association*, 103(481), 248–258. doi: 10.1198/016214507000000446

Temporal ERGMs

Krivitsky, P.N., Handcock, M.S,(2014). A separable model for dynamic networks *JRSS Series B-Statistical*

Methodology, 76(1):29-46. doi: 10.1111/rssb.12014

Krivitsky, P. N., M. S. Handcock and M. Morris (2011). Adjusting for Network Size and Composition Effects in Exponential-family Random Graph Models, *Statistical Methodology* 8(4): 319-339. doi: 10.1016/j.stamet.2011.01.005

Multiple and Multilayer ERGMS

Goeyvaerts, N., Santermans, E. Potter, G., Torneri, A., Van Kerckhove, K., Lander, W., Aerts, M., Beutels, P., and Hens, N. (2018). Household Members Do Not Contact Each Other at Random: Implications for Infectious Disease Modelling. *Proceedings of the Royal Society B: Biological Sciences*, 285(1893): 20182201. doi: 10.1098/rspb.2018.2201

Krivitsky, P. N., Coletti, P., and Hens, N. (2023). A Tale of Two Datasets: Representativeness and Generalisability of Inference for Samples of Networks. *Journal of the American Statistical Association*, 118(544): 2213–2224. doi: 10.1080/01621459.2023.2242627

Krivitsky, P. N., Koehly, L. M., and Marcum, C. S. (2020) Exponential-family Random Graph Models for Multi-layer Networks. *Psychometrika*, 85(3): 630-659. doi: 10.1007/s11336-020-09720-7

Missing Data

Handcock, M. S. and Gile, K. J. (2010). Modeling Social Networks from Sampled Data. *Annals of Applied Statistics*, 4(1), 5—25. doi:10.1214/08-AOAS221

Karwa, V., Krivitsky, P. N., and Slavković, A. B., (2017). Sharing Social Network Data: Differentially Private Estimation of Exponential-Family Random Graph Models. *Journal of the Royal Statistical Society C*, 66(3), 481–500. doi: 10.1111/rssc.12185

Krivitsky, P. N., Kuvelkar, A. R., and Hunter, D. R. (2022d). Likelihood-based Inference for Exponential-Family Random Graph Models via Linear Programming. *Electronic Journal of Statistics*, 17(2), 3337–3356. doi: 10.1214/23-ejs2176