Assignment 3 - Network Analysis 2022

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Contents

Conceptual Questions

Question 1 (1 point)

Are the following statements true or false? Explain why (0.5 point per statement).

1. If ergodicity holds, results from between-person analysis are expected to equal results from within-person analysis.

   Yes, if ergodicity holds, there should be no difference in between-person level, and correspondingly it aligns with the within-person analysis of every individual (Molenaar, 2004).

2. It is generally recommended to always remove trends (such as linear trends) prior to analyzing your N = 1 time series.

   No, even though some simulation stuides show detrending helps increasing the performance of estimated networks (Epskamp et al., 2018), it is often the case that these changing trends are of main interest. So it is not correct to say it is *always* recommended to detrend (Isvoranu et al., 2022).

Question 2 (1.5 points)

Suppose a therapist measures a patient about 75 times on a set of depression symptoms, including a question on "suicidal thought". Suppose that you estimate a graphical VAR model from this data and find that the node "suicidal thought" is not connected to any of the other nodes in your network, neither in the temporal nor in the contemporaneous network.

List three potential reasons why the node "suicidal thought" may be disconnected in the resulting network.

1. Probably the patient answered "no" every time on "suicidal thought, since it is quite an extreme symptom to develop. It is likely that the patient never developed"suicidal thought" and that leads to no variance, which will result in no connections in the network.

2. It could be the case that the data is missing completely on "suicidal thought". For example, the patient felt pressure or some sorts of discomfort to answer the question on "suicidal thought" and left the question always unanswered. Then, the item would have only *NAs*, which would likely to result in no variation on that item.

3. Lastly, another potential scenario is that the measurement period was too short to capture the occurrence in "suicidal thought". For example, the 75 times of measurement was performed every 2 hrs in a day over 2 weeks or so, which is quite a short period of time. It could be that the patient only started having "suicidal thought" after the measurement period ends and hence left the item score on "suicidal thought" constant.

Question 3 (1 point)

Give an example of a relationship that can only be studied at the *between-person* level.

Things that can only be studied at the *between-person* level have to be something that stay stable and do not change over time (i.e., no deviations / fluctuations over time). One example relationship that can be studied only in *between-person* level is: the relationship between the education level and different races. Another example could be the difference in personality trait between people with different zodiac sign.

(place of birth, sex at birth, gene?..., nationality).

According to Denny, (Isvorano: child abuse study can only be done in between level) Child abuse .. cannot really stuided within-person level, as it does not make sense bereavement . partner dies. blood type zodiac sign

Question 4 (2 points)

During the lecture we discussed multiple challenges regarding time-series modeling in the network approach. Pick your favorite challenge and explain this challenge in your own words. Make sure to not only explain what the challenge is, but also why this is a challenge: in what way may this challenge impact your results (i.e., the network model you estimate) and how may this jeopardize your conclusions? You can use additional literature to back up your argument, but this is not required. If you choose to use additional literature, make sure to include a reference list (max 250 words).

One of the challenges in time-series network modelling is the difficulty of incorporating variables that operate on different time-scale. For example, the symptom network (e.g., network consist of symptoms) evolves relatively fast, as symptoms generally fluctuate over days or weeks. Whereas, psychological resilience, which is an important protective factor against developing mental disorder, evolves rather slowly and gradually (Lunasky, 2020). Obviously, resilience is part of the dynamic of psychopathology, but there exists no such model that can incorporate variables operating on the different time-scale and enable us to analyze the whole network that integrates the slow-changing variable (e.g., resilience) with the fast-changing symptoms. Note that Lunasky et al.(2020) look into the interaction between slow and fast network processes but it was studied in such a way that have the slow changing variable influence the node in the symptom network but not incorporating them all in one network model, per se.

According to Borsboom (2021), omitting this relevant factor that operate on slower time-scale from the symptom network could lead to a much denser network. The reasoning is as follows. If the slow-changing variable is omitted in the network model, then the edges will be estimated without controlling for the SV. Assuming that SV has consistent influences on the symptoms, not controlling for the SV is likely to exaggerate the edges (i.e., partial correlations) between the symptoms. Therefore, it is expected that the symptom network model excluding the SV would appear denser (i.e., many thicker edges) than the integrated network model including the SV.

Hence, basing the network model only on the symptoms without incorporating the relevant SV can result in misleading model that overestimates the strength of relationships between symptoms. This could be especially detrimental to studies that look into a particular connection between two symptoms. If a SV that has a considerable influence on the symptom dynamics is not included in the model, the researcher may draw a conclusion based on one of the spurious connections in the network, which are resulted from overlooking the effects of the SV.[1]

Question 5 (2 points)

In a recent study by Haslbeck et al., (preprint) it was shown that use of a VAS or Likert scale has an affect on the observed distributions. Take a look at their article. Give (a) a short summary of the problem described in their paper, (b) reflect on this problem (e.g., why is this an issue and how does it affect the interpretation of our results?) and (c) think of a study to specifically test whether this phenomenon (different scales lead to different distributions) is a methodological artifact or a "true" phenomenon (max 250 words).

Haselbeck et al.(preprint) assessed the distributional modality and skewness in emotional measurements using seven different emotion ESM datasets and investigated whether there are any patterns of the distributional forms on the level of items, individuals, and measurement designs. They found that skewed unimodal distributions as well as multimodality are highly prevalent across the datasets. In addition, the presence of multimodality was found to be strongly associated with the measurement designs such that multimodality was more prevalent in VAS (visual analog scale) than in the Likert scales (e.g., $1 - 5$, or $1 - 7$) and some other association on the time level such as negative emotions exhibit higher skewness than position emotions.

This has a great implication on multiple aspects. First, with regard to theorizing emotion dynamics, if the found multimodality and high skewness is indeed true dynamics of emotion, then it implies that perhaps a person experiences emotions such that going through multiple states (intensity) instead of experiencing it one typical intensity

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[1] ***Note.*** Reference list can be found at the end of the document.

all the time (i.e., unimodal). Additionally, if we presume the multimodality, then the following measurement design should preferably include a broader scale (e.g., VAS with 0 – 100 scale) rather than such a limited Likert scale of 1 – 5 so that it can capture the variabilities across multiple peaks. Lastly, the VAR model might not be deemed appropriate if the true underlying dynamic follows a skewed/multimodal distribution as VAR model assumes a single equilibrium state that is drawn from a normal distribution. Accordingly, a VAR model will fit poorly on the skewed or multimodally-distributed time-series emotion data, and interpretating its parameters would be misleading.

However, it is difficult to reason whether the found result actually reflects the true emotion dynamics or it is just some sorts of methodological artifacts (e.g., specific measurement design induce multimodality). In order to test this, we could design a study such that participants are asked to report on each item with different measurement scales. For example, a participant reports each item twice, once with VAS and once with Likert scale at every occasion and in the end we can compare the distribution of items to see if they approximate to each other or not. If the distributions of item based on VAS and Likert-scale are similar, then we can be more confident in presuming that the found multimodality and skewness do reflect the true phenomenon.

