CONNECT: CONTINGENCY MEASURE BASED NETWORKS FOR BINARY TIME SERIES

Nadja Bodner^{1*} & Eva Ceulemans¹

Version 1/7/2020

¹Quantitative Psychology and Individual Differences Research Group, KU Leuven (University of Leuven), Leuven, Belgium

Author Note

* **Corresponding author:** Nadja Bodner, Quantitative Psychology and Individual Differences Research Group, Faculty of Psychology and Educational Studies, Tiensestraat 102 – Box 3713, 3000 Leuven, Belgium, Tel: +32 16 30 10 41, nadja.bodner@kuleuven.be.

Acknowledgment: We thank Guy Bosmans (KU Leuven), Peter de Jonge (RU Groningen), and Lisa Sheeber (Oregon Research Institute) and their teams for collecting and sharing the data. The research leading to the results reported in this paper was sponsored by research grants from the Research Council of KU Leuven (C14/19/054, PDM/20/062, iBOF/21/090).

1 Abstract

Dynamic networks are valuable tools to depict and investigate the concurrent and temporal interdependencies of various variables across time. Although several software packages for computing and drawing dynamic networks have been developed, software that allows investigating the bivariate relationships between a set of binary intensive longitudinal variables is still missing. To fill this gap, this paper introduces an R-package that yields contingency measure based networks (ConNEcT). ConNEcT implements different contingency measures: proportion of agreement, corrected and classic Jaccard index, phi correlation coefficient, Cohen's Kappa, odds ratio, and log odds ratio. Moreover, users can easily add alternative measures, if needed. Importantly, ConNEcT also allows conducting non-parametric significance tests on the obtained contingency values that correct for the inherent serial dependence in the time series, through a permutation approach or model-based simulation. In this paper, we provide an overview of all available ConNEcT features and showcase their usage. Addressing a major question that users are likely to have, we also discuss similarities and differences of the included contingency measures.

Keywords: contingency measures, dynamic networks, binary time series, network approach, bivariate relationships

2 Introduction

During the last decennium, a surge of network methods washed up on the shores of the behavioral sciences. Networks offer valuable tools to depict and investigate the complex interdependencies of various variables. The variables constitute the nodes of the obtained networks and the (partial) relations between the variables are represented through the edges that connect the nodes. Network methods have been applied to a wide range of problems, including affective dynamics (e.g., Bodner et al., 2018; Bringmann et al., 2016), attitudes (e.g., Dalege et al., 2016), beliefs (e.g., Brandt et al., 2019), psychopathology (Borsboom, 2008, 2017; Borsboom & Cramer, 2013; Cramer et al., 2010; Fried et al., 2017), and parent-child interactions (Bodner et al., 2018, 2019; Van der Meer et al., 2019).

Network methods come in variations. First, the underlying data can be cross-sectional (i.e., many individuals are measured once) or intensive longitudinal (i.e., one or more individuals are measured frequently). Psychopathological networks, for example, were initially built based on cross-sectional data, facilitating insight into how symptoms relate across individuals (e.g., Boschloo et al., 2015; Cramer et al., 2016; Isvoranu et al., 2016). Complementing these cross-sectional networks with dynamic networks, built on intensive longitudinal data, sheds additionally light on the within-subject relations between variables over time (e.g., Bringmann et al., 2013; Bulteel et al., 2018; Epskamp, Waldorp, et al., 2018; Hamaker et al., 2018). Second, the underlying data can be continuous or binary (e.g., absence or presence of a variable). While most methods have been developed for continuous data (e.g., Epskamp, Waldorp, et al., 2018) and mixed data (Haslbeck & Waldorp, 2020), attention has also been paid to binary data (e.g., van Borkulo et al., 2014). Third, most network methods focus on partial variable relations, quantified through partial correlations (e.g., Epskamp, Borsboom, et al., 2018; LaFit et al., 2019) or regression weights (e.g., Bulteel et al., 2016a). Yet, networks have also been useful to investigate simple bivariate relations (e.g., Bodner, Bringmann, et al., in press). Importantly, bivariate relations are not affected by the composition of the variable set, whereas partial relations may change when a variable is added or excluded.

Scrutinizing the available software with the above three distinctions in mind, the development focused on partial-relation-based approaches for continuous cross-sectional data (e.g., Epskamp & Fried, 2018). Software for the analysis of binary data (e.g., mgm, Haslbeck & Waldorp, 2020; IsingFit, van Borkulo et al., 2014) and intensive longitudinal data (e.g., mlvar, Epskamp, Waldorp, et al., 2018) has also been proposed. However, software for bivariate relation based networks of binary intensive longitudinal variables is still missing, although such approaches have led to meaningful insights when investigating micro-coded parent-child interactions (Bodner et al., 2018, 2019; Van der Meer et al., 2019) and longitudinal depression symptom reports (Bodner, Bringmann, et al., in press). Therefore, we propose an R-package for building such contingency measure based networks, which we called ConNEcT. The ConNEcT package includes seven contingency measures: Proportion of agreement, the classic and the corrected Jaccard index, phi correlation coefficient, Cohen's kappa, odds ratio, and log odds ratio. Other contingency measures can be easily added, as we will demonstrate. The package can be used to investigate concurrent associations as well as temporal sequences (i.e., the presence of behavior X at time point t is associated with the presence of behavior Y at time point $t+\delta$). The ConNEcT software also provides a tailor-made significance testing framework (Bodner et al., 2020). Finally, the package allows the visualization of the results in network figures.

The paper is organized into four modules, focusing on data requirements and exploration, contingency measure selection and computation, significance testing, and network visualization, respectively. Each module first gives a theoretical introduction to the topic, where we also delve deeper into some so far unanswered questions, such as the similarities and differences of the included contingency measures. Next, we explain how to use the ConNEcT R-Package using

illustrative examples. Figure 1 gives a visual overview of the four modules, making use of intensive longitudinal depression symptom data from a patient included in the study by Hosenfeld et al. (2015), which was also analyzed by Bodner, Bringmann et al. (in press).

Figure 1

Overview of the four ConNEcT modules using the data of weekly reported depression symptoms

Note. This example patient (Hosenfeld et al., 2015) reported the presence or absence of eight depression symptoms (**C**ore symptoms, lack of **E**nergy, **E**ating problems, **S**leeping problems, psychom**O**tor problems, feelings of **G**uilt, **C**ognitive problems, and preoccupation with **D**eath) for 145 weeks. a) Line plot of the depression symptoms over weeks, where elevated line segments indicate presence and segments that coincide with the reference line indicate absence. b) heatmap of the strength of the pairwise classic Jaccard values, quantifying concurrent contingency, c) histogram of the sampling distribution of the classic Jaccard value; the solid line indicates the observed Jaccard value and the dashed line the 95th percentile, d) network of the significant ($\alpha=0.05$) contingencies; the node size reflects the relative frequency of the variables, while the saturation and width of the undirected edges represent the strength of the concurrent contingency.

3 Module 1: Data requirements and exploration

ConNEcT has been developed to investigate bivariate contingencies in binary time series data. Such data show up in different forms in the behavioral sciences. To acknowledge this variety, we will make use of three data examples to illustrate the possibilities. The datasets are also included in the package.

(1) Symptom Data

The depression symptom data (see Figure 1) stem from a patient in the study of Hosenfeld et al. (2015), also used in Bodner, Bringmann et al. (in press). The patient reported each week on the presence or absence of eight depression symptoms (**Core** symptoms, lack of **energy**, **eating** problems, **sleeping** problems, **psychomotor** problems, feelings of **guilt**, **cognitive** problems, and preoccupation with **death**) for 145 weeks. This dataset is used in the introduction and in Modules 1 and 2.

(2) Family Data

These data, collected by Sheeber et al. (2012) and re-analyzed by Bodner et al. (2018), stem from a family interaction between two parents and their adolescent son or daughter during a nine-minute problem-solving interaction. The presence and absence of expressions of 'anger', 'dysphoric' feelings, and 'happiness' were coded for each family member in an event-based way (i.e., noting when a certain behavior starts and when it stops). The codes were subsequently restructured into second-to-second interval data, resulting in a 540 seconds by nine variables binary dataset. This dataset is used in modules 2 and 4.

(3) Attachment Data

In an attachment study (Bodner et al., 2019; Dujardin et al., 2016), a mother and her child (aged eight to 12) were videotaped while working on a three minutes stressful puzzle task. The interaction was coded in two-second intervals for the presence and absence of positive, negative, or task-related behavior. The dataset contains seven variables ('Mother positive', 'Mother negative', 'Mother working alone', 'Mother and child working together', 'Child positive', 'Child negative' and 'Child working alone') and 90-time points. This dataset will be used in Module 4.

3.1 Theory

3.1.1 Number of variables and time points

Before starting the analysis, we recommend careful consideration of which variables should be included. The more variables are considered, the more bivariate associations have to be quantified, implying that the network may become a complex, hard to interpret tangle of links and nodes. To avoid this, one should only consider those variables that are relevant to the question at hand. Further, variables with very high or very low relative frequencies may not be very informative, especially, since the absolute values of many contingency measures become hard to interpret in case of extreme relative frequencies (see Module 3).

The optimal number of time points depends on two different types of considerations. The first consideration is the frequency and length with which the variables of interest are assumed to be present. In case one is interested in rare and short-lived behaviors, the time series should be long and fine-grained, whereas for longer-lasting and more frequently occurring variables shorter and coarser time series may do. The second type of considerations pertains to statistical power. Longer time series will increase the available amount of information and decrease the estimation

uncertainty of the contingency strength, and thus increase the power of significance tests (see Module 3).

3.1.2 Relative frequency and serial dependence

During data exploration, two characteristics of time series data are especially important to consider: the relative frequency (i.e., the proportion of 1s; see higher and Module 3) and the serial dependence (or auto-dependence) of each variable. Serial dependence refers to the tendency of behaviors to be present for more than one time point. We can quantify it by calculating conditional probabilities and comparing them to each other or to the relative frequencies. Specifically, if the probability that a '1' is observed given that a '1' has been observed the timepoint before, $p(X_t=1 | X_{t-1}=1)$ or $p_{1|1}$ for ease of notation, differs from the probability that a '1' is shown given a zero at the previous time point, $p(X_t=1 | X_{t-1}=0)$ or $p_{1|0}$, or from the relative frequency of ones, $p(X_t=1)$ or p_1 , this suggests that serial dependence is present. Accounting for such serial dependence is important, to avoid false positives during significance testing (Bodner et al., 2020).

3.2 Tutorial

The ConNEcT package offers some data exploration features. Users can visualize the course of the raw data over time, as well as calculate and visualize relative frequency and auto-dependence.

3.2.1 Basics of the conData function

The **input** for the conData function is the raw data, structured in a time-points-by-variable matrix. Missing values need to be retained because certain operations (e.g., lagging the data; see Module 2) might lead to erroneous contingencies when missing values have already been removed. The function removes columns that contain non-binary values (e.g., identity number or time interval counting) and calculates the relative frequency and conditional probabilities $p_{1|1}$ and $p_{1|0}$ of each variable (see 3.2.3). The **output** is a conData object, containing **\$data**: the raw data, after removing continuous and non-binary variables, and **\$probs**, a table containing the relative frequencies and conditional probabilities of all variables. The labels of the variables are stored in **\$varNames**.

