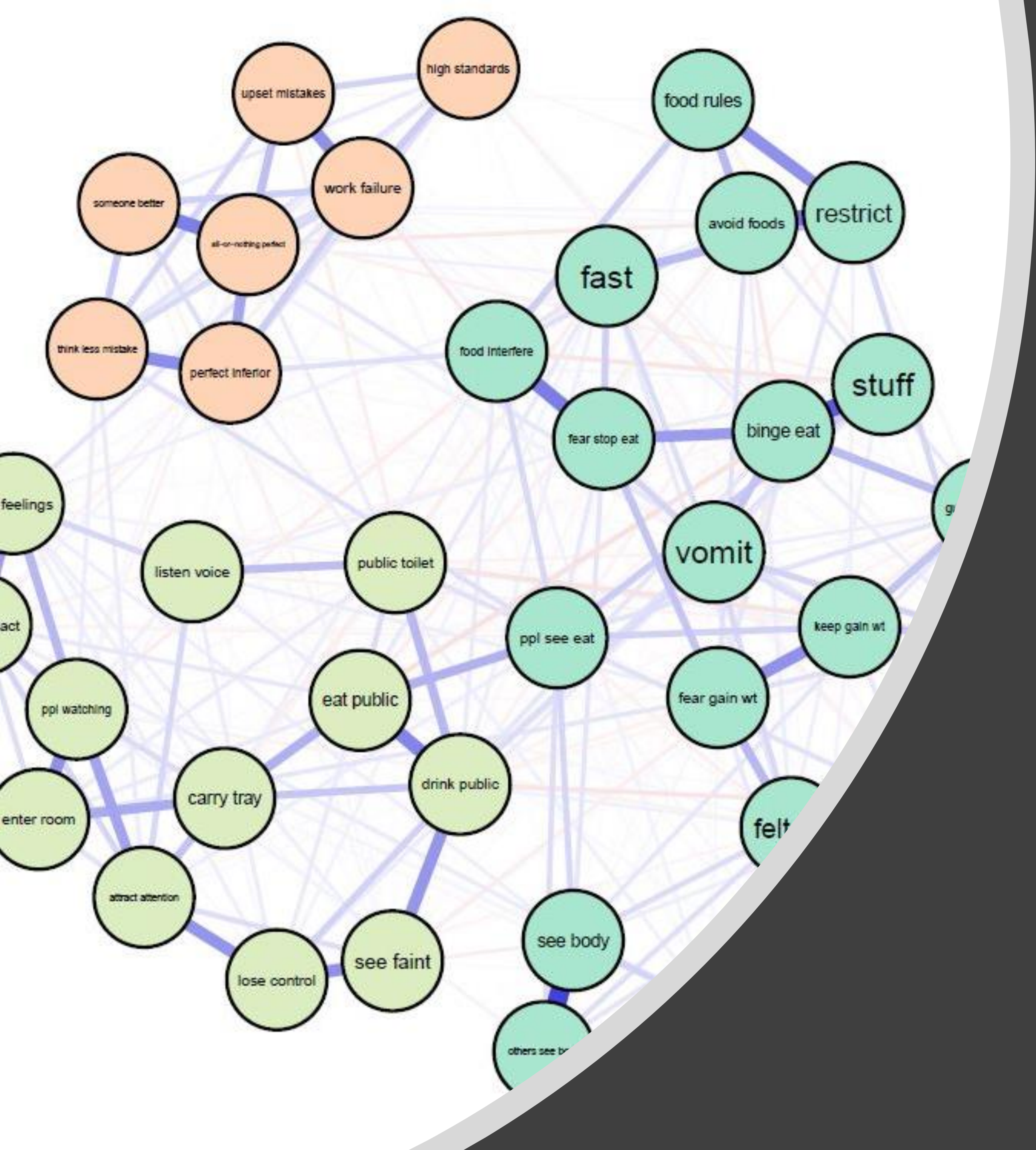

EAT LAB
EATING ANXIETY TREATMENT LABORATORY AND CLINIC

An Introduction to Network Analysis : Focus on Eating Disorders

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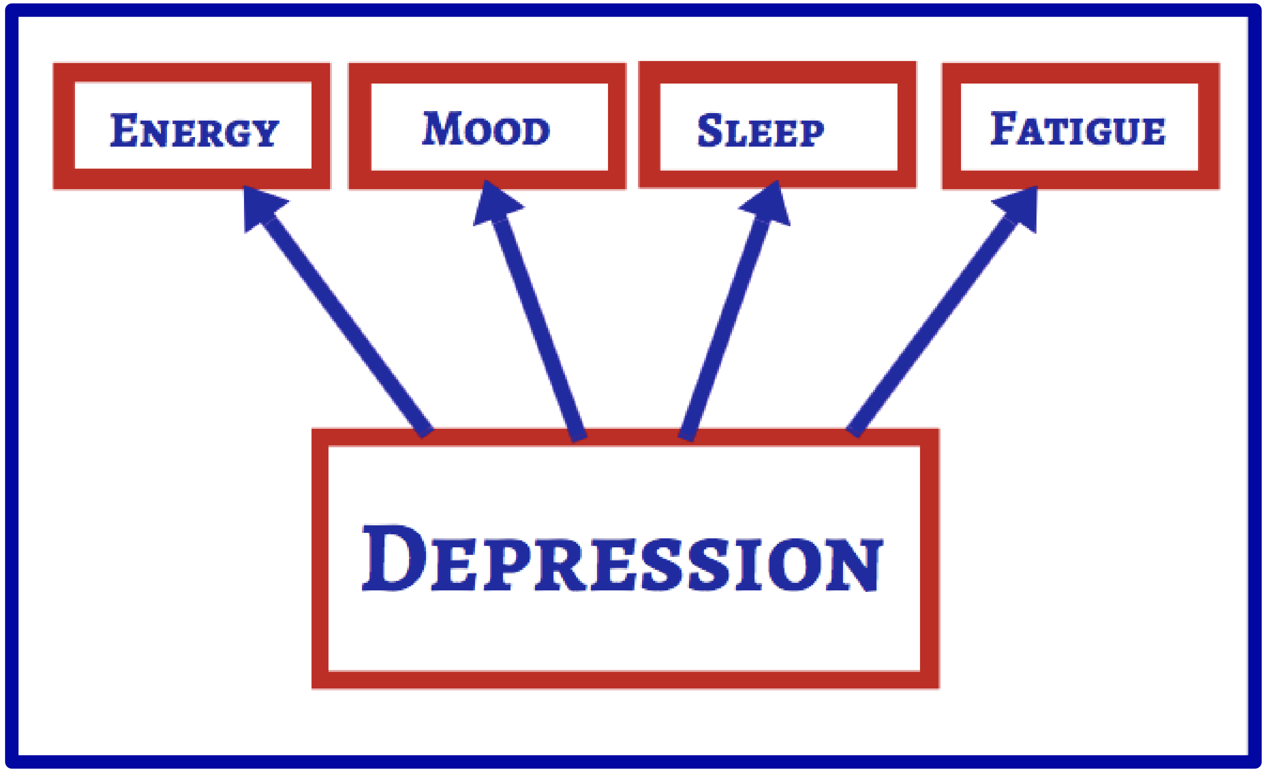
Outline

- Network Theory
- Understanding Network Models
- Cross-sectional Network Model in R
- Other Applications of Network Analysis
- Resources

Why Network Analysis?

Alternative to Latent Variable Theory

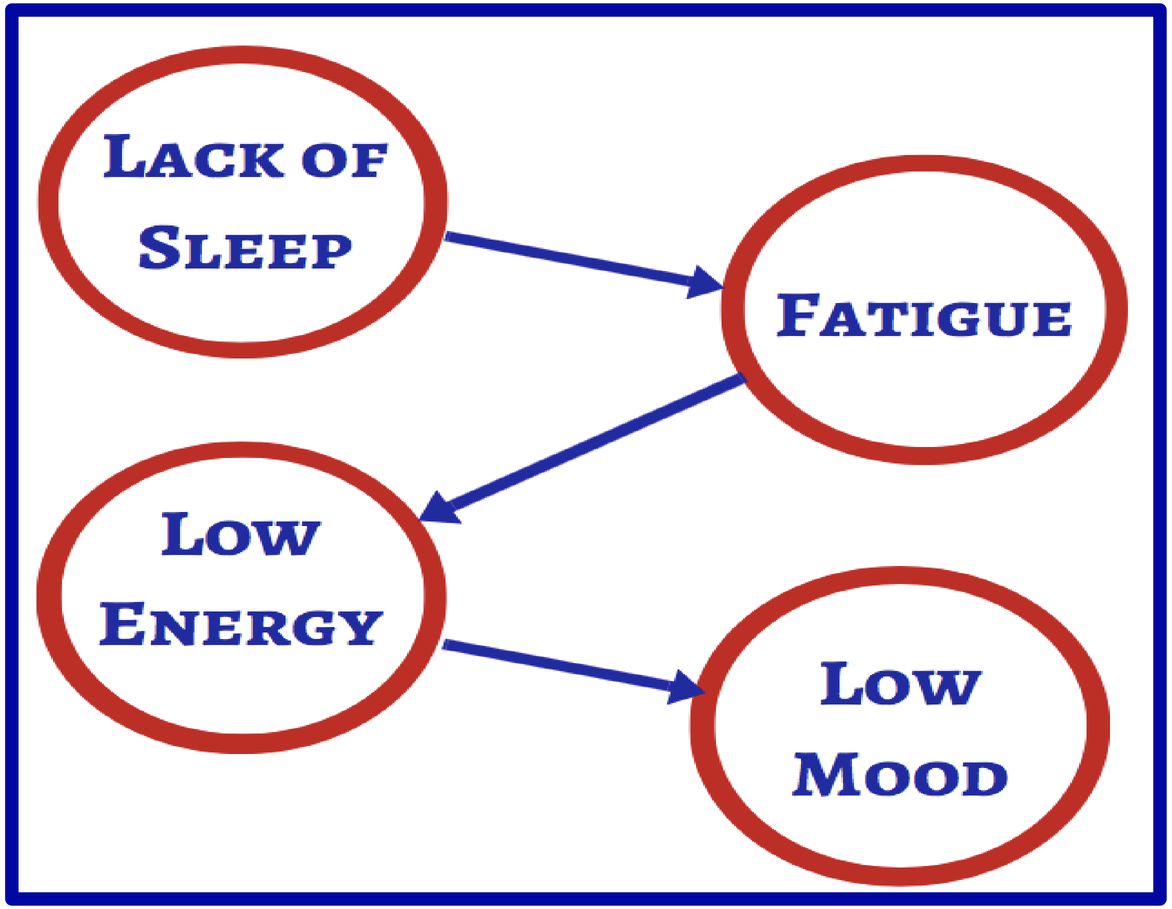
Traditional Disease Model: '*Depression*' is cause of all *Symptoms*



Borsboom & Cramer, 2013; Borsboom, 2017

Network Theory

Network Model of Disease: *Symptoms* are dynamical systems that cause *Depression*



Borsboom & Cramer, 2013; Borsboom, 2017

Why Network Analysis?

Symptoms as directly leading to one another

Takes into account unique relationships between symptoms

Targeted treatments based on symptoms

Creation of more refined theories

What Questions Can Network Analysis Answer

Testable:

- What are the most important symptoms in a network (disorder)?
- What symptoms connect two disorders (drive comorbidity)?
- How are symptoms uniquely related to one another?

Implications:

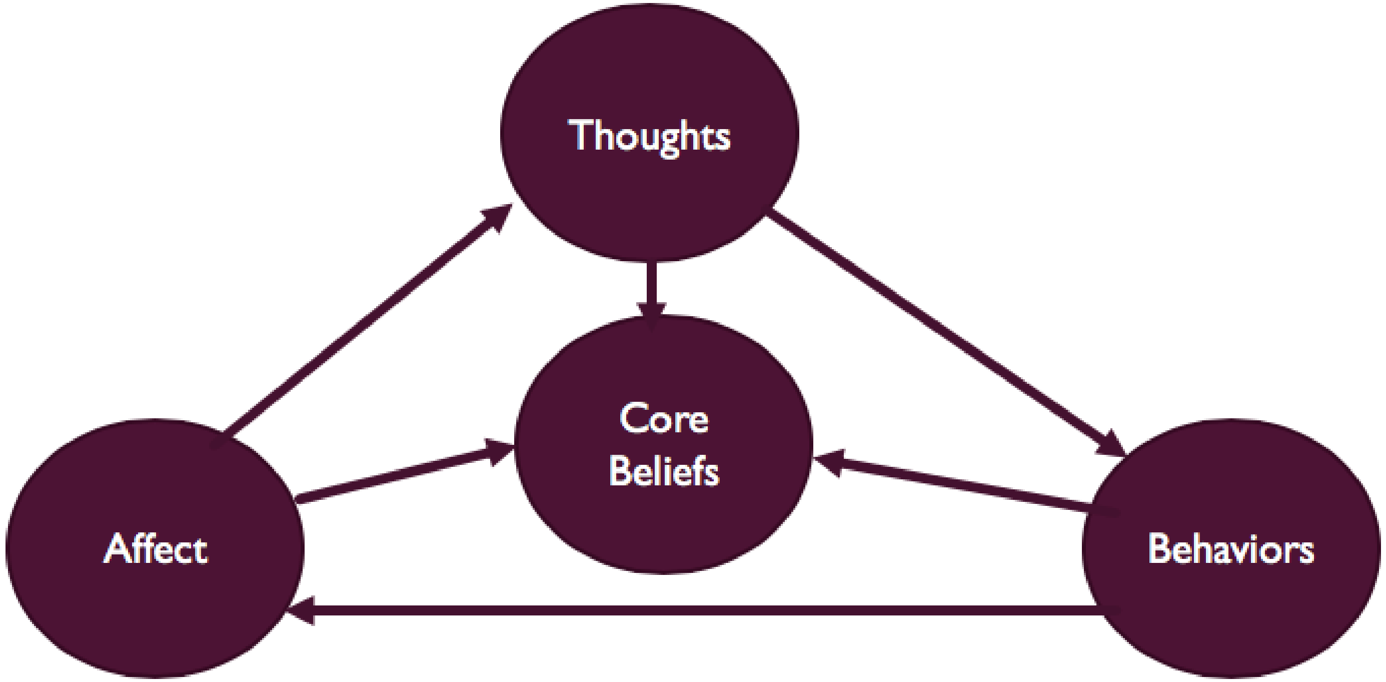
- How might symptom-level relationships inform theory/interventions?

Mapping onto Existing Theories

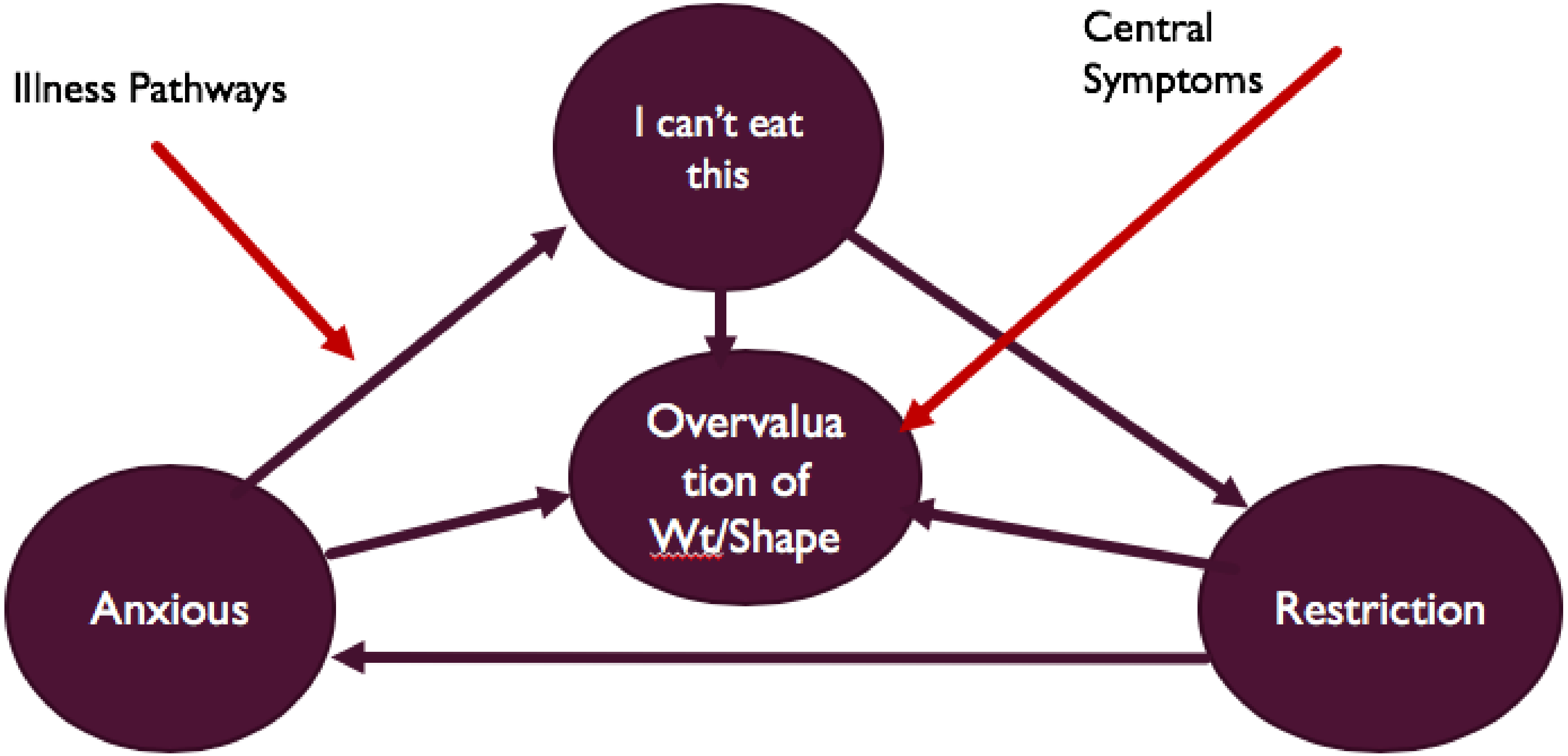
- Primary theory in EDs is CBT theory
- Most clinicians think about EDs as dynamical systems already

How do we conceptualize ED?

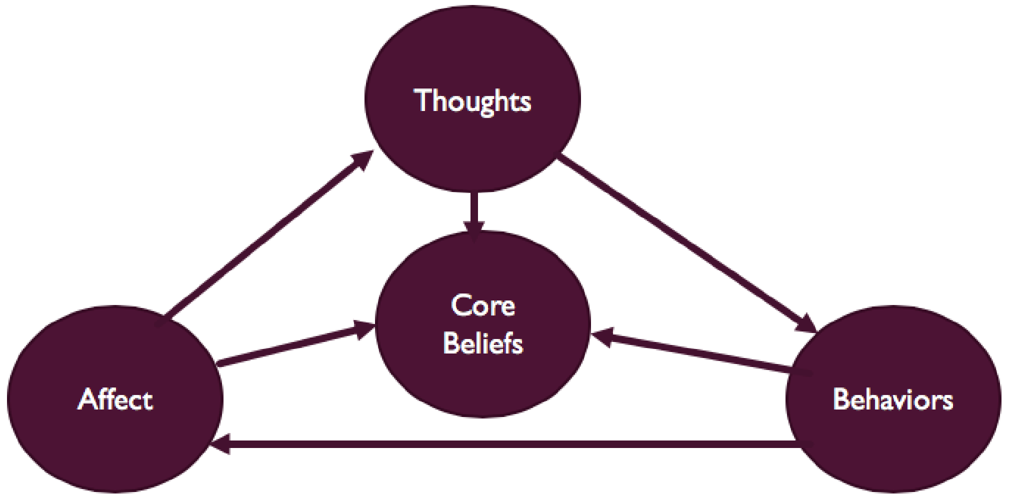
- Cognitive Behavioral Model



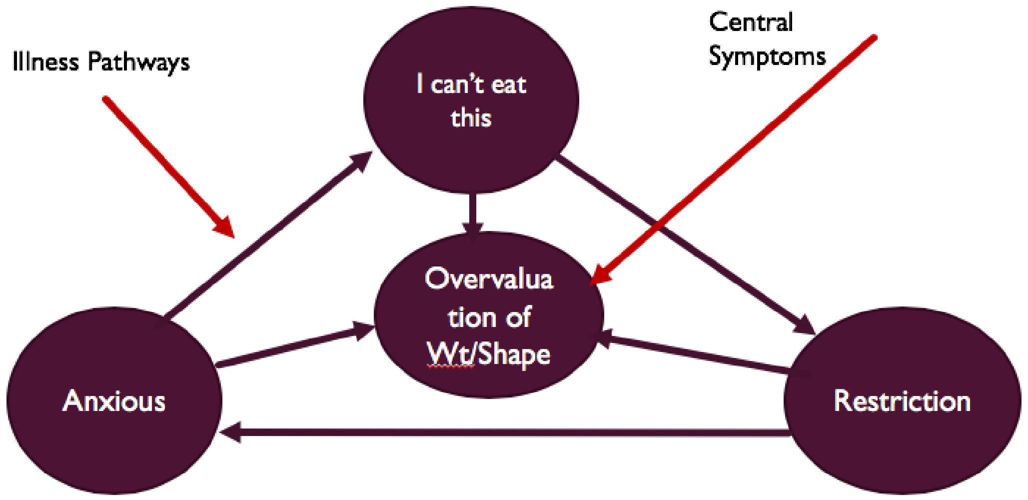
Network Analysis



CBT MODEL



NETWORK MODEL



Changing the Way We Think About EDs? Or Not?

- I would argue we have ALWAYS thought about EDs this way
  - But now we have methods we can use!

Cross-sectional Network Analyses

Focus today on cross-sectional networks

How do symptoms dynamically relate to other symptoms (but remember this is cross-sectional data!)

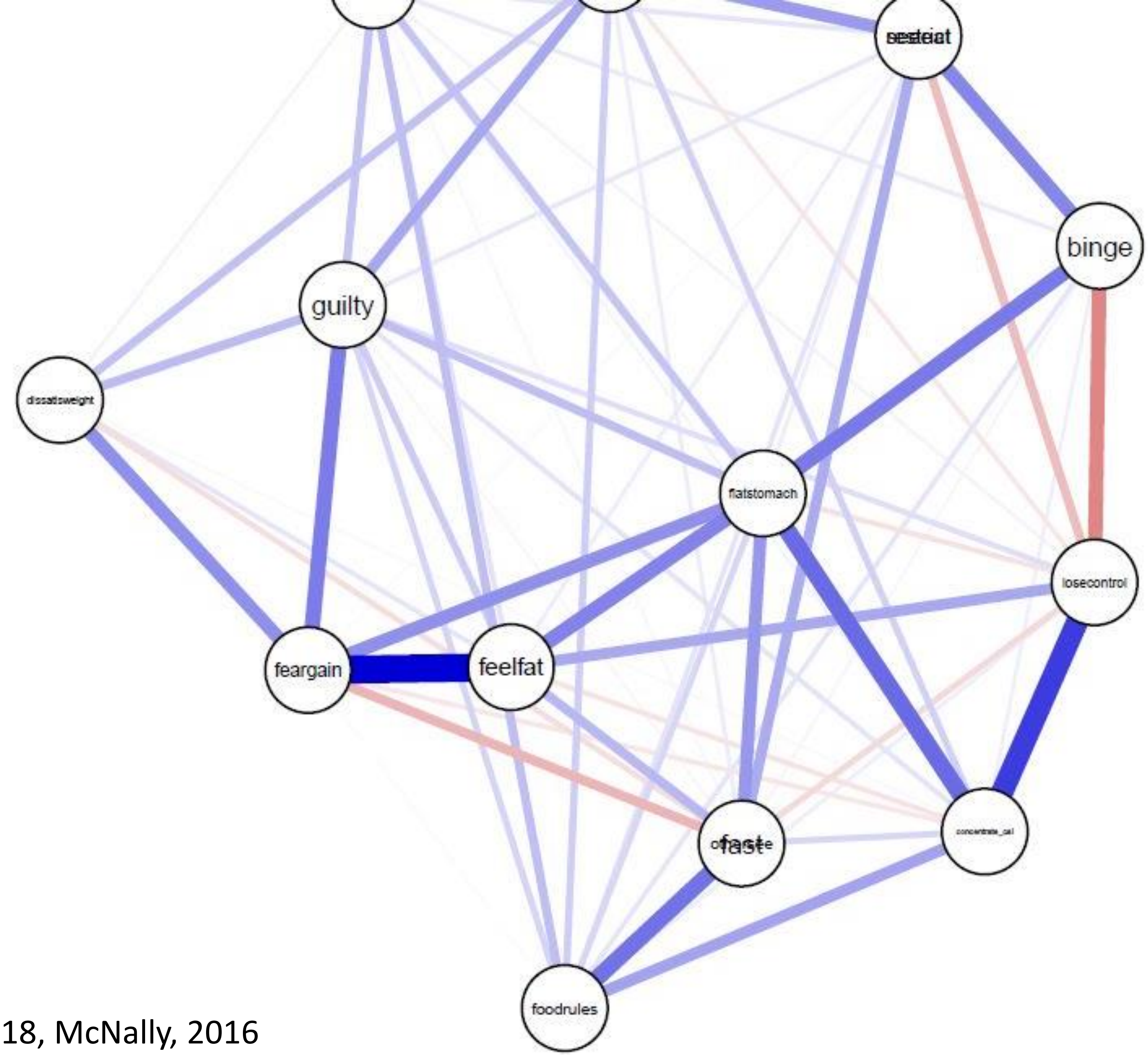
Many other applications though!!

Central symptoms are theorized to drive the maximum number of other symptoms meaning…

Intervention points!