Question 6 (1 point)

What do the *day* and *beep* arguments in the packages `graphicalVAR, psychonetrics,` and `mlVAR` do? Suppose you have a dataset containing only one observation per day for every weekday (but not weekends) in a year long study. Which argument would you use (and why) to make sure that measures from Mondays are not regressed on measures from Fridays?

- `dayvar` argument indicates assessment day and when you add this, it ensures that the first measurement of a day is not regressed on the last measurement of the previous day (it removes pairs of observations that cross a night). So it would be only sensible to add this argument when you have multiple observations per day.

- `beepvar` argument indicates the assessment beep per day, and when you add this, it will treat the non-consecutive beeps as missing (removes pairs of observations that are not consecutive).

- In this case, we want to regress measures of each weekdays on measures of the previous days but there is a break between Mondays and Fridays. We can then use `dayvar` argument and specify the same number to each week (e.g., Monday - Friday of week 1: `dayvar = 1` and Monday - Friday of week 2: `dayvar = 2, …`) then the measures from Mondays are not going to be regressed on the measures from Fridays of the previous week.

Practical Questions

```
# load data
load("clean_network.RData")

# Variables to investigate:
vars <- paste0("Q",1:18)

# Labels:
varLabs <- c("Relax","Irritable","Worry","Nervous","Future","Anhedonia",
"Tired","Hungry","Alone","Angry","Social_offline","Social_online",
"Music","Procrastinate","Outdoors","C19_occupied","C19_worry",
"Home")

# Rename columns in data:
```

```
names(Data2)[names(Data2) %in% vars] <- varLabs

# Remove items:
Data2 <- Data2 %>% select(-Hungry,-Angry,-Music,-Procrastinate)
varLabs <- varLabs[!varLabs %in% c("Hungry","Angry","Music","Procrastinate")]
```

N =1 time series

```
student_number <- 12183881
set.seed(student_number)
subject <- sample(Data2$id, 1)
my_data <- Data2[which(Data2$id == subject),]
```

I chose 4 variables: *"Irritable", "Worry", "Nervous", "Alone".*

```
chosen_var <- c("Irritable", "Worry", "Nervous", "Alone")
```

Question 7 (1.5 points)

Estimate a *saturated* (no model selection) GVAR model on your sampled subject using the 3 or 4 variables you chose above using `psychonetrics`. Plot the estimated temporal (partial directed correlations) and contemporaneous networks with the same layout (1 point). Which edges are significant (0.5 point)?

Tips:

- You can safely ignore warnings on non-positive definite matrices as long as the parameters you obtain look reasonable (e.g., no partial correlations near −1 and 1).

- The psychonetrics package models temporal effects using a matrix called beta, but also returns a standardized form back called PDC (partial directed correlations). Note that the PDC matrix is the standardized transpose of the beta matrix, allowing it to be plotted as a directed network. The significance of parameters in the beta matrix corresponds to the significance of parameters in the PDC matrix.

```
res1 <- gvar(my_data, vars = chosen_var, dayvar = "day", beepvar = "beep") %>% runmodel

# temporal network
temporal1 <- getmatrix(res1, "PDC") # PDC = Partial Directed Correlations
# contemporaneous network
contemporaneous1 <- getmatrix(res1, "omega_zeta")

# get average layout
L1 <- averageLayout(temporal1, contemporaneous1)

# Labels:
labs <- chosen_var

# plot networks
layout(t(1:2))
```
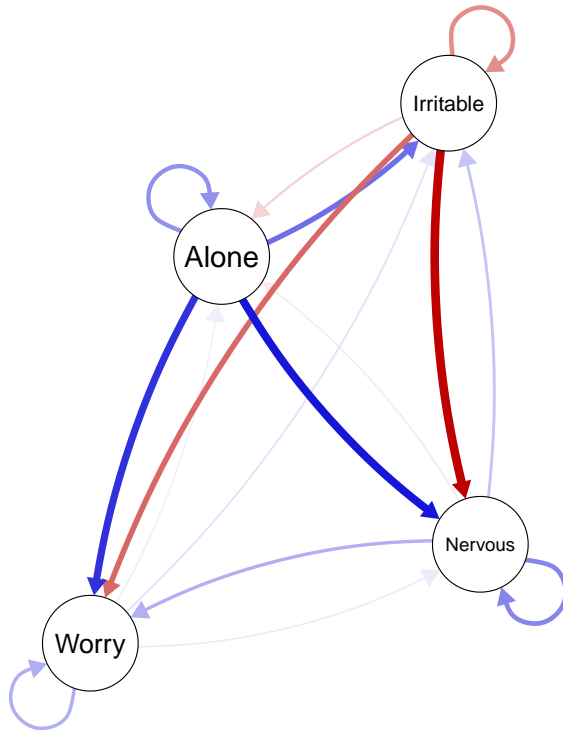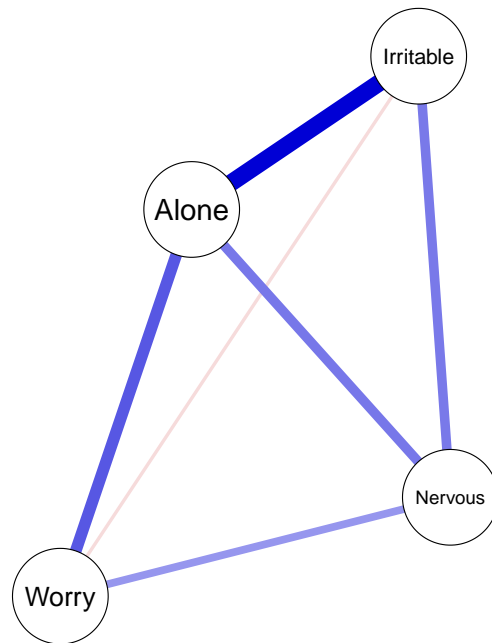
```r
qgraph(temporal1, layout = L1, theme = "colorblind", directed=TRUE, diag=TRUE,
       title = "Temporal", vsize = 12, mar = rep(6,4), asize = 5,
       labels = labs)
qgraph(contemporaneous1, layout = L1, theme = "colorblind",
       title = "Contemporaneous", vsize = 12, mar = rep(6,4), asize = 5,
       labels = labs)
```