3.2.2 Visualizing the course of the variables over time

The package provides different visualizations of the raw data that might reveal interesting characteristics, using the plot function. We will illustrate the function with the Symptom Data (see Figure 1). First, the conData function is applied to the data and the results are saved in a conData object that we call Sdata. The plot.conData function can simply be called by plot(Sdata). The plottype of the output can be specified as 'interval', 'line', or 'both'. Figure 2 shows the plot type 'interval', displaying a vertical tick each time a symptom was reported. The time intervals are indicated on the x-axis, while the y-axis represents the different symptoms. Alternatively, the plot type 'line' (see Figure 1a) shows the presence of a variable in terms of the height of the line, where the line is higher than (resp. coinciding with) the grey dotted auxiliary line indicates that the variable is present (resp. absent). It is also possible to choose 'both' to get a line plot with ticks at all intervals.

```
data(SymptomData)
Sdata <- conData(SymptomData)
fancy.col= c('purple','slateblue', 'royalblue', 'cyan4', 'green3',
'olivedrab3', 'orange', 'orangered')
#Figure 2:
plot(Sdata, plottype='interval',color=fancy.col)
#Figure 1a):
plot(Sdata, plottype='line',color=fancy.col)
```

Figure 2

Plot of the Symptom Data using the `plot.conData`-function, `plottype='interval'`

3.2.3 Relative frequency and serial dependence

To examine the relative frequency and the auto-dependence of each variable, we can examine the contents of the `probs` field of the `conData` object. The symptom *Death*, for example, is shown 65% of the time (i.e., 94 of the 145 time points). Moreover, this symptom is characterized by high auto-dependence, since almost every 1-score is followed by another 1-score (i.e., 90 out of the 94 times, resulting in a $p_{1|1}$ of .96 and $p_{0|1}$ of .04), while a 1-score rarely follows a 0-score (4 out of the 51 times, resulting in $p_{1|0}$ of .08 and $p_{0|0}$ of .92).

```
Sdata <- ConData(SymptomData)
Sdata$probs
```

Table 1

Relative frequencies and auto-dependences of the Symptom Data

	Relative frequency	$p_{1 1}$	$p_{1 0}$
Core	0.71	0.98	0.05
Energy	0.57	0.96	0.05
Eat	0.00	NaN	0.00
Sleep	0.93	0.99	0.20
Motor	0.93	0.99	0.20
Guilt	0.46	0.92	0.05
Cogn	0.71	0.98	0.05
Death	0.65	0.96	0.08

The relative frequencies can be visualized employing the barplot function¹. This function has two different plot types, plotting either only the relative frequency (plottype='RelFreq'; see Figure 3) or all three probabilities p_1 , $p_{1|1}$, and $p_{1|0}$ (plottype='All'; see Appendix).

```
Sdata <- conData(SymptomData)
FANCY= c('purple','slateblue', 'royalblue', 'cyan4', 'green3',
         'olivedrab3', 'orange', 'orangered')
barplot(Sdata,plottype='RelFreq', color = FANCY)
```

Figure 3

Barplot depicting the relative frequencies of the Symptom Data

¹ The function barplot.conData is an extension of the generic barplot function. When applying barplot() to a conData object (i.e., the output of the conData function), R will automatically call barplot.conData.

4 Module 2: Contingency measure selection and computation

4.1 Theory

To quantify the strength of the bivariate association between each pair of variables (X, Y), contingency values are computed. Seven popular contingency measures are included in the ConNECT-package: proportion of agreement, classic and corrected Jaccard index, Cohen's kappa, phi correlation coefficient, odds ratio, and log odds ratio. First, we will introduce the different contingency measures. Second, we will investigate how the measures relate to each other and discuss their similarities and differences. Third, we will explain how contingency measures can also be used to investigate the temporal relations between variables.

4.1.1 Introduction of the contingency measures

4.1.1.1 Notation

Table 2 shows the crosstabulation of a variable pair (X, Y), where a value of '1' indicates that a variable is present and a value of '0' that the variable is absent. In this table, a denotes the proportion of time points at which both variables equal '1', b the proportion that only variable X equals '1', c the proportion that only variable Y equals '1', and d the proportion that both variables equal '0'. We also use the relative frequencies p_1^X and p_1^Y that were introduced in module 1, and their complements p_0^X and p_0^Y . Note that these relative frequencies equal-weighted sums of a , b , c , and d . For example, $p_1^X = a + b$, $p_1^Y = a + c$, etc.

Table 2

Crosstabulation of two binary variables X and Y

		Variable Y		
		Value(Y)= 1	Value(Y)=0	Total Y
Variable X	Value(X)=1	a	b	p_1^X
	Value(X)=0	c	d	p_0^X
	Total X	p_1^Y	p_0^Y	1

4.1.1.2 Proportion of agreement

The proportion of agreement P_A quantifies the observed agreement, that is the proportion of time points at which both variables equal either '1' or '0':

$$P_A(X, Y) = a + d \quad (1)$$

This measure ranges from 0 to 1, with 1 indicating perfect agreement and 0 perfect non-agreement. The proportion of agreement attaches equal importance to co-absence and co-occurrence. This contingency measure is always defined.

4.1.1.3 Cohen's Kappa

Since the obtained proportion of agreement is affected by the relative frequencies of the variables (Bodner et al., 2020), Cohen's kappa (Cohen, 1960) refines it by correcting for chance agreement

$$\kappa(X, Y) = \frac{P_A - P_E}{1 - P_E}. \quad (2)$$

where P_E is computed as follows:

$$P_E(X, Y) = p_1^X p_1^Y + p_0^X p_0^Y. \quad (3)$$

Since $P_A = a + d$, see equation (1), and $p_1^X = a + b$, etc. we can simplify to (Warrens, 2008):

$$\kappa(X, Y) = \frac{2(ad-bc)}{p_1^X p_0^Y + p_0^X p_1^Y} \quad (4)$$

Cohen's kappa ranges from -1 to 1 with a value of 0 being interpreted as chance agreement. From equation (4) we derive that this situation occurs if ad equals bc . Moreover, kappa is not defined (*n.d.*) in the cases where both time series contain only '0's or '1's, as in such cases not only the numerator but also the denominator of (4) reduces to zero.

4.1.1.4 Classic Jaccard index

The Jaccard index was introduced by Jaccard (1901, 1912), to measure the ecological similarity of different geographical regions, based on the co-occurrence of specific species. It is calculated as:

$$J_A(X, Y) = \frac{a}{a+b+c} \quad (5)$$

The Jaccard index thus equals the proportion of time points at which both variables equal '1' over the proportion of time points at which at least one of them is shown. This means that the Jaccard index only depends on the co-occurrence of variables, but ignores their co-absence.

This measure may therefore be useful for behavioral science questions, for which the co-absence of variables is of less importance than their co-occurrence (Bodner, Bringmann, et al., in press; Brusco et al., 2019). For example, Main et al. (2016, p. 915) argue that they "do not wish to treat shared absence of a target emotion in two people as a kind of synchrony of that emotion." The co-absence of emotions and behaviors in micro-coded interaction data is indeed often a somewhat artificial result of assigning each coded event to a single coding category only, implying that the presence of one variable, automatically implies the absence of other variables (e.g., SPAFF, Coan & Gottman, 2007; LIFE, Hops et al., 1995). The Jaccard index ranges from 0 to 1 and is not defined if both time series have a relative frequency of 0.

4.1.1.5 Corrected Jaccard index

Like the proportion of agreement, the classic Jaccard measure (J_A) does not correct for chance agreement. Therefore, Bodner et al. (2019) developed a corrected Jaccard index (J_{Corr}), in which the classic Jaccard index is compared to an expected value (J_E), computed using the principles outlined in Albatineh & Niewiadomska-Bugaj (2011):

$$J_{Corr}(X, Y) = \frac{J_A - J_E}{1 - J_E} \quad (6)$$

J_E expresses the Jaccard value that we would expect if X and Y do not systematically co-occur. It only depends on the relative frequencies of X and Y :

$$J_E(X, Y) = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y} \quad (7)$$

Whereas a corrected Jaccard value of 0 implies that X and Y do not co-occur more than expected by chance, a negative value indicates that X and Y co-occur less than expected by chance. The corrected Jaccard is not defined if both time series have a relative frequency of 0 or of 1.

4.1.1.6 Odds ratio and log odds ratio

The odds ratio $OR(X, Y)$ and the log odds ratio $LOR(X, Y)$ are defined as

$$OR(X, Y) = \frac{ad}{bc} \quad (8)$$

$$LOR(X, Y) = \log \left(\frac{ad}{bc} \right). \quad (9)$$

The odds ratio ranges between 0 and +Infinity, with a value of 1 (i.e., $ad = bc$), indicating chance agreement. A value of +Infinity is observed, if b and/or c equals zero, implying that X or Y does not occur without the other (see also Bodner et al., 2020). The value is 0 when a and/or d equal zero, implying that X and Y do not co-occur or are not co-absent. In this cases, the value of the log odds ratio is -Infinity. The log odds ratio, therefore, ranges between -Infinity and +Infinity, with a value of zero indicating chance agreement. Finally, both indices are not defined if at least one of the variables has a relative frequency of 0 or 1.

4.1.1.7 Phi correlation coefficient

The phi correlation coefficient (Yule, 1912) equals the Pearson correlation coefficient computed on binary data. It can be calculated as:

$$r_\phi(X, Y) = \frac{ad - bc}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$$

The phi-correlation coefficient, therefore, has a value between -1 (perfect disagreement) and 1 (perfect agreement), with 0 indicating agreement on the chance level. Like the odds ratio and the log odds ratio, the formula of the phi correlation coefficient features a product in the denominator. As for them, variables with a frequency of 1 or 0 imply the phi value to be undefined. In contrast to those two measures, the phi correlation coefficient, however, never gets infinite.

Though the range in which the phi correlation coefficient is defined is narrower than that of Cohen's kappa (see Table 3 and appendix), some equalities between these two measures strike the eye. First, both Cohen's kappa and the phi correlation coefficient equals 0 if $ad = bc$ (if none of the variables has the frequency 0 or 1). Second, it can be derived that $r_\phi(X, Y)$ exactly equals $k(X, Y)$ whenever $p_1^X = p_1^Y$.

4.1.1.8 Other contingency measures

The discussed contingency measures are only a subset of all possible measures (see Warrens, 2008). Other measures have been proposed, such as Yule's Q (Bakeman et al., 1996; Bakeman & Quera, 2011) and the risk difference (Lloyd et al., 2016), the recurrence rate of cross-recurrence quantification analysis (Main et al., 2016) and Wampold's transformed kappa (Bakeman et al., 1996; Holloway et al., 1990). Measures that were developed for interrater reliability, like Gwet's AC (Gwet, 2014; Wongpakaran et al., 2013), Bangdiwala's B (Munoz & Bangdiwala, 1997) or Yule's Y (Yule, 1912), or measures developed for comparing partitions, like the Rand index (Rand, 1971) or the adjusted Rand Index (Hubert & Arabie, 1985) might also be suitable. In the Tutorial part, we will demonstrate how such alternative contingency measures can be added to the package.

4.1.2 Impact of the differences between the seven considered contingency measures

To investigate the impact of the differences between the seven contingency measures in practice, we calculated their values on real data. To this end, we analyzed 4860 time series pairs taken from the study from which also the Family Data (see Module 1) was taken. The data represents the interaction data of several different families. The variables have a prevalence ranging between 0 and .94 with a mean of .12.

Table 3 summarizes the conditions that lead to not defined (n.d.) or infinite (+Inf or -Inf) values in these 4860 variable pairs and their prevalence for the different contingency measures (as discussed in section 4.1.1). In the appendix, we discuss all potential cases that lead to not-defined or infinite values in more detail, also including those cases that are not shown in this data, for example, those for variables with prevalence 1 (see appendix Table A1, A2, A3).

