

The **qgraph** package for network visualizations of psychometric data in R

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All codes in these slides were run using R version 2.12.1 (2010-12-16) and **qgraph** version 0.4.8 and were made on Windows 7 x64 x86-64 build 7600.

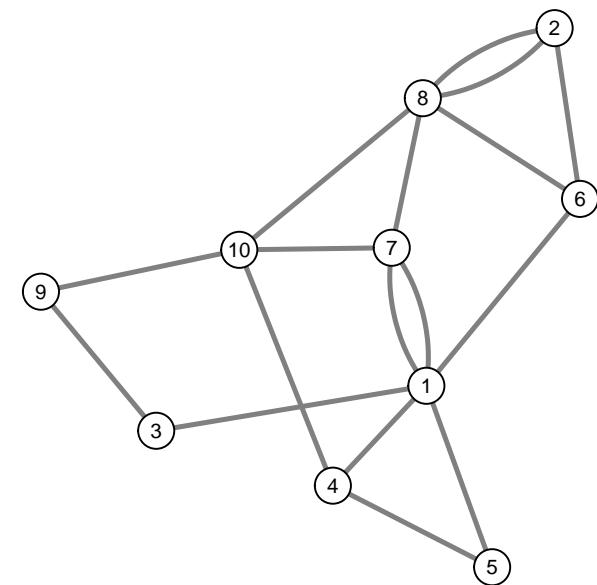
qgraph

- ▶ A R package (CRAN link)
- ▶ Can be used to plot various types of graphs
- ▶ Different from other R packages (e.g. **igraph** Csardi & Nepusz, 2006) in:
 - ▶ Focus on *weighted graphs*
 - ▶ Intended for visualization of data as graphs
 - ▶ Optimized for vector-type image files (e.g. PDF, SVG)
- ▶ Aims in **qgraph**
 - ▶ Simple input
 - ▶ Summarize a large amount of statistics without needing data reduction methods.
 - ▶ Visualize *relations between variables*
- ▶ Main idea: Show variables as nodes, relationships as edges

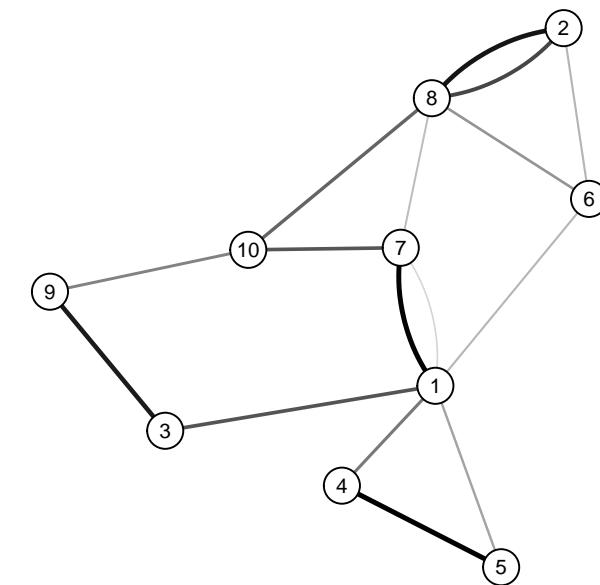
Graphs

- ▶ A graph is a *network* that consists of n nodes (or vertices) that are connected with m edges.
- ▶ Each edge has a *weight* indicating the strength of that connection
- ▶ An edge can be directed (have an arrow) or undirected

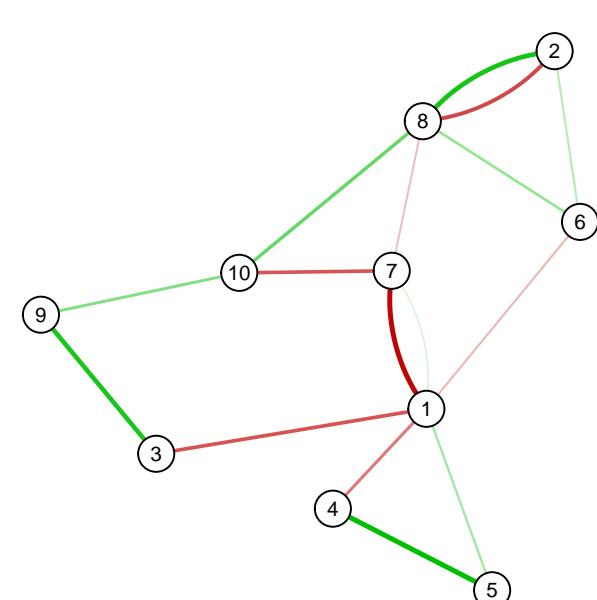
Unweighted graph



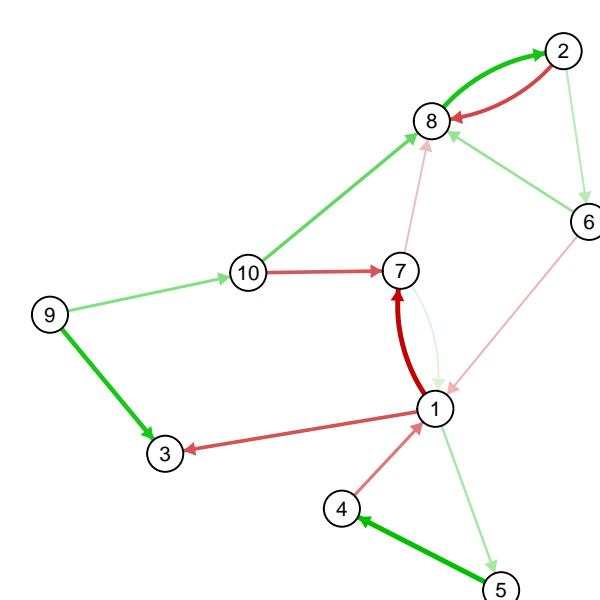
Weighted graph



Weighted graph



Directed graph

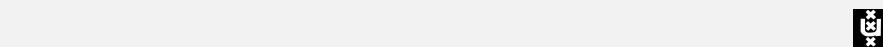


The qgraph() function

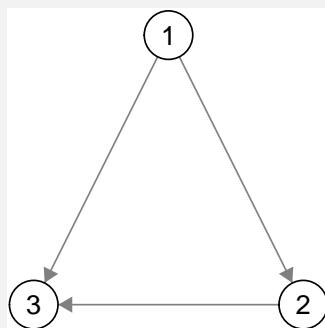
- ▶ The main function in **qgraph** is **qgraph()**
 - ▶ Most other functions are either wrapping functions using **qgraph()** or functions used in **qgraph()**
- ▶ The **qgraph()** function requires only one argument (**adj**)
- ▶ A lot of other arguments can be specified, but these are all optional

Usage:

```
qgraph( adj, ... )
```

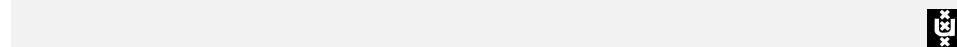


```
[,1] [,2] [,3]  
[1,] 0 1 1  
[2,] 0 0 1  
[3,] 0 0 0
```



The adjacency matrix

- ▶ The **adj** argument is the input. This can be an *adjacency matrix*
- ▶ An adjacency matrix is a square n by n matrix in which each element indicates the relationship between two variables
- ▶ Any relationship can be used as long as:
 - ▶ A 0 indicates no relationship
 - ▶ Absolute negative values are similar in strength to positive values
- ▶ Examples:
 - ▶ A 1 indicating a connection (unweighted graphs)
 - ▶ Correlations
 - ▶ Regression parameters
 - ▶ Factor loadings
- ▶ *Adjacency matrices occur naturally in statistics!*



Weighted graphs

$$\mathbf{Y} = \boldsymbol{\eta} \mathbf{A}^T + \boldsymbol{\Theta}$$

```
> set.seed(2)  
> eta <- matrix(rnorm(200 * 5), ncol = 5)  
> lam <- matrix(rnorm(50 * 5, 0, 0.15), 50,  
+ 5)  
> lam[apply(diag(5) == 1, 1, rep, each = 10)] <- rnorm(50,  
+ 0.7, 0.3)  
> th <- matrix(rnorm(200 * 50), ncol = 50)  
> Y <- eta %*% t(lam) + th
```



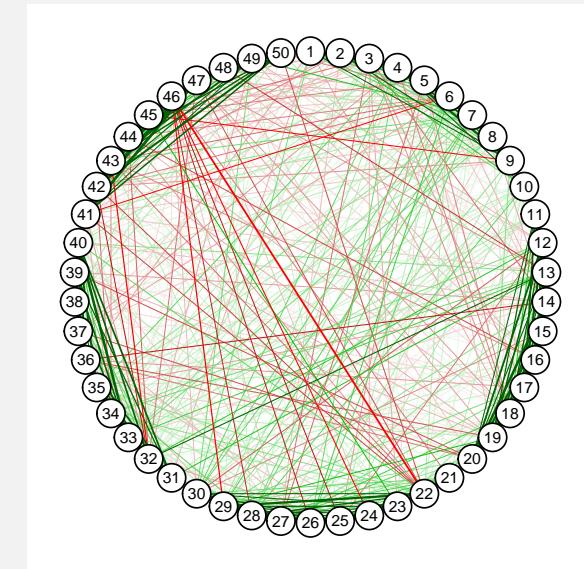
Weighted graphs

```
> cor(Y)[1:15, 1:3]
```