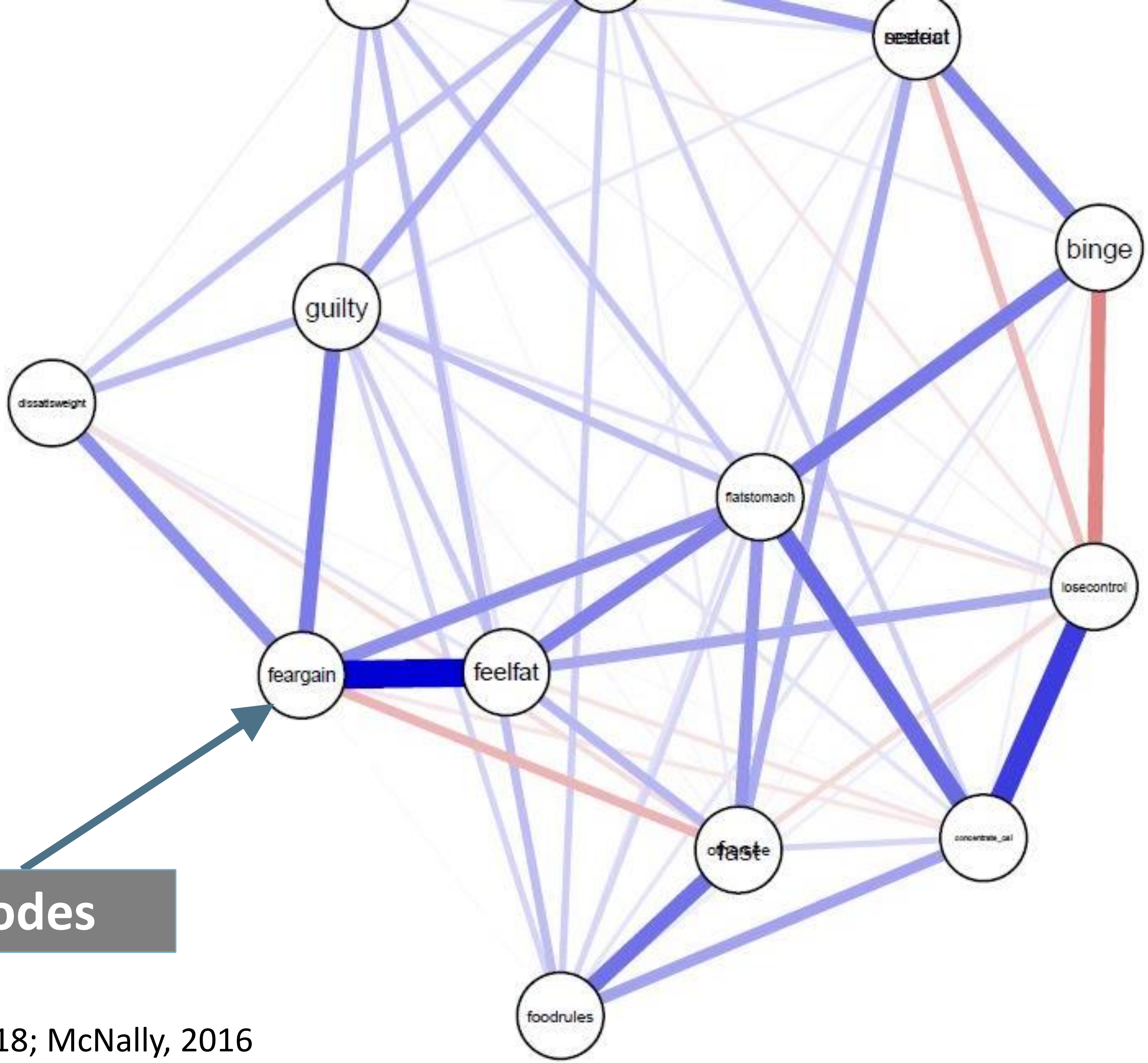
EDs are particularly well-suited for network analyses

Understanding (Partial) Network Models



Epskamp & Fried, 2018; Levinson et al., 2018, McNally, 2016

Understanding (Partial) Network Models

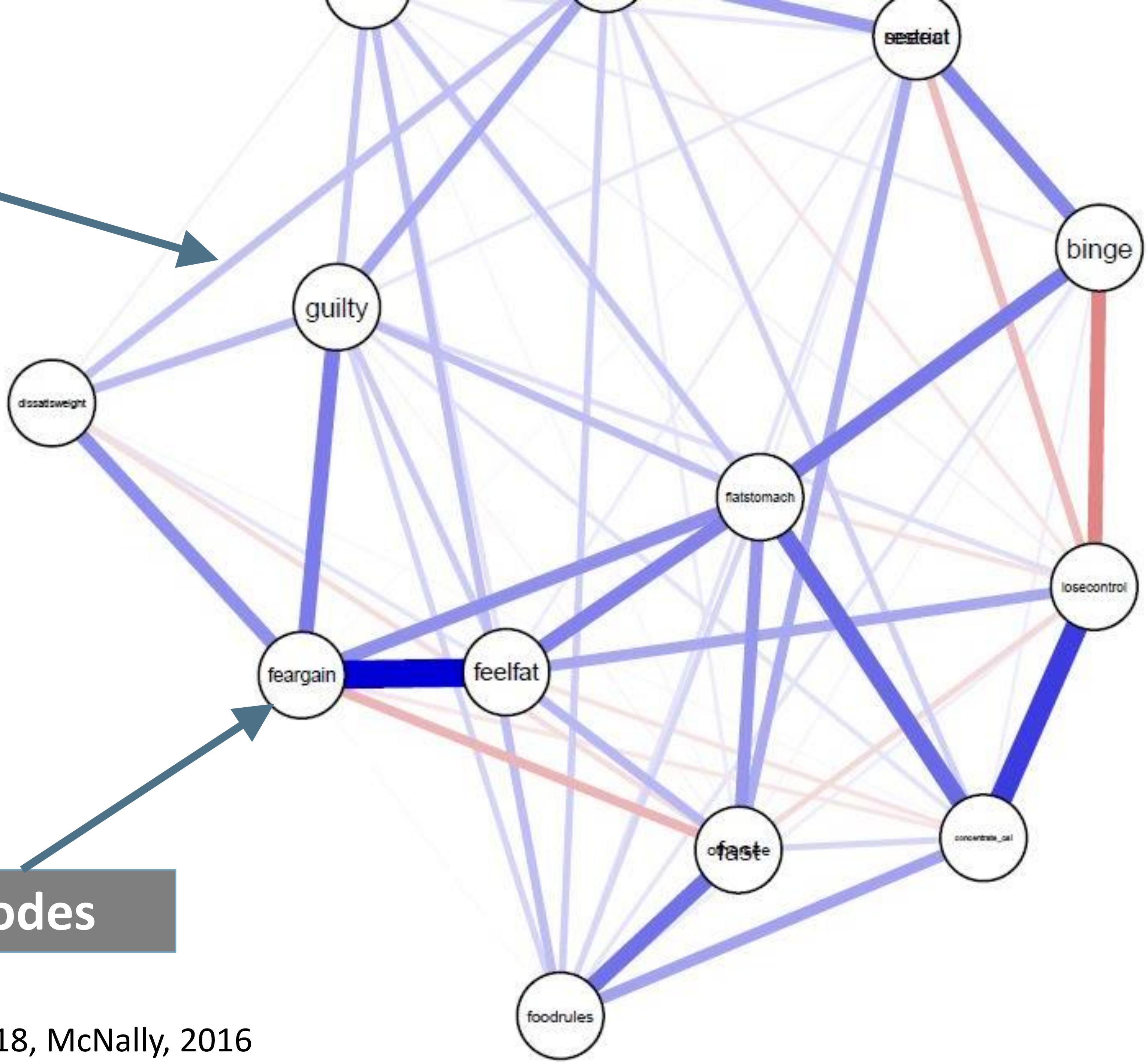


Symptoms = nodes

Epskamp & Fried, 2018; Levinson et al., 2018; McNally, 2016

Associations = edges

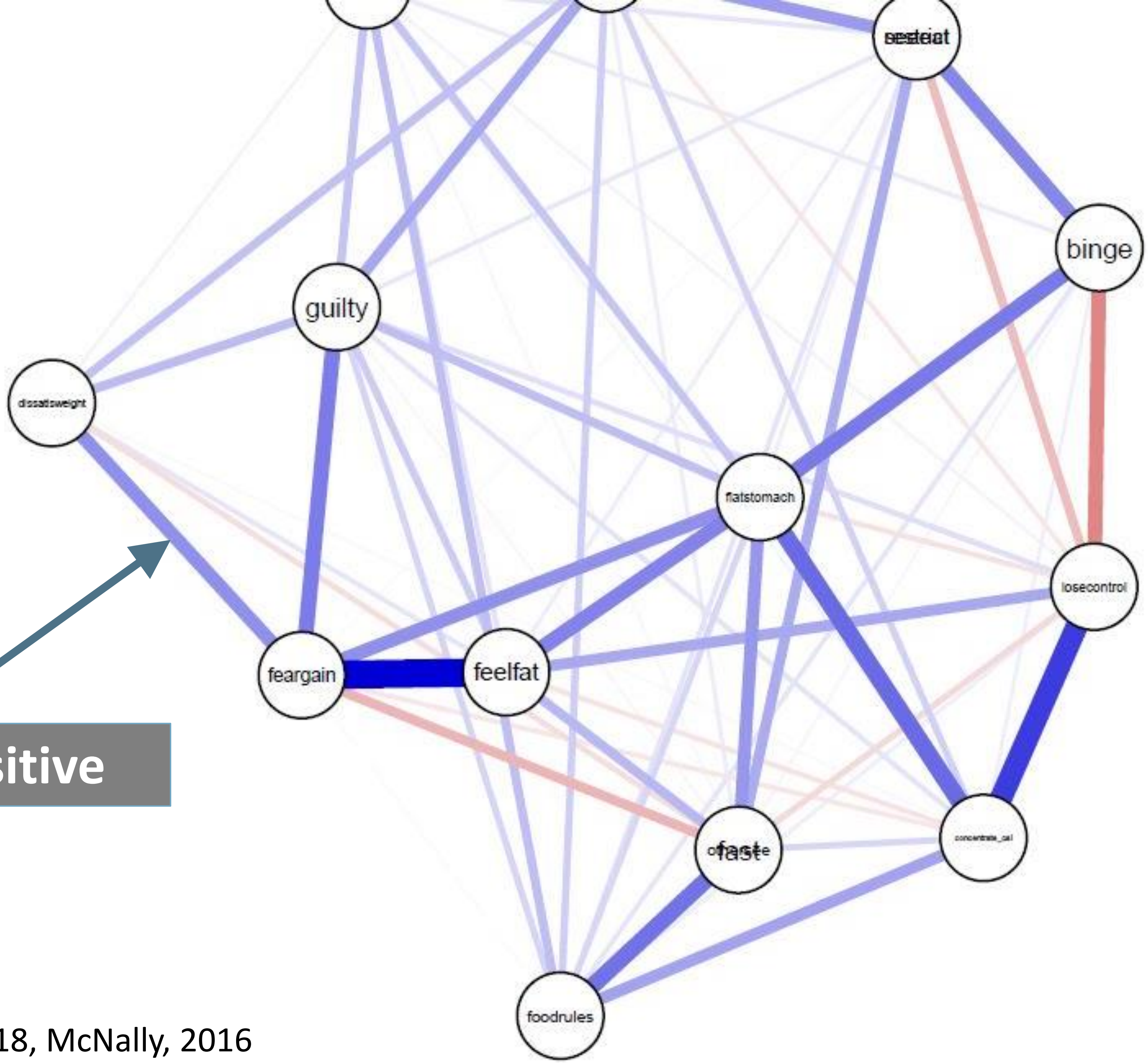
Understanding (Partial) Network Models



Symptoms = nodes

Epskamp & Fried, 2018; Levinson et al., 2018, McNally, 2016

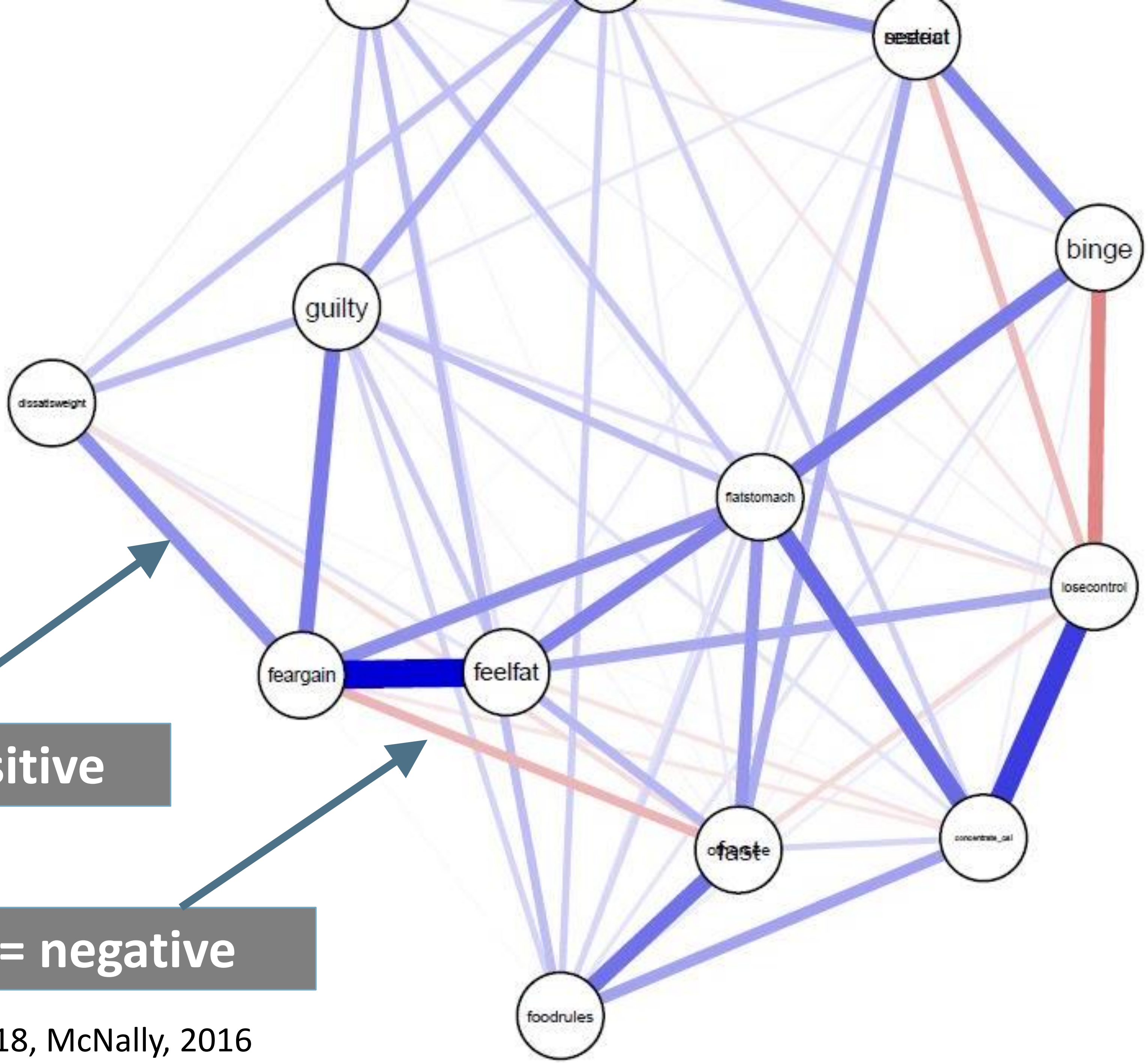
Understanding (Partial) Network Models



Blue (or green) edges = positive

Epskamp & Fried, 2018; Levinson et al., 2018, McNally, 2016

Understanding (Partial) Network Models

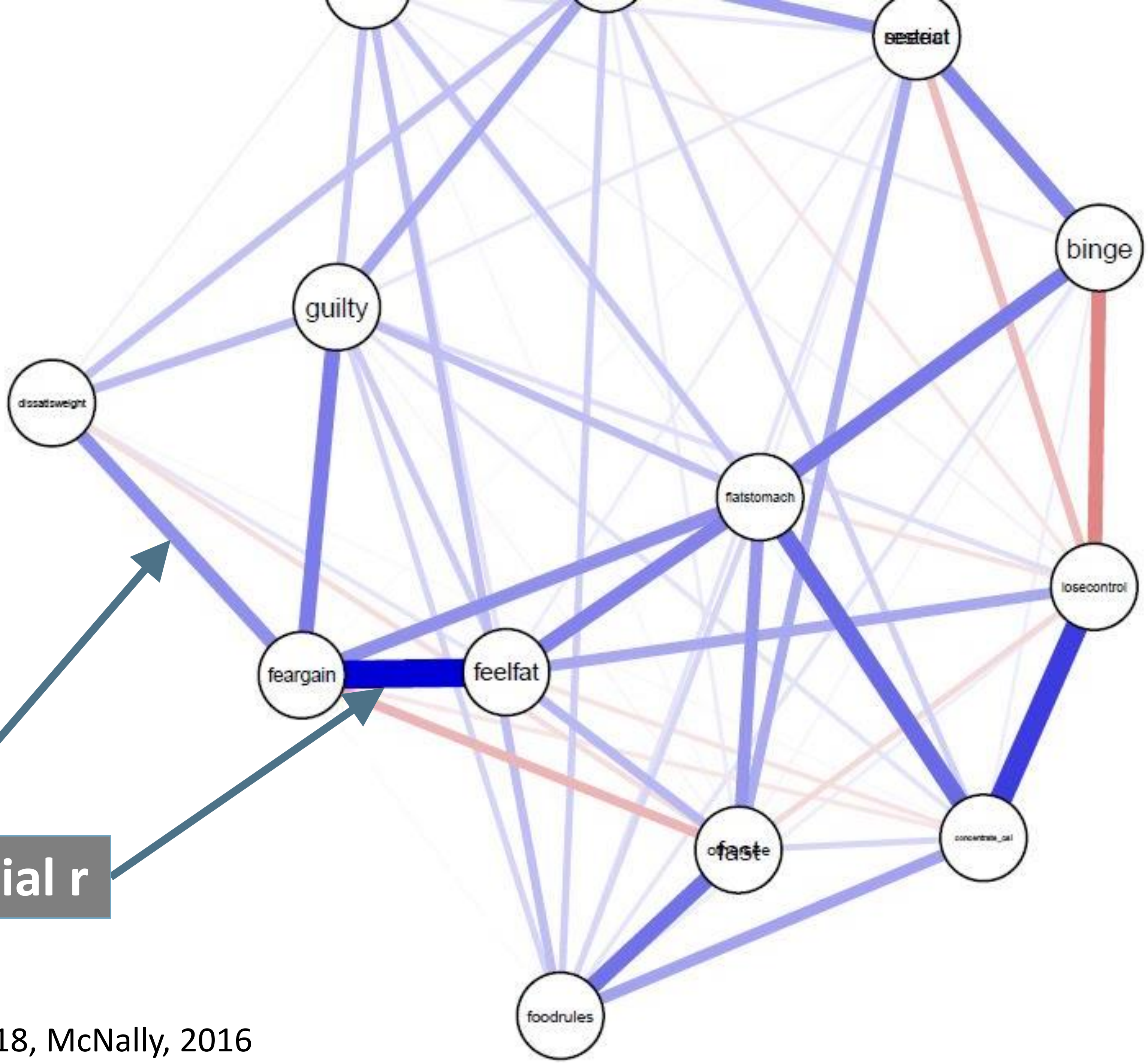


Blue (or green) edges = positive

Red edges = negative

Epskamp & Fried, 2018; Levinson et al., 2018, McNally, 2016

Understanding (Partial) Network Models



Thicker edges = larger partial r

Epskamp & Fried, 2018; Levinson et al., 2018, McNally, 2016

Different Types of Network Models

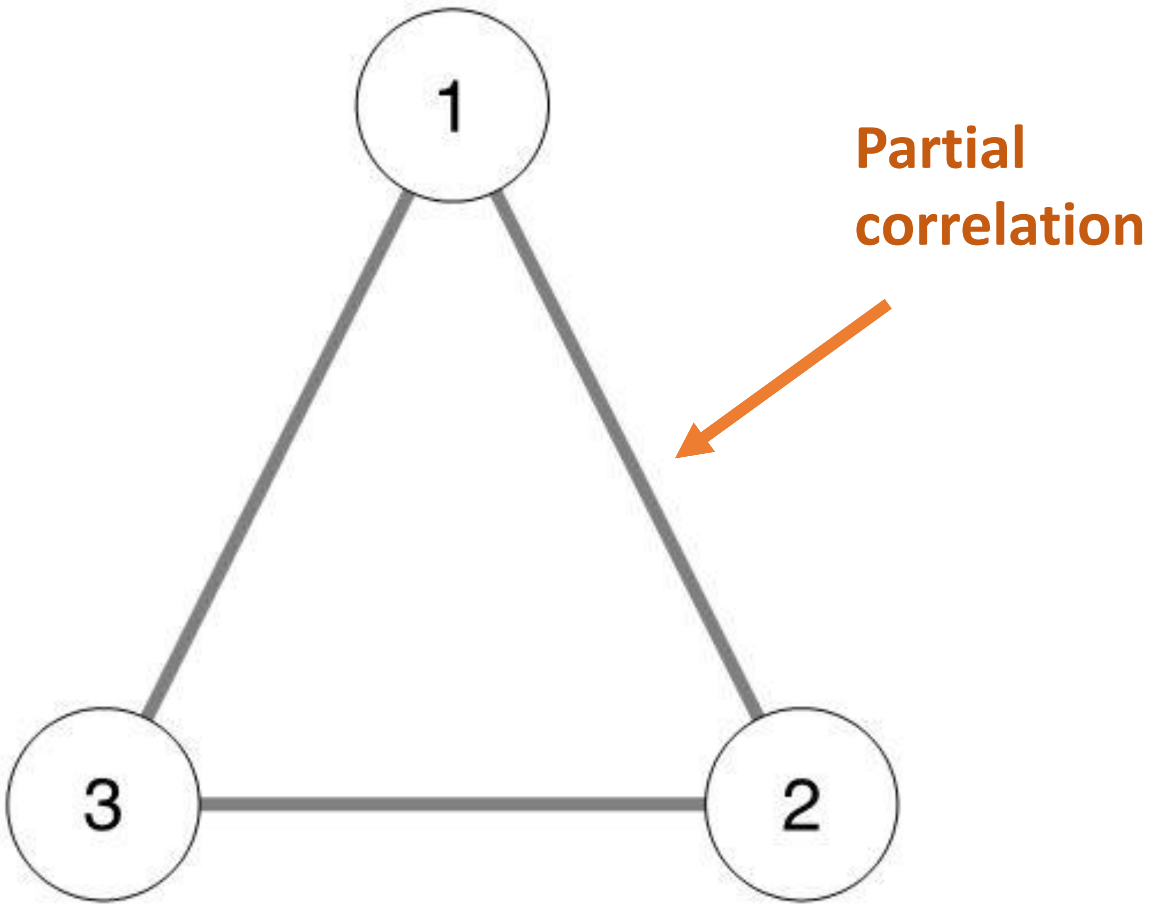
ASSOCIATION

PARTIAL CORRELATION

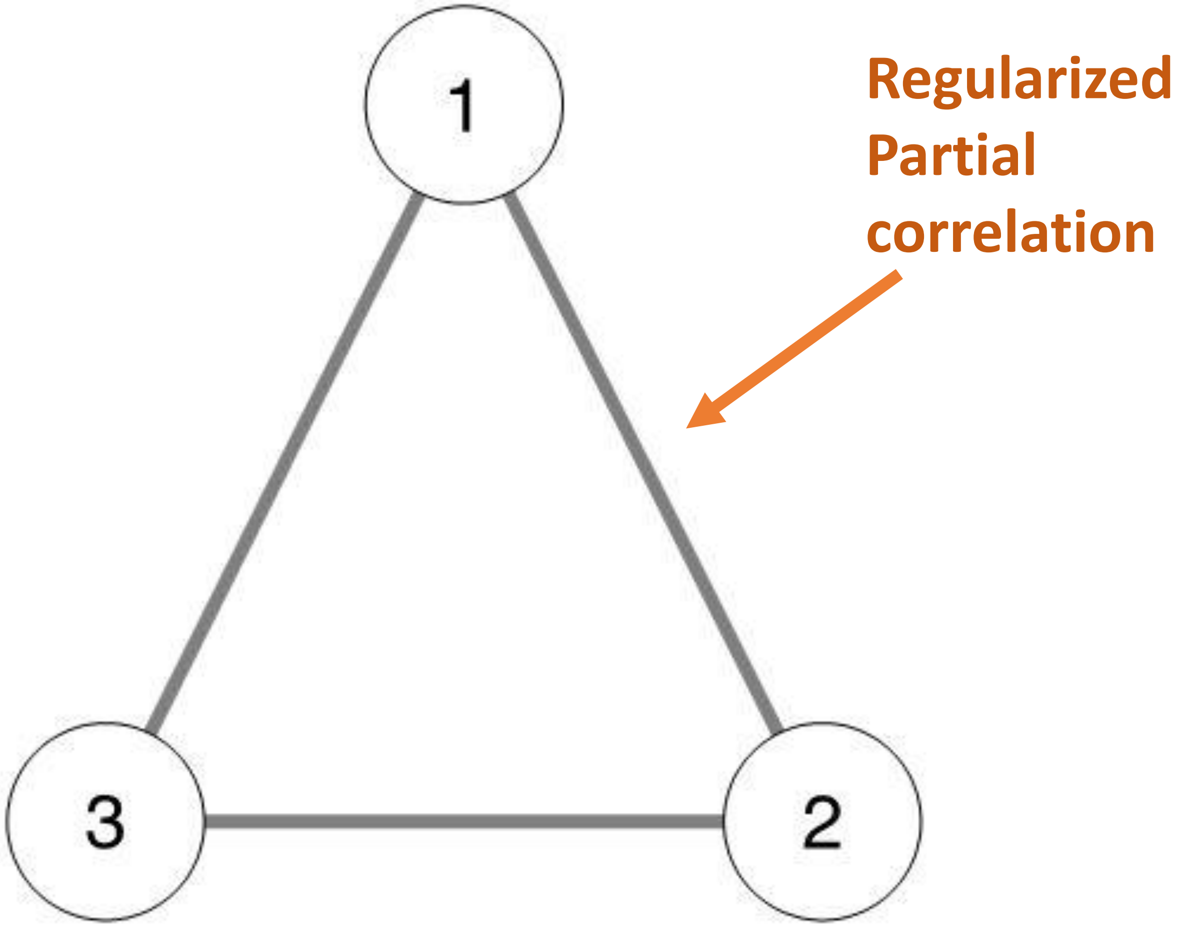
REGULARIZED PARTIAL CORRELATION

Borsboom & Cramer, 2013; Costantini et al., 2015; Epskamp, 2014;Epskamp et al., 2012; Epskamp & Fried, 2018; Levinson et al., 2018