Table 3

Which data characteristics lead to contingency values that are not defined (n.d.) or infinite(+Inf/-Inf), in the 4860 variable pairs taken from the family study

Contingency measure	Condition $p_1^X = 0$ and $p_1^Y = 0$	$p_1^X = 0$ or $p_1^Y = 0$	$b = 0$ and/or $c = 0$	$a = 0$ and/or $d = 0$
Proportion of agreement				
Classic Jaccard	n.d.			
Corrected Jaccard	n.d.			
Cohen's kappa	n.d.			
Phi correlation coefficient	n.d.	n.d.		
Odds ratio	n.d.	n.d.	+Inf	
Log odds ratio	n.d.	n.d.	+Inf	-Inf
Frequency	179	983	63	1144

We were also interested in how the different measures relate to each other. The values of the contingency measures, especially their means and standard deviations (Table 4), were quite different. As a direct comparison, therefore, was difficult, we investigated whether the rank order was comparable between measures by calculating the Spearman rank correlations across the 2491 binary variable pairs yielding defined and finite values for all contingency measure (2369 out of the 4860 variable pairs from the sample above, led to infinite or not defined values for at least one contingency measure; see Table 3). The corresponding scatter plot matrix and the distributions of the contingency values can be consulted in the appendix (Figure A1).

Table 4

Spearman rank order correlations between the contingency measures across the 2491 binary time series pairs that yielded defined and finite values for all contingency measures

Contingency measure	1	2	3	4	5	6	7
1 Proportion of agreement		.377	.648	.642	.656	.684	.684
2 Classic Jaccard			.850	.849	.853	.837	.837
3 Corrected Jaccard				1.000	.994	.967	.967
4 Cohen's kappa					.994	.964	.964
5 Phi correlation coefficient						.978	.978
6 Odds ratio							1.000
7 Log Odds ratio							
Mean(SD)	0.75 (.15)	0.15 (.17)	0.12 (.23)	0.09 (.17)	0.12 (.24)	12.8 (49.7)	0.7 (1.82)

Note. from the 4860 variable pairs of the sample above, 2369 variable pairs lead to infinite or non-defined values for at least one contingency measure (see Table 3).

Table 4 shows that Cohen's kappa, corrected Jaccard, and phi correlation coefficient have very high rank order correlations, whereas the proportion of agreement yields the most deviating ranking,

followed by the classic Jaccard. Figure 4 investigates the differences between kappa, the corrected Jaccard, and phi in more detail, by plotting their values as a function of the obtained kappa values. The figure reveals that the three indices coincide when kappa equals 0, but deviate elsewhere. Phi and kappa values are equal in some cases (e.g., when the relative frequencies of both variables equal each other), but in general phi yields higher absolute values. The corrected Jaccard, in contrast, yields less extreme values than kappa.

Figure 4

Relationship between Cohen's kappa, phi correlation coefficient and corrected Jaccard values

Note. Cohen's kappa, corrected Jaccard and phi correlation coefficient for 3698 pairs binary time series (1162 of the 4860 pairs of the original sample yielded not-defined values for at least one of the contingency measures; see Table 3). The triplets are sorted based on Cohen's kappa values.

4.1.3 From concurrent to temporal relations

So far, we only discussed concurrent bivariate relations. The temporal sequencing of variables can be used to investigate whether the presence of variable X at time point t is linked to the presence of variable Y one or more time points later, or vice versa. For instance, in coded interaction tasks the behavioral sequences between the interacting individuals are often studied (Bodner et al., 2018). Interestingly, such questions can be investigated by implementing the very same contingency measures, after appropriately lagging one of the two variables. For instance, to assess the strength of the association between X (at one time point) and Y (at the next time point), we calculate the contingency of X_t and Y_{t+1} , implying a lag of one on Y . Per pair (X, Y) , we always examine two temporal relations, one where only X is lagged and one where only Y is lagged; in both cases the same lag is used. This makes it, for example, possible to investigate whether both directions are significant or only one of them (or none).

One of the most pressing questions, however, is how to determine how large this lag should be. The answer to this question can be taken based on previous findings or the research hypothesis. When there are no clues, however, one can obtain a tentative answer by considering different lags and evaluating how the values of the contingency measure change across different lags, through the inspection of a contingency profile (based on the ideas laid out in Main et al., 2016). In Figure 5 two contingency profiles for the Family Data are plotted showing how the classical Jaccard index fluctuates across different lags. The contingency profile for the Jaccard association between ‘father happy’ and ‘adolescent happy’ (panel a), shows that the Jaccard value is maximal at a lag of 0 (dashed line), providing evidence of a concurrent association (e.g., they probably laugh a lot together). In panel b, the Jaccard value reaches its maximum at a lag of 4, suggesting a leader-follower behavioral sequence, where the adolescent’s anger leads to an angry reaction of the mother 4 seconds later. Although these contingency profiles shed interesting light on the temporal dependence structure, they also indicate that finding a one-lag-fits-all-associations-solution may not be very realistic. Therefore, it might make sense to apply the different indicated lags on the same data and compare the resulting networks, to shed light on which contingencies are concurrent and which are of a fast or slow-reacting nature (Van keer et al., 2019; Wilderjans et al., 2014).

Figure 5

Two Jaccard based contingency profiles for the Family Data.

Note. Whereas panel a provides evidence for a concurrent association (maximum at lag 0), panel b suggests a behavioral sequence, in which the maximum is reached if the angry behavior of the mother is lagged by four time points.

4.2 Tutorial

Using the Family Data, we first discuss the conMx-function that is provided to compute a **contingency matrix** and show how to visualize it in a heatmap using corplot (Wei & Simko, 2021). Second, we illustrate how to obtain contingency profiles. Finally, we explain how alternative contingency measures can be integrated into the package.

4.2.1 Basics of the conMx-function

The conMx-function takes the following **input** arguments:

- **data**: Raw time series data in a time-point-by-variable matrix. Before calculating the contingency values, the non-binary variables will automatically be removed using the conData-function (See Module1).
- **lag** (default lag=0, indicating co-occurrence of data) a not negative number, indicating the intervals for which the subsequent data shall be lagged. Lag=5 means that the contingency measure is calculated between all possible pairs X_t and Y_{t+5} (thus also between Y_t and X_{t+5}).
- **conFun**: The function used to calculate the contingency measure. For now, the classic Jaccard index (funClassJacc), corrected Jaccard (funCorrJacc), Cohen's kappa (funKappa), proportion of agreement (funPropAgree), odds ratio (funOdds) and log odds ratio (funLogOdds) and the phi correlation coefficient (funPhiCC) are included.

and yields a conMx-object as **output**, with two fields

- **\$value**, an V by V matrix, with V indicating the number of variables. If a lag larger than 0 is used, the rows of the asymmetric matrix indicate the leading variable, and the columns the following variable. If the lag equals zero, the matrix is symmetric.
- **\$para**, the parameters of the analyses, subdivided in the lag field (**\$lag**), the name of the contingency function (**\$funName**), and the names of the variables (**\$varNames**).

4.2.2 Calculating contingency matrices

Let us now take a look at the Family Data. We use a lag of 1 second to investigate the fast temporal sequencing of the emotional expressions, and the classic Jaccard measure to focus on the sequential co-occurrence of emotional reactions.

```
data(FamilyData)
conMx(FamilyData, lag=1, conFun=funClassJacc)

$value
      moanger faanger adanger modysph fadysph addysph mohappy fahappy adhappy
moanger 0.7872 0.0337 0.2607 0.0070 0.0000 0.0000 0.0131 0.0178 0.0233
faanger 0.0575 0.7778 0.0333 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
adanger 0.2869 0.0335 0.8566 0.0912 0.1204 0.0038 0.0473 0.1394 0.0185
modysph 0.0070 0.0000 0.0952 0.8308 0.1441 0.1806 0.0000 0.0000 0.0000
fadysph 0.0000 0.0000 0.1319 0.1835 0.8026 0.0106 0.0526 0.0129 0.0387
addysph 0.0000 0.0000 0.0038 0.1154 0.0106 0.6562 0.0426 0.0268 0.0085
mohappy 0.0000 0.0000 0.0612 0.0076 0.0448 0.0538 0.7654 0.2403 0.3016
fahappy 0.0178 0.0105 0.1233 0.0000 0.0130 0.0364 0.2231 0.8144 0.2245
adhappy 0.0000 0.0000 0.0122 0.0000 0.0526 0.0085 0.3252 0.2329 0.7864

$para
$para$lag
[1] 1

$para$funName
[1] "Classic Jaccard"

$para$varNames
[1] "moanger" "faanger" "adanger" "modysph" "fadysph" "addysph" "mohappy" "fahappy"
"adhappy"
```

To visualize the contingency matrix as a heatmap, we make use of the `corrplot`-function from the R package `corrplot` (Wei & Simko, 2021). The name of the contingency measure used to compute contingencies is added with a `mtext` to the plot after extracting it from the `conMx$para$funName` field.

```
if (!require(corrplot)) install.packages('corrplot')
library(corrplot)

conMx <- ConMx(FamilyData, lag=1, conFun=funClassJacc)

corrplot(conMx$value, method='color', addCoef.col='black',
         tl.col="black", tl.srt=45)

mtext(side=1, line=2, paste0("a) ", conMx$para$funName))
```

Panel a in Figure 6 shows the Jaccard contingency matrix. To find the contingency between ‘adolescent happy’ and ‘mother happy’ one second later we look for the $J(\text{adhappy}, \text{mohappy})$ value (in the last row and the seventh column) which equals .33. The other panels in Figure 6 provide the contingency matrices for Cohen’s kappa, the corrected Jaccard, and the phi correlation coefficient.

Figure 6

Heatmaps of the contingency matrices for different measures

Note. Heatmaps of the contingency matrices for a) classic Jaccard, b) corrected Jaccard, c) Cohen’s kappa, and d) the phi correlation coefficient, for the Family Data, using a lag of one.

4.2.3 Calculating and visualizing a contingency profile

To assess which lag is most suitable for investigating the temporal dependencies, we make use of contingency profiles (see Figure 5). A contingency profile plots the contingency between two variables for different lags. We can make this plot using the `conProf`-function, which needs as **input** the data (**data**) and the contingency measure of interest (**conFun**). We also need to specify the maximum lag of interest (**maxlag**). The **output** is a `conProf`-object that consists of a **\$value** that includes $(\text{maxlag} \times 2 + 1)$ contingency matrices for the different lags (ranging from $-\text{maxlag}$ over zero to $+\text{maxlag}$), the parameters (**\$para**) containing the maximum lag (`$maxLags`), the name of the contingency function (`$funName`) and the names of the variables (`$varNames`). The contingency profile is drawn using the following code²:

```
x <- conProf(FamilyData[7:9], 10, conFun=funcClassJacc)
plot(x)
```

The contingency profiles are arranged like a matrix. For instance, the second contingency profile in the first row pertains to the contingency between `mohappy` and `fahappy`. Whereas the positive lags indicate that `mohappy` leads and `fahappy` follows, the negative lags represent the values for the reverse direction (i.e., `fahappy` followed by `mohappy`). Therefore, the two off-diagonal plots per variable pair are mirrored versions of one another. The profiles on the diagonal are the auto-profiles, which reach their maximum at a lag of 0.

Figure 7

Contingency profile for the happy emotional expressions of mother, father, and adolescent

² The plot function here refers to the `plot.conProf` functions which is an extension of the generic `plot` function. When applying `plot()` to a `conProf` object (i.e., the output of the `conProf` function), R will automatically call `plot.conProf`.