	[,1]	[,2]	[,3]
[1,]	1.000000000	0.218987651	0.197325805
[2,]	0.218987651	1.000000000	0.231696634
[3,]	0.197325805	0.231696634	1.000000000
[4,]	0.464897112	0.346780772	0.279845144
[5,]	0.295912130	0.275030523	0.209220603
[6,]	0.235201044	0.272947122	0.197676521
[7,]	0.157314986	-0.001815960	-0.027551034
[8,]	0.234392422	0.212721700	0.192401237
[9,]	0.321680277	0.350685995	0.210808452
[10,]	0.204097076	0.277127339	0.148343574
[11,]	-0.072734280	-0.000913891	-0.085440215
[12,]	0.052842181	0.105870583	-0.056247479
[13,]	0.001850306	0.025604291	0.081077133
[14,]	-0.083391834	-0.088641129	-0.215127641
[15,]	-0.055847218	0.007651554	0.004209916

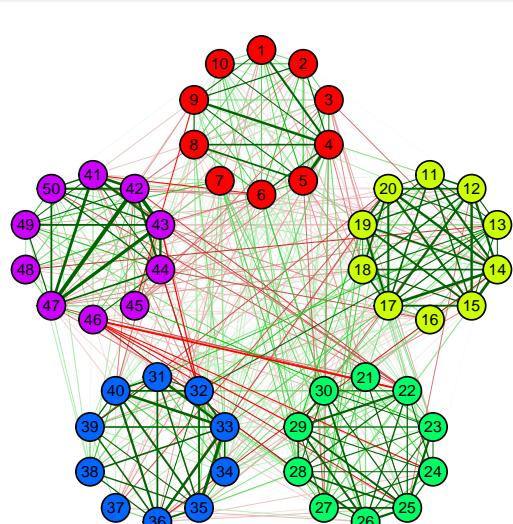
Weighted graphs

```
> qgraph(cor(Y))
```



Weighted graphs

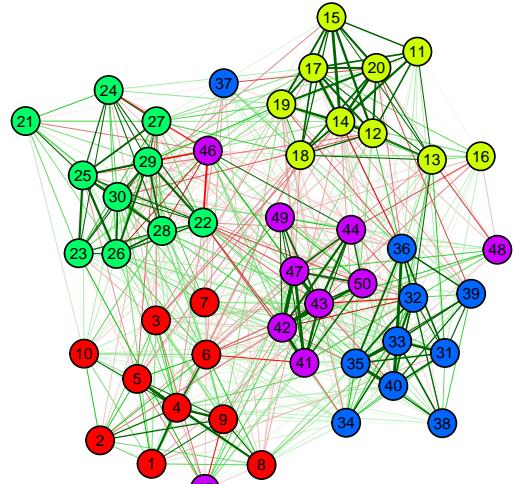
```
> gr <- list(1:10, 11:20, 21:30, 31:40, 41:50)
> qgraph(cor(Y), groups = gr)
```



Fruchterman-Reingold layout (20 iterations)

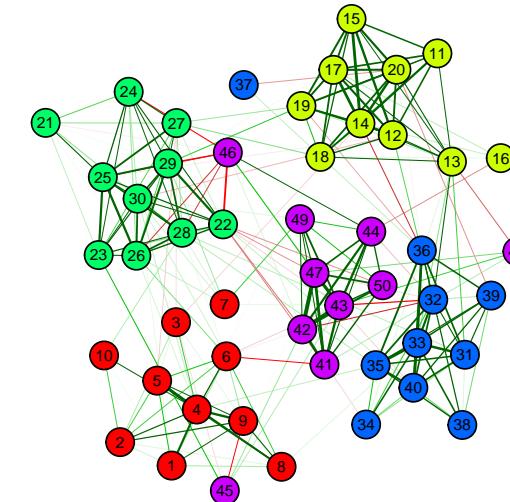
Fruchterman-Reingold layout (500 iterations)

```
> qgraph(cor(Y), groups = gr, layout = "spring")
```



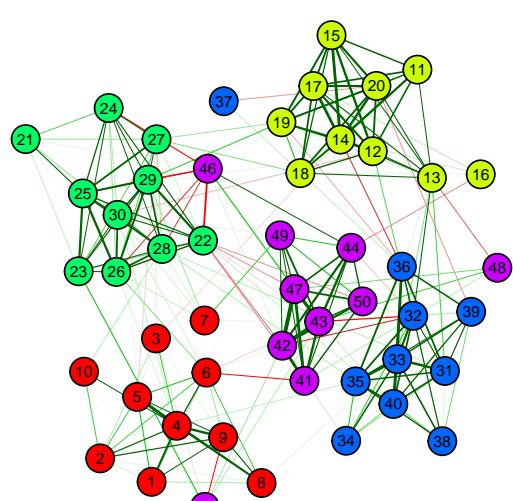
Saving arguments

```
> Q <- qgraph(cor(Y), groups = gr, layout = "spring",  
+               minimum = 0.2)
```



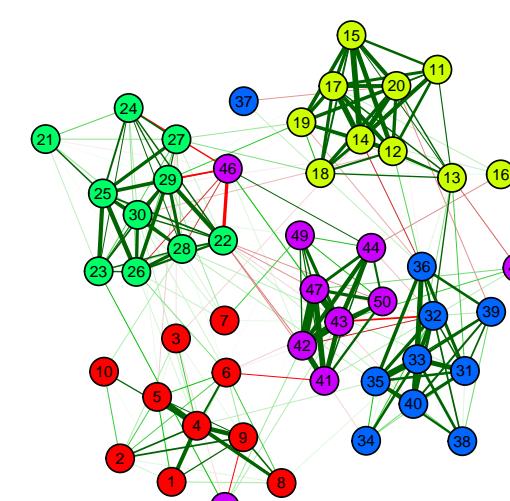
Saving arguments

```
> Q <- qgraph(Q)
```



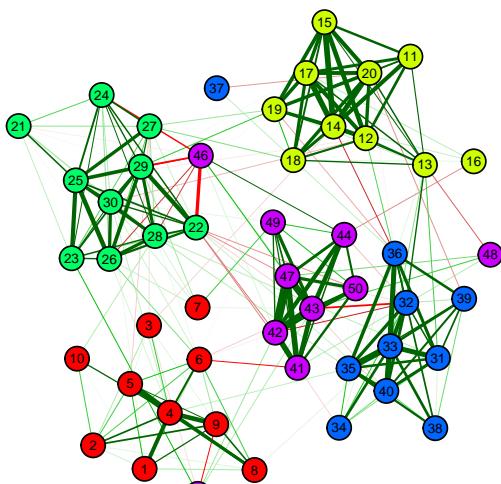
Graphical arguments

```
> Q <- qgraph(Q, esize = 10)
```



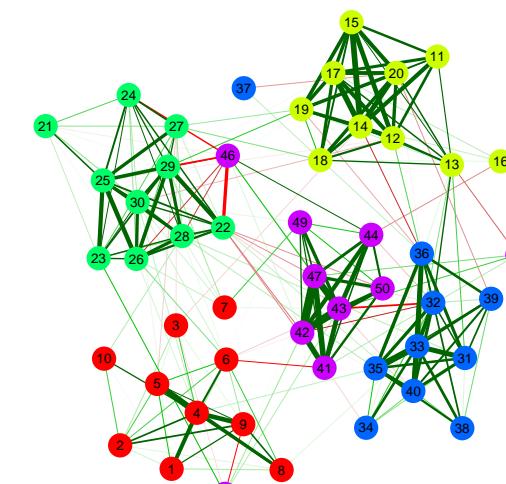
Graphical arguments

```
> Q <- qgraph(Q, vsize = 4)
```



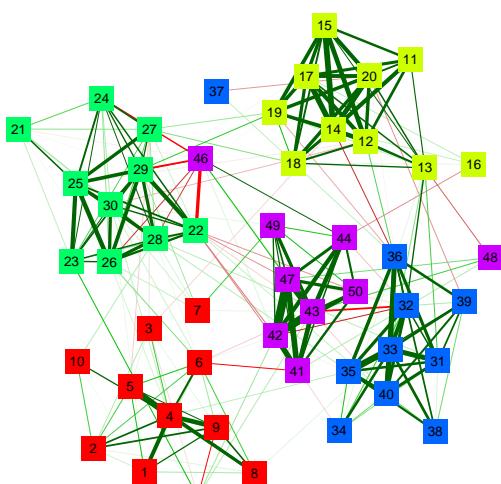
Graphical arguments

```
> Q <- qgraph(Q, borders = FALSE)
```



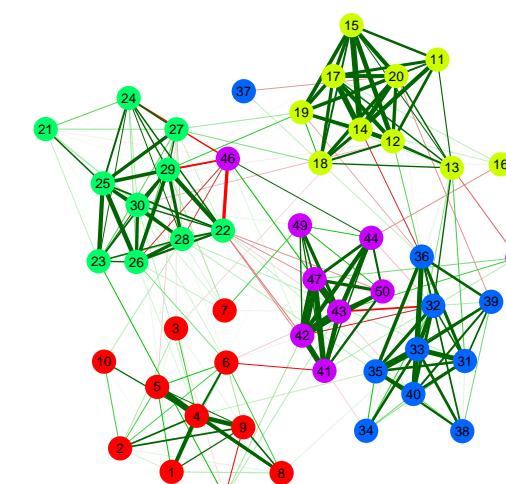
Graphical arguments

```
> Q <- qgraph(Q, shape = "square")
```