Temporal

Contemporaneous

Assuming that $\alpha = 0.05$, - the significant edge in the temporal network is: `Nervous <- Alone`. - the significant edges in the contemporaneous network are: `Nervous -- Irritable`, `Alone--Irritable`, `Nervous--Worry`, and `Alone -- Worry`.

```r
# get parameters
res1 %>% parameters()
```

```
Parameters for group fullsample
  - mu
          var1 op var2   est    se          p row col par
 Irritable_lag1 ~1        1.65  0.14 < 0.0001   1   1   1
    Worry_lag1 ~1        2.06  0.11 < 0.0001   2   1   2
  Nervous_lag1 ~1           2  0.13 < 0.0001   3   1   3
    Alone_lag1 ~1        1.41 0.094 < 0.0001   4   1   4
     Irritable ~1        1.56  0.13 < 0.0001   5   1   5
         Worry ~1        1.88  0.12 < 0.0001   6   1   6
       Nervous ~1        1.82  0.13 < 0.0001   7   1   7
         Alone ~1        1.26 0.086 < 0.0001   8   1   8
```

- exo_cholesky

var1	op	var2	est	se	p	row	col	par
Irritable_lag1	~chol~	Irritable_lag1	0.80	0.097	< 0.0001	1	1	9
Worry_lag1	~chol~	Irritable_lag1	0.17	0.11	0.11	2	1	10
Nervous_lag1	~chol~	Irritable_lag1	0.40	0.12	0.00092	3	1	11
Alone_lag1	~chol~	Irritable_lag1	0.22	0.090	0.016	4	1	12
Worry_lag1	~chol~	Worry_lag1	0.62	0.075	< 0.0001	2	2	13
Nervous_lag1	~chol~	Worry_lag1	0.32	0.10	0.0026	3	2	14
Alone_lag1	~chol~	Worry_lag1	0.23	0.082	0.0041	4	2	15
Nervous_lag1	~chol~	Nervous_lag1	0.57	0.069	< 0.0001	3	3	16
Alone_lag1	~chol~	Nervous_lag1	0.076	0.076	0.31	4	3	17
Alone_lag1	~chol~	Alone_lag1	0.44	0.053	< 0.0001	4	4	18

- beta

var1	op	var2	est	se	p	row	col	par
Irritable	<-	Irritable	-0.37	0.40	0.36	1	1	19
Worry	<-	Irritable	-0.37	0.36	0.30	2	1	20
Nervous	<-	Irritable	-0.82	0.45	0.069	3	1	21
Alone	<-	Irritable	-0.095	0.24	0.69	4	1	22
Irritable	<-	Worry	0.10	0.29	0.73	1	2	23
Worry	<-	Worry	0.22	0.26	0.41	2	2	24
Nervous	<-	Worry	0.062	0.31	0.84	3	2	25
Alone	<-	Worry	0.039	0.17	0.82	4	2	26
Irritable	<-	Nervous	0.20	0.29	0.48	1	3	27
Worry	<-	Nervous	0.20	0.26	0.44	2	3	28
Nervous	<-	Nervous	0.37	0.32	0.25	3	3	29
Alone	<-	Nervous	-0.052	0.17	0.76	4	3	30
Irritable	<-	Alone	0.74	0.56	0.19	1	4	31
Worry	<-	Alone	0.82	0.53	0.12	2	4	32
Nervous	<-	Alone	1.12	0.63	0.077	3	4	33
Alone	<-	Alone	0.38	0.34	0.26	4	4	34

- omega_zeta (symmetric)

var1	op	var2	est	se	p	row	col	par
Worry	--	Irritable	-0.070	0.20	0.73	2	1	35
Nervous	--	Irritable	0.26	0.23	0.26	3	1	36
Alone	--	Irritable	0.50	0.15	0.00096	4	1	37
Nervous	--	Worry	0.20	0.35	0.56	3	2	38
Alone	--	Worry	0.33	0.21	0.12	4	2	39
Alone	--	Nervous	0.27	0.24	0.26	4	3	40

- delta_zeta (diagonal)

var1	op	var2	est	se	p	row	col	par
Irritable	~/~	Irritable	0.50	0.063	< 0.0001	1	1	41
Worry	~/~	Worry	0.43	0.078	< 0.0001	2	2	42
Nervous	~/~	Nervous	0.45	0.10	< 0.0001	3	3	43
Alone	~/~	Alone	0.32	0.057	< 0.0001	4	4	44

```
# sig_pars <- res1 %>% parameters() %>%
#   filter(par >= 19, par <=40) %>%
#   select(var1, op,var2, est, se, p) %>%
```

```
#   filter(p < 0.05)
# sig_pars
```

Question 8 (1 point)

Estimate a GVAR model on your sampled subject using the 3 or 4 variables you chose above using the graphicalVAR package (use $\gamma = 0$), and compare your results to the results of the previous question.

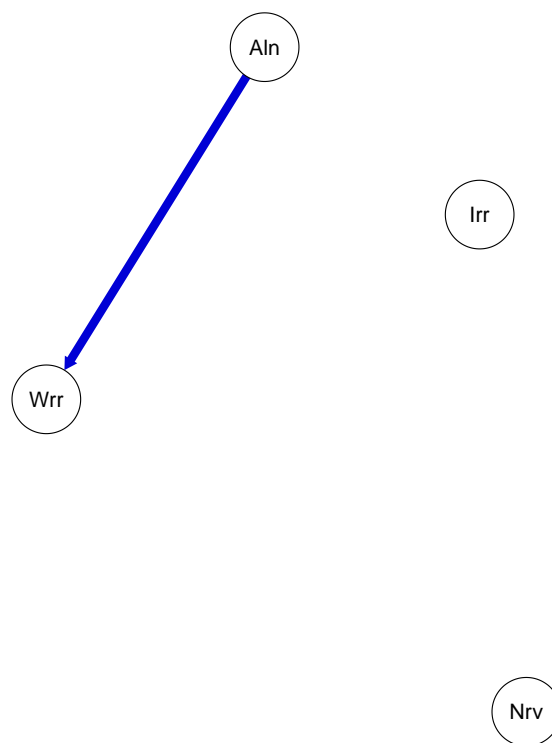It is more sparse, because the network is estimated with LASSO using BIC ($\gamma = 0$).

```
# run graphicalVAR
res2 <- graphicalVAR(my_data, vars = chosen_var, gamma = 0, dayvar = "day", beepvar = "beep")

# Plot results:
#layout(t(1:2))
plot(res2, include = c("PCC", "PDC"), titles = TRUE, sameLayout = TRUE, theme = "colorblind")
```
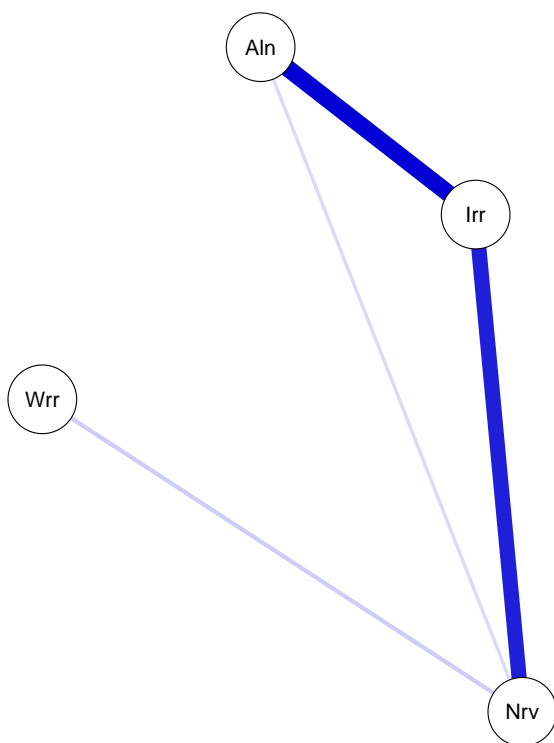