Partial Correlation

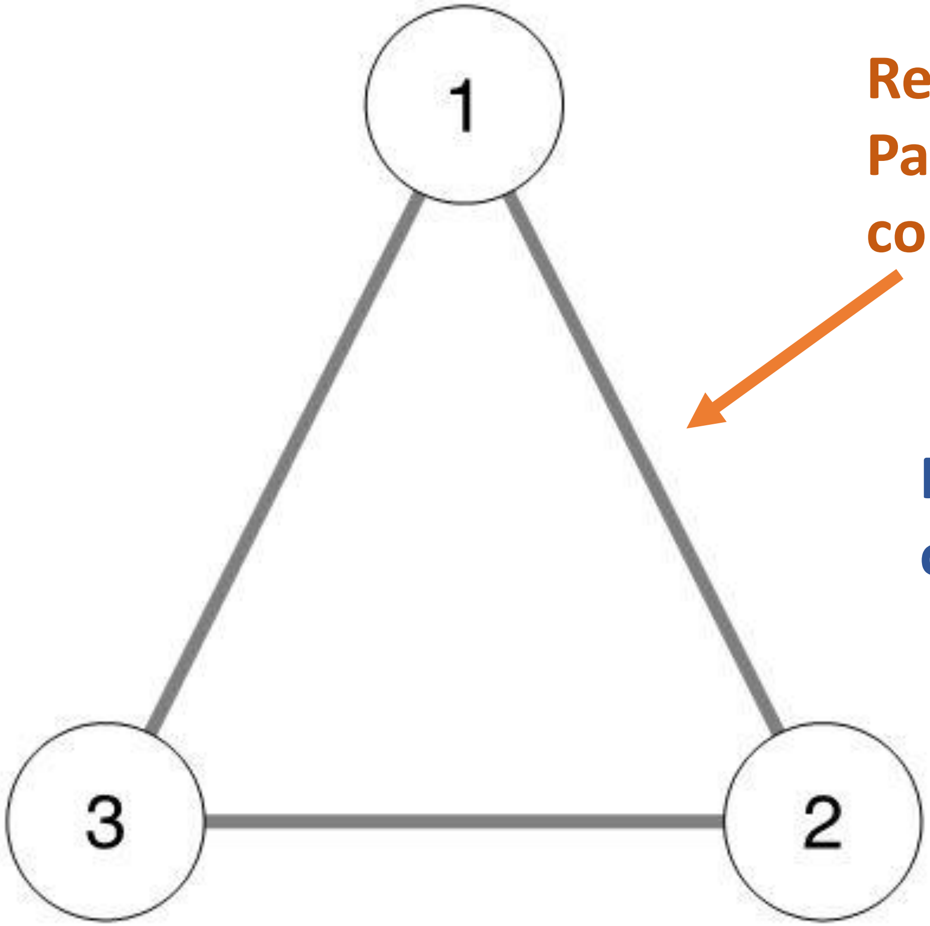


Glasso Networks



Friedman, Hastie, & Tibshirani, 2008

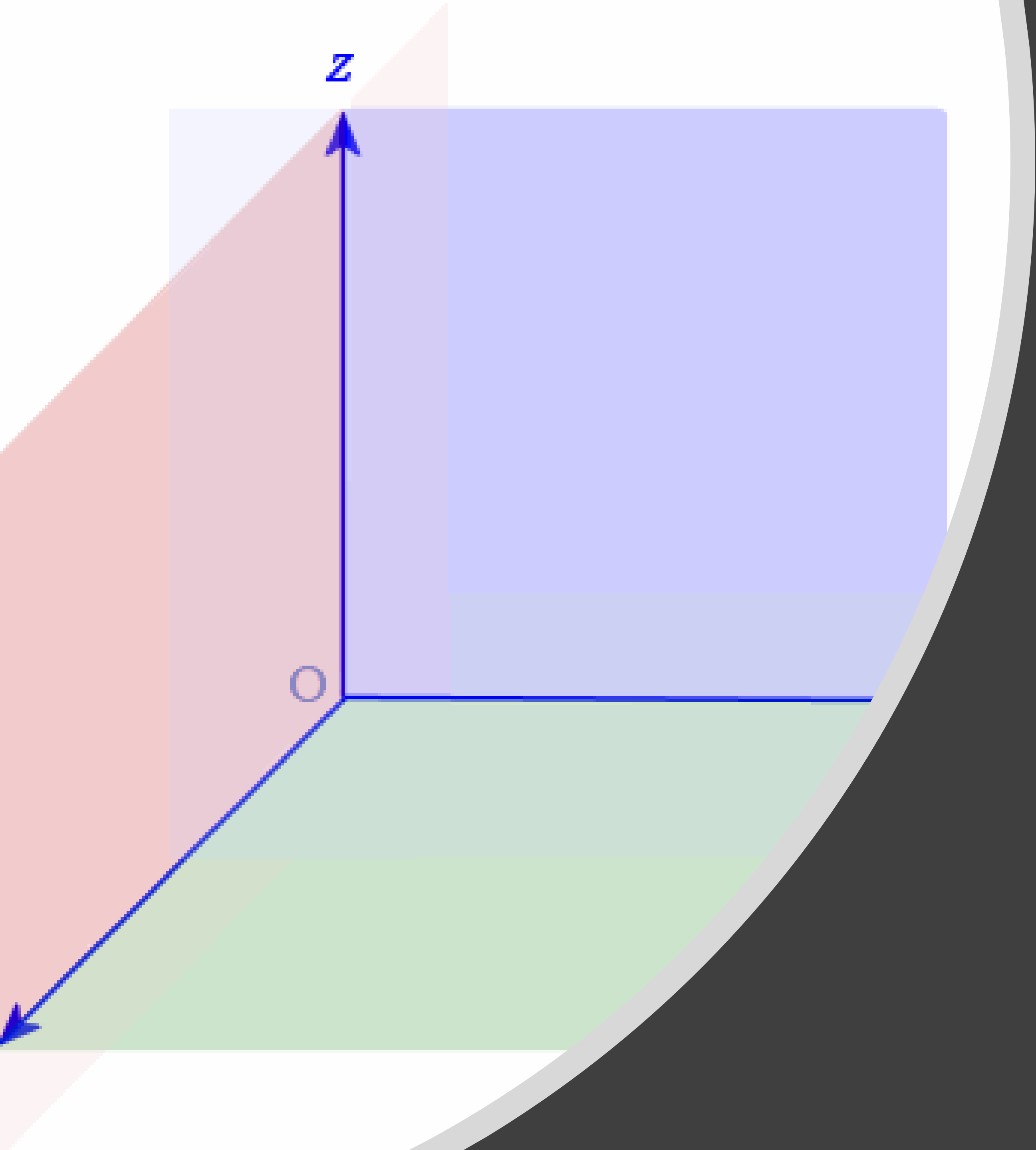
Glasso Networks



Regularized Partial correlation

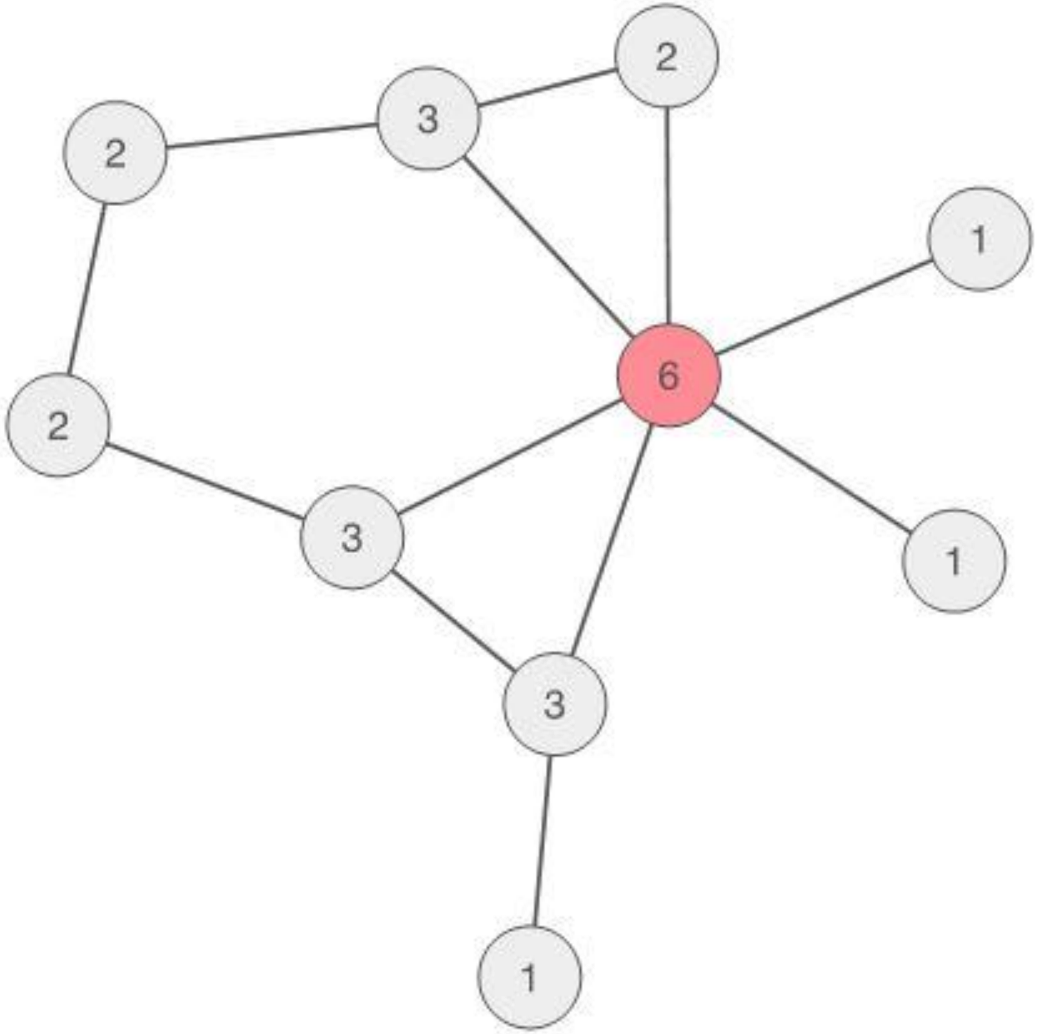
Polychoric or Spearman

Friedman, Hastie, & Tibshirani, 2008



YOU CANNOT INTERPRET NETWORKS VISUALLY

Centrality Indices

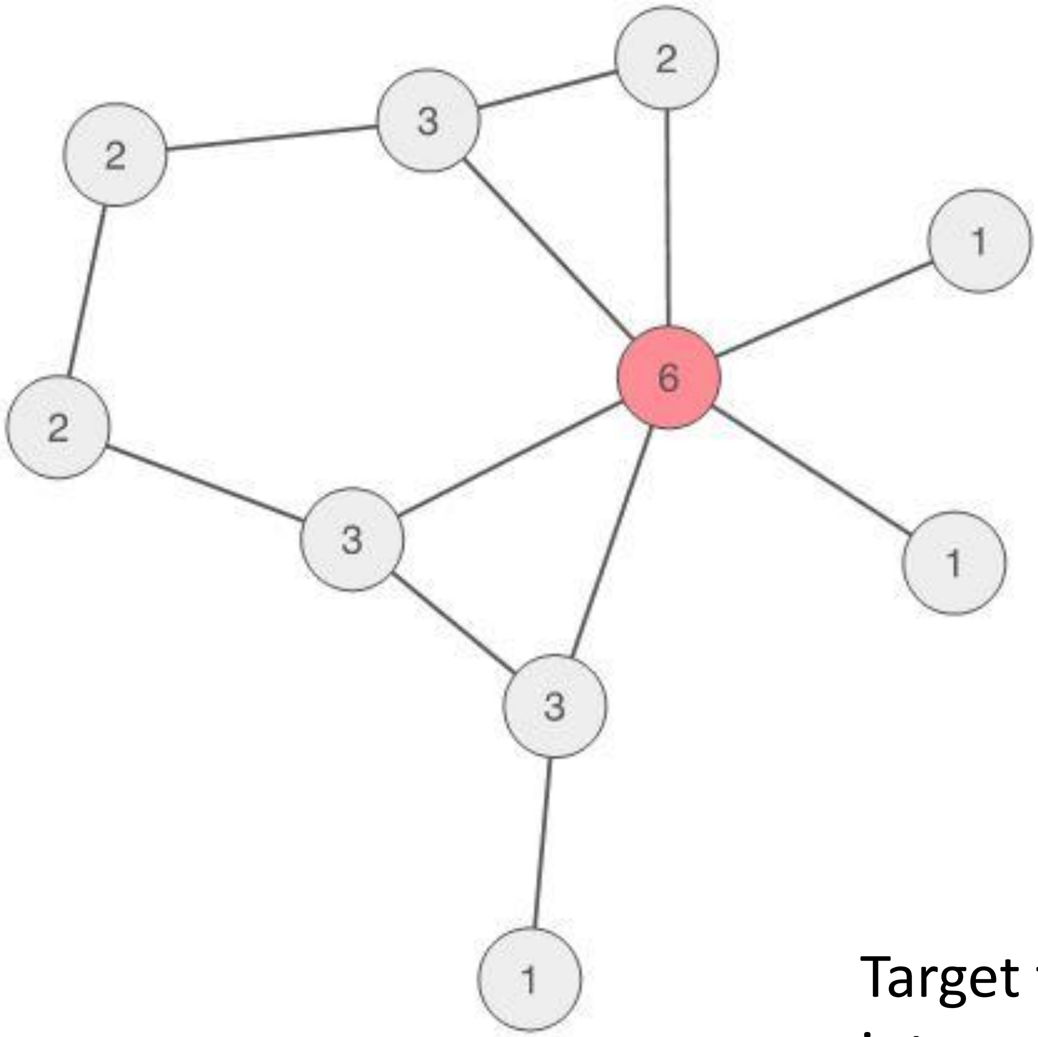


Epskamp, Borsboom, & Fried, 2018; Fried et al., 2017

Centrality Indices

Most “important” symptom

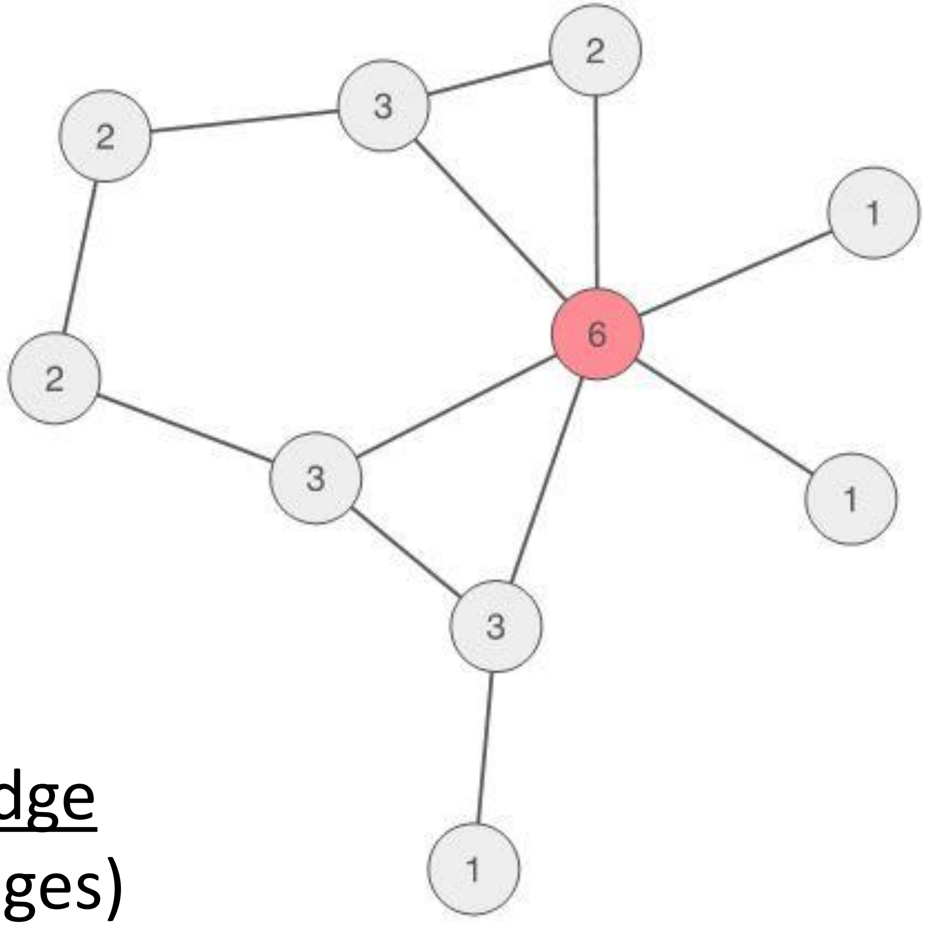
Maintaining symptom?



Target for intervention?

1) **Strength** = the sum of the absolute edge weights between a focal node and all other nodes to which it is connected in the network.

Centrality Indices



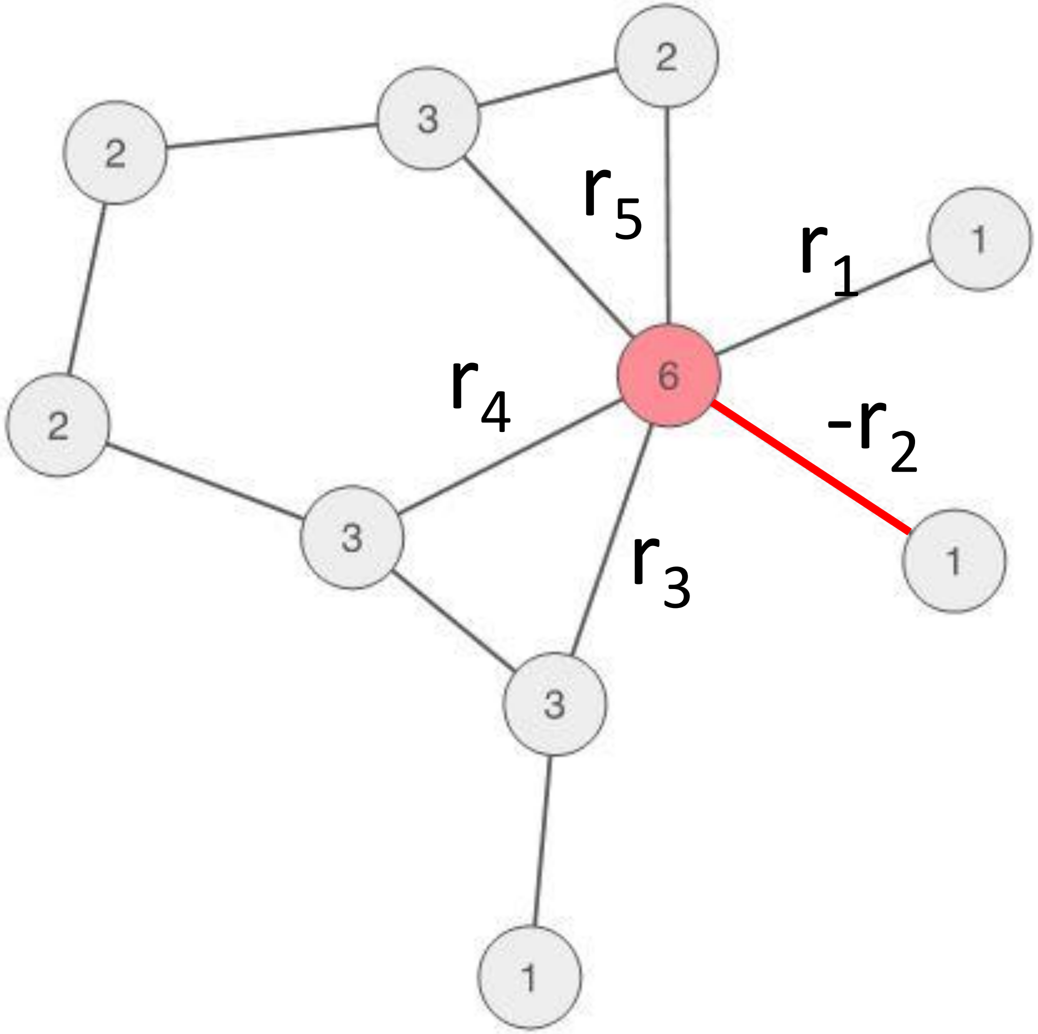
2) **Expected Influence** = sum of edge weights (accounts for negative edges)

Epskamp, Borsboom, & Fried, 2018; Fried et al., 2017; Jones, 2017

Calculating Centrality

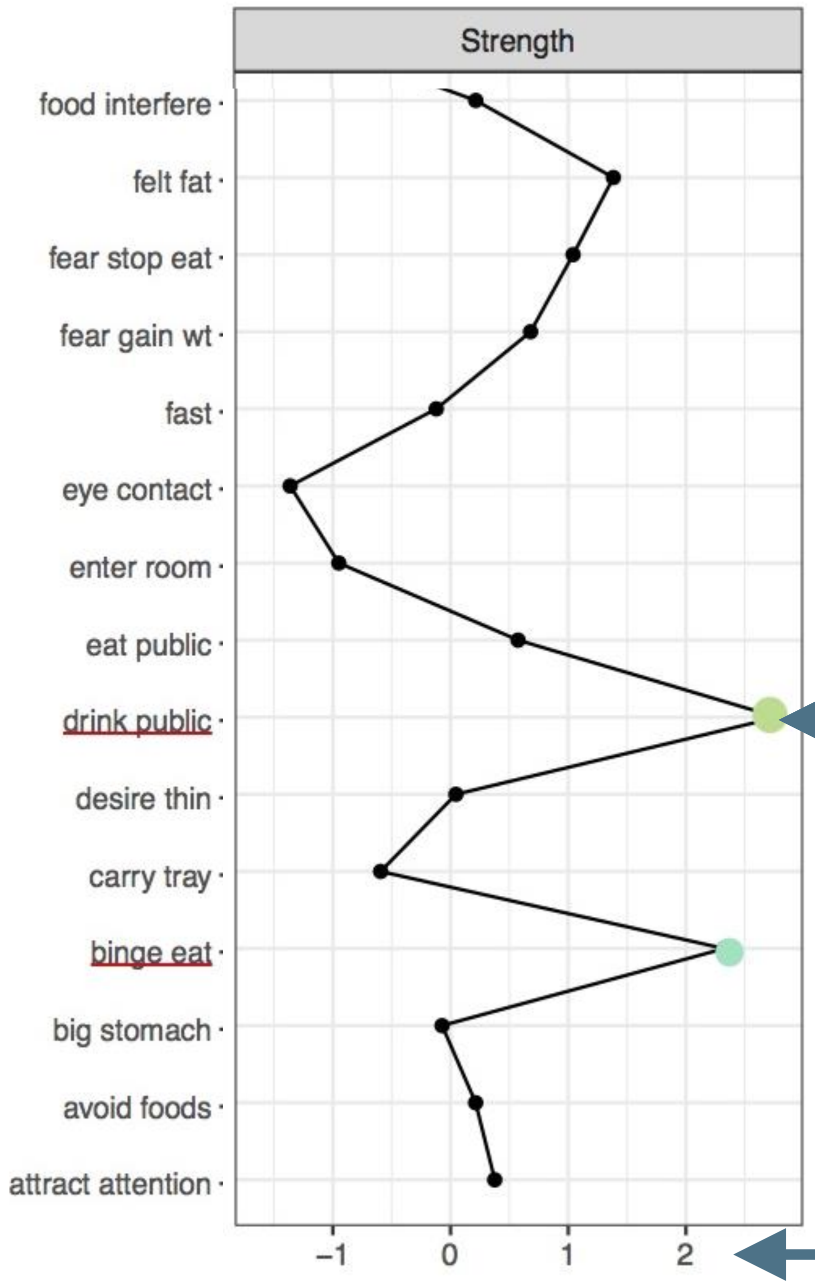
Strength centrality = $|r_1| + |-r_2| + |r_3| + |r_4| + |r_5|$

