ARTICLE IN PRESS
PAID-08391; No of Pages 11
Personality and Individual Differences xxx (2017) xxx–xxx
Contents lists available at ScienceDirect
Personality and Individual Differences
journal homepage: www.elsevier.com/locate/paid

# Stability and variability of personality networks. A tutorial on recent developments in network psychometrics

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ARTICLE INFO

*Article history:*
Received 1 April 2017
Received in revised form 30 May 2017
Accepted 10 June 2017
Available online xxxx

*Keywords:*
Network analysis
Fused Graphical Lasso
Centrality
Agency
Communion

ABSTRACT

Networks have been recently proposed for modeling dynamics in several kinds of psychological phenomena, such as personality and psychopathology. In this work, we introduce techniques that allow disentangling *between-subject* networks, which encode dynamics that involve stable individual differences, from *within-subject* networks, which encode dynamics that involve momentary levels of certain individual characteristics. Furthermore, we show how networks can be simultaneously estimated in separate groups of individuals, using a technique called the Fused Graphical Lasso. This technique allows also performing meaningful comparisons among groups. The unique properties of each kind of network are discussed. A tutorial to implement these techniques in the "R" statistical software is presented, together with an example of application.


Networks allow representing complex phenomena in terms of a set of elements that interact with each other. Networks include two basic components, the nodes, which represent the elements of a system, and the edges, that connect nodes and represent their pairwise interactions. Networks have been recently proposed as a model of complex psychological phenomena such as individual differences in psychopathology (Borsboom & Cramer, 2013; Schmittmann et al., 2013) and personality (Costantini, Epskamp, et al., 2015; Costantini & Perugini, 2016b; Cramer et al., 2012). From the network perspective, broad patterns of individual differences in both normal personality and psychopathology can be conceptualized as phenomena that emerge from the interactions among certain behaviors, cognitions, motivations, and emotions. For example, individual differences in depression could arise from, and could be maintained by, vicious cycles of mutual relationships among symptoms. A depression symptom such as insomnia can cause another symptom, such as fatigue, which in turn can determine concentration problems and worrying, which can result in more insomnia and so on (Borsboom & Cramer, 2013; Fried & Cramer, 2017). Similarly, broad personality traits such as conscientiousness and extraversion in the network perspective are not seen as explanations of basic individual differences, such as the time an individual spends attending parties and her number of friends (McCrae & Costa, 2008). Instead, individual differences in broad personality traits are considered phenomena to explain in terms of dynamic interactions. For instance, a researcher could focus on the fact that people who like to go to parties tend to meet more people and therefore to gain more friends, people who have more friends get invited to parties more often, and so on (Cramer et al., 2012). In this way, networks provide an explanation of individual differences that connects their structure to potential underlying processes and dynamics (Baumert et al., 2017).

The growing interest in conceptualizing individual differences in dynamic terms has led research to use intensive longitudinal data (Walls & Schafer, 2006), that is, many repeated measurements for multiple persons. Examples of intensive longitudinal data research designs include diary reports, observational methods, and ecological momentary assessment (EMA; Trull & Ebner-Priemer, 2013), which have become highly feasible and efficient thanks to the widespread use of electronic devices such as tablets and smartphones. The defining characteristics of these methods are that the assessment is both ecological (i.e., experiences are measured in the participant's natural environment) and momentary (i.e., assessment captures information about immediate or near immediate experiences and requires minimal retrospection; Shiffman, Stone, & Hufford, 2008).

In this work, we provide a primer on both established and new methods for computing and analyzing networks in psychology and investigating individual differences (e.g., in personality and psychopathology) and their patterns of stability and variability in two main ways. First, individual differences, for instance in personality characteristics, have been shown to vary around a stable central tendency according to the characteristics of the occasion (Fleeson, 2001). For example, it has been shown that individuals, independent of their typical level of extraversion, act in a more extraverted way when their goal is to be at the center of attention and in a less extraverted way when they want

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http://dx.doi.org/10.1016/j.paid.2017.06.011
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to "recharge their batteries" (McCabe & Fleeson, 2016). We present both techniques that allow analyzing dynamics involving the stable component of individual differences and techniques that allow investigating the dynamics characterizing the transient variability among different occasions. Focusing on stable between-subject differences is particularly relevant if one is interested in the dynamics that involve one individual's typical levels of a trait, whereas if one's interest is in the dynamics that involve the momentary level of certain characteristics in individuals, one should focus on the variability between occasions (Epskamp, Waldorp, Mõttus, & Borsboom, 2017).