Partial Contemporaneous Correlations   Partial Directed Correlations

Question 9 (1.5 points)

We can use the time variable (in this case we use `conc` as a proxy for the time of measurement) to check for trends in the data. To test if the variable "C19_worry" features a trend, we can run a linear regression on time:

```
lm_c19_worry <- lm(C19_worry ~ conc, data = my_data)
summary(lm_c19_worry)
```

```
Call:
lm(formula = C19_worry ~ conc, data = my_data)

Residuals:
     Min       1Q   Median       3Q      Max
-1.03552 -0.30191 -0.01976  0.16423  1.32564

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.103235   0.152314   13.81  < 2e-16 ***
conc        -0.022572   0.004542   -4.97 8.58e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5011 on 49 degrees of freedom
  (5 observations deleted due to missingness)
Multiple R-squared:  0.3351,    Adjusted R-squared:  0.3216
F-statistic:  24.7 on 1 and 49 DF,  p-value: 8.576e-06
```

This effect is significant. We can now "detrend" the variable worry as follows:

```
my_data$C19_worry[!is.na(my_data$C19_worry)] <- residuals(lm_c19_worry)
```

Test for significant trends ($\alpha = 0.05$) for your selected variables and detrend these variables if the trends are significant. Then, re-estimate the networks using either `graphicalVAR` or `psychonetrics`. Did your estimated networks change?

Note: if the participant you picked did not show any significant trends for the variables you picked, either pick a different participant or pick new variables that do show a significant trend.

```
# run lms on chosen variables
lms <- chosen_var %>%
  paste(., '~ conc') %>%
  map(as.formula) %>%
  map(lm, data=my_data)
names(lms) <- chosen_var

# get the summary
lapply(lms, summary)


$Irritable

Call:
.f(formula = .x[[i]], data = ..1)

Residuals:
    Min      1Q  Median      3Q     Max
-0.6114 -0.4959 -0.4076  0.4905  2.4611

Coefficients:
```

9

```
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.624942   0.223492   7.271 2.53e-09 ***
conc        -0.004527   0.006664  -0.679      0.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.7353 on 49 degrees of freedom
  (5 observations deleted due to missingness)
Multiple R-squared:  0.00933,   Adjusted R-squared:  -0.01089
F-statistic: 0.4615 on 1 and 49 DF,  p-value: 0.5001
```

$Worry

```
Call:
.f(formula = .x[[i]], data = ..1)

Residuals:
     Min       1Q   Median       3Q      Max
-1.19171 -0.57716  0.04182  0.28764  1.28764

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.22859    0.20458  10.894 1.09e-14 ***
conc        -0.01229    0.00610  -2.015   0.0494 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6731 on 49 degrees of freedom
  (5 observations deleted due to missingness)
Multiple R-squared:  0.07651,   Adjusted R-squared:  0.05767
F-statistic:  4.06 on 1 and 49 DF,  p-value: 0.04942
```

$Nervous

```
Call:
.f(formula = .x[[i]], data = ..1)

Residuals:
     Min       1Q   Median       3Q      Max
-1.27329 -0.48327  0.01729  0.33512  2.25339

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.364097   0.218806  10.805 1.45e-14 ***
conc        -0.018161   0.006524  -2.784  0.00762 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.7199 on 49 degrees of freedom
```

```
  (5 observations deleted due to missingness)
Multiple R-squared:  0.1365,    Adjusted R-squared:  0.1189
F-statistic: 7.748 on 1 and 49 DF,  p-value: 0.007617


$Alone

Call:
.f(formula = .x[[i]], data = ..1)

Residuals:
    Min      1Q  Median      3Q     Max
-0.3968 -0.3236 -0.2433  0.6550  1.6675

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.400390   0.153096   9.147 3.56e-12 ***
conc        -0.003570   0.004565  -0.782    0.438
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Residual standard error: 0.5037 on 49 degrees of freedom
  (5 observations deleted due to missingness)
Multiple R-squared:  0.01233,    Adjusted R-squared:  -0.007827
F-statistic: 0.6117 on 1 and 49 DF,  p-value: 0.4379
```

Since we found significant effects in `Worry` ($p < 0.05$) and `Nervous` ($p < 0.01$), we can detrend the variables as below.

```
my_data$Worry[!is.na(my_data$Worry)] <- residuals(lms$Worry)
my_data$Nervous[!is.na(my_data$Nervous)] <- residuals(lms$Nervous)
```