Expected influence = $r_1 + (-r_2) + r_3 + r_4 + r_5$



Epskamp, Borsboom, & Fried, 2018; Fried et al., 2017; Jones, 2017

Understanding Centrality Graphs

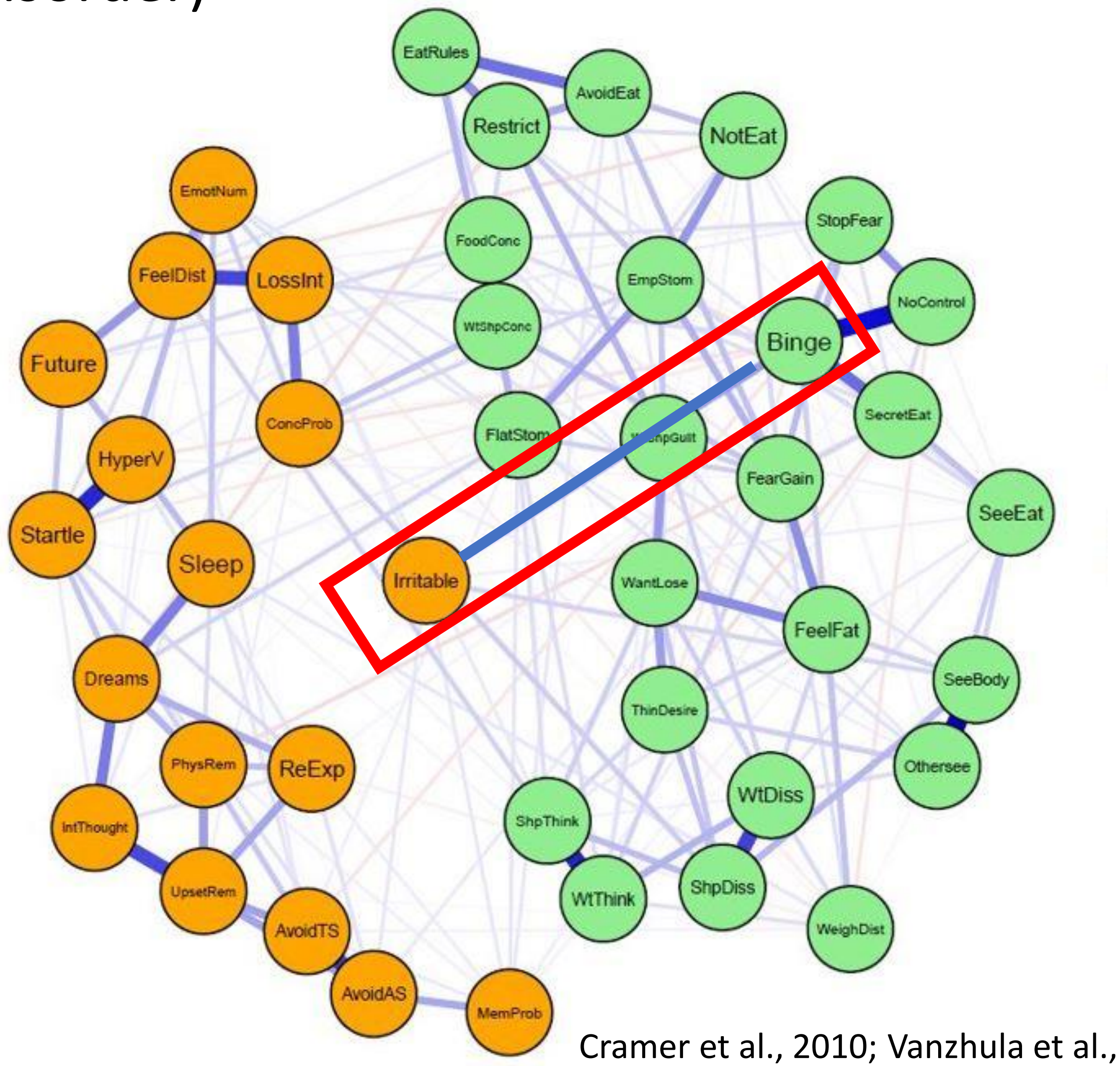


Higher centrality = more important

X-axis = *z*-scores

Bridge Symptoms: May Explain How Comorbidity is Maintained

Bridge: Irritability (PTSD) – Binge (Eating Disorder)

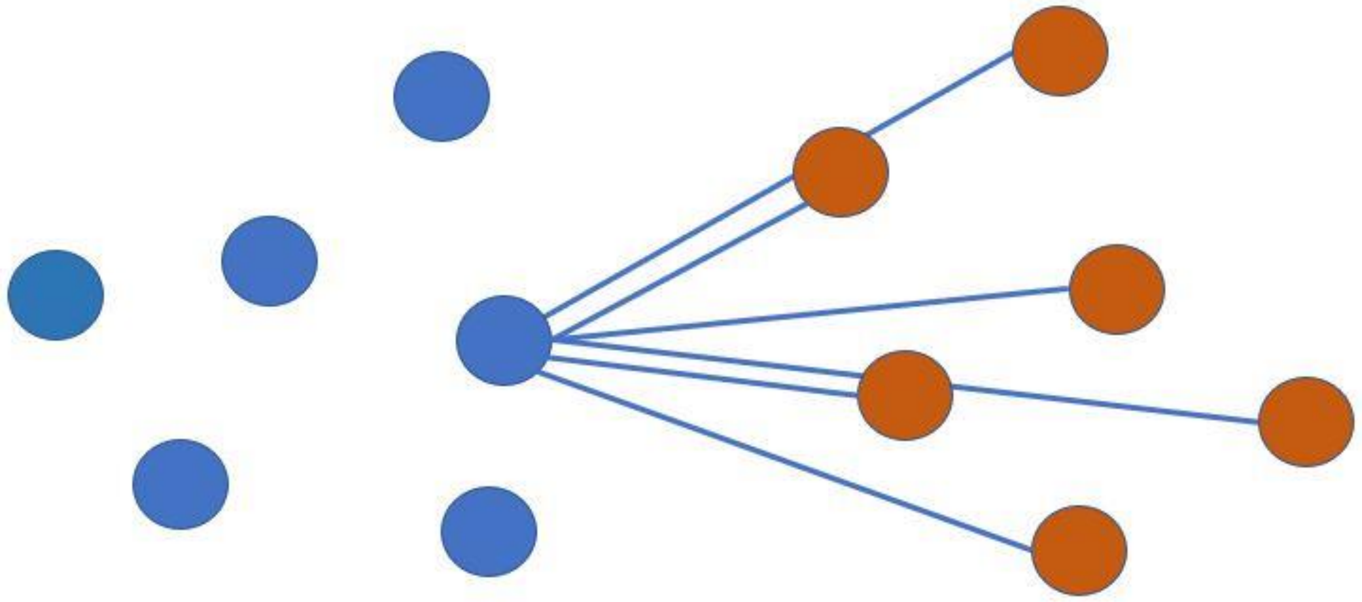


Cramer et al., 2010; Vanzhula et al., 2018

Bridge Symptoms: May Explain How Comorbidity is Maintained

nct

Bridge Symptom – Which symptom in one cluster (ex: eating disorder symptoms) is most strongly connected to all symptoms in a different cluster (ex: all PTSD symptoms)?



Cramer et al., 2010; Jones, 2017; Jones & McNally, 2018; Levinson et al., 2018b

Network Comparison Test

Network Structure Invariance: Is the way the nodes within the network are connected differs across samples?

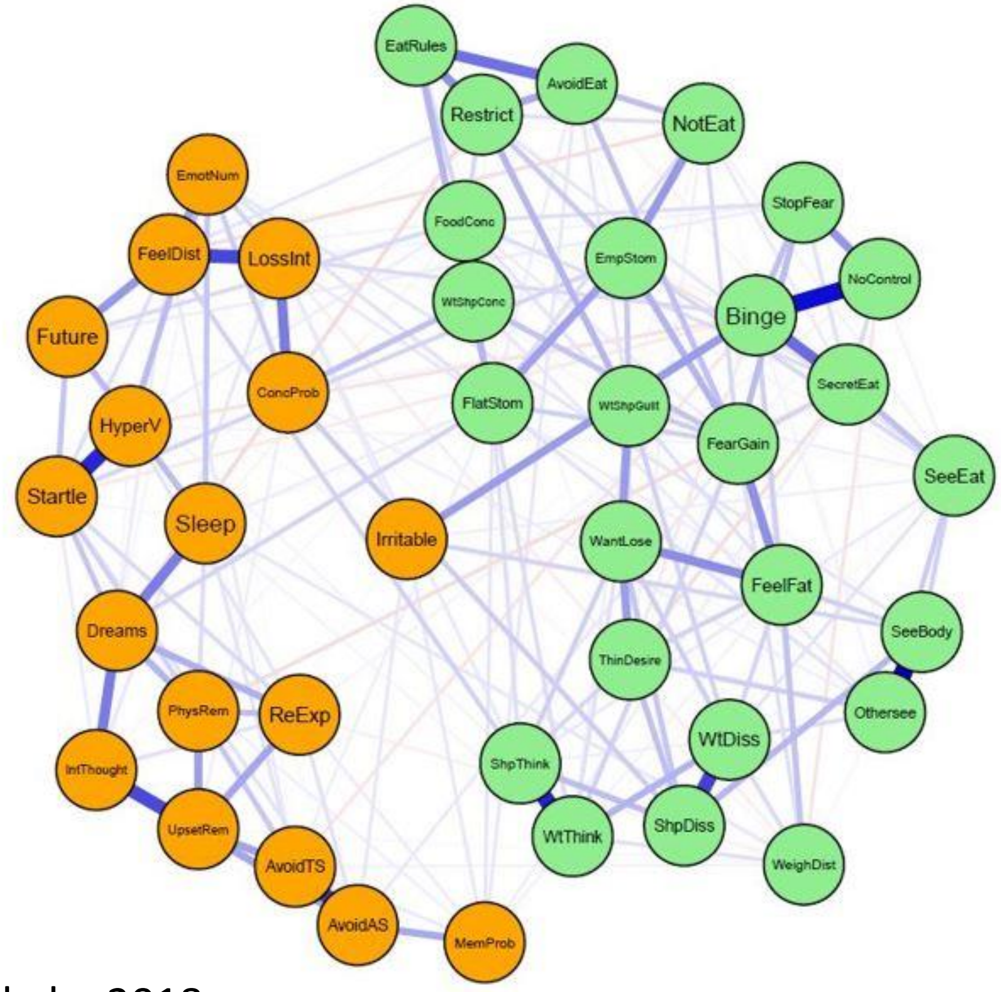
Specific Edge Invariance: Are the edges between 2 specific symptoms different between the two networks?

Global Strength Invariance: Is the sum of the strengths of all edges in the network (i.e., network density) differs across samples

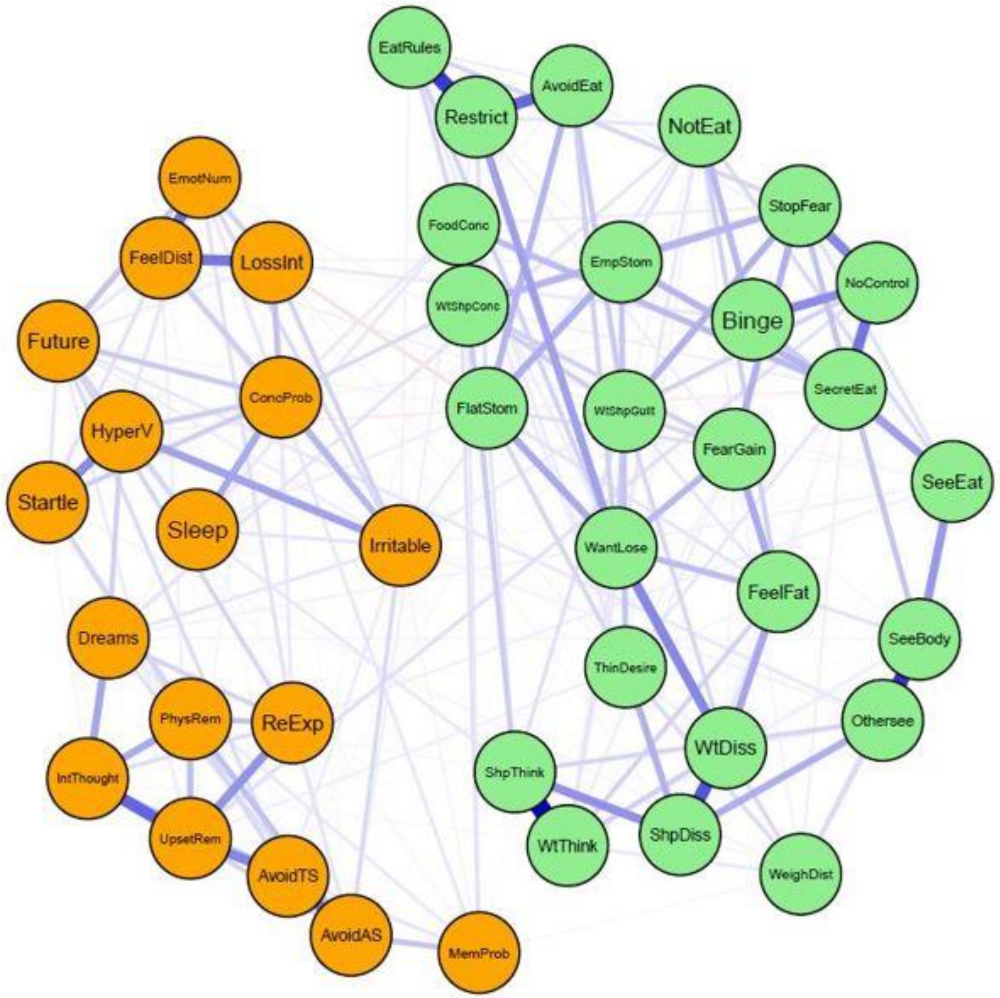
van Borkulo, 2018

Network Comparison Test

Clinical Network



Non-clinical Network



van Borkulo, 2018

Compare Networks Pre-Post Treatment

Psychological Medicine

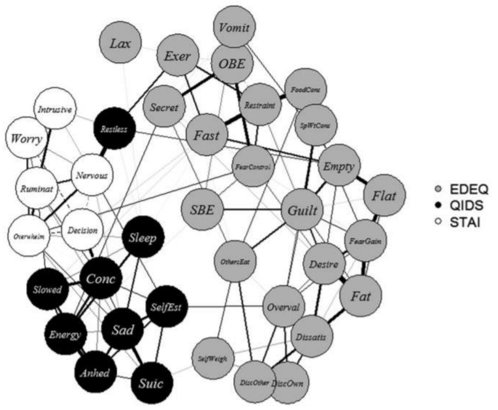
cambridge.org/psm

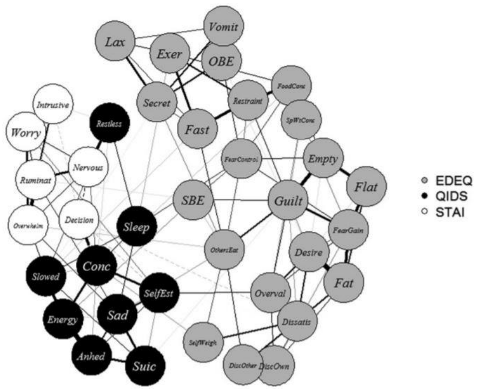
Original Article

Cite this article: Smith KE *et al* (2018). A comparative network analysis of eating disorder psychopathology and co-occurring depression and anxiety symptoms before and after treatment. *Psychological Medicine* **49**,

A comparative network analysis of eating disorder psychopathology and co-occurring depression and anxiety symptoms before and after treatment

Kathryn E. Smith[1,2], Tyler B. Mason[3], Ross D. Crosby[1,2], Li Cao[1], Rachel C. Leonard[4], Chad T. Wetterneck[4], Brad E. R. Smith[4], Nicholas R. Farrell[4], Bradley C. Riemann[4], Stephen A. Wonderlich[1,2] and Markus Moessner[5]





Item Selection Consideration

Network model = what you put in it

Similar symptoms => artificially inflated centrality (e.g., judge self based on shape/weight)

Factor structure

Variable type (count items in EDEQ require mgm)

Item Selection Methods

THEORETICAL

STATISTICAL (GOLDBRICKER)

COMBINATION

Jones, 2017

Levinson et al. (2018). Social anxiety and eating disorder comorbidity and underlying Vulnerabilities.

2. Sample size

- Depends on number of items included
- General rule: 3 participants per parameter
  - 23 items = 750 participants
- Can be lower if network is stable

Epskamp, Borsboom, & Fried, 2018; Fried et al., 2017; Fried & Cramer, 2016

Assumptions?

No "official" assumptions

Multicollinearity

Several items measuring the same thing ("sad" and "blue")

Skewed data (i.e., ceiling effect)

Epskamp, Borsboom, & Fried, 2018; Fried et al., 2017; Fried & Cramer, 2016

Missing Data

- Excluded listwise during analysis
- Can impute if desired

Van Buuren & Groothuis-Oudshoorn, 2011

Network Stability

Accuracy of network model

Model fit: Will not interpret model with poor fit

How is Stability Tested?

bootnet()

- Bootstrapping to create confidence intervals
- Dropping cases from dataset and estimating correlation between parameters in new and original dataset

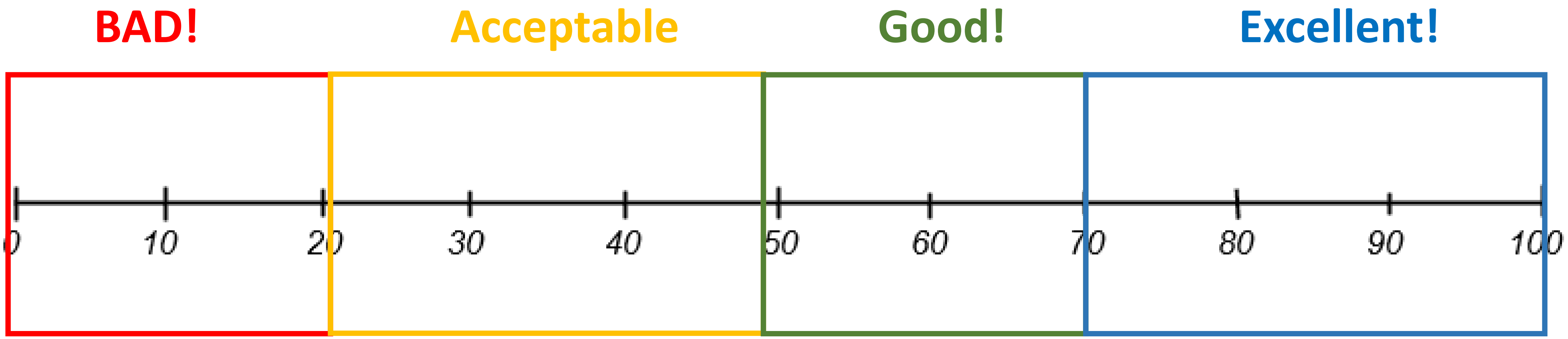
Behav Res
DOI 10.3758/s13428-017-0862-1

CrossMark

Estimating psychological networks and their accuracy: A tutorial paper

Sacha Epskamp[1] · Denny Borsboom[1] · Eiko I. Fried[1]

Coefficients

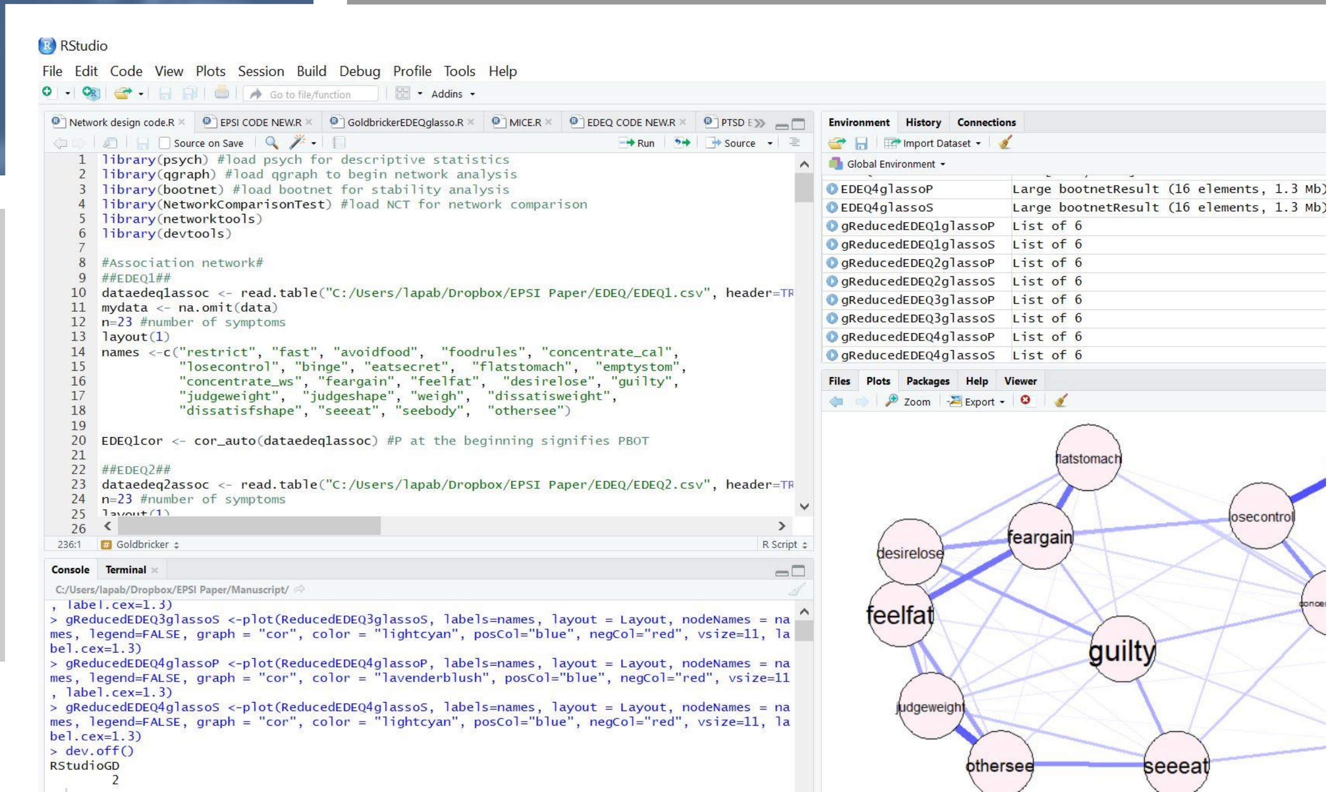


Data Analysis Demonstration

Network Estimation and Stability

Products

RStudio
Open source and enterprise-ready professional software for R



RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Addins
Network design code.R
EPSI CODE NEW.R
GoldbrickerEDEQglasso.R
MICE.R
EDEQ CODE NEW.R
Source on Save
Run
Source
library(psych) #load psych for descriptive statistics
library(qgraph) #load qgraph to begin network analysis
library(bootnet) #load bootnet for stability analysis
library(NetworkComparisonTest) #load NCT for network comparison
library(networktools)
library(devtools)
#Association network#
##EDEQ1##
dataedeq1assoc <- read.table("C:/Users/lapab/Dropbox/EPSI Paper/EDEQ/EDEQ1.csv", header=TR
mydata <- na.omit(data)
n=23 #number of symptoms
layout(1)
names <-c("restrict", "fast", "avoidfood", "foodrules", "concentrate_cal",
"losecontrol", "binge", "eatsecret", "flatstomach", "emptystom",
"concentrate_ws", "feargain", "feelfat", "desirelose", "guilty",
"judgeweight", "judgeshape", "weigh", "dissatisweight",
"dissatisfshape", "seeeat", "seebody", "othersee")
EDEQ1cor <- cor_auto(dataedeq1assoc) #P at the beginning signifies PBOT
##EDEQ2##
dataedeq2assoc <- read.table("C:/Users/lapab/Dropbox/EPSI Paper/EDEQ/EDEQ2.csv", header=TR
n=23 #number of symptoms
Goldbricker
R Script
Console Terminal
C:/Users/lapab/Dropbox/EPSI Paper/Manuscript/
> gReducedEDEQ3glassoS <-plot(ReducedEDEQ3glassoS, labels=names, layout = Layout, nodeNames = names, legend=FALSE, graph = "cor", color = "lightcyan", posCol="blue", negCol="red", vsize=11, label.cex=1.3)
> gReducedEDEQ4glassoP <-plot(ReducedEDEQ4glassoP, labels=names, layout = Layout, nodeNames = names, legend=FALSE, graph = "cor", color = "lavenderblush", posCol="blue", negCol="red", vsize=11, label.cex=1.3)
> gReducedEDEQ4glassoS <-plot(ReducedEDEQ4glassoS, labels=names, layout = Layout, nodeNames = names, legend=FALSE, graph = "cor", color = "lightcyan", posCol="blue", negCol="red", vsize=11, label.cex=1.3)
> dev.off()
RStudioGD
2
Environment History Connections
Import Dataset
Global Environment
EDEQ4glassoP Large bootnetResult (16 elements, 1.3 Mb)
EDEQ4glassoS Large bootnetResult (16 elements, 1.3 Mb)
gReducedEDEQ1glassoP List of 6
gReducedEDEQ1glassoS List of 6
gReducedEDEQ2glassoP List of 6
gReducedEDEQ2glassoS List of 6
gReducedEDEQ3glassoP List of 6
gReducedEDEQ3glassoS List of 6
gReducedEDEQ4glassoP List of 6
gReducedEDEQ4glassoS List of 6
Files Plots Packages Help Viewer
Zoom Export
flatstomach
losecontrol
feargain
desirelose
feelfat
guilty
judgeweight
othersee
seeeat

Preparing Data

Name	Name variables
Save	Save as .csv
Code	Code all missing data as NA

	A	B	C	D	E	F	G	H	I	J
1	restrict	fast	avoidfood	foodrules	concentrate_cal	losecontrol	binge	eatsecret	flatstomach	emptystom
2	4	0.00	4.00	4.00	4.00	4.00	4.00	4.00	5.00	4.00
3	2	2.00	0.00	3.00	0.00	1.00	1.00	0.00	6.00	5.00
4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
5	0	0.00	0.00	2.00	3.00	1.00	2.00	3.00	3.00	0.00
6	3	0.00	6.00	6.00	1.00	2.00	1.00	1.00	1.00	1.00
7	1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
8	3	1.00	4.00	1.00	1.00	5.00	5.00	1.00	6.00	5.00
9	0	0.00	3.00	0.00	0.00	2.00	3.00	3.00	6.00	6.00
10	6	4.00	4.00	6.00	6.00	6.00	5.00	0.00	6.00	6.00
11	1	0.00	6.00	6.00	1.00	0.00	0.00	0.00	6.00	6.00
12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
13	5	0.00	5.00	5.00	6.00	6.00	1.00	2.00	3.00	4.00
14	6	0.00	6.00	6.00	4.00	6.00	3.00	0.00	6.00	6.00
15	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
16	0	0.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00
17	6	1.00	6.00	6.00	6.00	3.00	2.00	2.00	6.00	6.00
18	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
19	6	0.00	6.00	4.00	5.00	4.00	1.00	0.00	6.00	5.00

Orientation to R

- Packages
  - Functions
  - Arguments
- Objects
  - <- symbol is used to assign object a name

Package: bootnet

Function: estimateNetwork

Arguments

`data`	A data frame or matrix containing the raw data. Must be numeric, integer or ordered factors.
`nBoots`	Number of bootstraps
`default`	A string indicating the method to use. See documentation at `estimateNetwork`.
`type`	The kind of bootstrap method to use.
`nCores`	Number of cores to use in computing results. Set to 1 to not use parallel computing.
`statistics`	Vector indicating which statistics to store. Can contain `"edge"`, `"strength"`, `"closeness"`, `"betweenness"`, `"length"` and `"distance"`. By default, length and distance are not stored.
`model`	The modeling framework to use. Automatically detects if data is binary or not.
`fun`	A custom estimation function, when no default set is used. This must be a function that takes the data as input (first argument) and returns either a weights matrix or a list containing the elements `"graph"` for the weights matrix, `"intercepts"` for the intercepts (optional) and `"results"` for the full estimation results (optional).