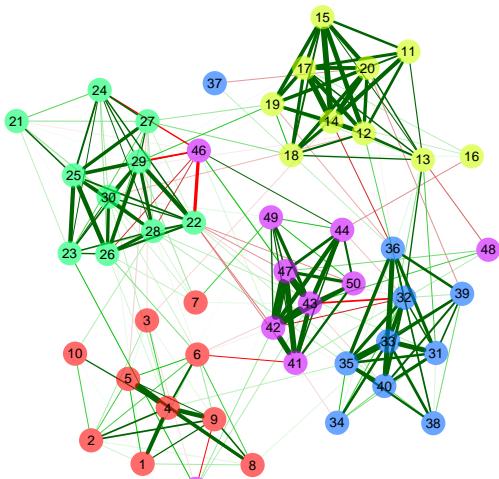
Graphical arguments

```
> Q <- qgraph(Q, shape = "circle")
```



Graphical arguments

```
> Q <- qgraph(Q, vTrans = 150)
```



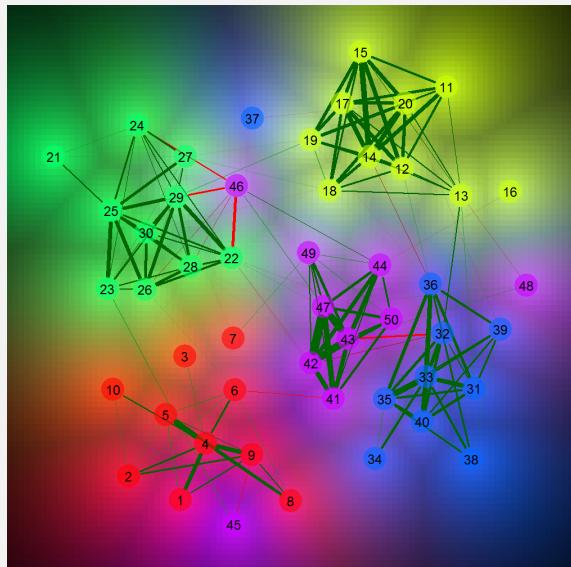
Graphical arguments

```
> qgraph(Q, transparency = T, bg = T, bgcontrol = 5,  
+         filetype = "png", filename = "bg", res = 144,  
+         width = 7, height = 7)
```

```
[1] "Output stored in C:/Users/Sacha/Documents/Work/qgraph/Psych
```

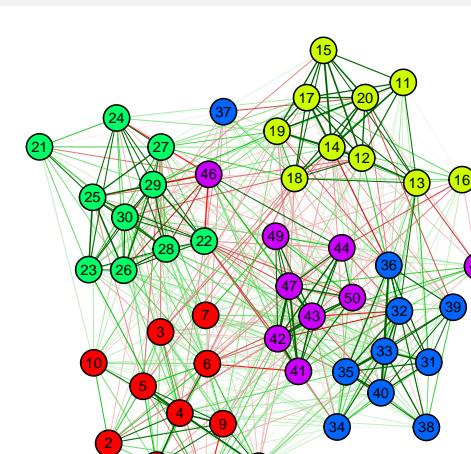


Graphical arguments



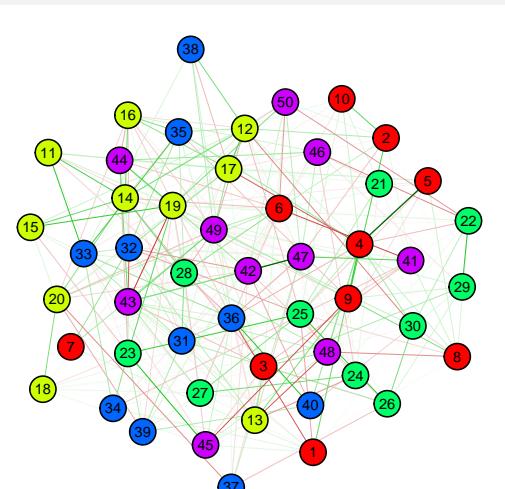
Correlations

```
> qgraph(cor(Y), layout = "spring", groups = gr,  
+         cut = 0.3, minimum = 0.1, maximum = 1,  
+         graph = "association")
```



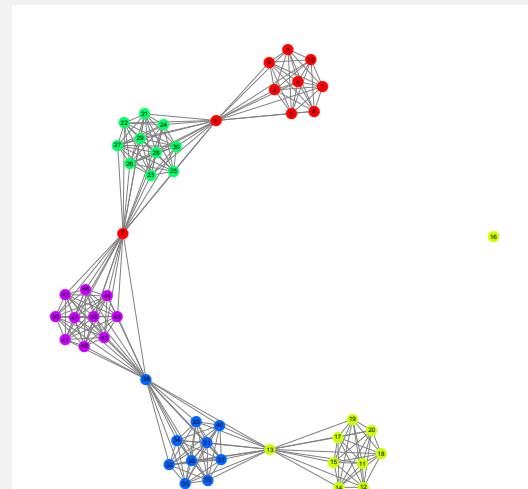
Partial correlations

```
> qgraph(cor(Y), layout = "spring", groups = gr,
+       cut = 0.3, minimum = 0.1, maximum = 1,
+       graph = "concentration")
```



Factorial graph

```
> qgraph(cor(Y), layout = "spring", groups = gr,
+       cut = 0.2, vsize = 2, esize = 1, borders = F,
+       graph = "factorial")
```

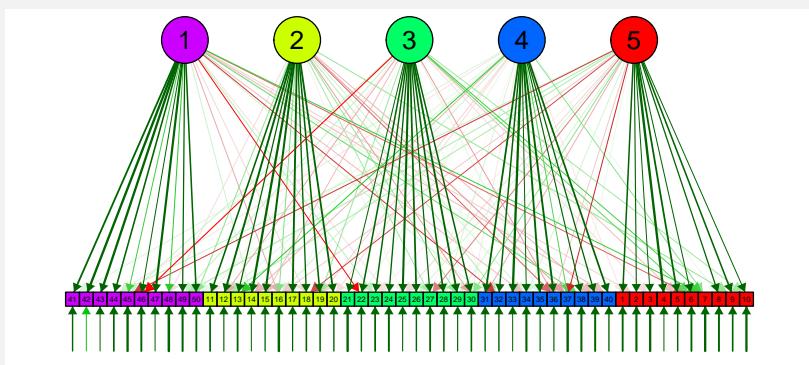


Factor loadings

- ▶ A factor loadings matrix can be visualized using `qgraph.loadings()`
- ▶ There are two wrapper functions that perform an analysis and send the results to `qgraph.loadings()`:
 - ▶ `qgraph.efa()` performs an exploratory factor analysis (EFA) using `stats:::factanal`
 - ▶ `qgraph.pca()` performs a principal component analysis (PCA) using `psych:::principal` (Revelle, 2010)
- ▶ These functions use a correlation or covariance matrix as input

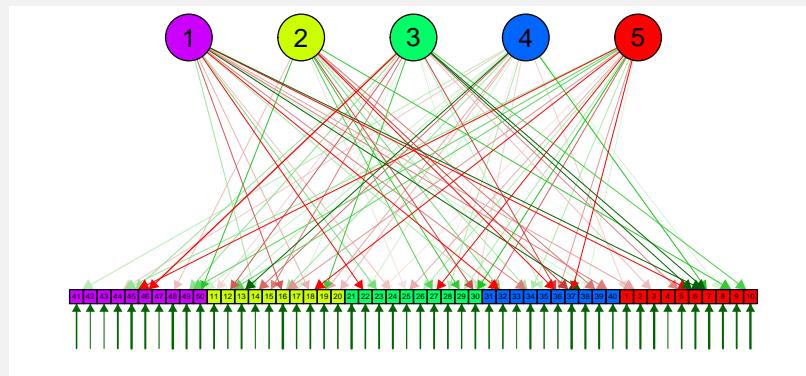
Factor loadings: EFA

```
> qgraph.efa(cor(Y), 5, rotation = "promax",
+             layout = "tree", vsize = c(3, 10), groups = gr)
```



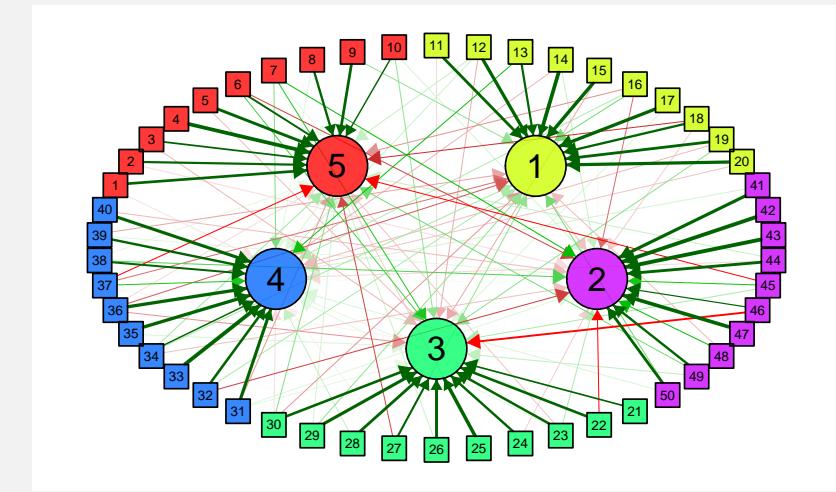
Factor loadings: EFA crossloadings

```
> qgraph.efa(cor(Y), 5, rotation = "promax",
+   layout = "tree", crossloadings = TRUE,
+   vsizes = c(3, 10), groups = gr, cut = 0.2)
```



Factor loadings: PCA

```
> qgraph.pca(cor(Y), 5, rotation = "promax",
+   vsize = c(4, 10), groups = gr, vTrans = 200)
```