4.2.4 Experts' excursion: How to integrate another contingency measure.

The functions that are already included in the package cover a wide range of possibilities. However, a specific research question (e.g., an extension to existing research) might ask for a specific contingency measure that is not yet included. The ConNEcT package allows to include other contingency measures. We will showcase this by including the calculation of Gwet's AC1 (Gwet, 2014; Wongpakaran et al., 2013), an interrater agreement measure for binary data, that corrects for chance agreement. In the first step, the calculation of the measure should be specified, either manually or by calling a function. Here we make use of the function `gwet.ac1.raw` of the `irrCAC`-package (Gwet, 2019). The value for Gwet's AC can be retrieved by `gwet.ac1.raw(x)$est$coeff.val` and is stored in the `$value` field. Second, the function must be given a name, both in the `$funName` field and in the title. Finally, the function should be saved in an R -file using the same name (`funGwet.R`).

```
funGwet<- function(vec1, vec2){
  #Calculate the value
  value<- gwet.ac1.raw(cbind(vec1,vec2))$est$coeff.val
  funName <- "Gwet's AC1"
  result <- list(value,funName)
  names(result)<-c('value','funName')
  return(result)
}
```

The function needs to be loaded using `source()`, and the dependencies installed and loaded before running any function on the newly created contingency measures function.

```
if (!require(irrCAC)) install.packages('irrCAC')
library(irrCAC)

source(funGwet.R)

conMx(FamilyData,conFun=funGwet)
```

5 Module 3: Testing Significance

5.1 Theory

Many network methods prune network edges to avoid that further investigations are influenced by links of which the value is mainly an artifact of the modeling technique (e.g., Epskamp & Fried, 2018). This is often achieved through a regularization approach (e.g., Bulteel et al., 2016b; Kuismin & Sillanpää, 2017; Lafit et al., 2019). Implementing such approaches is not possible, however, when no modeling approach is used. It might nevertheless be interesting to prune a network that relies on simple bivariate relations. One alternative strategy that one might think of is to simply prune edges based on the contingency strength, using some overall threshold value. We do not recommend this strategy, because contingency strength may strongly depend on the relative frequency and auto-dependence of the variables.

Figure 8 (first row) illustrates the relationship between the contingency measures and the relative frequency by plotting the contingency strength for two independently generated variables without auto-dependence as a function of their relative frequency. We observe a U-shaped relation for the proportion of agreement and an upward trend for the classic Jaccard. The mean of the chance corrected contingency measures-- kappa, corrected Jaccard, phi – remains close to zero, as desired. While the mean of the log odds ratio values also remains stable, their observed range is much higher for the extreme relative frequencies. The second to fourth rows of Figure 8 further put the spotlight on the range of the obtained values, now focusing on auto-dependence. These rows show the distribution of the obtained values for two independent variables with a relative frequency of .5 with raising auto-dependence in each variable, increasing from none (second row) over moderate (third row) to strong (fourth row). The range of the obtained values increases for higher levels of auto-dependence. This makes sense as auto-dependence may artificially install co-occurrence since variables that co-occur at least once and contain longer periods of ones are likely to co-occur on several adjacent time points.

Figure 8

Dependence of contingency values on the relative frequency and serial dependence.

Note. The first row plots **the contingency values** as a function of relative frequencies, with the different lines representing the mean (solid line), ± 1 sd (dashed lines), and min/max (dotted lines). The values are calculated based on simulated, independent variables X and Y ($p_1^X = p_1^Y$ range between 0.05 and 0.95; each pair contains 500 time points) without auto-dependency ($p_1^X = p_{1|1}^X = p_{1|0}^X = p_1^Y = p_{1|1}^Y = p_{1|0}^Y$). Row 2-4: Distributions of the contingency measures. While the relative frequency of X and Y always equals .5, their auto-dependency varies across the rows, in that in the second row $p_{1|1} = p_{1|0} = 0.5$ (light-grey), in the third row, $p_{1|1} = 0.8$ (middle-grey), and in the bottom row $p_{1|1} = 0.95$ (black). Each panel is based on 100 replicates of the pairwise independent variables X and Y (each consisting of 500 time points) on which contingency values were calculated for all 10000 possible pairs.

Therefore, we propose to prune network edges using the non-parametric significance testing procedure introduced and extensively validated by Bodner et al. (in press). This procedure investigates whether a certain contingency value is bigger than would be expected by chance, given the relative frequency and auto-dependency of the data. In what follows we briefly summarize the main principles of the test and explain the different variants that are included in ConNEcT.

5.1.1 Basic principles

The significance test consists of five steps, depicted in Figure 9. After collecting the time series data (step 1) and calculating the chosen contingency measure on a pair of variables (step 2), N samples or replicates of surrogate variable pairs are generated (step 3), under the null hypothesis that both variables are independent. This generation mechanism of the surrogate data retains the most important characteristics of the separate original variables (i.e., relative frequency and serial dependence), but breaks down the pairwise interdependence between the two variables, to be in line with the null hypothesis. The two generation mechanisms implemented in ConNEcT are discussed in the following subsections. Next, the same contingency measure is computed for each of the N by N surrogate variable pairs, yielding a sampling distribution of the contingency measure under the null hypothesis (step 4). In the fifth and last step, we compare this sampling distribution of the contingency values for the surrogate data with the value obtained in step 2. We consider the latter to be significantly stronger if it exceeds a certain percentile of the distribution, with the chosen percentile reflecting the adopted significance level.

Figure 9

Schematic overview of the significance test

5.1.2 Permutation-based data generation

As illustrated by Figure 10, the permutation-based approach cuts the original variables into ten roughly equal-sized segments of adjacent time points and subsequently permutes these segments (Moulder et al., 2018). The variables are permuted independently. As a result, the pairwise association between them is broken down, while the relative frequency is left untouched and the serial dependence is also largely kept because sequences within the variables are often moved as a whole.

Figure 10

Schematic representation of the permutation-based data generation

Note. The two observed time series (Variable 1 and Variable 2) are first cut in ten rather equally sized segments. These segments are randomly rearranged per variable yielding 100 permuted versions. To distinguish the solutions, we colored the second, fourth, sixth, and 10th segment in different shades of gray. The contingency measure of interest is computed for each pair of permuted variables.

5.1.3 Model-based data generation

In the model approach, the surrogate data is generated by simulating new data using characteristics of the original data. Specifically, the score for the first time point of the variable X is sampled from a Bernoulli distribution using the relative frequency p_1^X as parameter. Next, all other scores X_t are drawn from a Bernoulli distribution using the observed conditional probability $p_{1|0}^X$ if $X_{t-1}=0$ or the conditional probability $p_{1|1}^X$ if $X_{t-1}=1$. The scores on Y are generated correspondingly. Note that the relative frequencies and auto-dependence of the thus generated data may differ somewhat from the intended values due to sampling fluctuations.

5.1.4 Differences between the two data generating mechanisms

Both generation mechanisms often, but not always lead to the same test result. These differences can be understood by realizing that the permutation-based test keeps the relative frequency exactly the same for all surrogate data, whereas the model-based test generated surrogate data show some variation in relative frequency and auto-dependence. On the one hand, the choice of which test to use should therefore be based on whether or not we consider the relative frequency of the observed data to be fixed or variable. On the other hand, the choice may also have practical implications. The model-based generation will yield a wider range of contingency values for the surrogate data, but also a smoother sampling distribution, due to the variation in relative frequency across the surrogate samples, as is illustrated in Figure 11. Yet, in contrast to the permutation-based generation, this feature may generate surrogate data without observations for variables with a low relative frequency. If both variables, however, have a relative frequency of 0, many contingency measures cannot be calculated (see Module 2). It is therefore good practice to take a critical look at the sampling distributions of the significance test.

Figure 11

Comparison of the sampling distributions

Note. Sampling distributions of a) the model-based and b) the permutation-based data generation, using the classic Jaccard to quantify the contingency (lag=1) between the variables mother's positive and Child's positive behavior from the Attachment Data.

5.2 Tutorial

5.2.1 Basics of the conTest function

Both significance tests are implemented in the conTest-function. Like the conMx-function, this function requires the specification of data, lag, conFun (see Module 2). Moreover, one should also set the following parameters:

- **typeOfTest**: specifies whether a model-based ('model') or permutation-based ('permut'; default) data generation mechanism is used
- **adCor**: Logical parameter indicating whether (TRUE) or not (FALSE) the test should correct for auto-dependency, with TRUE being the default. If this parameter is set to FALSE, the test does not correct for serial dependence, because the surrogate data are generated based on the relative frequency only or by using segments of size 1. Although Bodner et al. (2020) showed that using these tests with time series data leads to an inflation of the type 1 error, we provide the option for comprehensiveness.
- **nBlox**: the number of segments used in the permutation-based test; the default value of this parameter equals 10
- **nReps** indicates the number of replicates or surrogate samples that are generated for each variable (default=100).

The output of the function is an S3 object of class 'conTest', containing:

- **allLinks**: contingency values (see conMx output)
- **percentile**: percentile of the sampling distribution where the observed contingency value is located
- **pValue**: p-value for the one-sided significance test calculated as 1 minus the percentile.
- **para**: the parameter settings for
 - **typeOfTest**
 - **adCor**
 - **nBlox**

- **nReps**
- **funName**
- **lag**
- **varNames**
- **samples:** the generated surrogate samples per \$variable1Name\$variable2Name combination

5.2.2 Applying the significance test

We will illustrate the usage of the function employing the Symptom Data on the not-lagged data (default lag=0). We apply the permutation-based test (typeOfTest = 'permut'), correcting for serial dependence (default adCor = TRUE) to the observed classic Jaccard values (conFun = funClassJacc). For each variable in the observed data set 100 replicates (nReps=100) of surrogate data will be generated. On all possible pairs of the surrogate data, the contingency measures are calculated, resulting in a sampling distribution consisting of 10.000 values. From the output test.result, we retrieve the classic Jaccard values in the observed data (test.result\$allLinks) and the one-sided upper p-value (test.result\$pValue).

```
data(SymptomData)

test.result <- ConTest(SymptomData, conFun=funClassJacc,
                      typeOfTest='permut', nBlox=10, nReps=100)

test.result$allLinks
test.result$pValue
```

```
> round(test.result$allLinks,4)
      Core Energy Eat Sleep Motor Guilt Cogn Death
Core   1.0000 0.8058  0 0.7372 0.7372 0.5794 1.0000 0.8411
Energy 0.8058 1.0000  0 0.5912 0.5912 0.3925 0.8058 0.6542
Eat    0.0000 0.0000 NaN 0.0000 0.0000 0.0000 0.0000 0.0000
Sleep  0.7372 0.5912  0 1.0000 0.8881 0.4672 0.7372 0.6715
Motor  0.7372 0.5912  0 0.8881 1.0000 0.4672 0.7372 0.6715
Guilt  0.5794 0.3925  0 0.4672 0.4672 1.0000 0.5794 0.6327
Cogn   1.0000 0.8058  0 0.7372 0.7372 0.5794 1.0000 0.8411
Death  0.8411 0.6542  0 0.6715 0.6715 0.6327 0.8411 1.0000

> round(test.result$pvalue,4)
      Core Energy Eat Sleep Motor Guilt Cogn Death
Core   0.0100 0.0000  1 0.1799 0.0638 0.0034 0.0000 0.0000
Energy 0.0000 0.0100  1 0.2886 0.1427 0.2650 0.0001 0.0066
Eat    1.0000 1.0000 NaN 1.0000 1.0000 1.0000 1.0000 1.0000
Sleep  0.1799 0.2886  1 0.0120 0.1903 0.3536 0.1901 0.1839
Motor  0.0638 0.1427  1 0.1903 0.0102 0.3072 0.0641 0.0997
Guilt  0.0034 0.2650  1 0.3536 0.3072 0.0100 0.0033 0.0003
Cogn   0.0000 0.0001  1 0.1901 0.0641 0.0033 0.0100 0.0000
Death  0.0000 0.0066  1 0.1839 0.0997 0.0003 0.0000 0.0100
```

From this output, we may, for example, conclude that the concurrent contingency between Guilt and Death has a Jaccard of value .63, which is significant with a p-value of .0003³. The function returns the exact p-value, without correction for multiple testing, allowing the user to implement a multiple testing correction of choice.