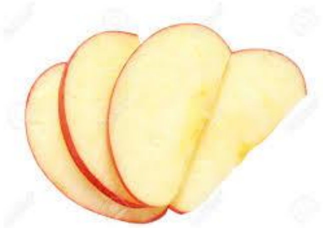
Function (object, details for how function will work…)

Example:

Upload.object(apple) 

Cut (apple, pieces = 4, removeseeds=TRUE) 

CutApple <- Cut (apple, pieces = 4, removeseeds=TRUE)

Display (CutApple) 

Packages

bootnet – Run all basic network analyses

qgraph – Visualize the network

networktools – Bridge symptoms, Goldbricker

NetworkComparisonTest – Compare networks

Find documentation online https://cran.r-project.org/web/packages

Current Sample

N = 823

Individuals with eating disorder diagnosis

Mean age = 23.07 (9.69)

#load required packages

library(bootnet)

library(networktools)

library(NetworkComparisonTest)

library(qgraph)

Assign datafile to object

File directory on your computer

#Load data

Irinadata <- read.table("C:/Users/lapab/Dropbox/EAT Lab/AED Webinar/clinicaldata.csv", header=TRUE, sep=",", na = "NA")

#check data

summary(Irinadata)

Object name for vector of variable names

```
#Assign names to nodes
mynames <- c("restrict", "fast",  "avoidfood", "foodrules",
"concentrate_cal",  "losecontrol",  "binge",  "eatsecret", "flatstomach",
"emptystom", "concentrate_ws",  "feargain",  "feelfat“, "desirelose“,
"guilty", "judgeweight", "judgeshape", "weigh", "dissatisweight",
"dissatisfshape", "seeeat",  "seebody", "othersee")
```

Object name for our network

Use the name of the object you assigned to your datafile

```
#Estimate network using default methods
mynetwork <- estimateNetwork(Irinadata, default="EBICglasso")

#Use Spearman correlation
mynetwork <- estimateNetwork(Irinadata, default="EBICglasso",
corMethod = "cor", corArgs = list(method = "spearman", use =
"pairwise.complete.obs"))
```

#Plot network

Use network object name

Select type of network layout

Node size

Node border color

```
plot(mynetwork, layout="spring", vsize=6, border.color="black", nodeNames = mynames,
color="lightblue“, legend=FALSE)
```

Node background color

Assign variable names as node names

See *qgraph* package documentation for more customization options

```
#set directory for where to save file
setwd("C:/Users/lapab/Dropbox/EAT Lab/AED Webinar")
```

Name for pdf

```
#Save plot as pdf
pdf("MyNetwork.pdf")
myplot <- plot(mynetwork, layout="spring", vsize=6, border.color="black",
nodeNames = names, color="lightblue“, legend=FALSE)
dev.off()
```

Assign name “plot1” to our graph

```
#Create centrality plot (will show strength centrality)
pdf("MyCentrality.pdf",width=4)
c1 <- centralityPlot(myplot)
dev.off()
```

Use plot object name

```
#Expected influence plot
pdf("MyExpectedInfluence.pdf", width=4)
c2 <- centralityPlot(myplot, include = "ExpectedInfluence")
dev.off()
```

Use network object name

```
#Save centrality values
CentralityTable <- centralityTable(mynetwork)
write.csv(CentralityTable, "MyCentralityTable.csv")
```

Name the file where centrality values will be saved

More boots = better accuracy

How many cores computer will use

```
#Estimating Network Stability
b1 <- bootnet(mynetwork, boots=1000,nCores=4, statistics=c("strength", "expectedInfluence", "edge"))
b2 <- bootnet(mynetwork, boots=1000,nCores=4, type="case", statistics=c("strength", "expectedInfluence", "edge"))
```

Indicate which statistics you want to bootstrap

```
#Save bootstrapped files
save(b1, file = "b1.Rdata")
save(b2, file = "b2.Rdata")
```

Save files so don't have to run again in the future

```
#load bootstrapped files after they have been previously saved
setwd("C:/Users/lapab/Dropbox/EAT Lab/AED Webinar")
load("b1.Rdata")
load("b2.Rdata")
```

```
#Get centrality stability coefficient
corStability(b2)

#Save edge stability graph
pdf("EdgeStability.pdf")
plot(b1, labels = FALSE, order = "sample")
dev.off()

#Save centrality stability graph
pdf("CentrStability.pdf")
plot(b2)
dev.off()
```

```
# Strength Centrality diff test
pdf("CentraityDifference.pdf")
plot(b1, "strength", order="sample",
labels=TRUE)
dev.off()
```

Indicate statistic

```
# EI diff test
pdf("EIDifference.pdf")
plot(b1, "expectedInfluence", order="sample",
labels=TRUE)
dev.off()

#Edge weights diff test
pdf("EdgeDifftest.pdf")
plot(b1, "edge", plot = "difference",
onlyNonZero = TRUE, order = "sample")
dev.off()
```

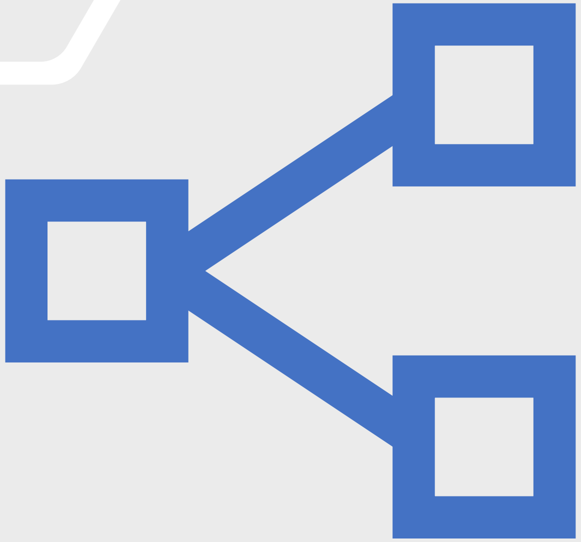
Interpreting Results

Two Types of Stability

Stability of **edge weights**

Stability of **centrality indices**

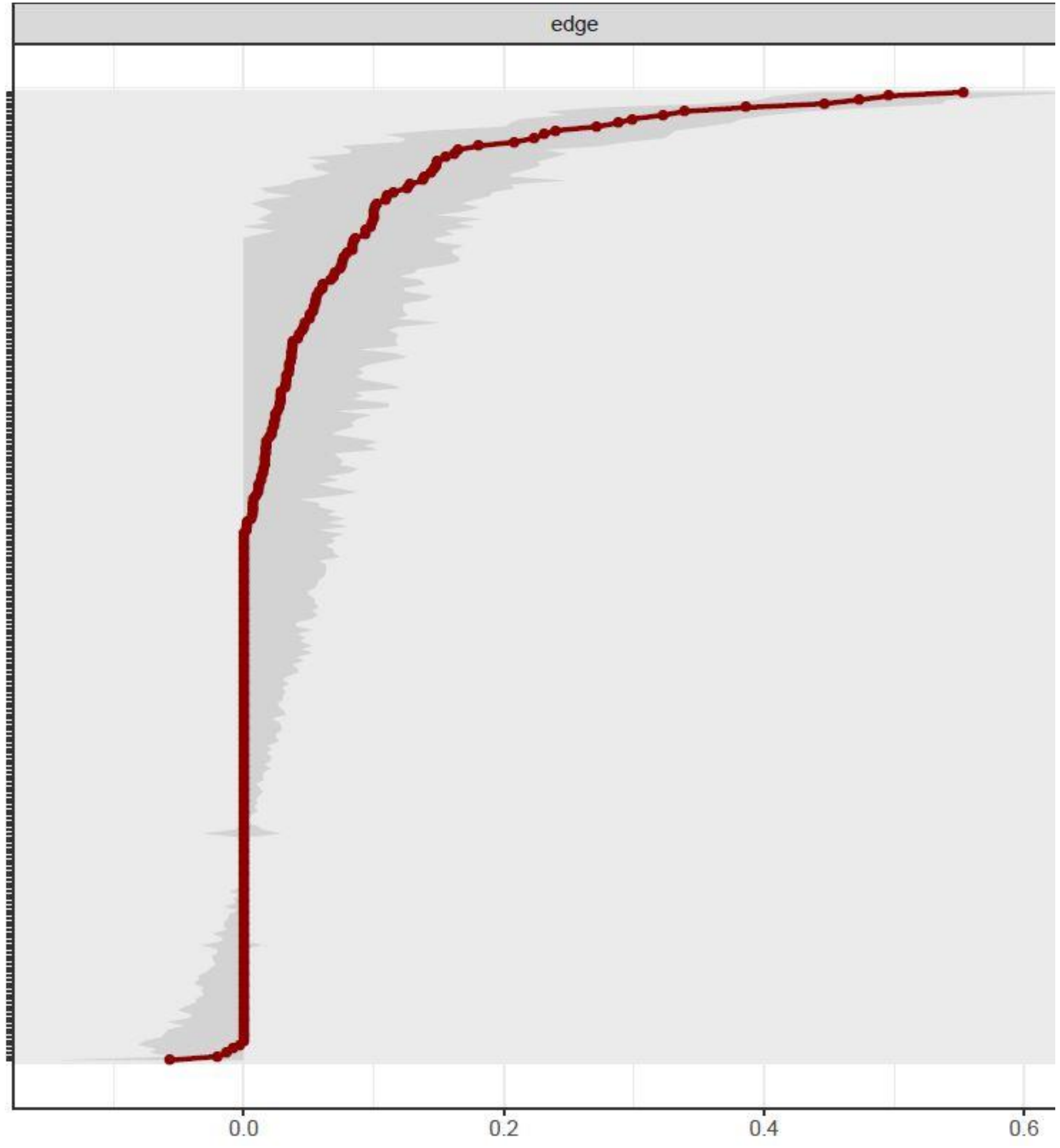
Is the network stable?



Edge Stability Graph

Edge Stability Coefficient = .75

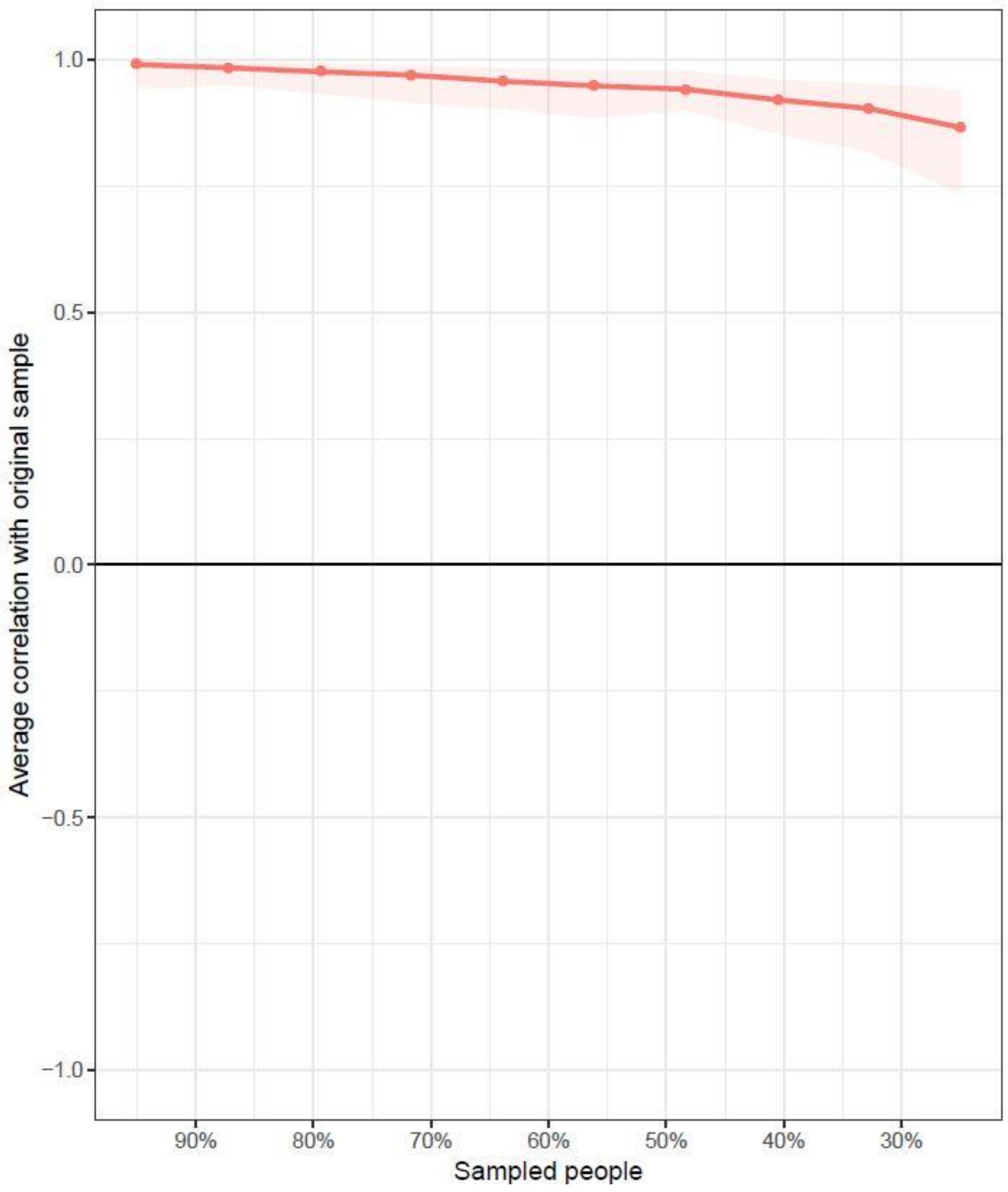
corStability()



Strength Centrality Stability Graph

Strength Centrality Stability Coefficient = .59

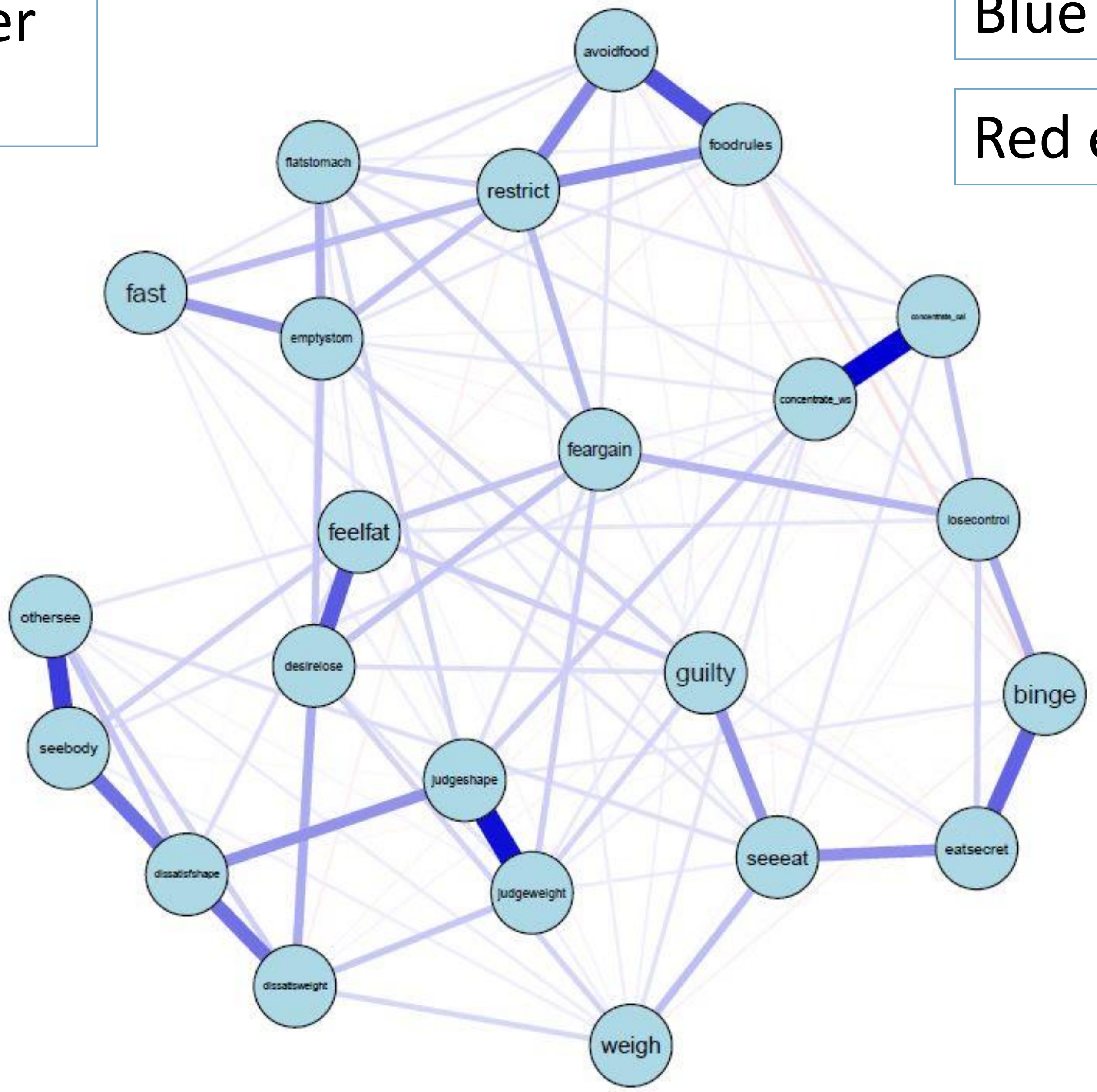
corStability()



Thick line = stronger correlation

Blue edges = positive

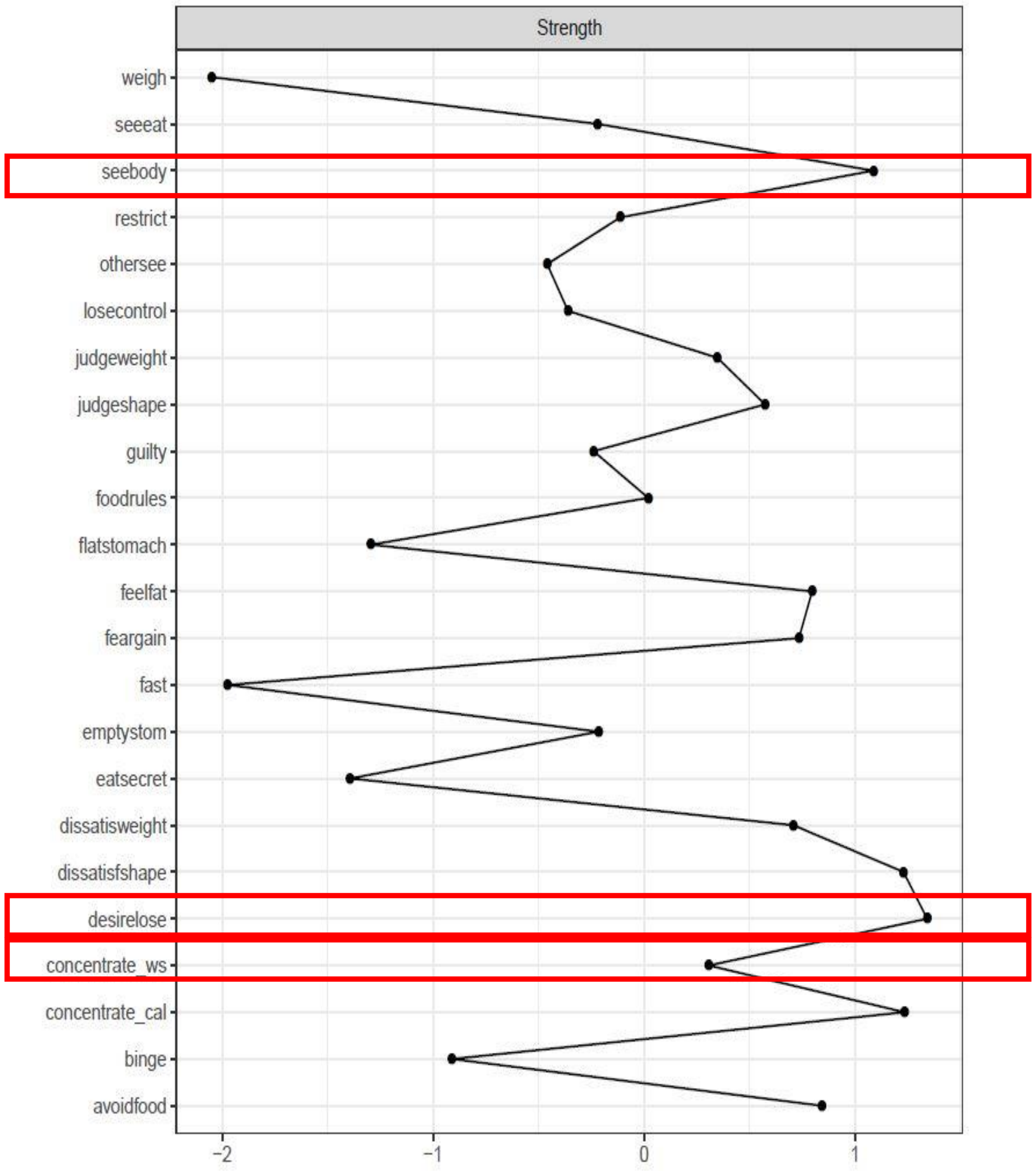
Red edges = negative



Strength Centrality and Expected Influence

Desire to lose weight
Trouble concentrating
Distress seeing your body

centralityPlot()



Standardized centrality estimates (mean=0, *SD*=1)

centralityTable()

	A	B	C	D	E	F
49	48	graph 1	NA	fast	Strength	-1.973543967
50	49	graph 1	NA	avoidfood	Strength	0.843065311
51	50	graph 1	NA	foodrules	Strength	0.020264902
52	51	graph 1	NA	concentrate_cal	Strength	1.235562168
53	52	graph 1	NA	losecontrol	Strength	-0.36003555
54	53	graph 1	NA	binge	Strength	-0.910418605
55	54	graph 1	NA	eatsecret	Strength	-1.393247749
56	55	graph 1	NA	flatstomach	Strength	-1.295289337
57	56	graph 1	NA	emptystom	Strength	-0.214487277
58	57	graph 1	NA	concentrate_ws	Strength	0.306833409
59	58	graph 1	NA	feargain	Strength	0.734370795
60	59	graph 1	NA	feelfat	Strength	0.797059986
61	60	graph 1	NA	desirelose	Strength	1.342398507
62	61	graph 1	NA	guilty	Strength	-0.239070017
63	62	graph 1	NA	judgeweight	Strength	0.347159576
64	63	graph 1	NA	judgeshape	Strength	0.574164883
65	64	graph 1	NA	weigh	Strength	-2.048551141
66	65	graph 1	NA	dissatisweight	Strength	0.707996772