Re-estimated networks after detrending are shown below. The ones estimated with `psychonetrics::gvar()` barely show any changes. And the ones estimated with `grahicalVAR()` shows a change, that is an additional edge between `Alone - Irritable` in the contemporaneous network. But all in all, there is barely any changes observed.

```
## after detrending, run psychonetrics gvar:
res3 <- gvar(my_data, vars = chosen_var) %>% runmodel
# temporal network
temporal3 <- getmatrix(res1, "PDC")
# contemporaneous network
contemporaneous3 <- getmatrix(res1, "omega_zeta")

# get average layout
L3 <- averageLayout(temporal3, contemporaneous3)

# plot networks
layout(t(1:2))
qgraph(temporal3, layout = L3, theme = "colorblind", directed=TRUE, diag=TRUE,
       title = "Temporal", vsize = 12, mar = rep(6,4), asize = 5,
       labels = labs)
```
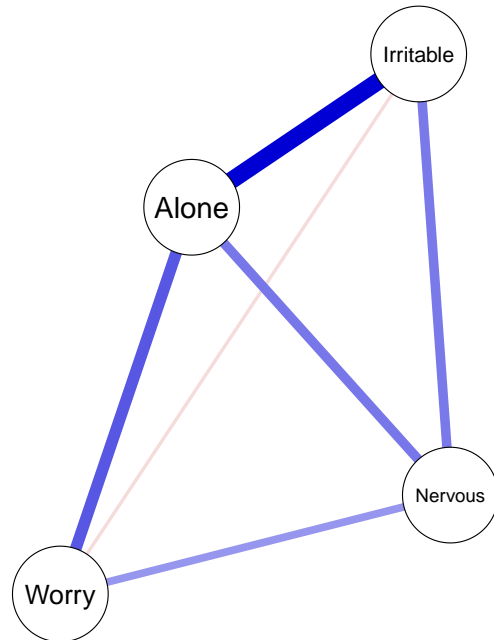
```
qgraph(contemporaneous3, layout = L3, theme = "colorblind",
       title = "Contemporaneous", vsize = 12, mar = rep(6,4), asize = 5,
       labels = labs)
```
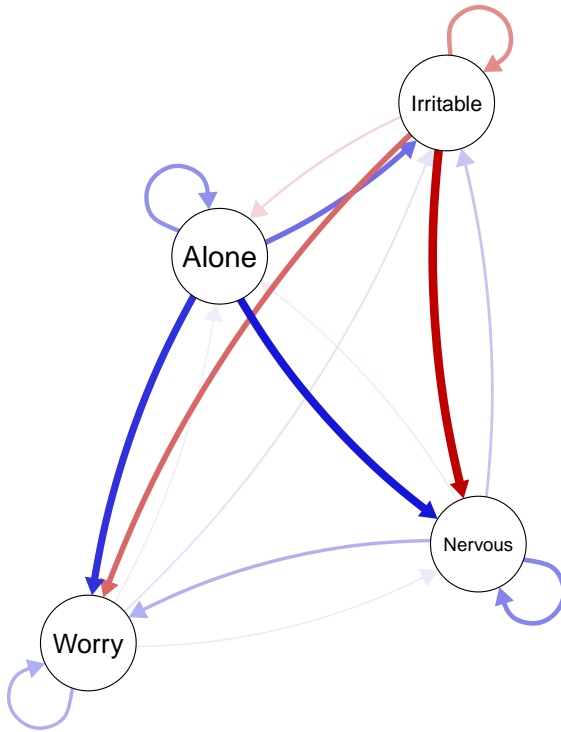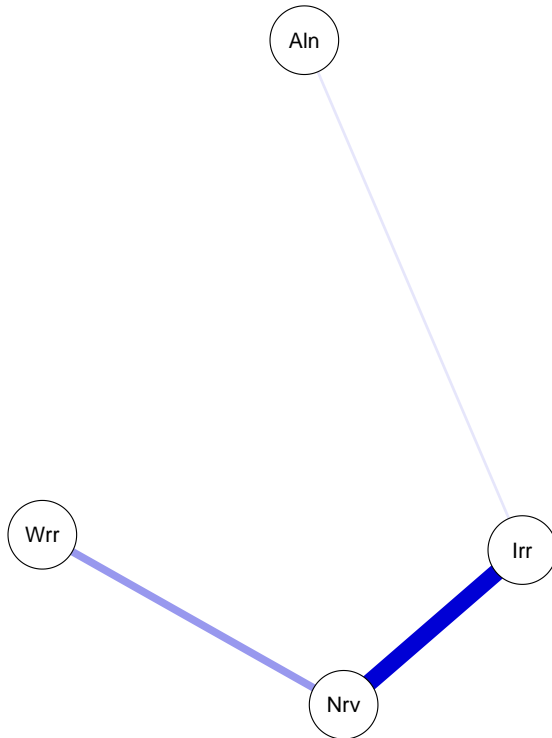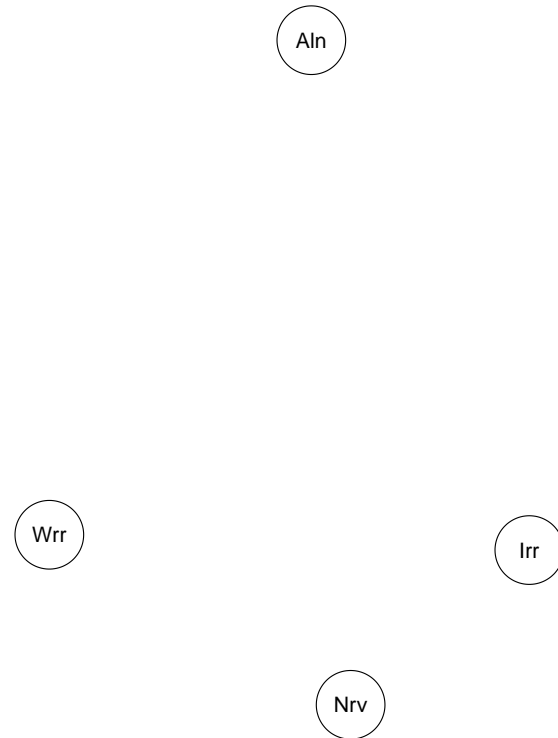

Temporal   Contemporaneous

```
## after detrending, run graphicalVAR:
res4 <- graphicalVAR(my_data, vars = chosen_var, gamma = 0)

# Plot results:
#layout(t(1:2))
plot(res4, include = c("PCC", "PDC"), titles = TRUE, sameLayout = TRUE, theme = "colorblind")
```

Partial Contemporaneous Correlations   Partial Directed Correlations

Question 10 (1 point)

For question 8 you estimated a graphical VAR network containing 3 or 4 variables for a sampled subject using the `graphicalVAR` package. Repeat this process for another subject, i.e., estimate an additional graphical VAR network containing the same 3 or 4 variables as before for another subject (for example, use the student number of a friend). Note here that you are not required to detrend the data prior to estimating the network structures. Now that you have estimated two graphical VAR models on non-detrended data, plot the resulting networks and inspect the similarities and differences between these estimated graphical VAR networks. Can you conclude there is heterogeneity between these two people? Why (not)?