5.2.3 Taking a closer look at the sampling distribution

As was already mentioned above, it is good practice to critically inspect the obtained sampling distribution. In our example, we might be interested in the concurrent relationships between Energy, Guilt, and Death, implying that we want to test three observed contingency values. To plot the

³ The p-value depends on the sampling distribution and may therefore slightly differ when the significance test is run several times, using different seeds.

associated matrix of sampling distributions, we first generate the corresponding `conTest` object. Second, we apply the `hist.conTest`-function⁴. In the case of concurrent data, the distributions in the upper triangle of the matrix are exactly the same as those in the lower triangle for lagged data, they differ of course. By default, the 95% percentile is added to each histogram as a dashed line. Other percentiles can be requested by specifying the parameter `signLev`. The observed contingency value is added as a full gray line.

```
test.result2 <- conTest(SymptomData[,c(2,6,8)], conFun=funClassJacc,
                        typeOfTest='permut', nBlox=10, nReps=100)
hist(test.result2, col='darkolivegreen2')
```

Figure 12

Sampling distributions of the pairwise contingencies

Note. Sampling distributions of pairwise concurrent contingencies between Energy, Guilt, and Death, from the Symptom Data, quantified using the classic Jaccard. The permutation-based test used 100 samples/replications.

⁴ The function `hist.conTest` is an extension of the generic `hist`-function. When applying `hist()` to an object of the class `conTest` (i.e., the output of the `conTest`-function), R will automatically call `hist.conTest`.

6 Module 4: Networks

6.1 Theory

Up to now, we have examined data characteristics, quantified concurrent and temporal relationships between the variables over time and investigated whether these relationships are significant. This final module focuses on depicting these results as a network. We will point towards some advantages of collecting the bivariate relations in a network and give some ideas about how the network could be analyzed.

6.1.1 The added value of drawing a network

The variables under consideration constitute the nodes of the ConNEcT networks, with the size reflecting their relative frequencies (Module 1). The edges between the nodes visualize the strength of the obtained contingency values for the different variable pairs (Module 2). Studying concurrent contingencies results in a network with undirected links, while focusing on temporal sequences leads to a network with directed links. Networks may include all contingency values or only the significant ones (Module 3). Networks are thus a perfect way to integrate all ConNEcT analyses in one plot.

Networks make it easier to discern contingency patterns that are sometimes difficult to spot in contingency matrices or heatmaps. Figure 13 illustrates this by showing the temporal sequences using a heatmap as well as a network. The strength of the sequencing (lag=1) was quantified using a corrected Jaccard. Positive values are depicted with blue full arrows and negative values with brown dashed arrows. The positive loops between negative child behavior (Cneg) and negative behavior of the mother (Mneg), between positive child behavior (Cpos) and positive maternal behavior (Mpos), and between positive child behavior (Cpos) and working on the task together (Togth) are easily traced in the network, whereas this is harder in the heatmap.

Figure 13

Visibility of contingency relations comparing a heatmap and a network figure

Note. Contingency values represented in a) a heatmap and b) a network figure. Contingency values are calculated using corrected Jaccard with a lag of one. Node size is adapted to relative frequency. Saturation of the edges is proportional to the value. Blueish full line arrows indicate positive Jaccard values, brownish dashed arrows negative values. Significant links are indicated with * ($p < .05$).

6.1.2 Network psychometrics

Networks can be described in various ways. Multiple descriptive measures have been put forward, such as the size of a network (i.e., the number of nodes) or centrality measures (see Epskamp et al., 2012). The latter measures have gained a lot of attention, especially in psychopathological symptom

networks. As discussed by Bringmann et al. (2019), the interpretation of these measures is, however, not as straightforward as it seems.

Some authors (e.g., Golino & Epskamp, 2017) have suggested screening the network for meaningful subgraphs. Subgraphs are subsets of the network, containing nodes and the links that connect them. Interesting are dense subgraphs, in which the nodes are all strongly interconnected, while the connections between the different subgraphs are then less strong. Indeed, the occurrence of clear subgraphs might reveal the underlying dimensionality of the data (Golino & Epskamp, 2017). The symptom network in Figure 1, for instance, has a size of 8 and falls apart into four components⁵, one comprising five nodes that co-occur, and the other three pertaining to single nodes. In the affective family network in Figure 14, the happy behaviors of all family members seem to form a dense subgraph. For the other non-zero connections it is difficult to discern which belong to a dense subgraph and which are more isolated. In the tutorial part, we will use this example to explain, how these dense subgraphs can be identified with a clustering method. Specifically, we will use the cluster walktrap algorithm (Pons & Latapy, 2005) from the igraph package (Csardi & Nepusz, 2006).

Figure 14

Heatmap and network of the Family Data

Note. Contingencies are calculated using the classic Jaccard with a lag of one.

6.2 Tutorial

All the analysis steps that were explained in the previous modules (lagging the data, calculating contingencies, and testing for significance) can be executed separately, but they can also be executed at once using the conNECT function, which additionally yields a network.

6.2.1 The conNECT function

The conNECT function has the same input arguments as the ConTEsT function (Module 3), the conMx function (Module 2) and the conData function (Module 1): **data**, **lag**, **conFun**, **typeOfTest**, **adCor**, **nBlox**, **nReps**. On top of that, one should specify whether the significance test should be executed (**test=TRUE**; default: FALSE), and if so, with which significance level (**signLev**; default=0.05). The function returns an S3 object of class 'conNECT', comprising the following fields:

- **\$allLinks**: The obtained contingency value matrix

⁵ Components are subgraphs that are totally separated from each other.

- **\$signLinks**: A contingency value matrix that only includes the significant contingencies; all other contingency values are set to zero (if no significance test is executed this matrix contains only NAs)
- **\$pValue**: A matrix holding the p-values for the one-sided significance test (if no significance test is executed, all p-values are set to NA)
- **\$para (Parameters)**: Saving the settings of \$lags, \$test, \$typeOfTest, \$adCor \$nBlox, \$nReps, \$funName, \$varNames
- **\$probs**: a table containing the relative frequencies and conditional probabilities of all variables (see Module 1).

6.2.2 Example

We show the usage of the conNEcT function by applying it to the Family Data. We calculate the classic Jaccard (conFun=funClassJacc) on lagged data (lag=1; default: lag=0) and execute a permutation-based significance test (test=TRUE and typeOfTest='permut', default) that accounts for serial dependence (adCor = TRUE, default) using 10 Segments (nBlox=10, default) and 100 replications (nReps=100, default) with a significance level of 5% (signLev=0.05, default).

```
data(FamilyData)
conNEcT(FamilyData, lag=1, conFun=funClassJacc, test=TRUE)
```

```
$allLinks
      moanger faanger adanger modysph fadysph addysph mohappy fahappy adhapp
moanger 0.7872 0.0337 0.2607 0.0070 0.0000 0.0000 0.0131 0.0178 0.0233
faanger 0.0575 0.7778 0.0333 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
adanger 0.2869 0.0335 0.8566 0.0912 0.1204 0.0038 0.0473 0.1394 0.0185
modysph 0.0070 0.0000 0.0952 0.8308 0.1441 0.1806 0.0000 0.0000 0.0000
fadysph 0.0000 0.0000 0.1319 0.1835 0.8026 0.0106 0.0526 0.0129 0.0387
addysph 0.0000 0.0000 0.0038 0.1154 0.0106 0.6562 0.0426 0.0268 0.0085
mohappy 0.0000 0.0000 0.0612 0.0076 0.0448 0.0538 0.7654 0.2403 0.3016
fahappy 0.0178 0.0105 0.1233 0.0000 0.0130 0.0364 0.2231 0.8144 0.2245
adhappy 0.0000 0.0000 0.0122 0.0000 0.0526 0.0085 0.3252 0.2329 0.7864
```

```
$signLinks
      moanger faanger adanger modysph fadysph addysph mohappy fahappy adhapp
moanger 0.7872      0 0.2607 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
faanger 0.0000      0 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
adanger 0.2869      0 0.8566 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
modysph 0.0000      0 0.0000 0.8308 0.0000 0.1806 0.0000 0.0000 0.0000
fadysph 0.0000      0 0.0000 0.0000 0.8026 0.0000 0.0000 0.0000 0.0000
addysph 0.0000      0 0.0000 0.0000 0.0000 0.6562 0.0000 0.0000 0.0000
mohappy 0.0000      0 0.0000 0.0000 0.0000 0.0000 0.7654 0.2403 0.3016
fahappy 0.0000      0 0.0000 0.0000 0.0000 0.0000 0.2231 0.8144 0.2245
adhappy 0.0000      0 0.0000 0.0000 0.0000 0.0000 0.3252 0.2329 0.7864
```

```
$pvalue
      moanger faanger adanger modysph fadysph addysph mohappy fahappy adhapp
moanger 0.0012 0.3609 0.0161 0.7582 1.0000 1.0000 0.9468 0.9767 0.8460
faanger 0.3111 0.0538 0.4391 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
adanger 0.0036 0.4496 0.0071 0.3296 0.2840 0.8711 0.9890 0.7450 1.0000
modysph 0.7602 1.0000 0.2733 0.0017 0.1922 0.0098 1.0000 1.0000 1.0000
fadysph 1.0000 1.0000 0.2250 0.1117 0.0066 0.6637 0.6010 0.8803 0.8083
addysph 1.0000 1.0000 0.9045 0.0865 0.7579 0.0026 0.3089 0.1697 0.8496
mohappy 1.0000 1.0000 0.9487 0.8948 0.6473 0.1882 0.0005 0.0016 0.0024
fahappy 0.9742 0.3779 0.8229 1.0000 0.8661 0.0925 0.0036 0.0008 0.0116
adhappy 1.0000 1.0000 1.0000 1.0000 0.7579 0.8325 0.0007 0.0056 0.0021
```

```
$para
$para$lag
[1] 1
```

```
$para$test
[1] TRUE
```

```
$para$typeOfTest
[1] "permut"
```

```

$para$adCor
[1] TRUE

$para$nBlox
[1] 10

$para$nReps
[1] 100

$para$funName
[1] "Classic Jaccard"

$para$varNames
[1] "moanger" "faanger" "adanger" "modysph" "fadysph" "addysph" "mohappy" "fahappy"
[9] "adhappy"

$probs
      rel.freq  p1|1  p1|0
moanger  0.1564 0.8810 0.0221
faanger  0.0149 0.8750 0.0019
adanger  0.4469 0.9247 0.0640
modysph  0.1117 0.9153 0.0126
fadysph  0.1285 0.8841 0.0150
addysph  0.0503 0.7778 0.0098
mohappy  0.1341 0.8611 0.0194
fahappy  0.1639 0.8977 0.0201
adhappy  0.1713 0.8804 0.0248

attr(,"class")
[1] "conNECT"

```

6.2.3 Plotting the network

A conNECT object can be plotted as a network by calling the `qgraph.conNECT`⁶ function. The plot shows each variable as a node. The node size is adapted to the relative frequency. Default only the significant links are shown (`signOnly=TRUE`, default)⁷; to display all links set `signOnly` to `FALSE`. Auto-loops are often uninformative and can be suppressed by adding `diag=F`. Since the `qgraph` function is taken from the R package `qgraph` (Epskamp et al., 2012), all features from `qgraph` can be used to optimize the plot (see examples for the networks in Figure 1, Figure 13 en Figure 14 in supplementary material)

```

FamNet <- conNECT(FamilyData, lag=1, conFun=funcClassJacc, test=T)
qgraph.conNECT(FamNet, signOnly=F, diag=F)

```

To look for clusters in a network, we can, for example, use the `cluster_walktrap`-function (Pons & Latapy, 2005) from the `igraph` package (Csardi & Nepusz, 2006). Our application of the function makes use of the `qgraph` and the `igraph` package which need to be installed first. Then we run the `conNECT` function on the data. Here we chose to rely on all links (not only the significant ones) and to remove the diagonals. Clustering the contingency matrix reveals that there are three clusters, each consisting of the three adjacent nodes.

```

if (!require(qgraph)) install.packages('qgraph')
library(qgraph)

```

⁶ Unfortunately, `qgraph` is not (yet) a generic function, which means that we cannot simply call `qgraph` with a `conNECT` object to call `qgraph.conNECT`.