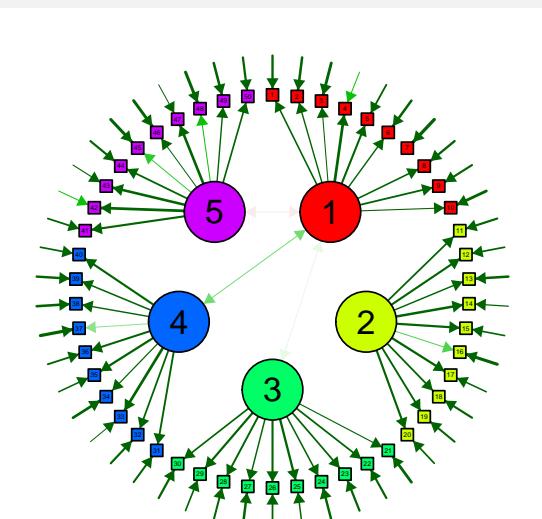


Confirmatory Factor Analysis

- ▶ `qgraph.cfa()` can be used to fit a simple confirmatory factor model
 - ▶ Each variable loads on only one factor
 - ▶ Factors are correlated
 - ▶ Scaling by fixing first loading of each factor to 1
- ▶ This is done with the **sem** (Fox, 2010) package
- ▶ Returns a "sem" object
- ▶ Results can be send to `qgraph.sem()` for a full report

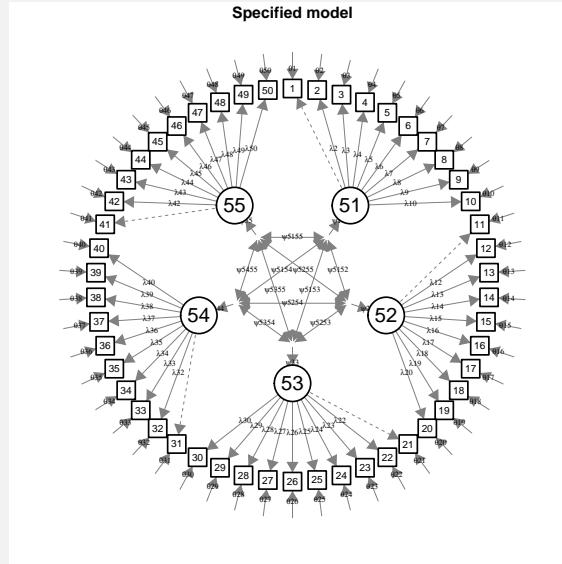
Confirmatory Factor Analysis

```
> res <- qgraph.cfa(cov(Y), N = 200, groups = gr,
+   vsize = c(2, 10))
```



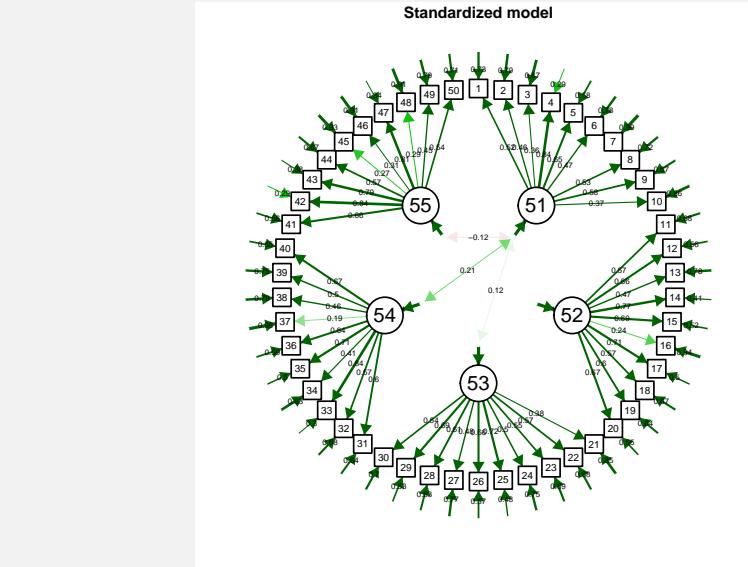
Confirmatory Factor Analysis

```
> qgraph.semModel(res, edge.label.cex = 0.6)
```



Confirmatory Factor Analysis

```
> qgraph(res, edge.label.cex = 0.6)
```

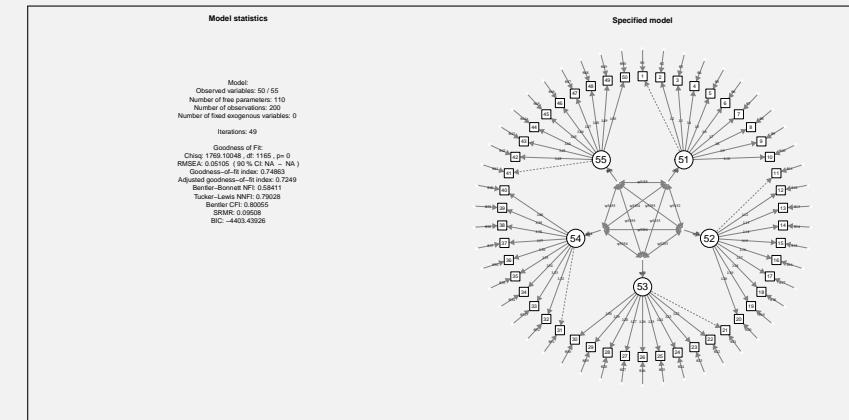


Confirmatory Factor Analysis

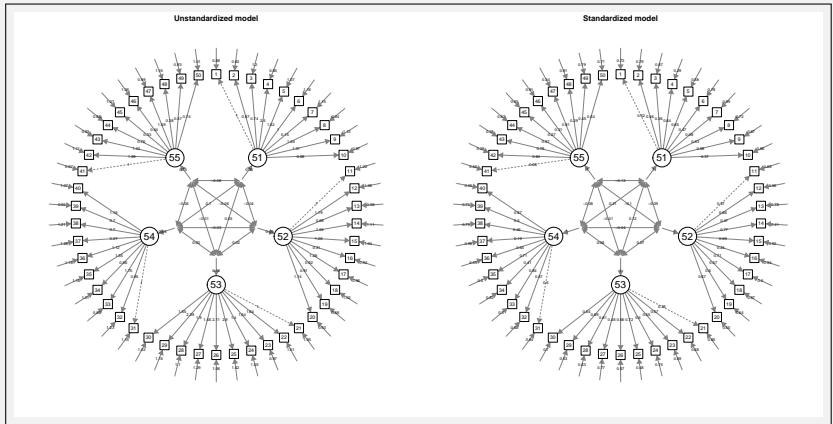
```
> qgraph.sem(res, filename = "sem%03d", onefile = F,
+   panels = 2, legend = FALSE, groups = gr,
+   edge.label.cex = 0.6)
```