Just at a glance, it seems two people are different as the estimated networks look different. However, we cannot really conclude that there is heterogeneity based on visually comparing the network structures, because we cannot ensure the these estimated GVAR models are reliable. It could be that they are just random noises, then we would compare a set of random noises to another set of random noises. According to Hoekstra et al. (2022), even when the generating structure is the same, it is likely that we would find different network structures. Hence, it is not advisable to interpret the differences between individual network models as an evidence for heterogeneity, especially when the networks are sparse as in this case!

```
## another seed
set.seed(13294889)
subject2 <- sample(Data2$id, 1)
my_data2 <- Data2[which(Data2$id == subject2),]

# run graphicalVAR
res5 <- graphicalVAR(my_data2, vars = chosen_var, gamma = 0)

# Plot results:
```
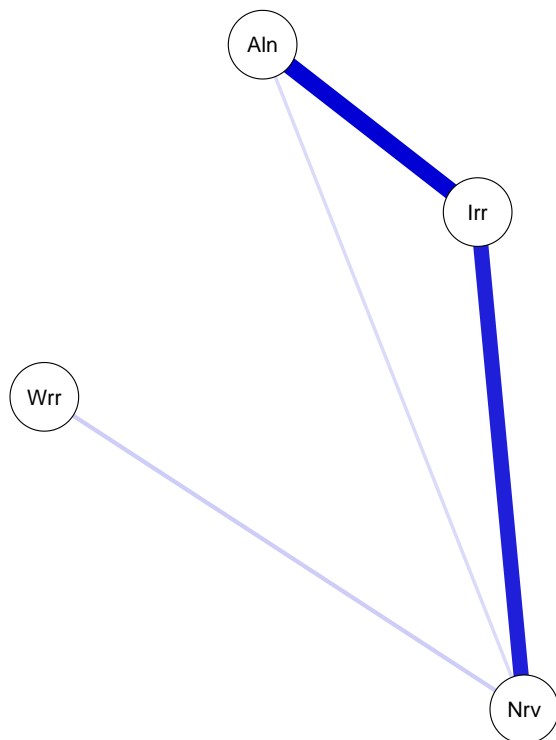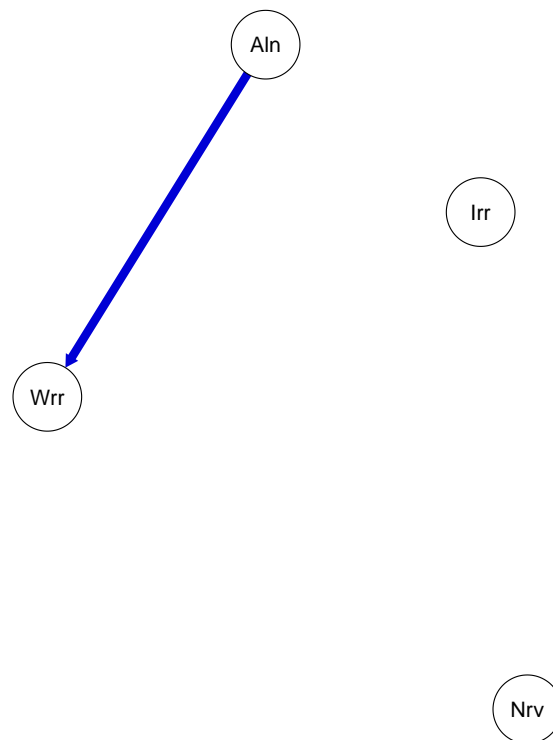
```
### LAYOUT the same fix!
par(mfrow=c(2,1))
plot(res2, include = c("PCC", "PDC"), titles = TRUE, sameLayout = TRUE, theme = "colorblind", main = "pers
```

Partial Contemporaneous Correlations   Partial Directed Correlations
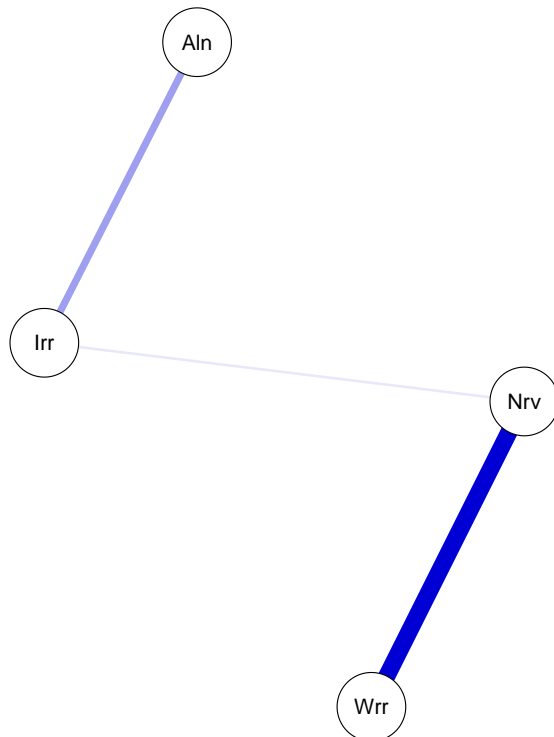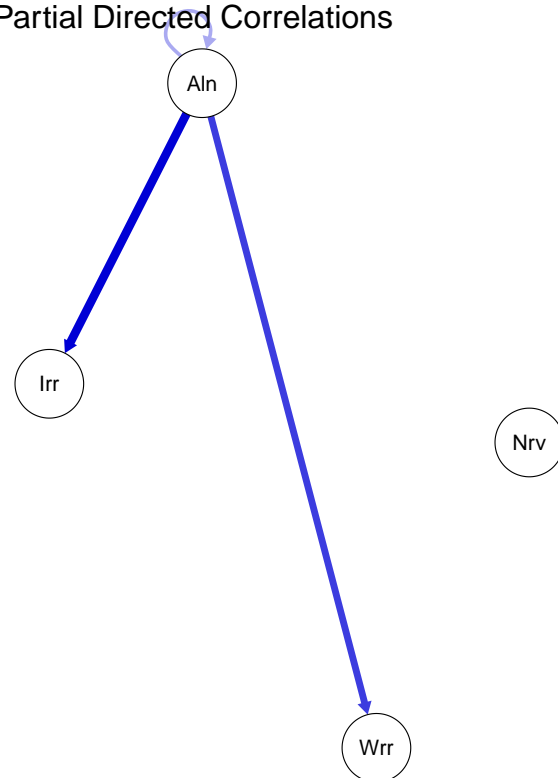


```
plot(res5, include = c("PCC", "PDC"), titles = TRUE, sameLayout = TRUE, theme = "colorblind", main = "pers
```

Partial Contemporaneous Correlations   Partial Directed Correlations

N > 1 time-series

Question 11 (1 point)

Look at the help file for the `mlVAR` function and estimate a multilevel GVAR model on the entire dataset on 4 to 6 variables of your choice.

```
## choose 5 variables
chosen_var2 <- c("Irritable", "Worry", "Nervous", "Alone", "C19_worry")
## estimate mlGVAR model
mlVAR_res <- mlVAR(Data2, vars = chosen_var2, idvar = "id" , beepvar = "beep", dayvar="day", contemporaneo
```

Question 12 (1 point)