⁷ If the significance test had not been called when generating the `conNECT` function (`test=FALSE`), but the plot opts for only significant links option (`signOnly=TRUE`), a warning message is displayed.

```

if (!require(igraph)) install.packages('igraph')
library(igraph)

FamNet <- conNECT(FamilyData, lag=1, conFun=funClassJacc, test=T)
Links <- FamNet$allLinks
diag(Links) <- 0
Graph <- as.igraph(qgraph(Links, DoNotPlot=TRUE))
CWT <- cluster_walktrap(Graph)

```

CWT

IGRAPH clustering walktrap, groups: 3, mod: 0.32

```

+ groups:
  $1
  [1] 1 2 3

  $2
  [1] 4 5 6

  $3
  [1] 7 8 9

```

As we might consider this result slightly suboptimal in that we still have to look up the names of the variables, we might be tempted to add the variable names in an automated way. For example with the following code:

```

index <- unique(CWT$membership)
groups <- vector(mode = "list", length = length(index))
groupnames <- c()

for(i in index){
  numbers.temp <- which(CWT$membership==i)
  groups[[i]] <- FamNet$para$varNames[numbers.temp]
  groupnames <- c(groupnames, paste0("group", i))
}

names(groups) <- groupnames

```

```

> groups
$group1
[1] "moanger" "faanger" "adanger"

$group2
[1] "modysph" "fadysph" "addysph"

$group3
[1] "mohappy" "fahappy" "adhappy"

```

7 Conclusions

We introduced the R-package ConNECT that implements the contingency measures based network approach for binary intensive longitudinal data. We showed in four modules (1) how the data can be explored, (2) how to compute pairwise contingencies among the variables, (3) how to investigate the significance of these contingency values, and (4) how to plot them in a network. Additionally, we gave first answers to some open questions: what are the similarities and differences of the included contingency measures, should the data be lagged, and if so, how to get an idea of the appropriate lag, and how to detect patterns in the final network.

8 References

- Albatineh, A. N., & Niewiadomska-Bugaj, M. (2011). Correcting Jaccard and other similarity indices for chance agreement in cluster analysis. *Advances in Data Analysis and Classification*, 5(3), 179–200. <https://doi.org/10.1007/s11634-011-0090-y>
- Bakeman, R., McArthur, D., & Quera, V. (1996). Detecting group differences in sequential association using sampled permutations: Log odds, kappa, and phi compared. *Behavior Research Methods, Instruments, & Computers*, 28(3), 446–457. <https://doi.org/10.3758/BF03200524>
- Bakeman, R., & Quera, V. (2011). *Sequential analysis and observational methods for the behavioral sciences*. Cambridge University Press.
- Bodner, N., Bosmans, G., Sannen, J., Verhees, M., & Ceulemans, E. (2019). Unraveling middle childhood attachment-related behavior sequences using a micro-coding approach. *PLOS ONE*, 14(10), e0224372. <https://doi.org/10.1371/journal.pone.0224372>
- Bodner, N., Bringmann, L., Tuerlinckx, F., De Jonge, P., & Ceulemans, E. (in press). ConNEt: A novel network approach for investigating the co-occurrence of binary psychopathological symptoms over time. *Psychometrika*. <https://doi.org/10.1007/s11336-021-09765-2>
- Bodner, N., Kuppens, P., Allen, N. B., Sheeber, L. B., & Ceulemans, E. (2018). Affective family interactions and their associations with adolescent depression: A dynamic network approach. *Development and Psychopathology*, 30(4), 1459–1473. <https://doi.org/10.1017/S0954579417001699>
- Bodner, N., Tuerlinckx, F., Bosmans, G., & Ceulemans, E. (2020). Accounting for auto-dependency in binary dyadic time series data: A comparison of model- and permutation-based approaches for testing pairwise associations. *British Journal of Mathematical and Statistical Psychology*, bmsp.12222. <https://doi.org/10.1111/bmsp.12222>
- Bodner, N., Tuerlinckx, F., Bosmans, G., & Ceulemans, E. (in press). Accounting for auto-dependency in binary dyadic time series data: A comparison of model- and permutation-based

- approaches for testing pairwise associations. *British Journal of Mathematical and Statistical Psychology*, bmsp.12222. <https://doi.org/10.1111/bmsp.12222>
- Borsboom, D. (2008). Psychometric perspectives on diagnostic systems. *Journal of Clinical Psychology*, 64(9), 1089–1108. <https://doi.org/10.1002/jclp.20503>
- Borsboom, D. (2017). A network theory of mental disorders. *World Psychiatry*, 16(1), 5–13. <https://doi.org/10.1002/wps.20375>
- Borsboom, D., & Cramer, A. O. J. (2013). Network Analysis: An Integrative Approach to the Structure of Psychopathology. *Annual Review of Clinical Psychology*, 9(1), 91–121. <https://doi.org/10.1146/annurev-clinpsy-050212-185608>
- Boschloo, L., Borkulo, C. D. van, Rhemtulla, M., Keyes, K. M., Borsboom, D., & Schoevers, R. A. (2015). The Network Structure of Symptoms of the Diagnostic and Statistical Manual of Mental Disorders. *PLOS ONE*, 10(9), e0137621. <https://doi.org/10.1371/journal.pone.0137621>
- Brandt, M. J., Sibley, C. G., & Osborne, D. (2019). What Is Central to Political Belief System Networks? *Personality and Social Psychology Bulletin*, 45(9), 1352–1364. <https://doi.org/10.1177/0146167218824354>
- Bringmann, L. F., Elmer, T., Epskamp, S., Krause, R. W., Schoch, D., Wichers, M., Wigman, J. T. W., & Snippe, E. (2019). What do centrality measures measure in psychological networks? *Journal of Abnormal Psychology*, 128(8), 892–903. <https://doi.org/10.1037/abn0000446>
- Bringmann, L. F., Pe, M. L., Vissers, N., Ceulemans, E., Borsboom, D., Vanpaemel, W., Tuerlinckx, F., & Kuppens, P. (2016). Assessing Temporal Emotion Dynamics Using Networks. *Assessment*, 1073191116645909. <https://doi.org/10.1177/1073191116645909>
- 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>

- Brusco, M. J., Steinley, D., Hoffman, M., Davis-Stober, C., & Wasserman, S. (2019). On Ising models and algorithms for the construction of symptom networks in psychopathological research. *Psychological Methods*, 24(6), 735–753. <https://doi.org/10.1037/met0000207>
- Bulteel, K., Tuerlinckx, F., Brose, A., & Ceulemans, E. (2016a). Using Raw VAR Regression Coefficients to Build Networks can be Misleading. *Multivariate Behavioral Research*, 51(2–3), 330–344. <https://doi.org/10.1080/00273171.2016.1150151>
- Bulteel, K., Tuerlinckx, F., Brose, A., & Ceulemans, E. (2016b). Clustering Vector Autoregressive Models: Capturing Qualitative Differences in Within-Person Dynamics. *Frontiers in Psychology*, 7. <https://doi.org/10.3389/fpsyg.2016.01540>
- Bulteel, K., Tuerlinckx, F., Brose, A., & Ceulemans, E. (2018). Improved Insight into and Prediction of Network Dynamics by Combining VAR and Dimension Reduction. *Multivariate Behavioral Research*, 53(6), 853–875. <https://doi.org/10.1080/00273171.2018.1516540>
- Coan, J. A., & Gottman, J. M. (2007). Coan, J. A., & Gottman, J. M. (2007). The Specific Affect Coding System (SPAFF). In J. A. Coan & J. J. B. Allen (Eds.), (p. 267–285). Oxford University Press. In J. A. Coan & J. J. B. Allen, *Handbook of emotion elicitation and assessment* (pp. 267–285). Oxford University Press.
- Cohen, J. (1960). A Coefficient of Agreement for Nominal Scales. *Educational and Psychological Measurement*, 20(1), 37–46. <https://doi.org/10.1177/001316446002000104>
- Cramer, A. O. J., Borkulo, C. D. van, Giltay, E. J., Maas, H. L. J. van der, Kendler, K. S., Scheffer, M., & Borsboom, D. (2016). Major Depression as a Complex Dynamic System. *PLOS ONE*, 11(12), e0167490. <https://doi.org/10.1371/journal.pone.0167490>
- Cramer, A. O. J., Waldorp, L. J., Maas, H. L. J. van der, & Borsboom, D. (2010). Comorbidity: A network perspective. *Behavioral and Brain Sciences*, 33(2–3), 137–150. <https://doi.org/10.1017/S0140525X09991567>
- Csardi, G., & Nepusz, T. (2006). The igraph software package for complex network research. *InterJournal, Complex Systems*, 1695.

- Dalege, J., Borsboom, D., van Harreveld, F., van den Berg, H., Conner, M., & van der Maas, H. L. J. (2016). Toward a formalized account of attitudes: The Causal Attitude Network (CAN) model. *Psychological Review*, 123(1), 2–22. <https://doi.org/10.1037/a0039802>
- Dujardin, A., Santens, T., Braet, C., De Raedt, R., Vos, P., Maes, B., & Bosmans, G. (2016). Middle Childhood Support-Seeking Behavior During Stress: Links With Self-Reported Attachment and Future Depressive Symptoms. *Child Development*, 87(1), 326–340. <https://doi.org/10.1111/cdev.12491>
- Epskamp, S., Borsboom, D., & Fried, E. I. (2018). Estimating psychological networks and their accuracy: A tutorial paper. *Behavior Research Methods*, 50(1), 195–212. <https://doi.org/10.3758/s13428-017-0862-1>
- Epskamp, S., Cramer, A. O. J., Waldorp, L. J., Schmittmann, V. D., & Borsboom, D. (2012). qgraph: Network Visualizations of Relationships in Psychometric Data. *Journal of Statistical Software*, 48(4), 1–18.
- Epskamp, S., & Fried, E. I. (2018). A tutorial on regularized partial correlation networks. *Psychological Methods*, 23(4), 617–634.
- Epskamp, S., Waldorp, L. J., Möttus, R., & Borsboom, D. (2018). The Gaussian Graphical Model in Cross-Sectional and Time-Series Data. *Multivariate Behavioral Research*, 53(4), 453–480. <https://doi.org/10.1080/00273171.2018.1454823>
- Fried, E. I., Borkulo, C. D. van, Cramer, A. O. J., 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), 1–10. <https://doi.org/10.1007/s00127-016-1319-z>
- Golino, H. F., & Epskamp, S. (2017). Exploratory graph analysis: A new approach for estimating the number of dimensions in psychological research. *PLOS ONE*, 12(6), e0174035. <https://doi.org/10.1371/journal.pone.0174035>