Strength Centrality

Desire to lose weight

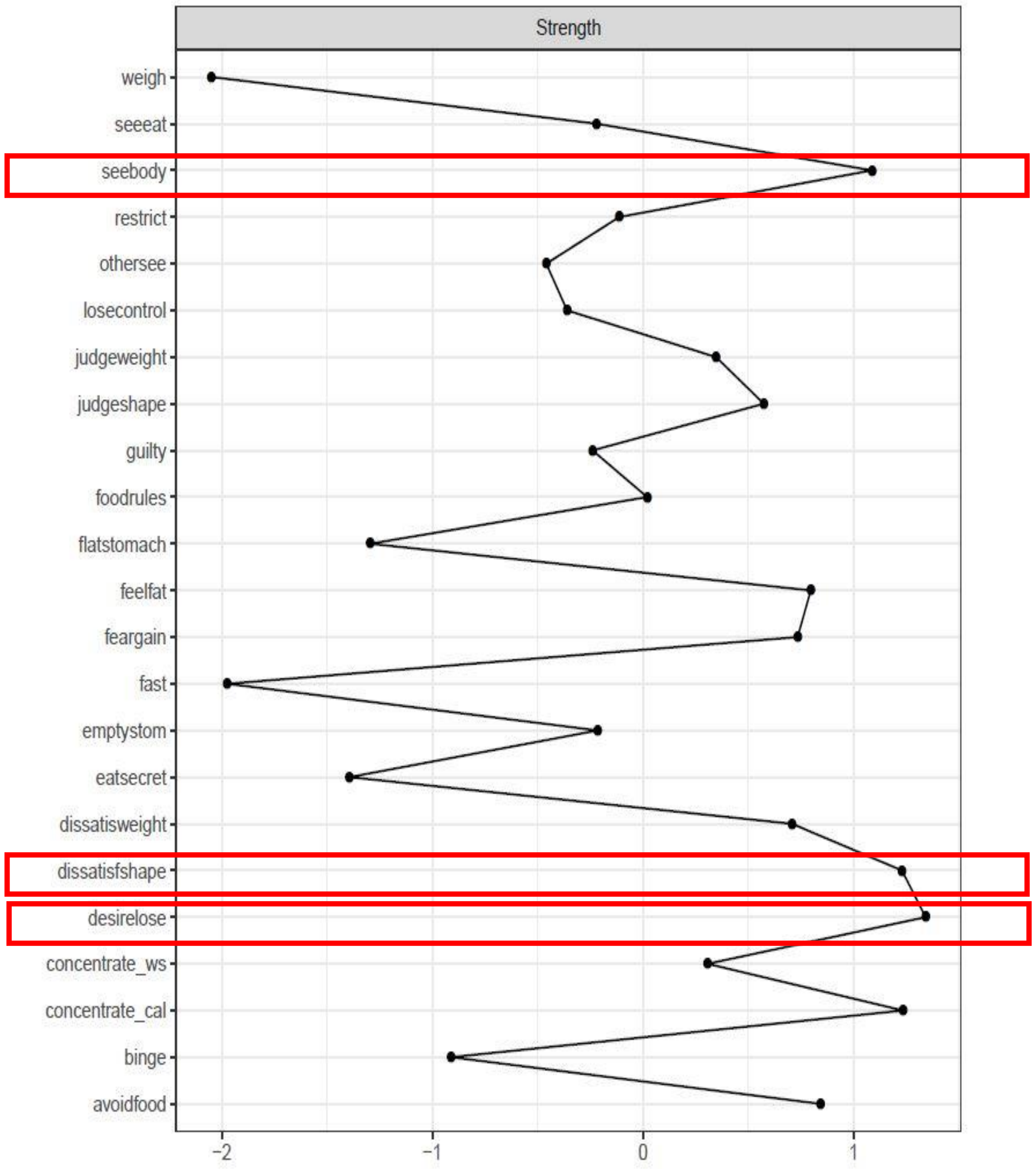
SC = 1.34

Trouble concentrating

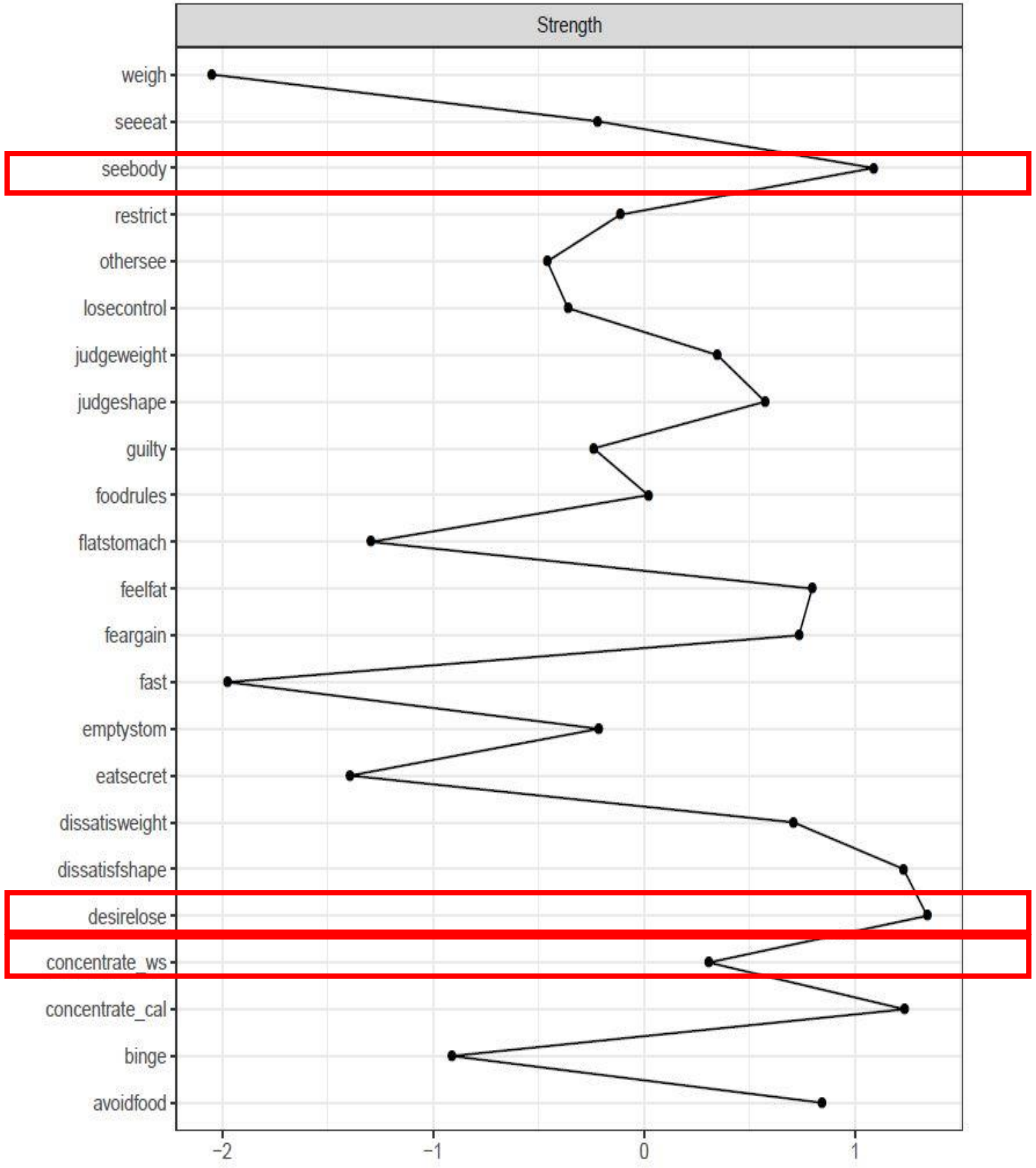
SC = 1.23

Distress seeing your body

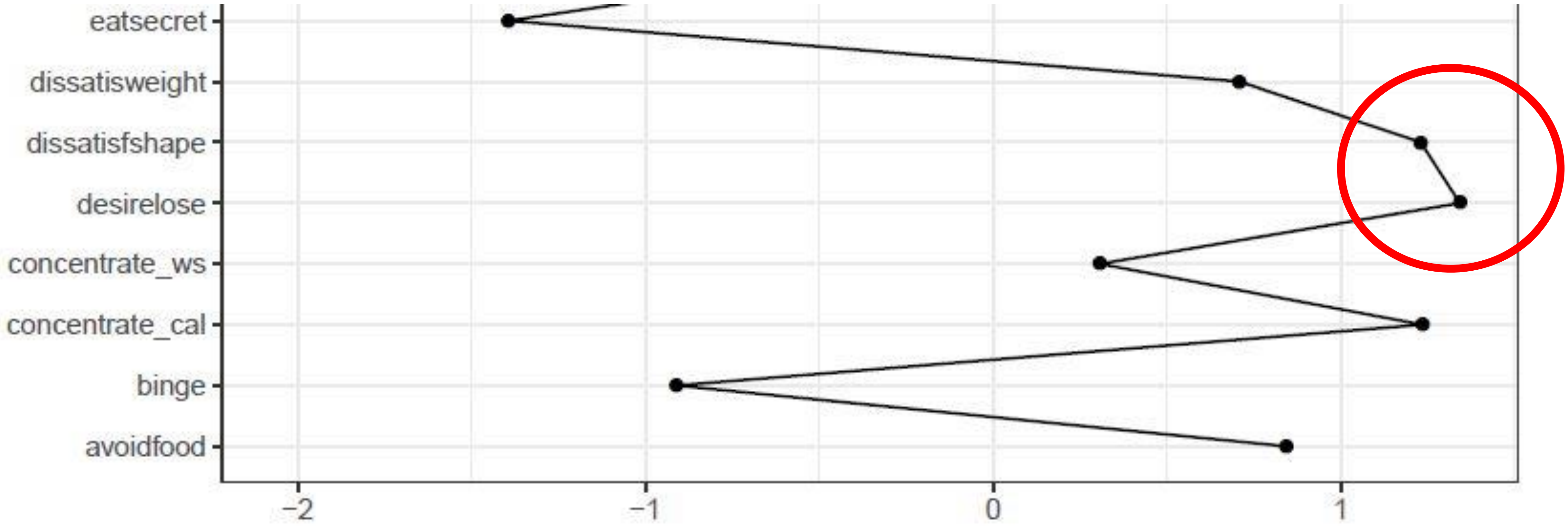
SC = 1.09



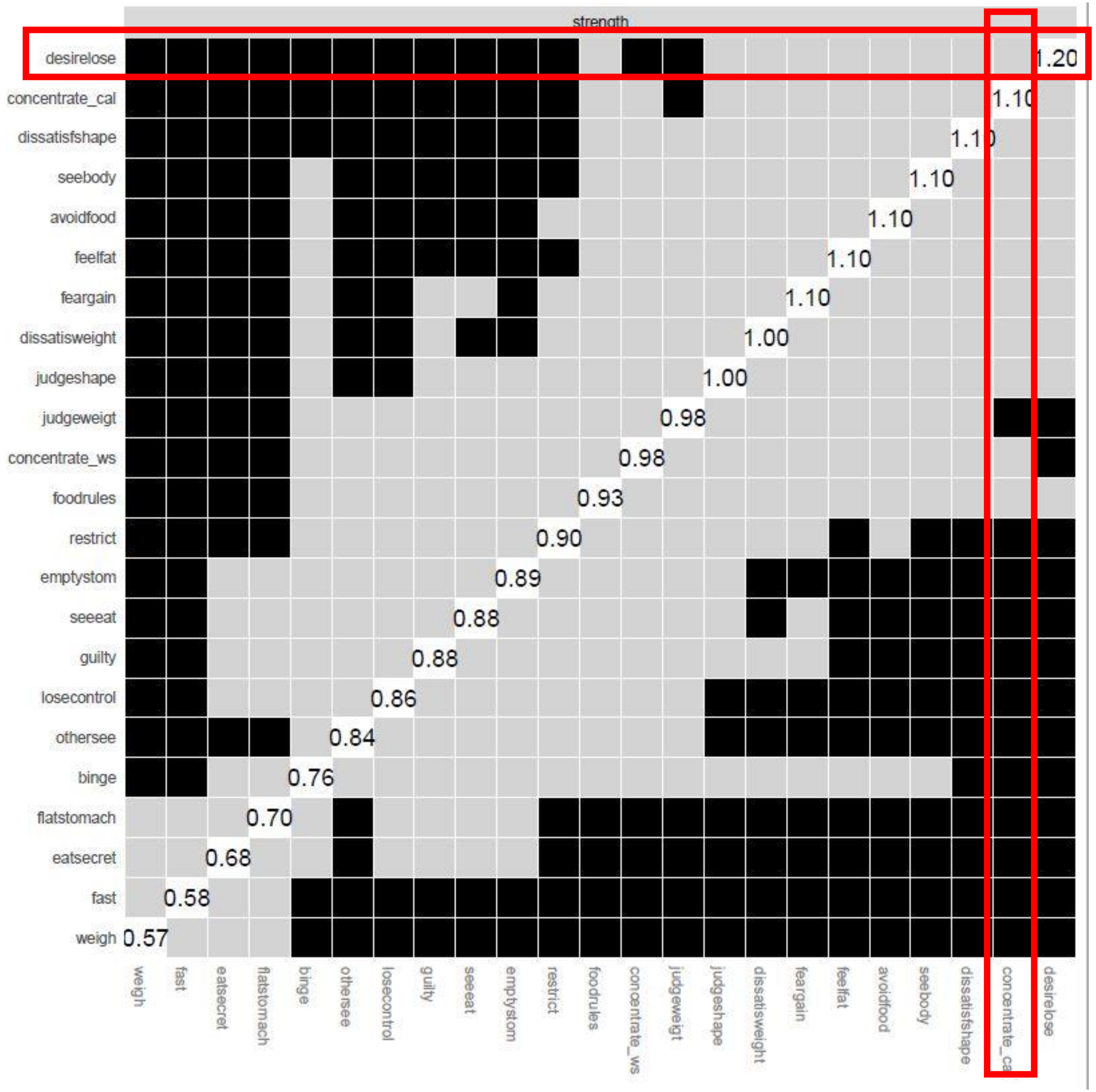
Just because a symptom is more central does not mean it is substantially more central!



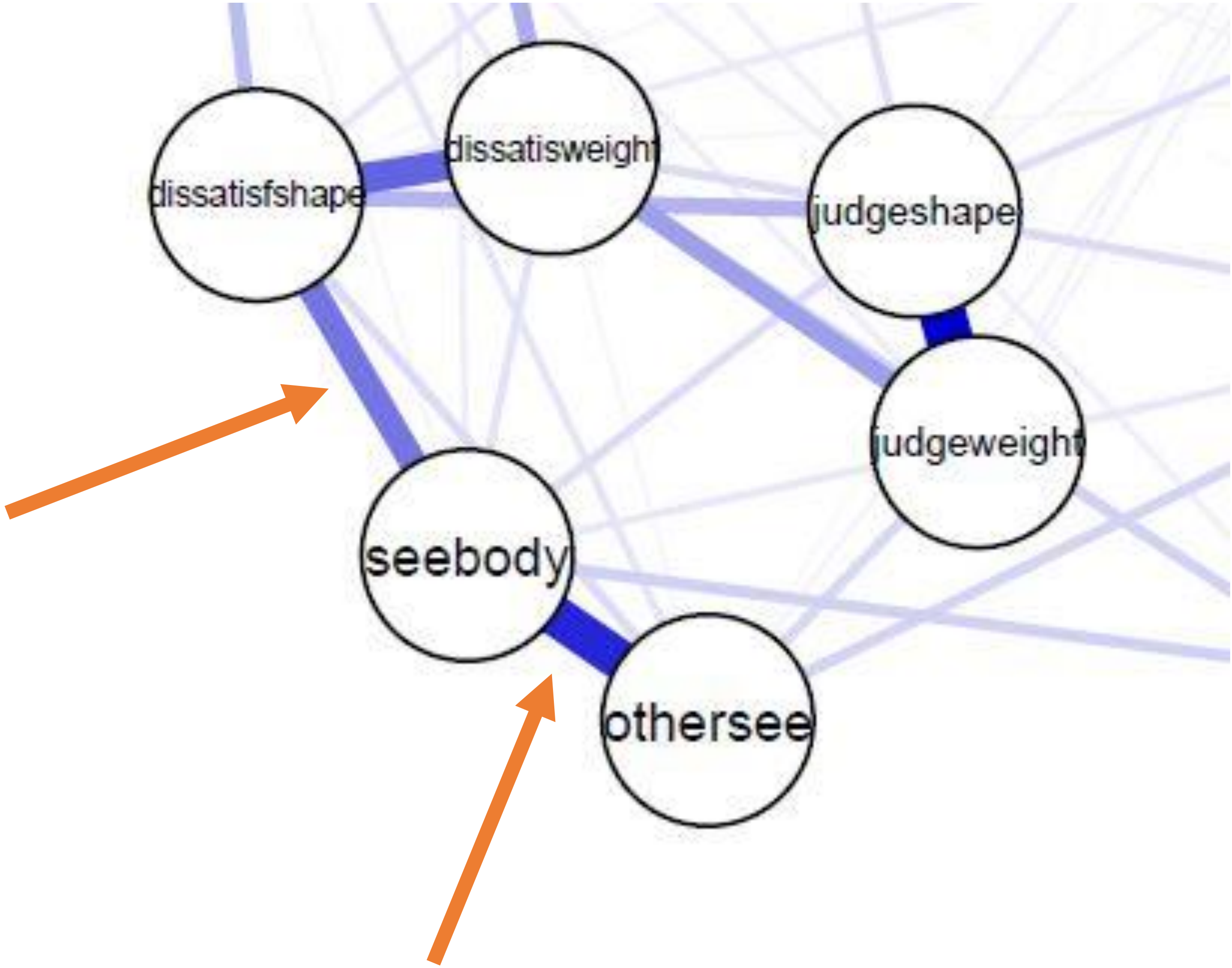
Centrality Stability: Is one node significantly more central than another?



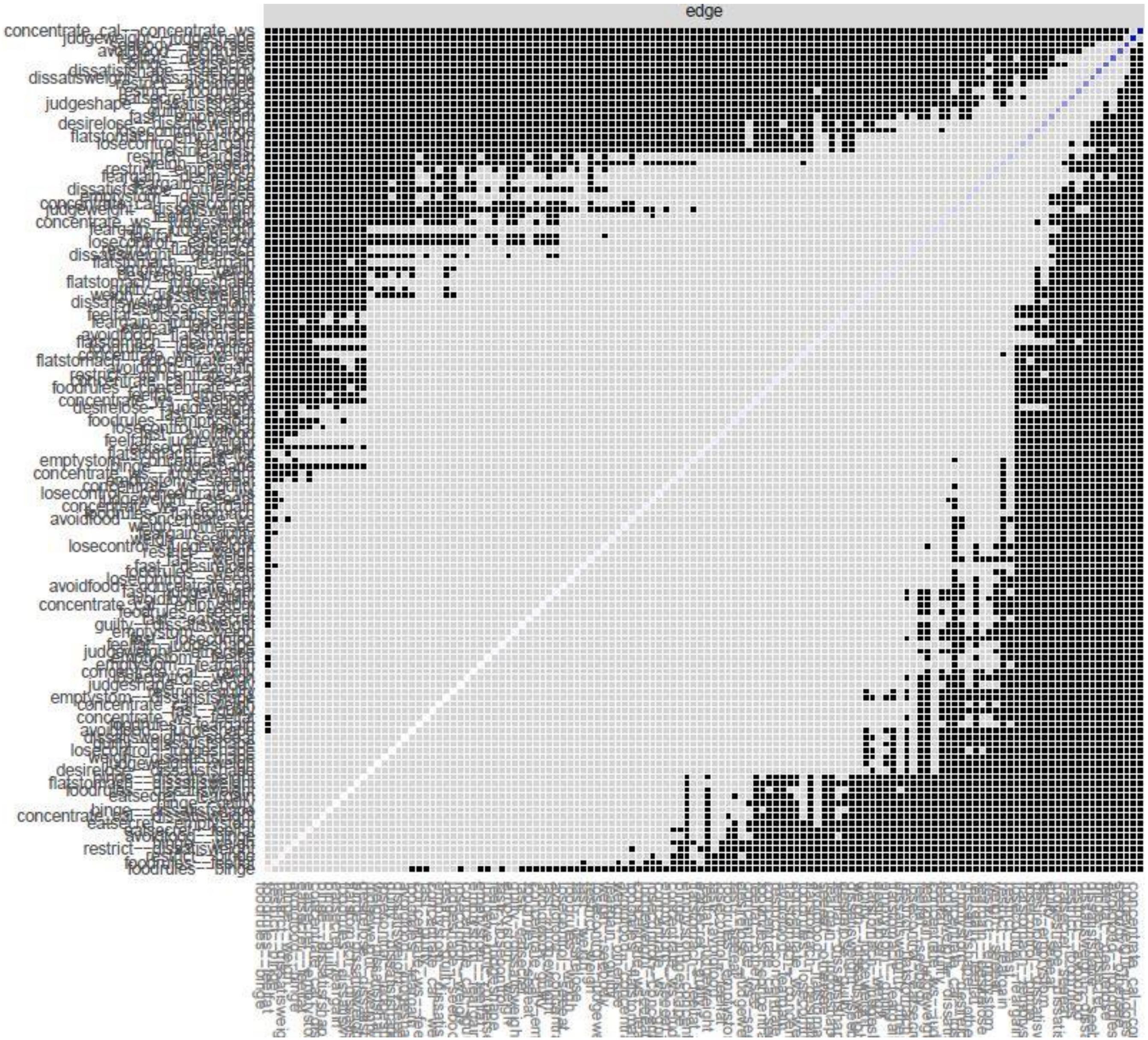
Centrality Difference Test



Edge Stability: Are these 2 edges significantly different from each other?

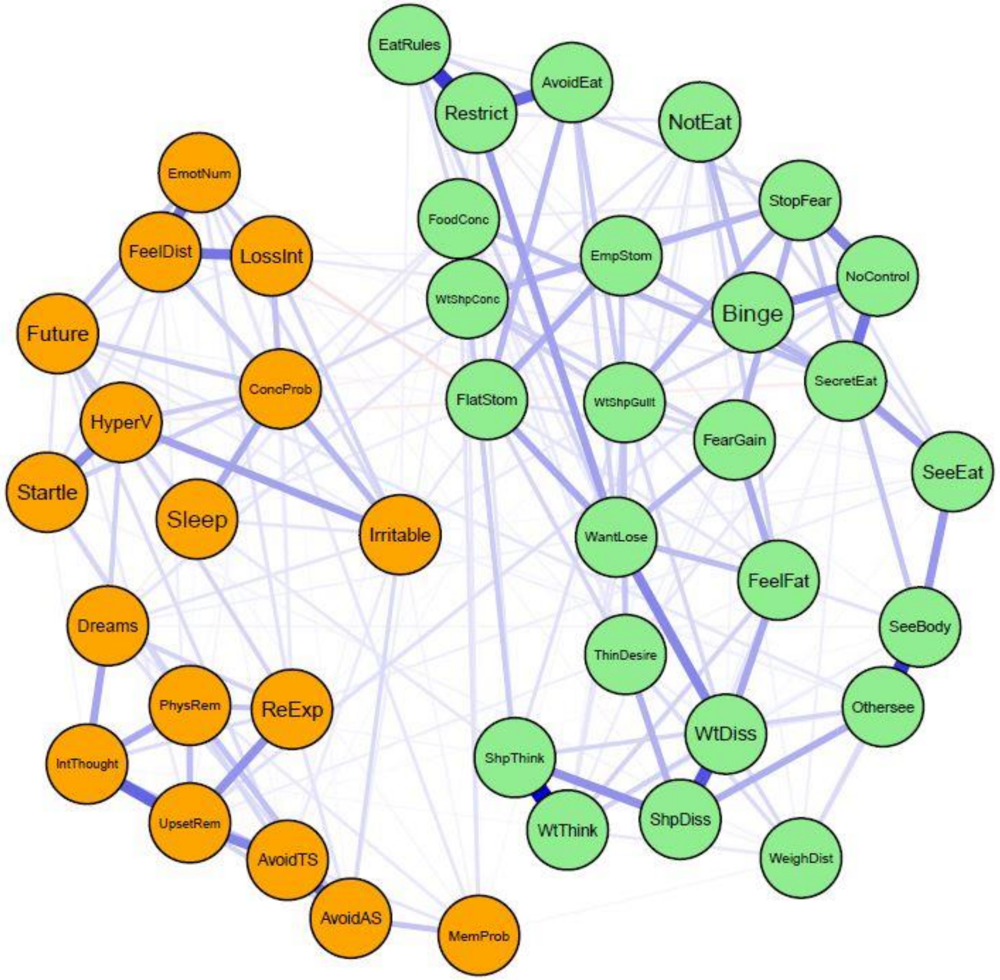


Edge Difference Test



Bridge Symptoms

Bridge Symptoms



Repeat same steps to estimate and plot network

```
Irinadata <- read.table("C:/Users/lapab/Dropbox/EAT Lab/AED Webinar/bridgedata.csv", header=TRUE, sep=",", na = "NA")
```

```
mynames  <- c("Restrict", "NotEat",
"AvoidEat","EatRules","FoodConc","StopFear",
"NoControl","Binge","SecretEat","FlatStom“,"EmpStom","WtShpConc","F
earGain","FeelFat", "WantLose”, “WtShpGuilt","WtThink","ShpThink“,
"WeighDist","WtDiss“,"ShpDiss", "ThinDesire","SeeEat","SeeBody",
"Othersee","IntThought","Dreams", "ReExp","UpsetRem", "PhysRem",
"AvoidTS","AvoidAS","MemProb", "LossInt","FeelDist","EmotNum",
"Future", "Sleep", "Irritable", "ConcProb", "HyperV", "Startle")
```

Repeat same steps to estimate and plot network

Assign items to groups: 1-25 are ED symptoms and 26-42 are PTSD symptoms

```
mygroups=list("ED"=c(1:25),"PTSD"=c(26:42))
mynetwork <- estimateNetwork(Irinadata, default="EBICglasso")
myplot <-plot(mynetwork, layout="spring", vsize=6, border.color="black", groups=mygroups, labels=mynames, color=c('#a8e6cf', '#dcedc1’))

#Constructing a partial correlation matrix
myedges <-getWmat(mynetwork)
write.csv(myedges, "MyNetworkEdges.csv")
```

Plot each group different color

Assign a number to each variable. Here all 25 ED items are “1” (community 1) and all 16 PTSD items are “2” (community 2)

```
#Estimate bridge values for each node
bridge(myplot, communities=c('1','1','1','1','1','1','1','1','1','1',
                    '1','1','1','1','1','1','1','1','1','1',
                    '1','1','1','1','1','2','2','2','2','2','2','2',
                    '2','2','2','2','2','2','2','2','2','2'), useCommunities = "all",
directed = NULL, nodes = NULL)
```