Look at the mlVAR plot method help file (`?plot.mlVAR`), and plot the estimated fixed-effect temporal, contemporaneous and between-subjects networks. Plot all networks with the same layout (circle layout or average layout), and hide (threshold) edges that are not significant at $\alpha = 0.05$. For the contemporaneous and between-subjects networks, use an "and"-rule to minimize type-1 error rate in showing edges.

```
# Get networks:
cont <- getNet(mlVAR_res, "contemporaneous", nonsig = "hide", rule = "and")
bet  <- getNet(mlVAR_res, "between", nonsig = "hide", rule = "and")
temp <- getNet(mlVAR_res, "temporal", nonsig = "hide")

# average layout
```

```
L <- averageLayout(cont,bet,temp)

## plot the networks
# par(mfrow=c(1,3))
# qgraph(cont, layout = L,
#        title="Contemporaneous", theme='colorblind', negDashed=FALSE,
#        legend.cex=0.4, details=TRUE, nodeNames = chosen_var2)
#
# qgraph(temp, layout = L,
#        title="Temporal, Lag-1", theme='colorblind', negDashed=FALSE,
#        legend.cex=0.4, details=TRUE, nodeNames = chosen_var2)
#
# qgraph(bet, layout = L,
#        title="Between",  theme='colorblind', negDashed=FALSE,
#        legend.cex=0.4, details=TRUE, diag = FALSE, nodeNames = chosen_var2)

par(mfrow=c(1,3))
plot(mlVAR_res, "temporal", title="(a) Temporal (Lag-1)", layout = L, nonsig = "hide", rule = "and", theme=

plot(mlVAR_res, "contemporaneous", title="(b) Contemporaneous", layout = L, nonsig = "hide", rule = "and",

plot(mlVAR_res, "between", title="(c) Between-subjects", layout = L, nonsig = "hide", theme='colorblind',
```
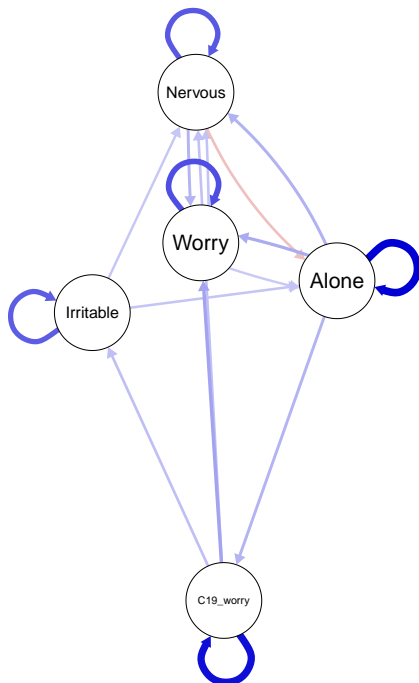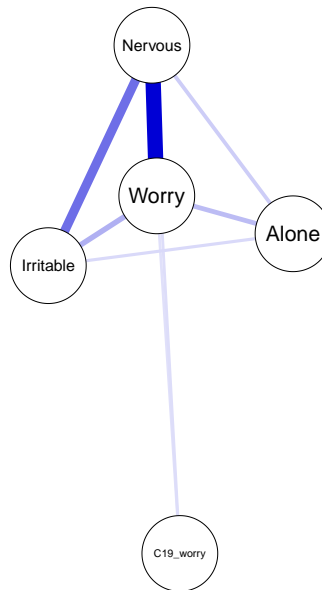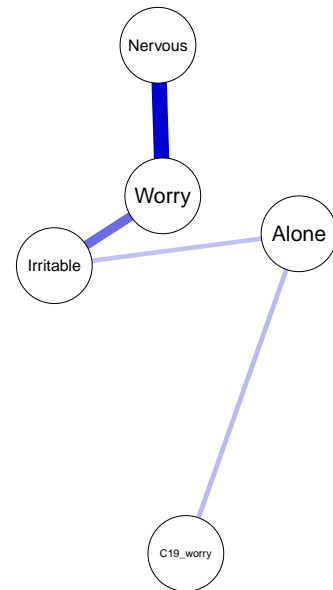

(a) Temporal (Lag−1)   (b) Contemporaneous   (c) Between−subjects

Question 13 (2 points)

Plot the estimated individual differences for both the temporal and the contemporaneous network. Explain what the edges in these networks represent. Inspect the plotted networks, what conclusion can you draw about heterogeneity within this sample based on these network structures?

Figure 1 shows the estimated networks of the individual differences, where the edges represent the standard deviation of random effects in the temporal and in the contemporaneous network, respectively.

In the temporal network, the `minimum` argument is set to 0.07, meaning that only the standard deviation of temporal random effects above 0.07 are shown with a non-transparent arrow, following the advice of Bringmann et al. (2013). We can see that in Figure 1 (a), the largest individual differences are found in the auto-regressions, given that the self-loops of `Alone`, and `C19-worry` are pronounced. It implies that there is a high individual variability over those items such that for some individuals, once they feel alone they tend to feel lonely for long time, but for the other individuals, it is rather momentary). Among the cross-lagged regressions, `Nervous -> Irritable` turns out to have relatively larger individual differences.

When looking at the contemporaneous network in in Figure 1 (b), the largest individual differences are found again in the relationship between `Nervous` and `Irritable`, followed by the relationship between `Nervous` and `Worry`.