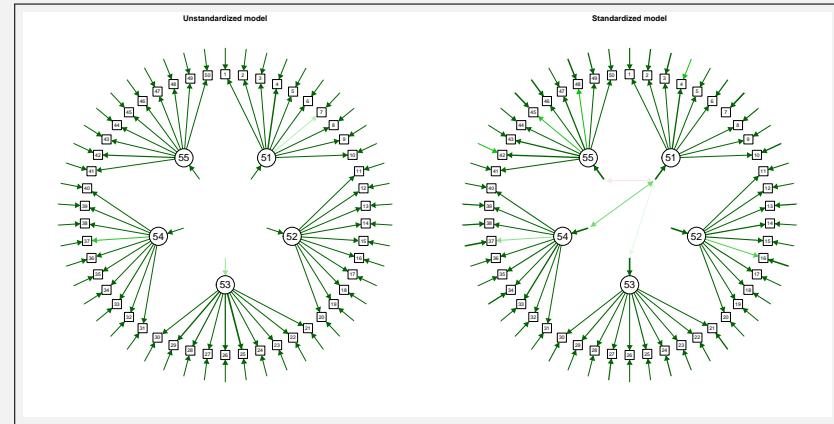
Confirmatory Factor Analysis



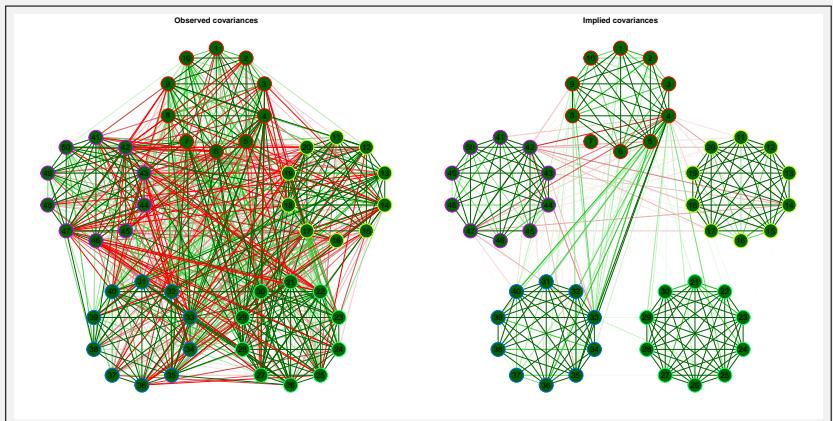
Confirmatory Factor Analysis



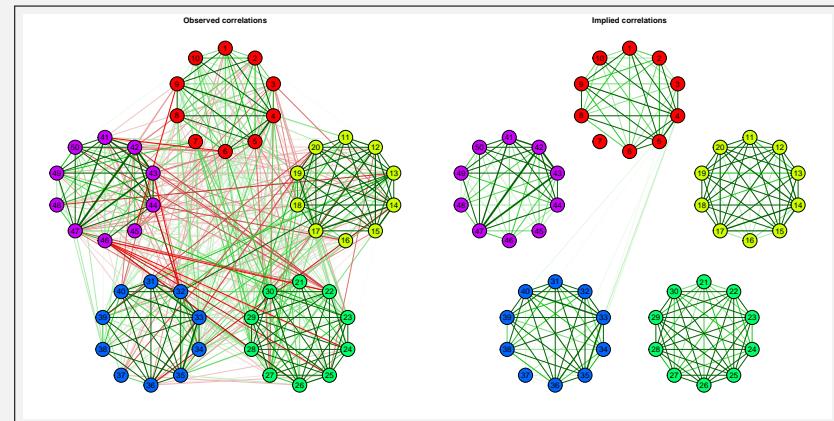
Confirmatory Factor Analysis



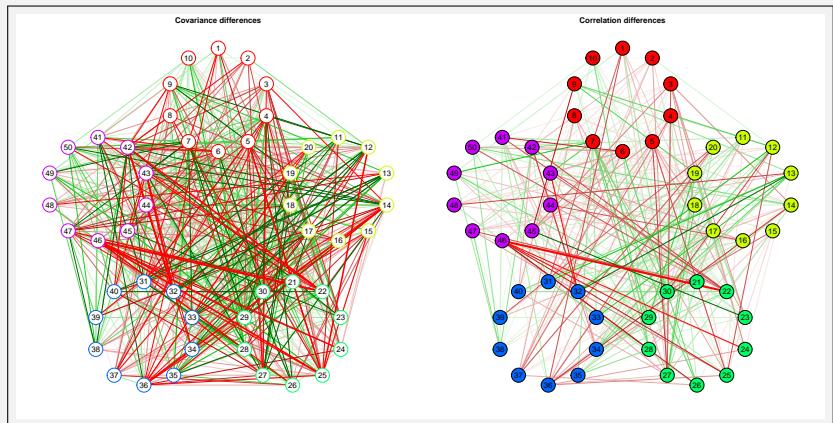
Confirmatory Factor Analysis



Confirmatory Factor Analysis



Confirmatory Factor Analysis



Structural Equation Modelling

- ▶ **qgraph** comes with a function that extends output from **sem** (Fox, 2010) with path diagrams and graphs visualizing the parameter estimates
- ▶ This is done with the **qgraph.sem()** function
- ▶ The output of **qgraph.sem()** is a multi-page pdf file
- ▶ We can use **sem** as usual and pass the output to **qgraph.sem()** with only two things to note:
 - ▶ It is best to limit variable names in the model to three characters
 - ▶ **qgraph** supports Greek letters, by adding an asterisk a label is printed in the symbol font

Structural Equation Modelling

```
> library('sem')
> R.thur <- read.moments(diag=FALSE, names=c('Sen', 'Voc',
+           'SC', 'FL', '4LW', 'Suf', 'LS', 'Ped', 'LG'))
1:   .828
2:   .776   .779
4:   .439   .493   .46
7:   .432   .464   .425   .674
11:  .447   .489   .443   .59   .541
16:  .447   .432   .401   .381   .402   .288
22:  .541   .537   .534   .35   .367   .32   .555
29:  .38    .358   .359   .424   .446   .325   .598   .452
37:
Read 36 items
```

Structural Equation Modelling

```
> model.thur <- specify.model()
1:   F1 -> Sen,   *l11, NA
2:   F1 -> Voc,   *l21, NA
3:   F1 -> SC,    *l31, NA
4:   F2 -> FL,    *l41, NA
5:   F2 -> 4LW,   *l52, NA
6:   F2 -> Suf,   *l62, NA
7:   F3 -> LS,    *l73, NA
8:   F3 -> Ped,   *l83, NA
9:   F3 -> LG,    *l93, NA
10:  F4 -> F1,    *g1,  NA
11:  F4 -> F2,    *g2,  NA
12:  F4 -> F3,    *g3,  NA
13:  Sen <-> Sen, q*1, NA
14:  Voc<-> Voc, q*2, NA
15:  SC <-> SC,  q*3, NA
```

Structural Equation Modelling

```

16:   FL <-> FL,    q*4,  NA
17:   4LW <-> 4LW,  q*5,  NA
18:   Suf<-> Suf,   q*6,  NA
19:   LS <-> LS,    q*7,  NA
20:   Ped<-> Ped,   q*8,  NA
21:   LG <-> LG,    q*9,  NA
22:   F1 <-> F1,    NA,    1
23:   F2 <-> F2,    NA,    1
24:   F3 <-> F3,    NA,    1
25:   F4 <-> F4,    NA,    1
26:

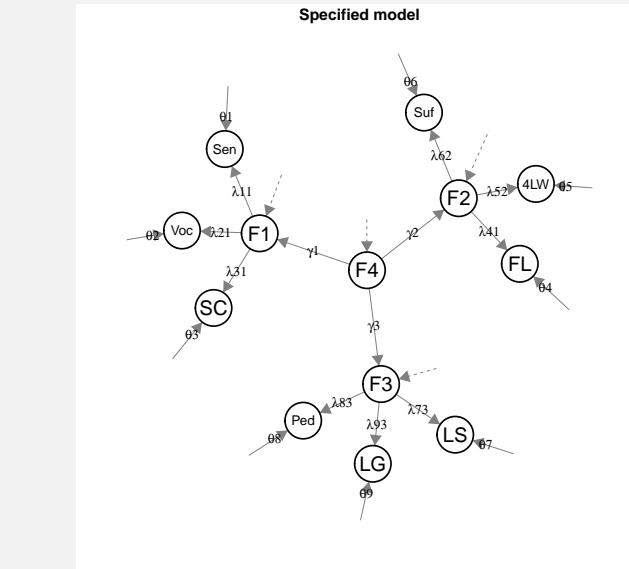
Read 25 records
> sem.thur <- sem(model.thur, R.thur, 213)

```



Structural Equation Modelling

> qgraph(model.thur)



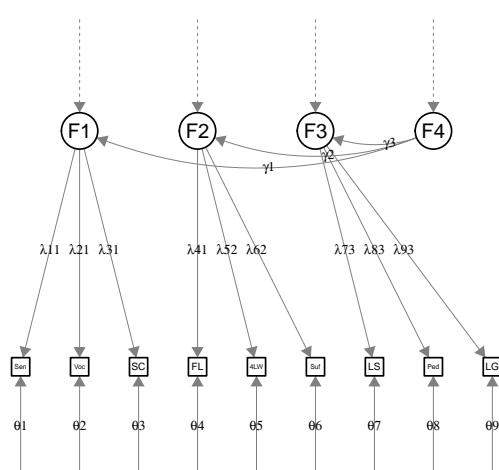
Structural Equation Modelling

```

> qgraph(model.thur, manifest = rownames(R.thur),
+         layout = "tree")

```

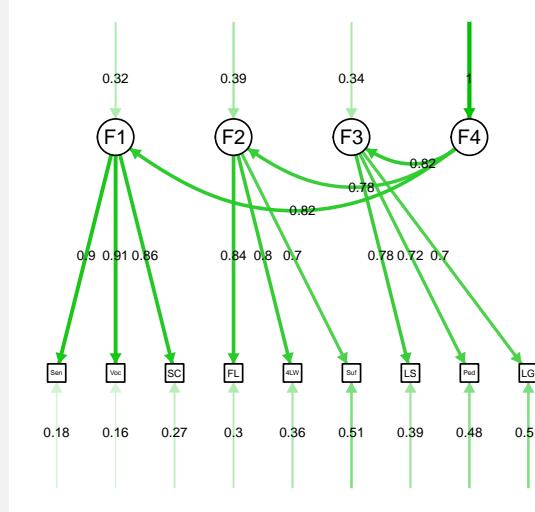
Specified model



Structural Equation Modelling

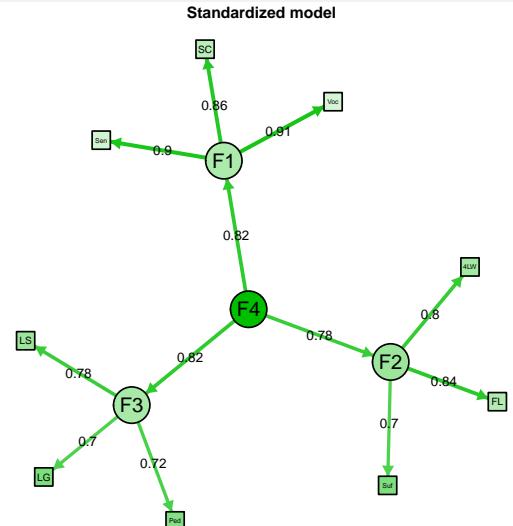
> qgraph(sem.thur, layout = "tree", curve = 0.4)

Standardized model



Structural Equation Modelling

```
> qgraph(sem.thur, layout = "spring", residuals = FALSE)
```



The big 5

```
> library(qgraph)
```

```
> data(big5)
```

```
> str(big5)
```

```
num [1:500, 1:240] 2 3 4 4 5 2 2 1 4 2 ...
- attr(*, "dimnames")=List of 2
..$ : NULL
..$ : chr [1:240] "N1" "E2" "O3" "A4" ...
```

```
> data(big5groups)
```