Use plot object from plotting the network

Indicate which communities you want to use. Can specify “1” and “2” if you have 3: useCommunities = c('1','3')

Console Terminal

C:/Users/lapab/Dropbox/EAT Lab/AED Webinar/

```
$ Bridge Strength
   Restrict      NotEat    AvoidEat    EatRules    FoodConc    StopFear   NoControl 
0.034406833 0.114433726 0.029641985 0.025339958 0.166498850 0.000000000 0.063491910 
      Binge   SecretEat   FlatStom     EmpStom   WtShpConc    FearGain     FeelFat 
0.071644327 0.041930735 0.096341047 0.041894741 0.135800298 0.011983521 0.000000000 
   WantLose  WtShpGuilt     WtThink    ShpThink   WeighDist      WtDiss     ShpDiss 
0.004297049 0.101002803 0.015363852 0.064056605 0.057808318 0.000000000 0.017486016 
 ThinDesire      SeeEat     SeeBody    Othersee  IntThought      Dreams       ReExp 
0.033850572 0.087339393 0.029993123 0.090367593 0.015363852 0.127559683 0.031207371 
   UpsetRem     PhysRem     AvoidTS     AvoidAS     MemProb     LossInt    FeelDist 
0.112103141 0.021093648 0.039841420 0.034988957 0.136110140 0.140793351 0.055497607 
    EmotNum      Future       Sleep   Irritable    ConcProb      HyperV     Startle 
0.039905411 0.080862032 0.127361351 0.149479505 0.120931138 0.078225517 0.023649129 
```

```
#Name our bridge object
mybridge <- bridge(myplot, communities=c('1','1','1','1','1','1','1','1','1','1',
                         '1','1','1','1','1','1','1','1','1','1',
                         '1','1','1','1','1','2','2','2','2','2','2','2',
                         '2','2','2','2','2','2','2','2','2','2'), useCommunities = "all", directed = NULL,
nodes = NULL)

#Create bridge graph
pdf("bridgecentrality.pdf", width=4)
plot(mybridge, include = "Bridge Strength")
dev.off()

#Create bridge expected influence graph
pdf("bridgeEI.pdf", width=4)
plot(mybridge, include = "Bridge Expected Influence (1-step)", width=4)
dev.off()
```

Specify which bridge centrality to plot

Same as b2 in earlier example

```
#Bridge stability part 1
caseDroppingBoot <- bootnet(network2, boots=1000, type="case",
                    statistics=c("bridgeStrength", "bridgeExpectedInfluence"),
                    communities=groups)
#get stability coefficients
corStability(caseDroppingBoot)

#Plot centrality stability
plot(caseDroppingBoot, statistics=" bridgeStrength ")
plot(caseDroppingBoot, statistics="bridgeExpectedInfluence")
```

Specify object for communities

Specify which centrality to bootstrap

b1

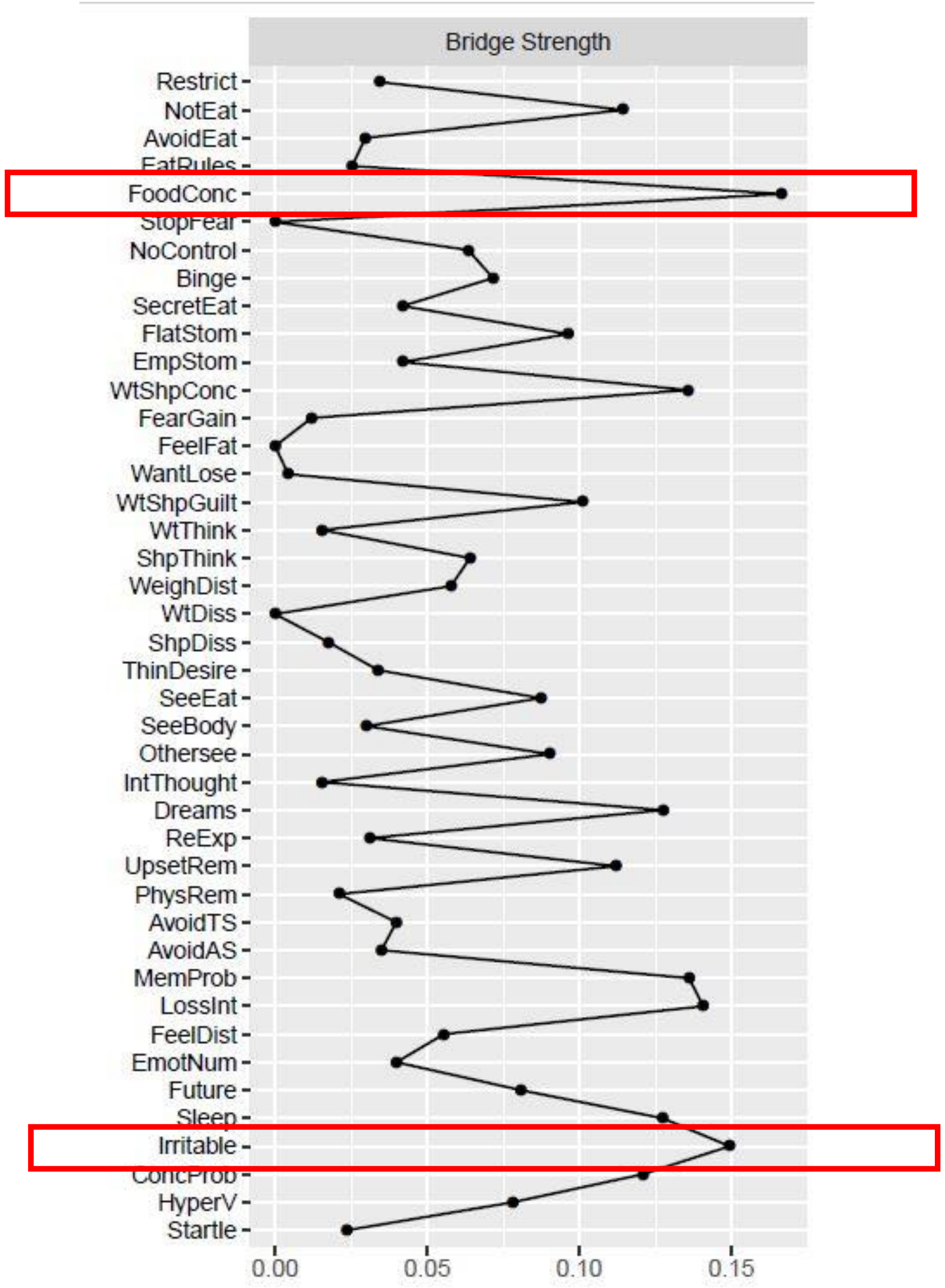
```
#Bridge stability part 2; centraity difference
nonParametricBoot <- bootnet(network2, boots=1000, type="nonparametric",
        statistics=c("bridgeStrength", "bridgeExpectedInfluence"), communities=groups)
#Plot centrality difference
plot(nonParametricBoot, statistics="bridgeExpectedInfluence", plot="difference")
plot(nonParametricBoot, statistics="bridgeStrength", plot="difference")
```

Interpreting Results

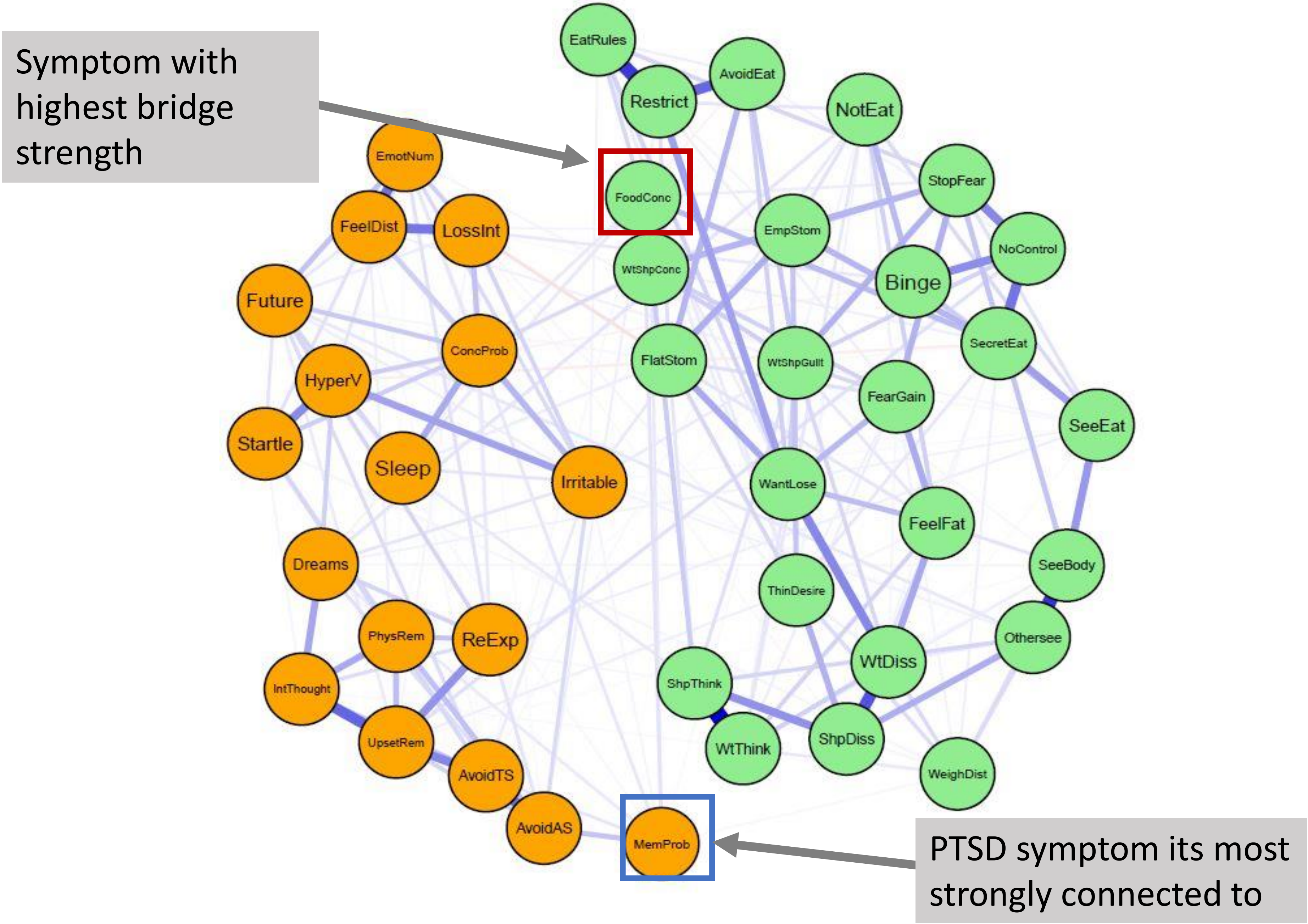
Bridge Strength

1) Identify symptom with the highest bridge centrality
2) Use partial correlation matrix to identify which symptom in the other community it is most strongly connected to
3) Repeat for symptoms with second highest centrality

Difficulty concentrating (ED) most strongly connected to *memory problems* (PTSD; part r = .07)

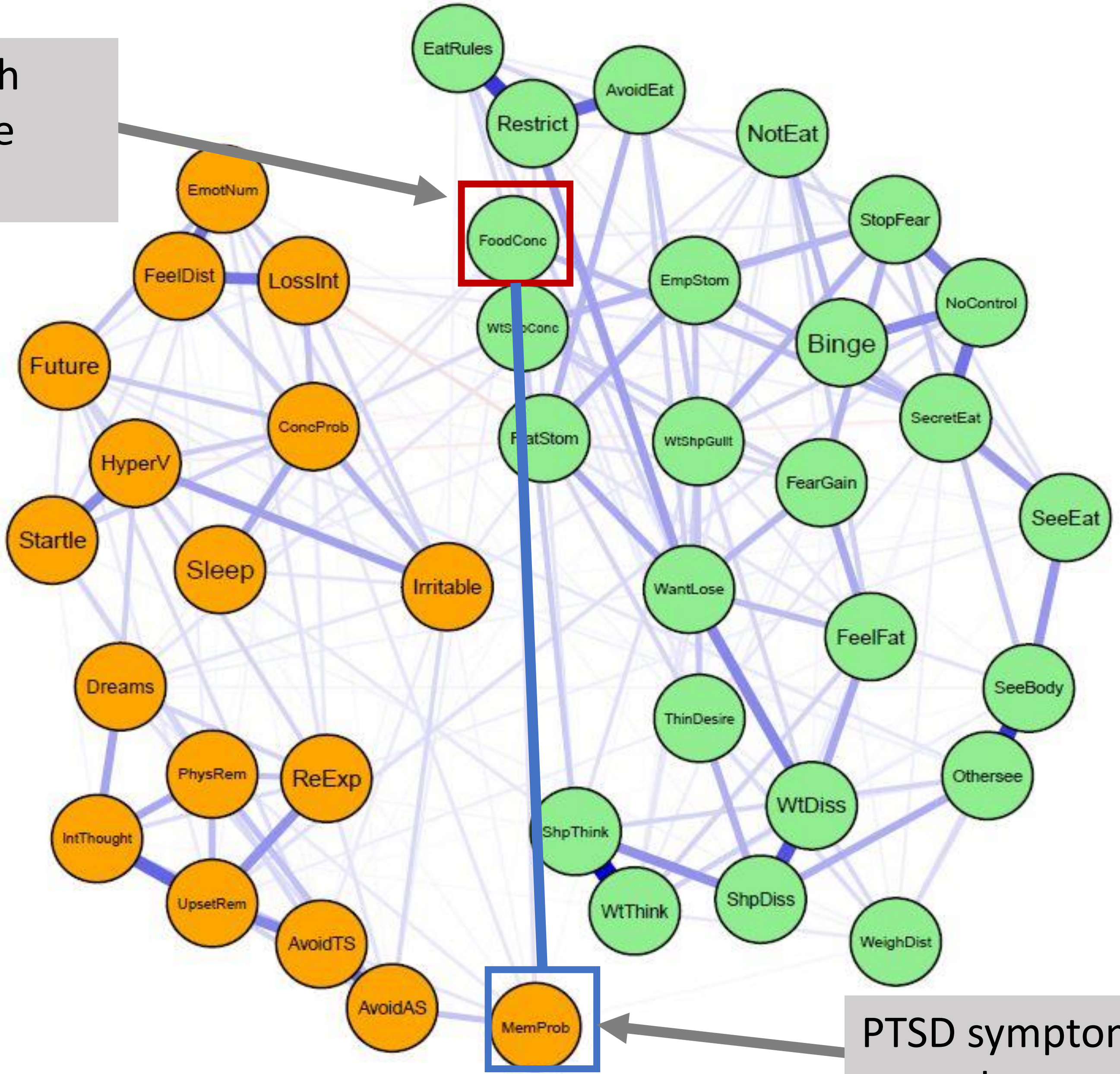


	A	B	C	D	E	F	G
1		restrict	fast	avoidfood	foodrules	concentra	losecontrc
2	restrict	0	0.154258	0.272495	0.251625	0.061362	0
3	fast	0.154258	0	0.051601	0	0	0.017253
4	avoidfood	0.272495	0.051601	0	0.392235	0.02276	0
5	foodrules	0.251625	0	0.392235	0	0.06021	0.064213
6	concentra	0.061362	0	0.02276	0.06021	0	0.129091
7	losecontrc	0	0.017253	0	0.064213	0.129091	0
8	binge	-0.02888	0	-0.02582	-0.05917	0	0.188568
9	eatsecret	0	0.019884	0	0	0	0.103656
10	flatstomac	0.103356	0	0.070113	0.038618	0	0
11	emptystor	0.140415	0.232303	0	0.056884	0.021821	0
12	concentra	0	0	0.037542	0	0.575426	0.041004
13	feargain	0.151819	0	0.063171	0.004237	0	0.165792
14	feelfat	0	0	0	-0.03086	0	0.055409
15	desirelose	0	0.031579	0	0	0	0



Symptom with highest bridge strength
PTSD symptom its most strongly connected to
EatRules
AvoidEat
Restrict
NotEat
EmotNum
StopFear
FoodConc
EmpStom
FeelDist
LossInt
NoControl
WtShpConc
Binge
Future
SecretEat
ConcProb
FlatStom
WtShpGuilt
HyperV
FearGain
SeeEat
Startle
Sleep
Irritable
WantLose
FeelFat
Dreams
SeeBody
ThinDesire
PhysRem
ReExp
Othersee
WtDiss
IntThought
ShpThink
UpsetRem
WtThink
ShpDiss
WeighDist
AvoidTS
AvoidAS
MemProb

Symptom with highest bridge strength

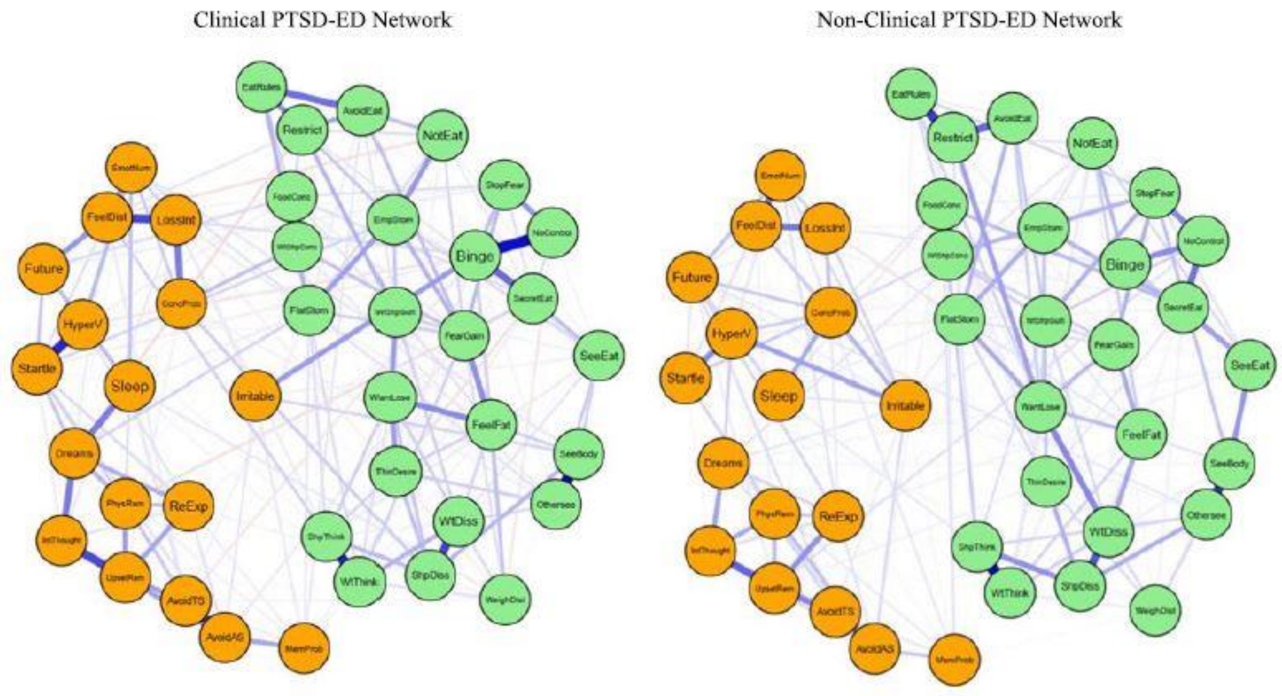


PTSD symptom its most strongly connected to

Network Comparison Test

NCT

1. Are the edges between the same nodes different?
2. If yes, which edges are different?
3. Are sums of all edges (global strength) different between networks?



```
#Load data
Irinadata1 <- read.table("C:/Users/lapab/Dropbox/EAT Lab/AED Webinar/clinicaldata.csv", header=TRUE, sep=",", na = "NA")
Irinadata2 <- read.table("C:/Users/lapab/Dropbox/EAT Lab/AED Webinar/nonclinicaldata.csv", header=TRUE, sep=",", na = "NA")

#Omit missing data
newdata1 <- na.omit(Irinadata1)
newdata2 <- na.omit(Irinadata2)

#Estimate networks
mynetwork1 <- estimateNetwork(newdata1, default="EBICglasso")
mynetwork2 <- estimateNetwork(newdata2, default="EBICglasso")
```

For NCT data can't be missing;
Omit missing data listwise

Can instead use datafile names; using network objects will capture all network settings

```
#Run NCT
MyNCT <- NCT(mynetwork1, mynetwork2, it=1000, weighted = TRUE, test.edges = FALSE, edges='ALL')
```

Number of iterations; 1000 is best

At first, set to FALSE; If Network invariance is significant, then change to TRUE to test specific edges

```
#Get results
summary(MyNCT)
```

Display results

Results

NETWORK INVARIANCE TEST

Test statistic M: 0.2651459

p-value 0.28

Edges are not different between networks;
No need to test individual edges

GLOBAL STRENGTH INVARIANCE TEST

Global strength per group: 12.77505 12.91559

Test statistic S: 0.140536

p-value 0.94

No difference in global strength

Results

- The network had excellent stability (edge stability coefficient = .75; strength centrality stability coefficient = .59). As seen in Figure 1, the following nodes with the highest strength centrality were identified: Desire to lose weight (strength coefficient [SC] = 1.34), trouble concentrating (SC = 1.23), and distress from seeing your body (SC = 1.09).

Other Useful Packages

Networktools	NetworkComparisonTest	MGM
• Expected Influence: *expectedInf()* • Bridge symptoms: *bridge()* • Identify redundant items: *goldbricker()*	• Compare 2 networks: *nct()*	• Network with dichotomous and count variables: *mgm()*
Jones, 2017	van Borkulo, 2018	Haslbeck & Waldrop, 2017

Other Useful Packages

mlVAR

- Longitudinal group-level modeling

Epskamp, Deserno, & Brigmann, 2017

graphicalVAR

- Longitudinal single-person modeling

Epskamp, 2017

psychonetrics

- Latent network models (combination of latent and network models)

Epskamp, 2018

What Else Can You Do?

Do Central Symptoms Predict Outcomes?