All in all, we can conclude that there is some amount of individual heterogeneity observed in our data. In general, auto-regressions have relatively larger individual differences compared to cross-lagged regressions and the relation between `Nervous` and `Irritable` seems to vary a lot across individuals, considering that it is pronounced in both temporal and contemporaneous networks.

```
## checked with summary result
summary(mlVAR_res)
```

```
mlVAR estimation completed. Input was:
    - Variables: Irritable Worry Nervous Alone C19_worry
    - Lags: 1
    - Estimator: lmer
    - Temporal: correlated

Information indices:
        var      aic      bic
  Irritable 6902.545 7091.918
      Worry 5998.146 6187.519
    Nervous 6268.447 6457.820
      Alone 5327.321 5516.694
  C19_worry 5739.716 5929.089


Temporal effects:
      from          to lag  fixed    SE     P ran_SD
  Irritable Irritable   1  0.162 0.030 0.000  0.162
  Irritable     Worry   1  0.017 0.019 0.354  0.031
  Irritable   Nervous   1  0.055 0.019 0.004  0.026
  Irritable     Alone   1  0.058 0.020 0.003  0.095
  Irritable C19_worry   1  0.008 0.020 0.676  0.077
      Worry Irritable   1  0.061 0.032 0.059  0.138
      Worry     Worry   1  0.176 0.028 0.000  0.124
      Worry   Nervous   1  0.060 0.026 0.022  0.075
      Worry     Alone   1  0.054 0.023 0.017  0.080
      Worry C19_worry   1 -0.015 0.026 0.555  0.120
    Nervous Irritable   1  0.059 0.035 0.093  0.174
    Nervous     Worry   1  0.075 0.030 0.013  0.149
    Nervous   Nervous   1  0.166 0.029 0.000  0.123
    Nervous     Alone   1 -0.063 0.025 0.012  0.120
```

```
    Nervous C19_worry   1  0.026 0.025 0.304  0.103
      Alone Irritable   1  0.064 0.035 0.065  0.157
      Alone     Worry   1  0.083 0.029 0.004  0.138
      Alone   Nervous   1  0.077 0.025 0.002  0.082
      Alone     Alone   1  0.253 0.034 0.000  0.198
      Alone C19_worry   1  0.074 0.026 0.005  0.112
  C19_worry Irritable   1  0.064 0.029 0.029  0.142
  C19_worry     Worry   1  0.092 0.024 0.000  0.108
  C19_worry   Nervous   1  0.061 0.027 0.022  0.137
  C19_worry     Alone   1  0.013 0.020 0.514  0.083
  C19_worry C19_worry   1  0.239 0.030 0.000  0.194


Contemporaneous effects (posthoc estimated):
        v1          v2 P 1->2 P 1<-2  pcor ran_SD_pcor   cor ran_SD_cor
    Worry Irritable  0.000  0.000 0.137       0.060 0.314      0.123
  Nervous Irritable  0.000  0.000 0.251       0.148 0.376      0.166
  Nervous     Worry  0.000  0.000 0.440       0.125 0.523      0.137
    Alone Irritable  0.005  0.010 0.065       0.046 0.153      0.072
    Alone     Worry  0.000  0.000 0.116       0.096 0.214      0.110
    Alone   Nervous  0.000  0.006 0.086       0.072 0.203      0.102
C19_worry Irritable  0.133  0.047 0.037       0.032 0.091      0.060
C19_worry     Worry  0.010  0.016 0.053       0.030 0.120      0.071
C19_worry   Nervous  0.023  0.011 0.058       0.072 0.125      0.093
C19_worry     Alone  0.072  0.081 0.035       0.019 0.070      0.046


Between-subject effects:
        v1          v2 P 1->2 P 1<-2  pcor   cor
    Worry Irritable  0.000  0.000 0.409 0.870
  Nervous Irritable  0.231  0.115 0.155 0.843
  Nervous     Worry  0.000  0.000 0.707 0.931
    Alone Irritable  0.138  0.041 0.175 0.655
    Alone     Worry  0.496  0.974 0.040 0.665
    Alone   Nervous  0.476  0.054 0.135 0.670
C19_worry Irritable  0.524  0.426 0.001 0.533
C19_worry     Worry  0.379  0.200 0.114 0.587
C19_worry   Nervous  0.416  0.486 0.082 0.581
C19_worry     Alone  0.030  0.087 0.188 0.517
```

```r
layout(t(1:2))
## temporal: random effects SD
temp_ran_sd <- mlVAR_res[["results"]][["Beta"]][["SD"]] # mlVAR_res$results$Beta$SD
tem_inddif <- cbind(rep(1:5,each=5), rep(1:5,5), weight=as.vector(temp_ran_sd))
qgraph(tem_inddif, layout = L, labels = chosen_var2, theme='colorblind', vsize = 12, asize = 4, mar = rep(

## contemporaneous: random effects SD
contemp_ran_sd <- mlVAR_res[["results"]][["Theta"]][["pcor"]][["SD"]]
qgraph(contemp_ran_sd, layout = L, labels = chosen_var2, theme='colorblind', vsize = 12, asize = 4, mar =
```
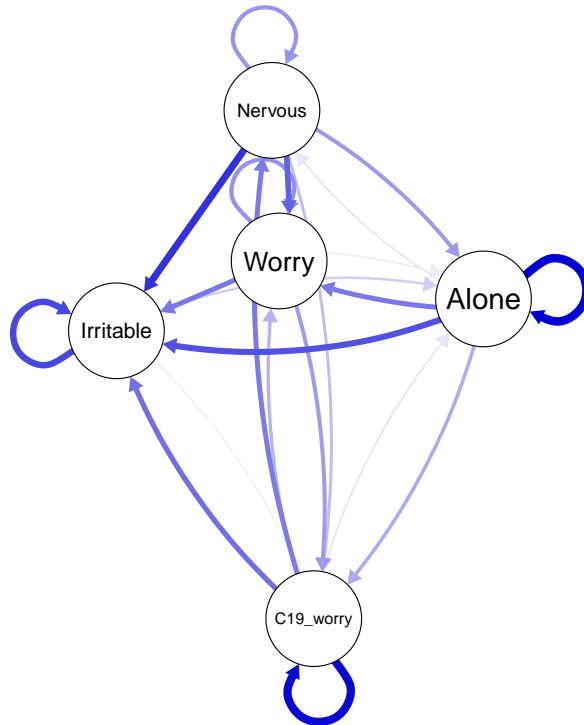
(a) Temporal (b) Contemporaneous

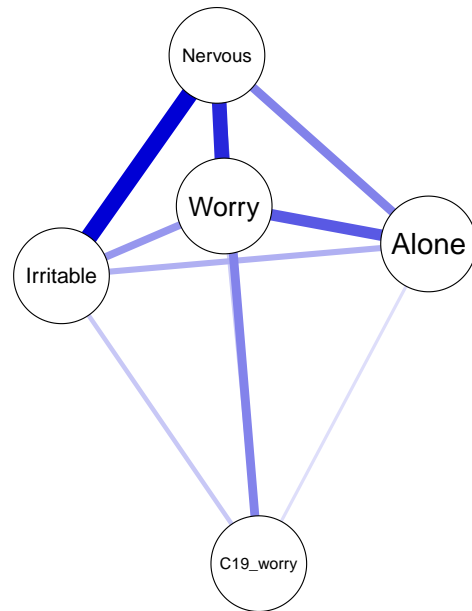Figure 1: Individual differences networks

Essay Question

Question 14 (2 points)

Let's revisit centrality measures: As we already explored in previous assignments, `qgraph` implements a number of centrality measures for networks. In addition, the Brain Connectivity Toolbox (see https://sites.google.com/site/bctnet/home) contains measures to inspect complex network structures. Inspect these network measures and choose one that would be interesting to compute on one of the estimated networks from any of the previous questions. Report your chosen measure and what it represents for the network you have chosen, explain your choice, and what research question it could answer in the form of a short essay (max 250 words).

Note: you do not need to compute the metric as not all of the centrality measures are also implemented into R (you are of course free to compute the measure nonetheless!).

References

Bringmann, L. F., Vissers, N., Wichers, M., Geschwind, N., Kuppens, P., Peeters, F., Borsboom, D., & Tuerlinckx, F. (2013). A Network Approach to Psychopathology: New Insights into Clinical Longitudinal Data. *PLOS ONE*, *8*(4), e60188. https://doi.org/10.1371/journal.pone.0060188

Epskamp, S., Borkulo, C. D. van, Veen, D. C. van der, 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*(3), 416–427.

Hoekstra, R. H. A., Epskamp, S., & Borsboom, D. (2022). Heterogeneity in Individual Network Analysis: Reality or Illusion? *Multivariate Behavioral Research*, 1–25. https://doi.org/10.1080/00273171.2022.2128020

Isvoranu, A.-M., Epskamp, S., Waldorp, L., & Borsboom, D. (2022). *Network psychometrics with r: A guide for behavioral and social scientists*. Routledge.

Molenaar, P. C. (2004). A manifesto on psychology as idiographic science: Bringing the person back into scientific psychology, this time forever. *Measurement*, *2*(4), 201–218.