- Gwet, K. L. (2014). *Handbook of inter-rater reliability: The definitive guide to measuring the extent of agreement among raters ; [a handbook for researchers, practitioners, teachers & students]* (4. ed). Advanced Analytics, LLC.
- Gwet, K. L. (2019). *IrrCAC: Computing Chance-Corrected Agreement Coefficients (CAC) version 1.0*.
<https://CRAN.R-project.org/package=irrCAC>
- Hamaker, E., Asparouhov, T., Brose, A., Schmiedek, F., & Muthén, B. (2018). At the Frontiers of Modeling Intensive Longitudinal Data: Dynamic Structural Equation Models for the Affective Measurements from the COGITO Study. *Multivariate Behavioral Research*, 53(6), 820–841.
<https://doi.org/10.1080/00273171.2018.1446819>
- Haslbeck, J. M. B., & Waldorp, L. J. (2020). mgm: Estimating Time-Varying Mixed Graphical Models in High-Dimensional Data. *ArXiv:1510.06871 [Stat]*. <http://arxiv.org/abs/1510.06871>
- Holloway, E. L., Wampold, B. E., & Nelson, M. L. (1990). Use of a paradoxical intervention with a couple: An interactional analysis. *Journal of Family Psychology*, 3(4), 385–402.
<http://dx.doi.org/10.1037/h0080552>
- Hops, H., Biglan, A., Tolman, A., Arthur, J., & Longoria, N. (1995). *Living in Family Environments (LIFE) coding system: (Reference manual for coders)*. Eugene, OR: Oregon Research Institute.
- Hosenfeld, B., Bos, E. H., Wardenaar, K. J., Conradi, H. J., van der Maas, H. L. J., Visser, I., & de Jonge, P. (2015). Major depressive disorder as a nonlinear dynamic system: Bimodality in the frequency distribution of depressive symptoms over time. *BMC Psychiatry*, 15(1), 222.
<https://doi.org/10.1186/s12888-015-0596-5>
- Hubert, L., & Arabie, P. (1985). Comparing partitions. *Journal of Classification*, 2(1), 193–218.
<https://doi.org/10.1007/BF01908075>
- Isvoranu, A.-M., Borsboom, D., van Os, J., & Guloksuz, S. (2016). A Network Approach to Environmental Impact in Psychotic Disorder: Brief Theoretical Framework. *Schizophrenia Bulletin*, 42(4), 870–873. <https://doi.org/10.1093/schbul/sbw049>

- Jaccard, P. (1901). Étude comparative de la distribution florale dans une portion des Alpes et des Jura. *Bulletin de La Société Vaudoise Des Sciences Naturelles*, 37, 547–579.
- Jaccard, P. (1912). The Distribution of the Flora in the Alpine Zone. *New Phytologist*, 11(2), 37–50.
<https://doi.org/10.1111/j.1469-8137.1912.tb05611.x>
- Kuismin, M. O., & Sillanpää, M. J. (2017). Estimation of covariance and precision matrix, network structure, and a view toward systems biology: Estimation of covariance and precision matrix, network structure, and a view toward systems biology. *Wiley Interdisciplinary Reviews: Computational Statistics*, 9(6), e1415. <https://doi.org/10.1002/wics.1415>
- Lafit, G., Tuerlinckx, F., Myin-Germeys, I., & Ceulemans, E. (2019). A Partial Correlation Screening Approach for Controlling the False Positive Rate in Sparse Gaussian Graphical Models. *Scientific Reports*, 9(1), 17759. <https://doi.org/10.1038/s41598-019-53795-x>
- Lloyd, B. P., Yoder, P. J., Tapp, J., & Staubitz, J. L. (2016). The relative accuracy and interpretability of five sequential analysis methods: A simulation study. *Behavior Research Methods*, 48(4), 1482–1491. <https://doi.org/10.3758/s13428-015-0661-5>
- Main, A., Paxton, A., & Dale, R. (2016). An Exploratory Analysis of Emotion Dynamics Between Mothers and Adolescents During Conflict Discussions. *Emotion*, 16(6), 913–928.
<https://doi.org/10.1037/emo0000180>
- Moulder, R. G., Boker, S. M., Ramseyer, F., & Tschacher, W. (2018). Determining synchrony between behavioral time series: An application of surrogate data generation for establishing falsifiable null-hypotheses. *Psychological Methods*, 23(4), 757–773.
<https://doi.org/10.1037/met0000172>
- Munoz, S. R., & Bangdiwala, S. I. (1997). Interpretation of Kappa and B statistics measures of agreement. *Journal of Applied Statistics*, 24(1), 105–112.
<https://doi.org/10.1080/02664769723918>

- Pons, P., & Latapy, M. (2005). Computing Communities in Large Networks Using Random Walks. In pınar Yolum, T. Güngör, F. Gürgen, & C. Özturan (Eds.), *Computer and Information Sciences—ISCIS 2005* (pp. 284–293). Springer. https://doi.org/10.1007/11569596_31
- Rand, W. M. (1971). Objective Criteria for the Evaluation of Clustering Methods. *Journal of the American Statistical Association*, 66(336), 846–850.
<https://doi.org/10.1080/01621459.1971.10482356>
- Sheeber, L. B., Kuppens, P., Shortt, J. W., Katz, L. F., Davis, B., & Allen, N. B. (2012). Depression is associated with the escalation of adolescents' dysphoric behavior during interactions with parents. *Emotion*, 12(5), 913–918. <https://doi.org/10.1037/a0025784>
- van Borkulo, C. D., Borsboom, D., Epskamp, S., Blanken, T. F., Boschloo, L., Schoevers, R. A., & Waldorp, L. J. (2014). A new method for constructing networks from binary data. *Scientific Reports*, 4. <https://doi.org/10.1038/srep05918>
- Van keer, I., Ceulemans, E., Bodner, N., Vandesande, S., Van Leeuwen, K., & Maes, B. (2019). Parent-child interaction: A micro-level sequential approach in children with a significant cognitive and motor developmental delay. *Research in Developmental Disabilities*, 85, 172–186.
<https://doi.org/10.1016/j.ridd.2018.11.008>
- Warrens, M. J. (2008). On Association Coefficients for 2×2 Tables and Properties That Do Not Depend on the Marginal Distributions. *Psychometrika*, 73(4), 777–789.
<https://doi.org/10.1007/s11336-008-9070-3>
- Wei, T., & Simko, V. (2021). *R package 'corrplot': Visualization of a Correlation Matrix. (Version 0.88)*.
<https://github.com/taiyun/corrplot>
- Wilderjans, T. F., Lambrechts, G., Maes, B., & Ceulemans, E. (2014). Revealing interdyad differences in naturally occurring staff reactions to challenging behaviour of clients with severe or profound intellectual disabilities by means of Clusterwise Hierarchical Classes Analysis (HICLAS): Clusterwise HICLAS to detect interdyad differences. *Journal of Intellectual Disability Research*, 58(11), 1045–1059. <https://doi.org/10.1111/jir.12076>

- Wongpakaran, N., Wongpakaran, T., Wedding, D., & Gwet, K. L. (2013). A comparison of Cohen's Kappa and Gwet's AC1 when calculating inter-rater reliability coefficients: A study conducted with personality disorder samples. *BMC Medical Research Methodology*, 13(1), 61. <https://doi.org/10.1186/1471-2288-13-61>
- Yule, G. U. (1912). On the Methods of Measuring Association Between Two Attributes. *Journal of the Royal Statistical Society*, 75(6), 579. <https://doi.org/10.2307/2340126>

9 Appendix:

9.1 Discussion of the cases that lead to undefined or non-finite values

We will now investigate in which cases the contingency values of X and Y will be undefined or non-finite. To this end, we will use the following equations and facts:

- (1) $p_1^x = a + b$
- (2) $p_0^x = d + c$
- (3) $p_1^y = a + c$
- (4) $p_0^y = b + d$

p_1^x and p_1^y indicate the prevalence of variable X and Y respectively, p_0^x and p_0^y their complements. a indicates the proportion of time points where both variables are present, etc. (see Table 2). p_1^x , p_1^y , p_0^x , p_0^y , a , b , c and d are all probabilities, and thus range between 0 and 1. As a consequence (see equation 1), $p_1^x = 0$ implies that $a = 0$ and $b = 0$.

We investigate the 15 scenarios in which at least one of the proportions in the four central cells (i.e., a , b , c , or d) of Table 2 is 0. We sorted these scenarios in function of how many contingency measures are affected (from many affected measures to few).

- (1) The theoretical case where $a = b = c = d = 0$ cannot occur (i.e., it would imply that the number of time points equals zero).
- (2) There are four scenarios where three proportions equal zero, and one equals one:
 - Case 1: $d = 1$ (none of the variables is shown)
 - Case 2: $a = 1$ (both variables have a relative frequency of 1)
 - Case 3: $b = 1$ (prevalence of X is 1 and that of Y is 0)
 - Case 4: $c = 1$ (prevalence of X is 0 and that of Y is 1)
- (3) There are 6 cases in which exactly two of the four proportions equal zero.
 - Case 5: $a = 0, b = 0$
 - Case 6: $a = 0, c = 0$
 - Case 7: $b = 0, d = 0$
 - Case 8: $c = 0, d = 0$
 - Case 9: $b = 0, c = 0$
 - Case 10: $a = 0, d = 0$
- (4) There are four scenarios in which exactly one proportion equals 0:
 - Case 11: $a = 0$
 - Case 12: $b = 0$
 - Case 13: $c = 0$
 - Case 14: $d = 0$

Table A1

Scenarios 1 to 4, which lead to not defined values for some measures (indicated in grey)