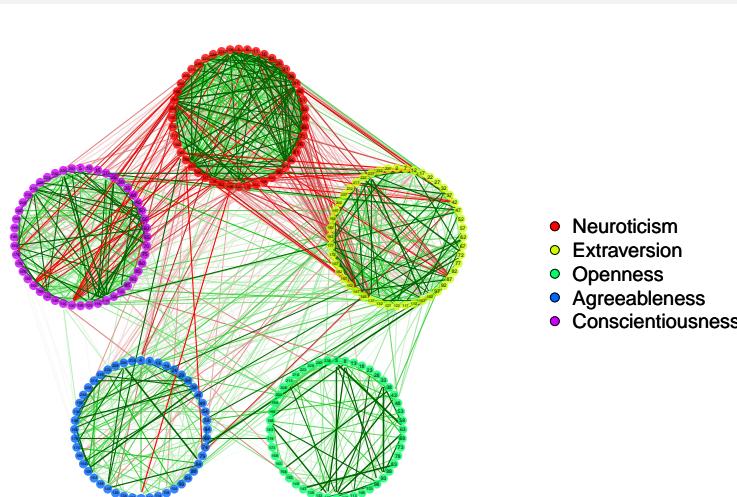
```
> str(big5groups)
```

List of 5

```
$ Neuroticism      : num [1:48] 1 6 11 16 21 26 31 36 41 46 ...
$ Extraversion     : num [1:48] 2 7 12 17 22 27 32 37 42 47 ...
$ Openness          : num [1:48] 3 8 13 18 23 28 33 38 43 48 ...
$ Agreeableness    : num [1:48] 4 9 14 19 24 29 34 39 44 49 ...
$ Conscientiousness: num [1:48] 5 10 15 20 25 30 35 40 ...
```

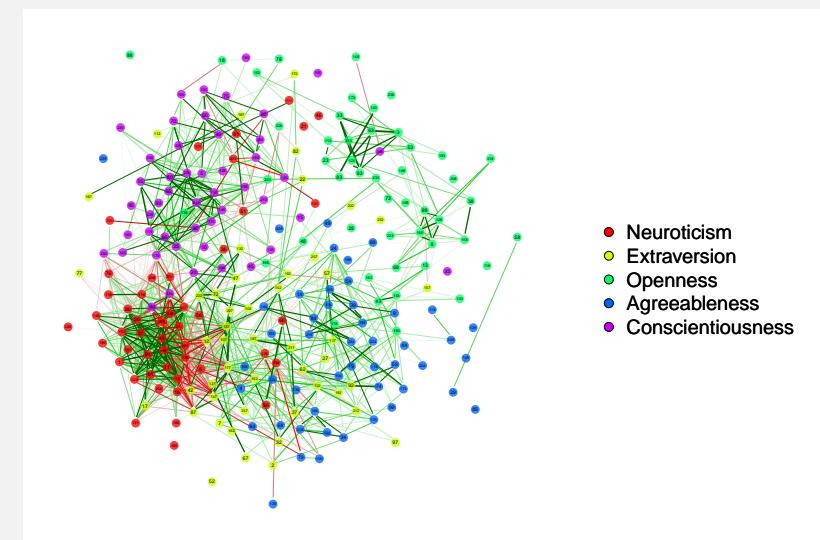
The big 5

```
> Q <- qgraph(cor(big5), minimum = 0.25, cut = 0.4,
+   vsize = 2, groups = big5groups, legend = T,
+   borders = F, vTrans = 200)
```



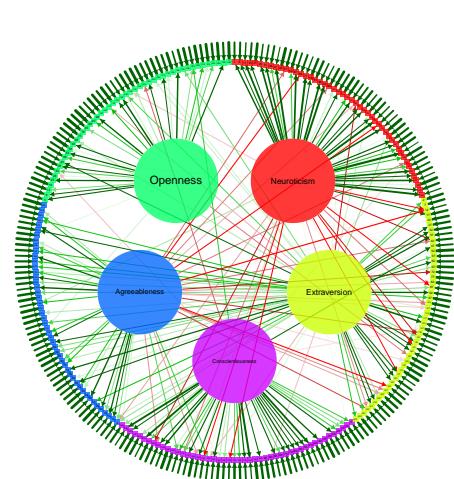
The big 5

```
> qgraph(cor(big5), Q, layout = "spring")
```



EFA

```
> qgraph.efa(cor(big5), factors = 5, Q, layout = "circle",
+   vsize = c(1, 15), borders = F, asize = 0.07,
+   esize = 4, rotation = "promax", residSize = 0.1)
```



Concluding comments

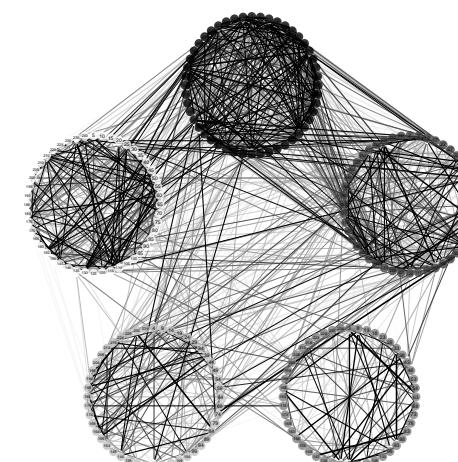
- ▶ **qgraph** is still work in progress
- ▶ Plans for the future:
 - ▶ More wrapper functions for different statistics (e.g. IRT)
 - ▶ More layout modes
 - ▶ Estimating and fitting causal models
- ▶ Some things I couldn't describe...



Layout constraints

Grayscale colors

```
> Q <- qgraph(cor(big5), minimum = 0.25, cut = 0.4,
+   vsize = 2, groups = big5groups, legend = T,
+   borders = F, vTrans = 200, gray = TRUE)
```

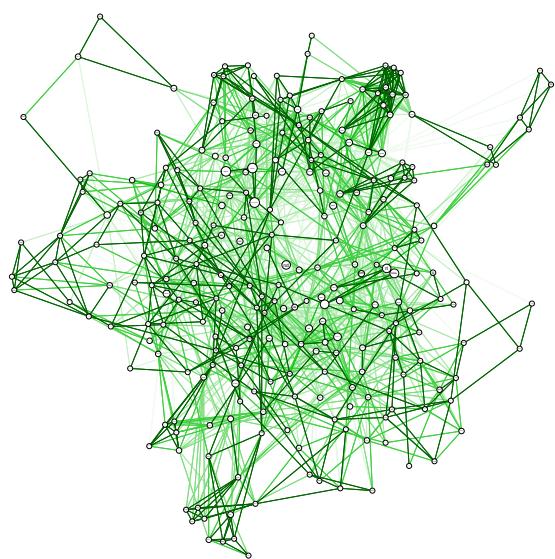


- Neuroticism
- Extraversion
- Openness
- Agreeableness
- Conscientiousness

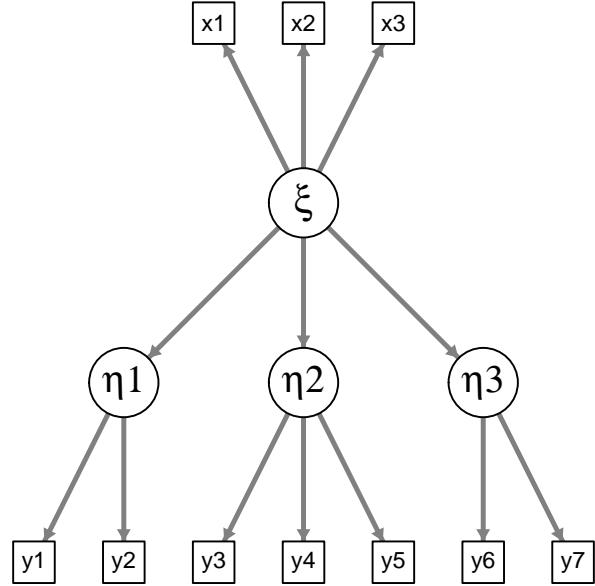


Tooltips

Link



Modelling



Concluding comments

Thank you for your attention!



References

- Butts, C. T. (2010). **sna**: Tools for social network analysis [Computer software manual]. Available from <http://CRAN.R-project.org/package=sna> (R package version 2.2-0)
- Csardi, G., & Nepusz, T. (2006). The **igraph** software package for complex network research. *InterJournal, Complex Systems*, 1695. Available from <http://igraph.sf.net>
- Fox, J. (2010). **sem**: Structural equation models [Computer software manual]. Available from <http://CRAN.R-project.org/package=sem> (R package version 0.9-21)
- Fruchterman, T., & Reingold, E. (1991). Graph drawing by force-directed placement. *Software: Practice and Experience*, 21(11), 1129–1164.
- Revelle, W. (2010). **psych**: Procedures for psychological, psychometric, and personality research [Computer software manual]. Evanston, Illinois. Available from <http://personality-project.org/r/psych.manual.pdf> (R package version 1.0-93)

Fruchterman-Reingold layout (20 iterations)



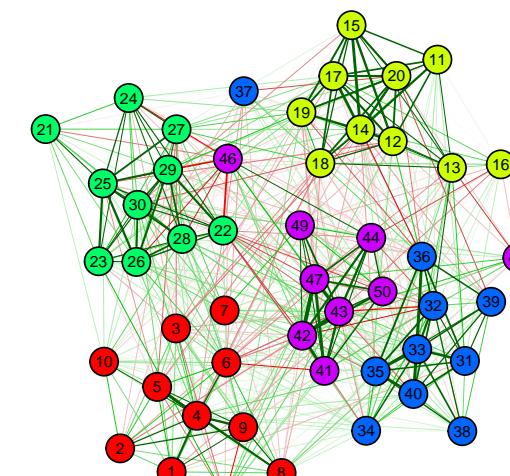
Layout modes

- ▶ The placement of the nodes is specified with the `layout` argument in `qgraph()`
- ▶ This can be a n by 2 matrix indicating the x and y position of each node
- ▶ `layout` can also be given a character indicating one of the two default layouts
- ▶ If `layout="circular"` the nodes are placed in circles per group (if the `groups` list is specified)
- ▶ If `layout="spring"` a force-embedded algorithm (Fruchterman & Reingold, 1991) is used for the placement
 - ▶ This is an iterative algorithm that clusters the nodes so that the length of the edges correspond to the absolute strength of the edges