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Central Symptoms Predict Post-Treatment Outcomes and Clinical Impairment in Anorexia Nervosa: A Network Analysis in a Randomized-Controlled Trial

AUTHORS
Haley Elliott, Payton Jones, Ulrike Schmidt

CREATED ON
November 13, 2018

LAST EDITED
December 29, 2018

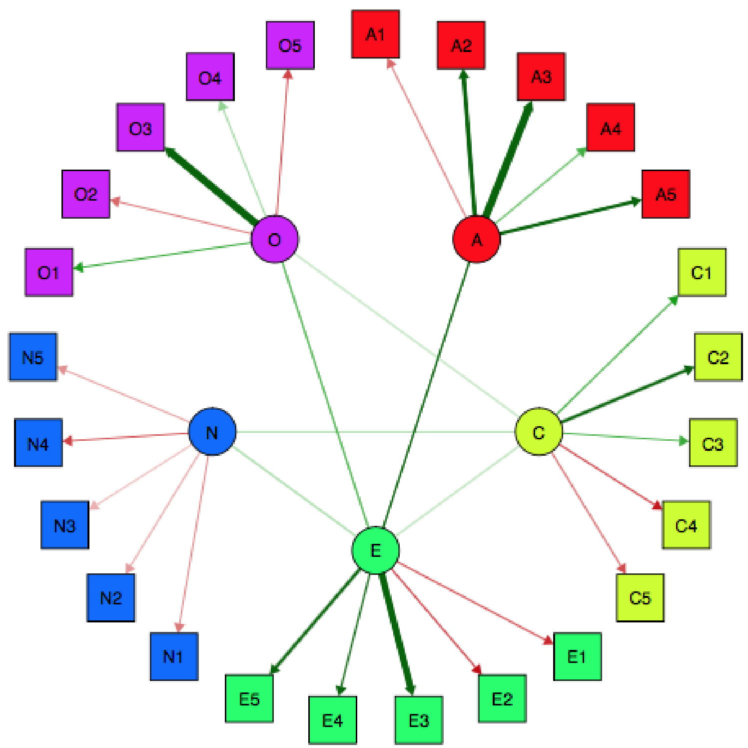
SUPPLEMENTAL MATERIALS
osf.io/et4sn/

Haslbeck & Waldrop, 2018; Olatunji, Levinson, & Calebs, 2018

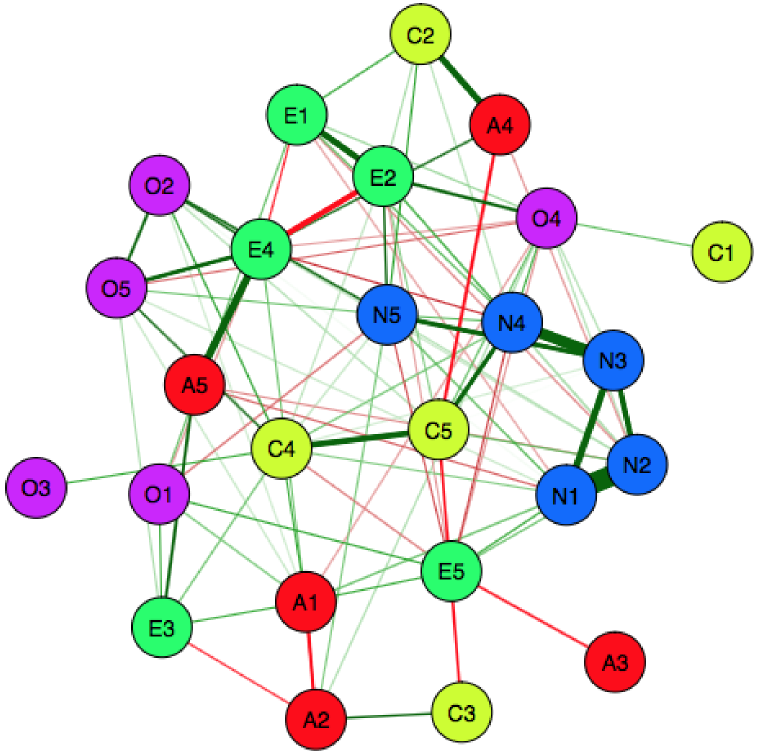
Latent Network Model

psychonetrics

Factor structure & latent network



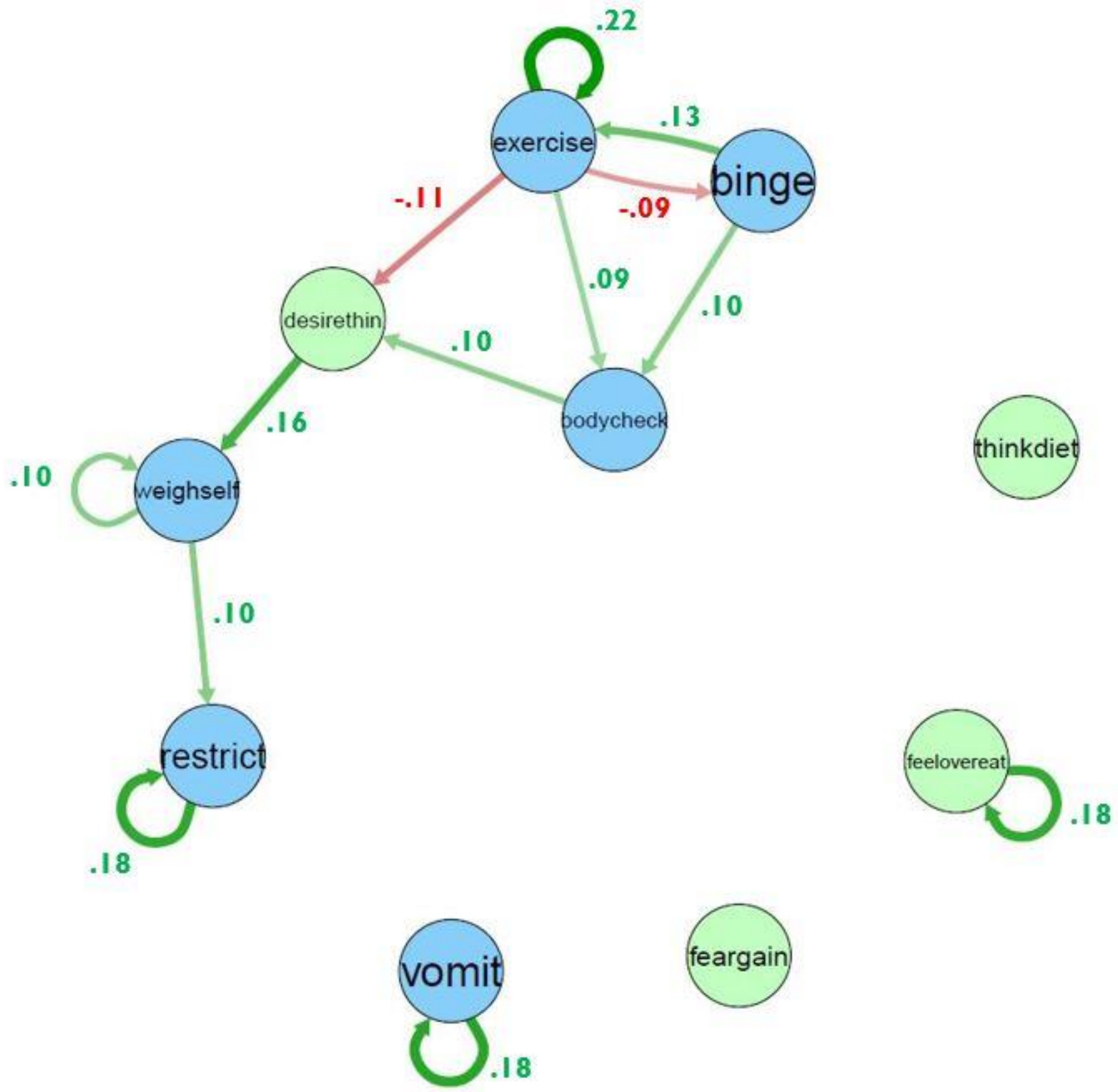
Residual network



Bringmann & Eronen, 2018; Epskamp, Rhemtulla, & Borsboom, 2018

Temporal Group Networks

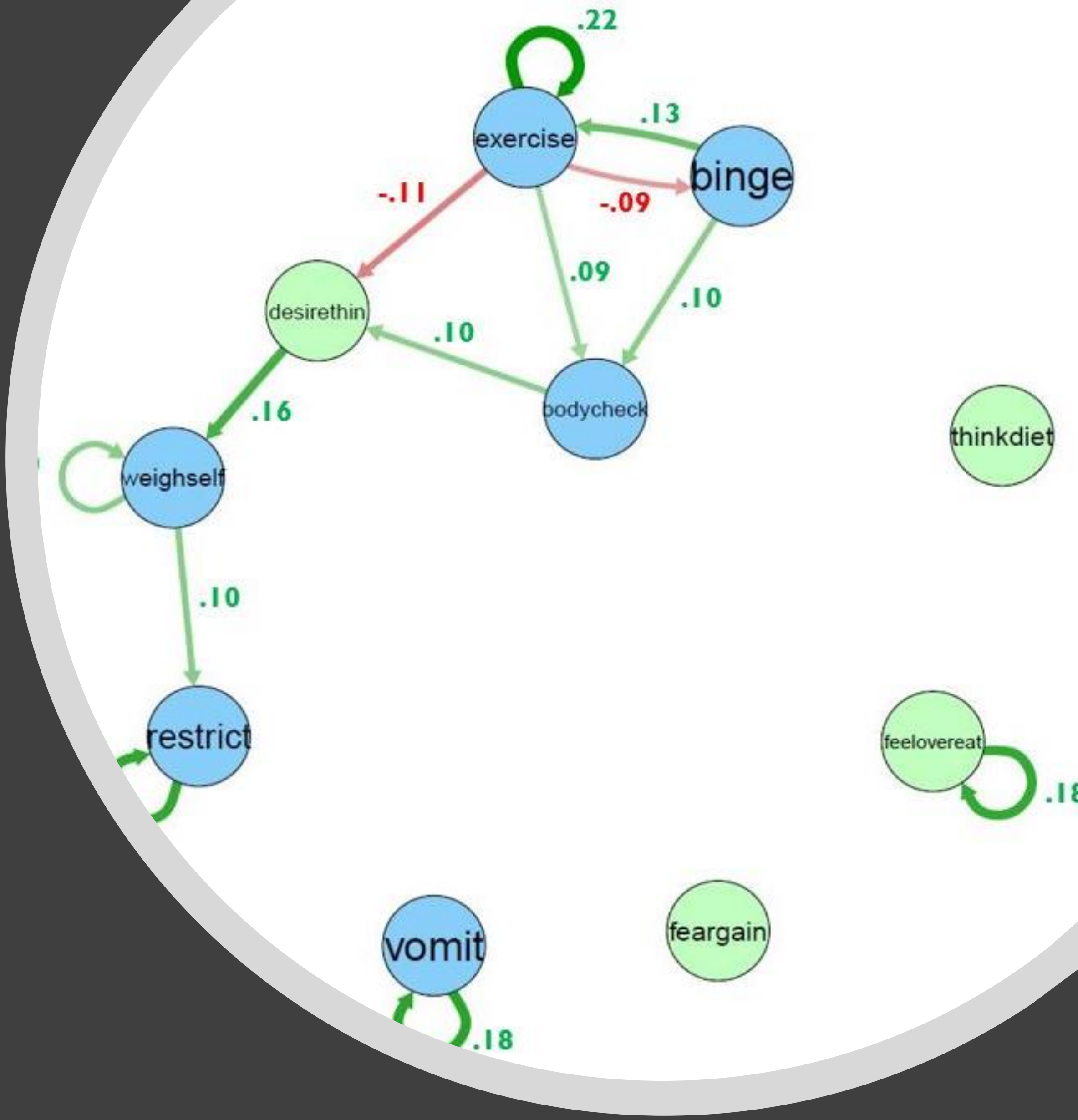
mlVAR



Epskamp et al., 2018

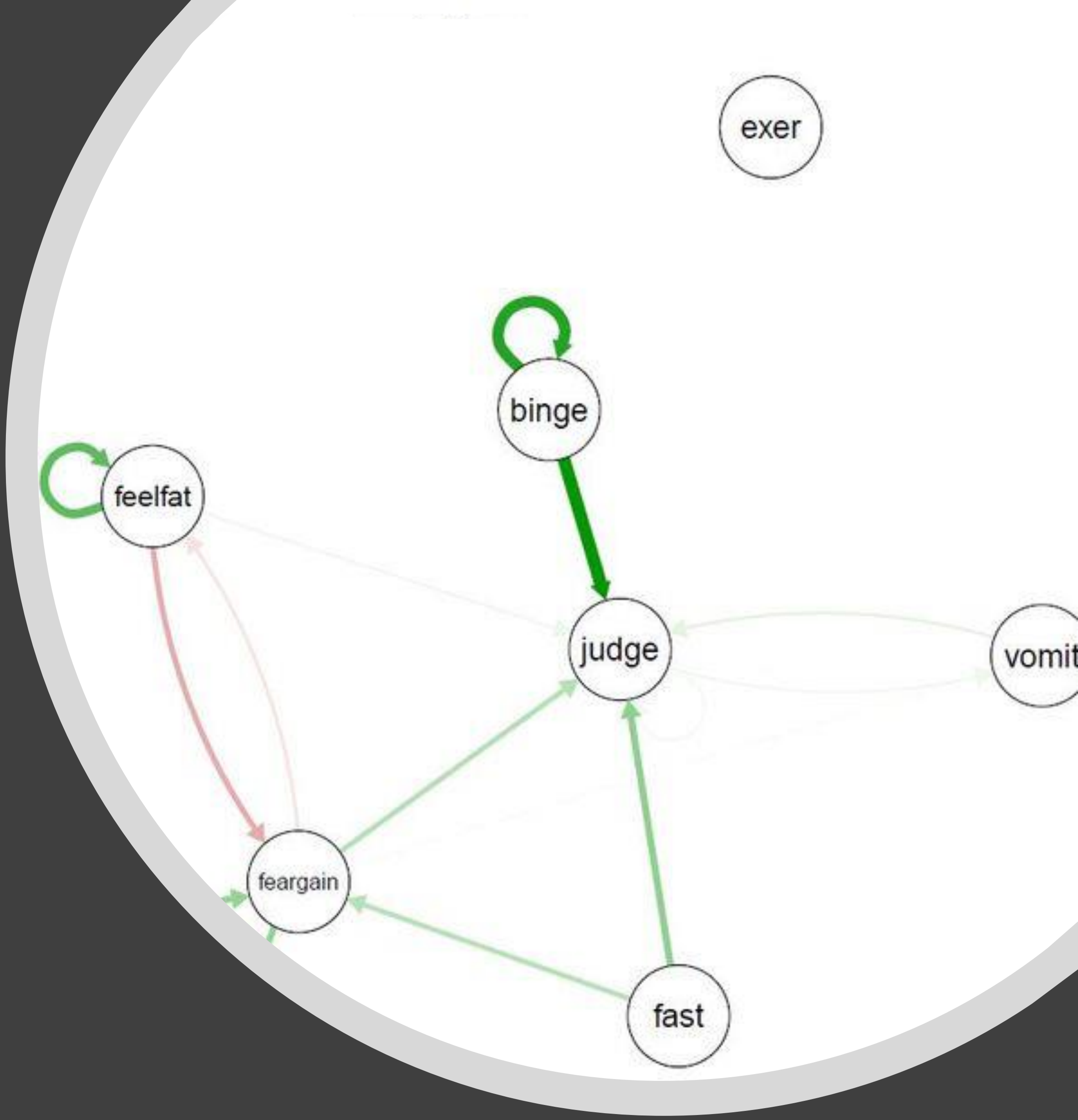
Temporal Group Networks

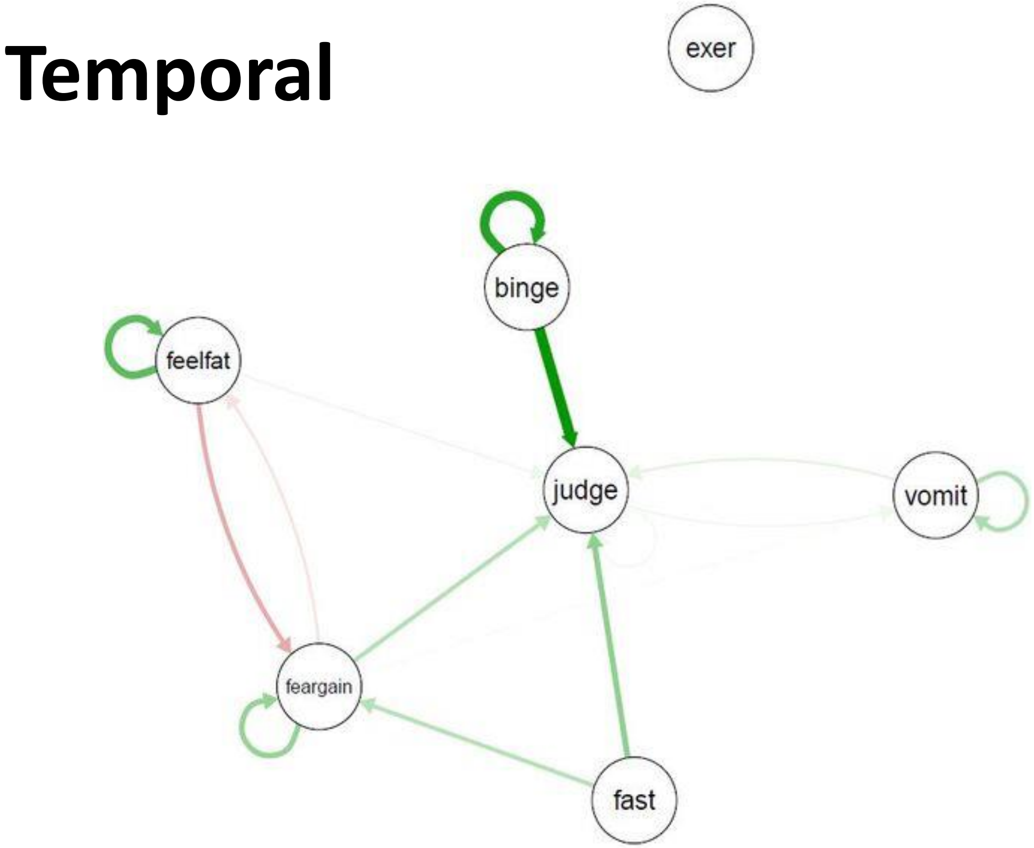
- How symptoms predict each other over time
- *N* = 62
- Ecological Momentary Assessment
- 48 Observations
  - 4 per day, 12 days

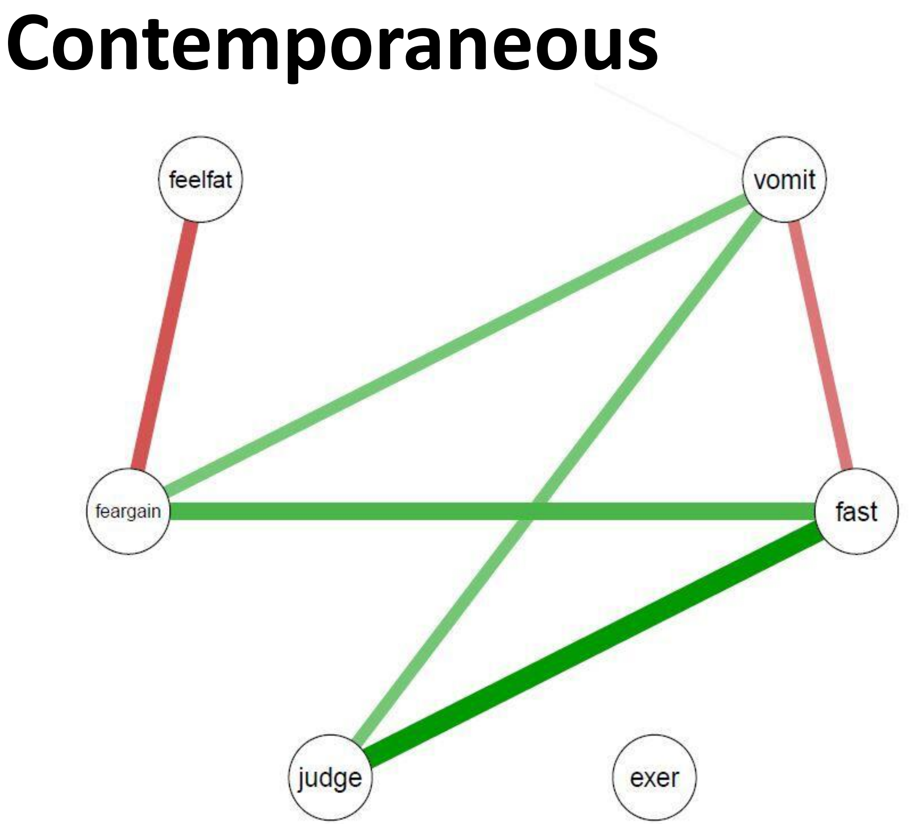


Individual Networks

- *N* = 1
- Ecological Momentary Assessment data
- 48 observations (4 times per day for 12 days)
- Individualized treatment!







Individual Networks

graphicalVAR

Epskamp et al., 2018; Fisher et al., 2017

Temporal

How symptoms predict each other over time (4 hours)

Contemporaneous

How symptoms are associated at the same time point while accounting for temporal relationships

Individual Networks

graphicalVAR

Other Uses

- Experimental manipulations
- Comparisons across treatment
- Task-based measures
- Pre-post treatment change
- Many more!

Resources: R Code

- Journal articles on network analysis
  - R code in supplemental materials
- Rdocumentation https://www.rdocumentation.org/
- Cran R packages https://cran.r-project.org/web/packages/
  - Change often!
- Developer's platform https://github.com/
  - Can ask code-related questions

Resources: New Developments

- Online Facebook community https://www.facebook.com/groups/PsychologicalDynamics/?ref=bookmarks
  - Can ask theory-related questions and stay updated on news
- Articles, blogs, presentations https://psych-networks.com/
- Websites of the developers http://sachaepskamp.com/; https://eiko-fried.com/
- PsychSystems Research Lab in Amsterdam http://psychosystems.org/people

Resources: Training

- Summer school in Amsterdam http://psychosystems.org/NetworkSchool
  - 1 week
- Statistics workshops in US http://reifmanintrostats.blogspot.com/
  - Few hours to a few days
- Network Analysis workshop through Curran & Bauer at UNC-Chapel Hill

https://curranbauer.org/training/network/
  - Five days

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References

Borsboom, D. (2017). A network theory of mental disorders. *World psychiatry*, *16*, 5-13.

Borsboom, D., & Cramer, A. O. J. (2013). Network Analysis: An Integrative Approach to the Structure of Psychopathology. *Annual Review of Clinical Psychology, 9*, 91–121. p https://doi.org/10.1146/ annurev-clinpsy-050212-185608.

Bringmann, L. F., & Eronen, M. I. (2018). Don't blame the model: Reconsidering the network approach to psychopathology. *Psychological Review*, *125*, 606-615.

Bringmann, L. F., Vissers, N., Wichers, M., Geschwind, N., Kuppens, P., Peeters, F., ... & Tuerlinckx, F. (2013). A network approach to psychopathology: new insights into clinical longitudinal data. *PloS one*, *8*, e60188.

Costantini, G., Epskamp, S., Borsboom, D., Perugini, M., Mõttus, R., Waldorp, L. J., & Cramer, A. O. (2015). State of the art personality research: A tutorial on network analysis of personality data in R. *Journal of Research in Personality, 54*, 13–29. https://doi.org/10.1016/j.jrp. 2014.07.003

Cramer, A. O. J., Waldorp, L. J.,van der Maas, H. L. J., & Borsboom, D. (2010). Comorbidity: A network perspective. *Behavioral and Brain Sciences, 33*, 137–150. p https://doi.org/10.1017/ S0140525X09991567

Elliott, H., Jones, P. J., & Schmidt, U. (2018). Central Symptoms Predict Post-Treatment Outcomes and Clinical Impairment in Anorexia Nervosa: A Network Analysis in a Randomized-Controlled Trial. https://doi.org/10.31234/osf.io/hw2dz

Epskamp, S. (2014). elasticIsing: Ising network estimation using Elastic net and k-fold cross-validation. R package version 0.1.

Epskamp, S., Borsboom, D., & Fried, E. I. (2018). Estimating psychological networks and their accuracy: A tutorial paper. *Behavior Research Methods, 50*, 195–212.

Epskamp, S., Cramer, A., Waldorp, L., Schmittmann, V. D., & Borsboom, D. (2012). qgraph: Network visualizations of relationships in psychometric data. *Journal of Statistical Software, 48*, 1–18. https://doi.org/10.18637/jss.v048.i04

Epskamp, S., & Fried, E. I. (2018). A tutorial on regularized partial correlation networks. *Psychological Methods, 23,* 617-634.

References

Epskamp, S., Rhemtulla, M., & Borsboom, D. (2017). Generalized network psychometrics: Combining network and latent variable models. *Psychometrika*, *82*, 904-927. https://doi.org/10.1007/s11336- 017-9557-x.

Epskamp, S., van Borkulo, C. D., van der Veen, D. C., Servaas, M. N., Isvoranu, A. M., Riese, H., & Cramer, A. O. (2018). Personalized network modeling in psychopathology: The importance of contemporaneous and temporal connections. *Clinical Psychological Science*, *6*, 416-427. https://doi.org/10.1177/2167702617744325.

Fisher, A. J., Reeves, J. W., Lawyer, G., Medaglia, J. D., & Rubel, J. A. (2017). Exploring the idiographic dynamics of mood and anxiety via network analysis. *Journal of abnormal psychology*, *126*, 1044-1056. https://doi.org/10.1037/abn0000311.

Fried, E. I., & Cramer, A. O. (2016). Moving forward: challenges and directions for psychopathological network theory and methodology. *Perspectives in Psychological Science* https://doi.org/10.17605/OSF.IO/MH3CF

Fried, E. I., van Borkulo, C. D., Cramer, A. O., Boschloo, L., Schoevers, R. A., & Borsboom, D. (2017). Mental disorders as networks of problems: A review of recent insights. *Social Psychiatry and Psychiatric Epidemiology, 52*, 1–10. https://doi.org/10.1007/s00127-016-1319-z.

Friedman, J., Hastie, T., & Tibshirani, R. (2008). Sparse inverse covariance estimation with the graphical lasso. *Biostatistics, 9*, 432–441. https://doi.org/10.1093/biostatistics/kxm045

Haslbeck, J., & Waldorp, L. J. (2017). mgm: Estimating time-varying mixed graphical models in high-dimensional data. *arXiv preprint arXiv:1510.06871*.

Haslbeck, J. M., & Waldorp, L. J. (2018). How well do network models predict observations? On the importance of predictability in network models. *Behavior Research Methods*, *50*(2), 853-861.

Jones, P. J. (2017). networktools: Assorted Tools for Identifying Important Nodes in Networks. R package version 1.1.0.

Jones, P. J., Ma, R., & McNally, R. J. (2018). Bridge centrality: A network approach to understanding comorbidity. Retrieved from osf.io/c5dkj

References

Levinson, C. A., Brosof, L. C., Vanzhula, I., Christian, C., Jones, P., Rodebaugh, T. L., ... & Menatti, A. (2018a). Social anxiety and eating disorder comorbidity and underlying vulnerabilities: Using network analysis to conceptualize comorbidity. *International Journal of Eating Disorders*, *51*, 693-709.

Levinson, C. A., Vanzhula, I. A., Brosof, L. C., & Forbush, K. (2018b). Network Analysis as an Alternative Approach to Conceptualizing Eating Disorders: Implications for Research and Treatment. *Current psychiatry reports*, *20*, 67-.

Levinson, C. A., Zerwas, S. C., Calebs, B., Marcus, M., Kordy, H., Hamer, R. M., Hofmeier, S. M., ... Bulik, C. M. (2017). The core symptoms of bulimia nervosa, anxiety, and depression: a network analysis. *Journal of Abnormal Psychology*, *126*, 340–354.. Doi 10.1037/abn0000254

McNally, R. J. (2016). Can network analysis transform psychopathology? *Behaviour Research and Therapy, 86*, 95–104. https://doi.org/10. 1016/j.brat.2016.06.006

Olatunji, B. O., Levinson, C., & Calebs, B. (2018). A network analysis of eat- ing disorder symptoms and characteristics in an inpatient sample. *Psychiatry Research, 262*, 270–281. https://doi.org/10.1016/j.psychres. 2018.02.027

Smith, K. E., Mason, T. B., Crosby, R. D., Cao, L., Leonard, R. C., Wetterneck, C. T., ... & Moessner, M. (2019). A comparative network analysis of eating disorder psychopathology and co-occurring depression and anxiety symptoms before and after treatment. *Psychological Medicine*, *49*, 314-324.

van Borkulo, C., Boschloo, L., Kossakowski, J., Tio, P., Schoevers, R., Borsboom, D., & Waldorp, L. (2017). Comparing network structures on three aspects: A permutation test. DOI: 10.13140/RG.2.2.29455.38569.

Van Buuren, S., & Groothuis-Oudshoorn, K. (2011). Mice: Multivariate imputation by chained equations in R. *Journal of Statistical Software, 45*, https://doi.org/10.18637/jss.v045.i03

Vanzhula, I., Calebs, B., Fewell, L., & Levinson C.A. (2018). Irritability and concentration difficulties are illness pathways between eating disorder and post traumatic stress disorder symptoms: understanding comorbidity with network analysis.