Contingency measure	Basic Equation	Case 1: Only $d \neq 0$, Both variables have a prevalence of 0	Case 2: Only $a \neq 0$ Both variables have a prevalence of 1	Case 3: Only $c \neq 0$	Case 3: Only $b \neq 0$
Implications:		$p_1^x = p_1^y = 0$ $\Rightarrow p_0^x = p_0^y = 1$ $\Rightarrow a = b = c = 0$ $\Rightarrow d = 1$	$p_1^x = p_1^y = 1$ $\Rightarrow p_1^x = p_1^y = 0$ $\Rightarrow b = c = d = 0$ $\Rightarrow a = 1$	$p_1^x = 0$ and $p_1^y = 1$ $\Rightarrow p_0^x = 1$ and $p_0^y = 0$ $\Rightarrow a = b = d = 0$ $\Rightarrow c = 1$	$p_1^x = 1$ and $p_1^y = 0$ $\Rightarrow p_0^x = 0$ and $p_0^y = 1$ $\Rightarrow a = c = d = 0$ $\Rightarrow b = 1$
Proportion of agreement	$P_A(X, Y) = a + d$	$P_A = 1$	$P_A = 1$	$P_A = 0$	$P_A = 0$
Cohen's Kappa	$P_E(X, Y) = p_1^x p_1^y + p_0^x p_0^y$ $\kappa(X, Y) = \frac{P_A - P_E}{1 - P_E}$	$P_E = 0 * 0 + 1 * 1 = 1$ $\kappa = \frac{1 - 1}{1 - 1} = n.d.$	$P_E = 1 * 1 + 0 * 0 = 1$ $\kappa = \frac{1 - 1}{1 - 1} = n.d.$	$P_E = 0 * 1 + 1 * 0 = 0$ $\kappa = \frac{0 - 0}{1 - 0} = 0$	$P_E = 1 * 0 + 0 * 1 = 0$ $\kappa = \frac{0 - 0}{1 - 0} = 0$
Jaccard	$J_A(X, Y) = \frac{a}{a+b+c}$	$J_A = \frac{0}{0+0+0} = n.d.$	$J_A = \frac{1}{1+0+0} = 1$	$J_A = \frac{0}{0+0+1} = 0$	$J_A = \frac{0}{0+1+0} = 0$
Corrected Jaccard	$J_E(X, Y) = \frac{p_1^x * p_1^y}{1 - p_0^x * p_0^y}$ $J_{Corr}(X, Y) = \frac{J_A - J_E}{1 - J_E}$	$J_E = \frac{0 * 0}{1 - 1 * 1} = n.d.$ $J_{Corr} = n.d.$	$J_E = \frac{1 * 1}{1 - 0 * 0} = 1$ $J_{Corr} = \frac{1 - 1}{1 - 1} = n.d.$	$J_E = \frac{0 * 1}{1 - 1 * 0} = 0$ $J_{Corr} = \frac{0 - 0}{1 - 0} = 0$	$J_E = \frac{1 * 0}{1 - 0 * 1} = 0$ $J_{Corr} = \frac{0 - 0}{1 - 0} = 0$
Phi correlation Coefficient	$r_\phi(X, Y) = \frac{ad - bc}{\sqrt{p_1^x p_0^x p_1^y p_0^y}}$	$r_\phi = \frac{0 * 1 - 0 * 0}{\sqrt{0 * 1 * 0 * 1}} = n.d.$	$r_\phi = \frac{1 * 0 - 0 * 0}{\sqrt{1 * 0 * 1 * 0}} = n.d.$	$r_\phi = \frac{0 * 0 - 0 * 1}{\sqrt{0 * 1 * 1 * 0}} = n.d.$	$r_\phi = \frac{0 * 0 - 1 * 0}{\sqrt{1 * 0 * 0 * 1}} = n.d.$
Odds ratio	$OR(X, Y) = \frac{ad}{bc}$	$OR = \frac{0 * 1}{0 * 0} = n.d.$	$OR = \frac{1 * 0}{0 * 0} = n.d.$	$OR = \frac{0 * 0}{0 * 1} = n.d.$	$OR = \frac{0 * 0}{1 * 0} = n.d.$
Log odds ratio	$LOR(X, Y) = \log\left(\frac{ad}{bc}\right)$	$LOR = \log\left(\frac{0 * 1}{0 * 0}\right) = n.d.$	$LOR = \log\left(\frac{1 * 0}{0 * 0}\right) = n.d.$	$LOR = \log\left(\frac{0 * 0}{0 * 1}\right) = n.d.$	$LOR = \log\left(\frac{0 * 0}{1 * 0}\right) = n.d.$

Table A2

Scenarios 5 to 8, which lead to not defined values for some measures (indicated in grey)

Contingency measure	Equation	Case 5: $a = b = 0$ $c \neq 0$ and $d \neq 0$	Case 6: $a = c = 0$ $b \neq 0$ and $d \neq 0$	Case 7: $b = d = 0$ $c \neq 0$ and $a \neq 0$	Case 8: $c = d = 0$ $a \neq 0$ and $b \neq 0$
Implications:		$p_1^x = 0$ $\Rightarrow p_0^x = 1$ $\Rightarrow a = b = 0$	$p_1^y = 0$ $\Rightarrow p_0^y = 1$ $\Rightarrow a = c = 0$	$p_0^x = 0$ $\Rightarrow p_1^x = 1$ $\Rightarrow b = d = 0$	$p_0^y = 0$ $\Rightarrow p_1^y = 1$ $\Rightarrow c = d = 0$
Proportion of agreement	$P_A(X, Y) = a + d$	$P_A = d \neq 1$	$P_A = d \neq 1$	$P_A = a \neq 1$	$P_A = a \neq 1$
Cohen's Kappa	$P_E(X, Y) = p_1^x p_1^y + p_0^x p_0^y$	$P_E = p_0^y \neq 1$	$P_E = p_0^x \neq 1$	$P_E = p_1^y \neq 1$	$P_E = p_1^x \neq 1$
	$\kappa(X, Y) = \frac{P_A - P_E}{1 - P_E}$	$\kappa = \frac{d - p_0^y}{1 - p_0^y}$	$\kappa = \frac{d - p_0^x}{1 - p_0^x}$	$\kappa = \frac{a - p_1^y}{1 - p_1^y}$	$\kappa = \frac{a - p_1^x}{1 - p_1^x}$
Jaccard	$J_A(X, Y) = \frac{a}{a+b+c}$	$J_A = \frac{0}{0+0+1} = 0$	$J_A = \frac{0}{0+1+0} = 0$	$J_A = \frac{a}{a+c+0}$	$J_A = \frac{a}{a+b+0}$
Corrected Jaccard	$J_E(X, Y) = \frac{p_1^x * p_1^y}{1 - p_0^x * p_0^y}$	$J_E = \frac{0}{1 - p_0^y} = 0$	$J_E = \frac{0}{1 - p_0^x} = 0$	$J_E = \frac{p_1^y}{1 - 0} = p_1^y$	$J_E = \frac{p_1^x}{1 - 0} = p_1^x$
	$J_{Corr}(X, Y) = \frac{J_A - J_E}{1 - J_E}$	$J_{Corr} = \frac{0 - 0}{1 - 0} = 0$	$J_{Corr} = \frac{0 - 0}{1 - 0} = 0$	$J_{Corr} = \frac{\frac{a}{a+c} - p_1^y}{1 - p_1^y}$	$J_{Corr} = \frac{\frac{a}{a+b} - p_1^x}{1 - p_1^x}$
Phi correlation Coefficient	$r_\phi(X, Y) = \frac{ad - bc}{\sqrt{p_1^x p_0^x p_1^y p_0^y}}$	$r_\phi = \frac{0 - 0}{\sqrt{0 * 1 * p_1^y p_0^y}} = n. d.$	$r_\phi = \frac{0 - 0}{\sqrt{0 * 1 * p_1^x p_0^x}} = n. d.$	$r_\phi = \frac{0 - 0}{\sqrt{1 * 0 * p_1^y p_0^y}} = n. d.$	$r_\phi = \frac{0 - 0}{\sqrt{1 * 0 * p_1^x p_0^x}} = n. d.$
Odds ratio	$OR(X, Y) = \frac{ad}{bc}$	$OR = \frac{0 * d}{0 * c} = n. d.$	$OR = \frac{0 * d}{0 * b} = n. d.$	$OR = \frac{a * 0}{0 * c} = n. d.$	$OR = \frac{a * 0}{0 * b} = n. d.$
Log odds ratio	$LOR(X, Y) = \log\left(\frac{ad}{bc}\right)$	$LOR = \log(n. d.) = n. d.$	$LOR = \log(n. d.) = n. d.$	$LOR = \log(nd) = n. d.$	$LOR = \log(nd) = n. d.$

Table A3

Scenarios 9 to 14, which lead to infinite values for some measures (indicated in grey)

Contingency measure	Equation	Case 9: $c = b = 0$ $a \neq 0$ and $d \neq 0$	Case 10: $a = d = 0$ $b > 0$ and $c > 0$	Case 11: Only $a = 0$	Case 12: Only $b = 0$	Case 13: Only $c = 0$	Case 14: Only $d = 0$
implications		Perfect co-occurrence	Perfect anti – co – occurrence	No co-occurrence	X never occurs without Y	Y never occurs without X	There is always one of the two shown
Proportion of agreement	$P_A(X, Y) = a + d$	$P_A = 1$	$P_A = 0$	$P_A = d$	$P_A = a + d$	$P_A = a + d$	$P_A = a$
Cohen's Kappa	$P_E(X, Y) = p_1^X p_1^Y + p_0^X p_0^Y$	$P_E = p_1^X p_1^Y + p_0^X p_0^Y$	$P_E(X, Y) = p_1^X p_1^Y + p_0^X p_0^Y$	$P_E(X, Y) = p_1^X p_1^Y + p_0^X p_0^Y$	$P_E = p_1^X p_1^Y + p_0^X p_0^Y$	$P_E = p_1^X p_1^Y + p_0^X p_0^Y$	$P_E(X, Y) = p_1^X p_1^Y + p_0^X p_0^Y$
	$\kappa(X, Y) = \frac{P_A - P_E}{1 - P_E}$	$\kappa = \frac{1 - P_E}{1 - P_E} = 1$	$\kappa(X, Y) = \frac{0 - P_E}{1 - P_E}$	$\kappa(X, Y) = \frac{d - P_E}{1 - P_E}$	$\kappa = \frac{P_A - P_E}{1 - P_E}$	$\kappa = \frac{P_A - P_E}{1 - P_E}$	$\kappa(X, Y) = \frac{a - P_E}{1 - P_E}$
Jaccard	$J_A(X, Y) = \frac{a}{a+b+c}$	$J_A = \frac{a}{a} = 1$	$J_A = \frac{0}{b+c} = 0$	$J_A = \frac{0}{b+c} = 0$	$J_A = \frac{a}{a+c}$	$J_A = \frac{a}{a+b}$	$J_A = \frac{a}{a+b+c}$
Corrected Jaccard	$J_E(X, Y) = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$	$J_E = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$	$J_E = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$	$J_E(X, Y) = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$	$J_E = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$	$J_E = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$	$J_E(X, Y) = \frac{p_1^X * p_1^Y}{1 - p_0^X * p_0^Y}$
	$J_{corr}(X, Y) = \frac{J_A - J_E}{1 - J_E}$	$J_{corr} = \frac{1 - J_E}{1 - J_E}$	$J_{corr} = \frac{0 - J_E}{1 - J_E}$	$J_{corr} = \frac{0 - J_E}{1 - J_E}$	$J_{corr} = \frac{J_A - J_E}{1 - J_E}$	$J_{corr} = \frac{J_A - J_E}{1 - J_E}$	$J_{corr} = \frac{J_A - J_E}{1 - J_E}$
Phi correlation Coefficient	$r_\phi(X, Y) = \frac{ad - bc}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$	$r_\phi = \frac{ad - 0}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$	$r_\phi = \frac{0 - cb}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$	$r_\phi = \frac{0 - cb}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$	$r_\phi = \frac{ad - 0}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$	$r_\phi = \frac{ad - 0}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$	$r_\phi = \frac{0 - cb}{\sqrt{p_1^X p_0^X p_1^Y p_0^Y}}$
Odds ratio	$OR(X, Y) = \frac{ad}{bc}$	$OR = \frac{a * d}{0} = +Inf$	$OR = \frac{0}{c * b} = 0$	$OR = \frac{0}{c * b} = 0$	$OR = \frac{a * d}{0} = +Inf$	$OR = \frac{a * d}{0} = +Inf$	$OR = \frac{0}{c * b} = 0$
Log odds ratio	$LOR(X, Y) = \log\left(\frac{ad}{bc}\right)$	$LOR = \log(+Inf) = +Inf$	$LOR = \log(0) = -Inf$	$LOR = \log(0) = -Inf$	$LOR = \log(+Inf) = +Inf$	$LOR = \log(+Inf) = +Inf$	$LOR = \log(0) = -Inf$

Note. We grouped these cases because they lead to + Inf or – Inf outcomes.

9.2 (Cor)Relations of the contingency measures

Figure A1

Combined scatter matrix, density plot, and spearman correlation for different contingency measures

Note. Combined scatter matrix, density plot, and spearman correlation for the proportion of agreement, classic Jaccard, Cohen's kappa, phi correlation coefficient, and log odds ratio, complementing Table 4 in the theory section of Module 2.