Fruchterman-Reingold layout (500 iterations)

```
> qgraph(cor(Y), groups = gr, layout = "spring")
```



Grid layout

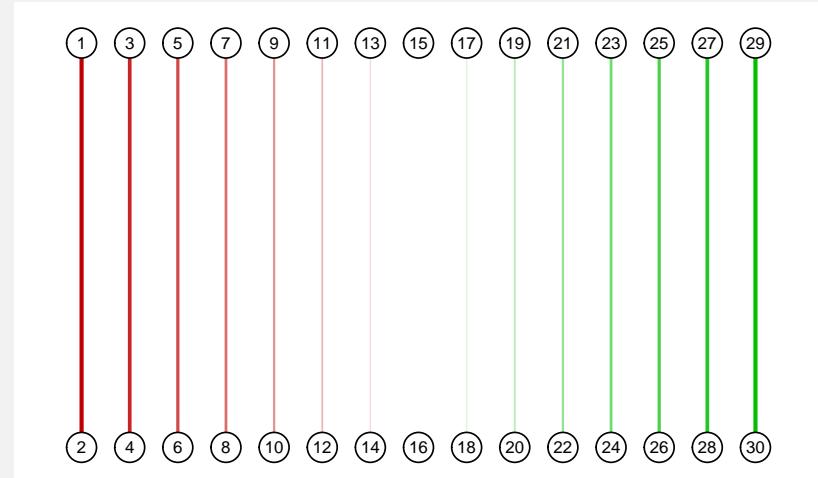
- ▶ A final option is to specify a grid as layout
- ▶ This can be done by specifying a matrix to layout with more than two columns
- ▶ This matrix contains zeros and a number for each node

```
> dat.3 <- matrix(c(1:15 * 2 - 1, 1:15 * 2),  
+ , 2)  
> dat.3 <- cbind(dat.3, round(seq(-0.7, 0.7,  
+ length = 15), 1))  
> L.3 <- matrix(1:30, nrow = 2)  
> L.3  
  
[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]  
[1,] 1 3 5 7 9 11 13 15 17  
[2,] 2 4 6 8 10 12 14 16 18  
[,10] [,11] [,12] [,13] [,14] [,15]  
[1,] 19 21 23 25 27 29  
[2,] 20 22 24 26 28 30
```



Grid layout

```
> qgraph(dat.3, layout = L.3, directed = FALSE)
```



Fruchterman-Reingold layout

- ▶ `layout="spring"` uses a force-embedded algorithm that was proposed by Fruchterman and Reingold (1991)
 - ▶ This layout was ported from the `sna` package (Butts, 2010)
 - ▶ A solution for weighted graphs was taken from `igraph` (Csardi & Nepusz, 2006)
- ▶ This is an iterative algorithm.
- ▶ The initial layout is a circle
- ▶ Then in each iteration:
 - ▶ Each node is repulsed by all other nodes
 - ▶ Connected nodes are also attracted to each other
 - ▶ The maximum displacement weakens each iteration
- ▶ After this process the layout is rescaled to fit the -1 to 1 xy -plane
- ▶ The unscaled layout is returned as `layout.orig`



Fruchterman-Reingold layout

- ▶ The Fruchterman-Reingold algorithm can be controlled with the `layout.par` argument
- ▶ This must be a list containing other arguments:
 - `niter` Number of iterations, default is 500
 - `max.delta` Maximum displacement, default is n
 - `area` The area of the plot, default is n^2
 - `cool.exp` Cooling exponent, default is 1.5
 - `repulse.rad` Repulse radius, default is $n \cdot \text{area}$
 - `init` Matrix indicating initial layout



Constraints in the Fruchterman-Reingold layout

- ▶ The Fruchterman-Reingold algorithm behaves like a chaotic system
- ▶ A small difference in initial setup can result in a completely different layout
- ▶ In **qgraph** the layout can be constrained to compensate this
- ▶ Hard constraints
 - ▶ Hard constraints can be used to fix the *x* and *y* position of certain nodes
 - ▶ This can be done with the `constraints` argument in `layout.par`
- ▶ Soft constraints
 - ▶ Soft constraints can be used to limit the displacement of certain nodes
 - ▶ This can be done with the `max.delta` and `init` arguments in `layout.par`



No constraints

```
> dat.3 <- matrix(c(1, 2, 1, 3, 2, 3), 3, 2,  
+      byrow = T)  
> L <- matrix(c(1:3, 1, 3, 1), 3, 2)  
> Q <- qgraph(dat.3, layout = L, vsize = 3,  
+      esize = 1)  
> par <- list(init = L)  
> set.seed(1)  
> for (i in 3:20) {  
+      dat.3 <- rbind(dat.3, c(sample(c(i, sample(1:i,  
+          1)), 1), i + 1))  
+      L <- rbind(L, 0)  
+      par$init <- L  
+      L <- qgraph(dat.3, Q, layout.par = par,  
+                  layout = "spring")$layout.orig  
+ }
```



No constraints



Hard constraints

```
> dat.3 <- matrix(c(1, 2, 1, 3, 2, 3), 3, 2,  
+      byrow = T)  
> L <- matrix(c(1:3, 1, 3, 1), 3, 2)  
> par <- list(max.delta = 10, area = 10^2,  
+      repulse.rad = 10^3)  
> Q <- qgraph(dat.3, layout = L, vsize = 3,  
+      esize = 1, layout.par = par)  
> set.seed(1)  
> for (i in 3:20) {  
+      dat.3 <- rbind(dat.3, c(sample(c(i, sample(1:i,  
+          1)), 1), i + 1))  
+      par$init <- rbind(L, 0)  
+      L <- rbind(L, NA)  
+      par$constraints <- L  
+      L <- qgraph(dat.3, Q, layout.par = par,  
+                  layout = "spring")$layout.orig  
+ }
```



Hard constraints



Soft constraints

```
> dat.3 <- matrix(c(1, 2, 1, 3, 2, 3), 3, 2,  
+      byrow = T)  
> L <- matrix(c(1:3, 1, 3, 1), 3, 2)  
> par <- list(max.delta = 10, area = 10^2,  
+      repulse.rad = 10^3)  
> Q <- qgraph(dat.3, layout = L, vsize = 3,  
+      esize = 1, layout.par = par)  
> set.seed(1)  
> for (i in 3:20) {  
+      dat.3 <- rbind(dat.3, c(sample(c(i, sample(1:i,  
+          1)), 1), i + 1))  
+      par$init <- rbind(L, 0)  
+      L <- rbind(L, NA)  
+      par$max.delta <- 10/(i + 1):1  
+      L <- qgraph(dat.3, Q, layout.par = par,  
+                  layout = "spring")$layout.orig  
+ }
```

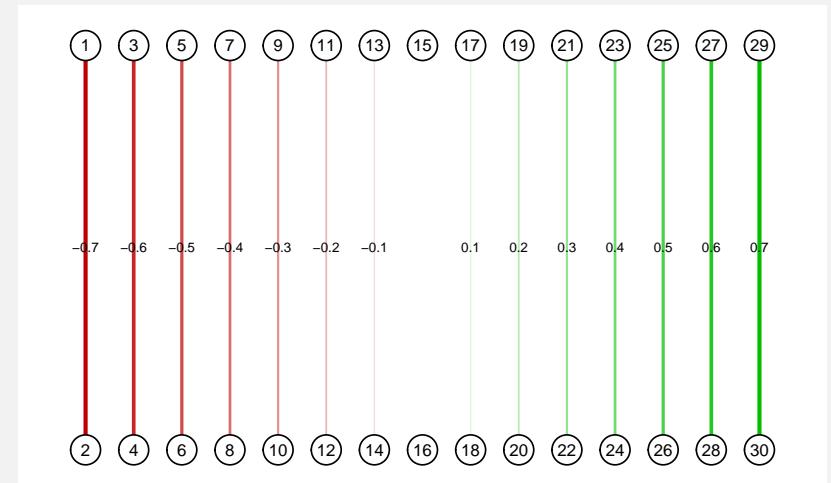


Soft constraints



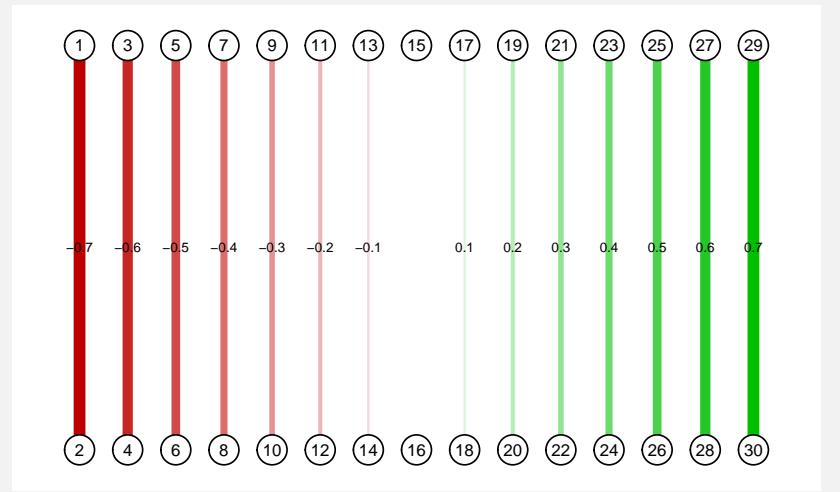
Interpreting weighted graphs

```
> qgraph(dat.3, layout = L.3, directed = FALSE,  
+      edge.labels = T)
```



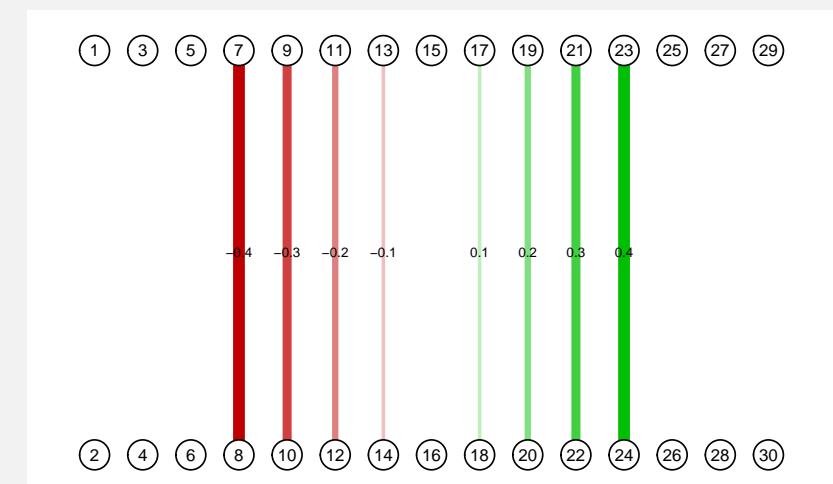
Interpreting weighted graphs

```
> qgraph(dat.3, layout = L.3, directed = FALSE,  
+         edge.labels = T, esize = 14)
```



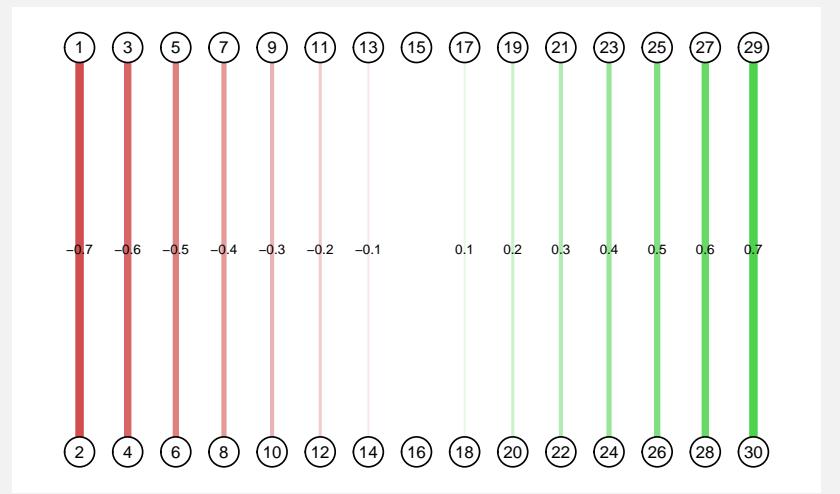
Interpreting weighted graphs

```
> qgraph(dat.3[-c(1:3, 13:15), ], layout = L.3,  
+         nNodes = 30, directed = FALSE, edge.labels = T,  
+         esize = 14)
```



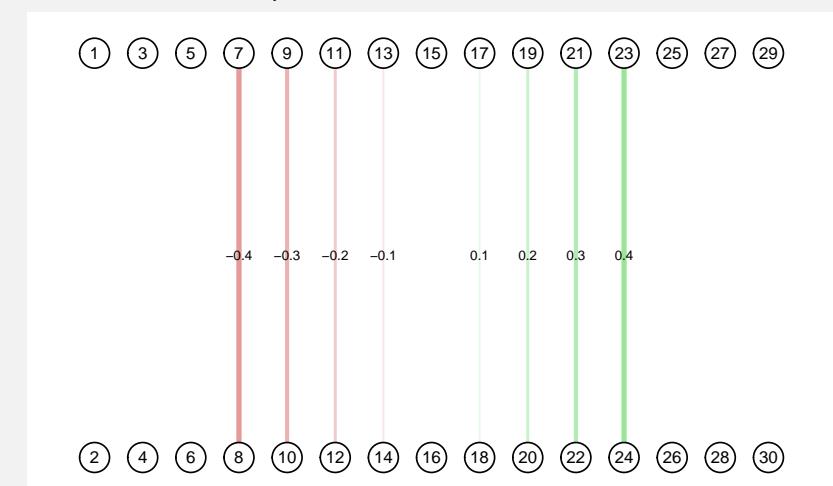
Interpreting weighted graphs

```
> qgraph(dat.3, layout = L.3, directed = FALSE,  
+         edge.labels = T, esize = 14, maximum = 1)
```



Interpreting weighted graphs

```
> qgraph(dat.3[-c(1:3, 13:15), ], layout = L.3,  
+         nNodes = 30, directed = FALSE, edge.labels = T,  
+         esize = 14, maximum = 1)
```



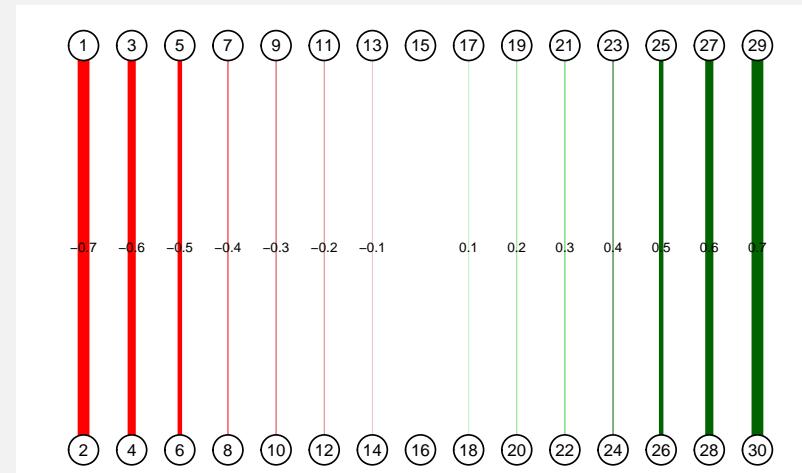
Interpreting weighted graphs

maximum must be set to be able to compare multiple graphs!



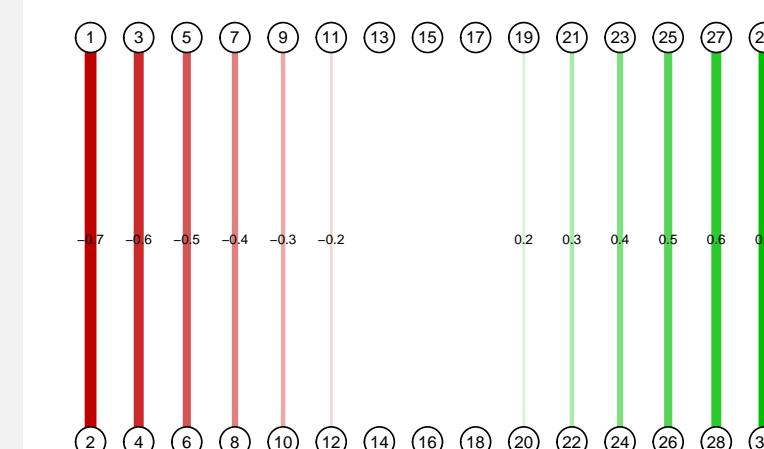
Interpreting weighted graphs

```
> qgraph(dat.3, layout = L.3, directed = FALSE,  
+         edge.labels = T, esize = 14, cut = 0.4)
```



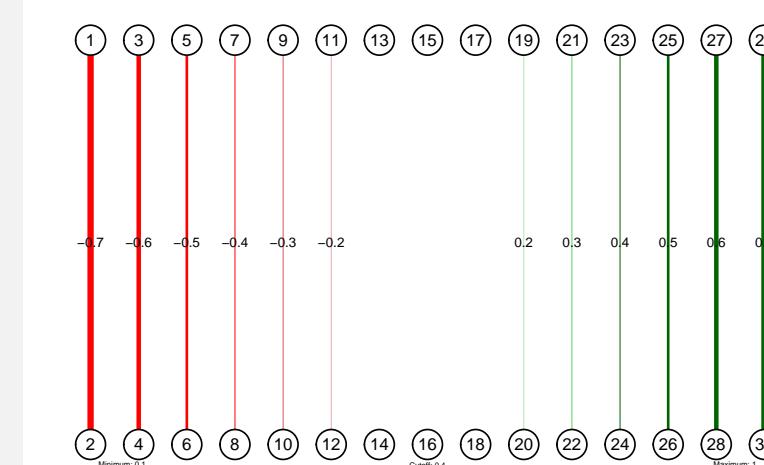
Interpreting weighted graphs

```
> qgraph(dat.3, layout = L.3, directed = FALSE,  
+         edge.labels = T, esize = 14, minimum = 0.1)
```



Interpreting weighted graphs

```
> qgraph(dat.3, layout = L.3, directed = FALSE,  
+         edge.labels = T, esize = 14, minimum = 0.1,  
+         maximum = 1, cut = 0.4, details = TRUE)
```



Interpreting weighted graphs

**Graphs can not be interpreted without knowing minimum, cut
and maximum!**