Second, individual differences and their dynamics can vary among groups. One could be interested in inspecting which dynamics are similar and which vary across individuals, for example who are addicted to different substances (Rhemtulla et al., 2016), who follow different types of psychotherapy (Bringmann, Lemmens, Huibers, Borsboom, & Tuerlinckx, 2015), who are diagnosed with a disorder or not (Richetin, Preti, Costantini, & De Panfilis, 2017) or who live in different countries (Costantini & Perugini, 2017). In psychopathology, this issue has been referred to as heterogeneity (Fried & Cramer, 2017; Mõttus et al., 2015). We present new techniques that allow simultaneously estimating networks from different groups of individuals and identifying patterns of similarities and differences in the dynamics characterizing these groups (Danaher, Wang, & Witten, 2014). Such methods allow inspecting whether between-subject and between-occasion dynamics are stable or vary among groups.

Once a network is computed, network analysis offers a powerful toolbox to summarize complex patterns of relationships. For instance, network analysis allows analyzing the global structural organization, or topology, of a phenomenon (e.g., Borsboom, Cramer, Schmittmann, Epskamp, & Waldorp, 2011; Costantini et al., 2015) or the role played by specific elements of the network, such as by identifying the most "central" or "peripheral" elements of a system (Costantini, Epskamp, et al., 2015; Freeman, 1978). In this work, we will introduce the most important network indices and show how they can be computed in R (R Core Team, 2017).

## 1. Estimating and analyzing networks in psychology

When investigating personality, nodes can represent symptoms (Borsboom & Cramer, 2013), behaviors, emotions, cognitions, and motivations that can vary across individuals or occasions. Nodes can be assessed by single items in questionnaires (Cramer et al., 2012) or by aggregates of items, for instance personality facets (Costantini & Perugini, 2016b). The choice of an appropriate level of investigation (e.g., items, facets, or even broader traits) depends on which level is most useful for investigating the phenomenon of interest (Costantini & Perugini, 2012).

Edges represent pairwise connections between nodes and can be characterized by three main properties: *weight*, *sign*, and *direction*. Weights encode information about the intensity of the relationships and are graphically represented by the thickness of the lines connecting the nodes. Signs allow distinguishing positive from negative relationships and are conventionally represented by colors: green (or blue) edges are positive and red edges are negative. For personality and psychopathology research, edge weights and signs are fundamental, because they allow distinguishing between intense and weak and between positive and negative associations among variables (Costantini & Perugini, 2014). Edge direction allows representing asymmetrical relationships between nodes and is typically represented by arrowheads. Edge direction has been used in psychology particularly for representing temporal dependencies (Bringmann et al., 2013, 2016, 2015).

The interpretation of the edges crucially depends on the method used for computing the network. In turn, not all methods can be applied to all kinds of datasets. Examples of sources of data in psychology include participants' rating on an object of interest (e.g., themselves, a peer, or a situation) collected only once (cross-sectional studies) or many times (e.g., as in EMA studies). Whereas networks can be computed both on cross-sectional and longitudinal datasets, disentangling the variation due to subjects (i.e., to their stable central tendency) from the variation due to the specific occasion requires repeated-measure data (Epskamp, Waldorp, et al., 2017). Moreover, group comparisons can be performed only if participants can be univocally assigned to different groups.

### 1.1. Estimating networks on cross-sectional data

Although correlation networks can be used (e.g., Cramer et al., 2012), the most common method for cross-sectional data has been to elaborate partial correlation networks (Costantini, Epskamp, et al., 2015; Epskamp, Borsboom, & Fried, 2017), which are equivalent to standardized Gaussian Graphical Models (GGM; Lauritzen, 1996; for a detailed presentation of the GGM in psychology, see Epskamp et al., 2017). In partial correlation networks, an edge between any two nodes is drawn if they correlate after controlling for all other variables in the network. The absence of an edge in partial correlation networks (i.e., a zero in the partial correlation matrix) indicates that two nodes are conditionally independent given the others, and therefore is particularly informative (Lauritzen, 1996). However, because exact zeros cannot be easily observed in sample partial correlation matrices and because in partial correlation networks an increase in the number of nodes can lead to overfitting and very unstable estimates (Babyak, 2004), such networks are usually estimated using regularization methods such as the least absolute shrinkage and selection operator (*lasso*; Tibshirani, 1996).

Partial correlations can be computed from the concentration (or precision) matrix, which is the inverse of the correlation matrix, via simple mathematical operations.[1] The *graphical lasso* (glasso) methodology estimates a concentration matrix by imposing a lasso regularization directly on its elements[2]: Instead of estimating the concentration matrix by maximizing the log-likelihood function, the glasso maximizes a penalized log-likelihood, the penalty being equal to the sum of the absolute values of the elements of the concentration matrix, multiplied by a tuning parameter $\lambda_1$ (Friedman, Hastie, & Tibshirani, 2008). The larger is the value of $\lambda_1$, the stronger is the penalization and the sparser will be the estimated concentration matrix (with many zero coefficients). The $\lambda_1$ parameter therefore regulates the sparsity of the resulting network: By setting the $\lambda_1$ parameter to zero (i.e., no regularization), one simply gets the maximum likelihood estimates of the partial correlations. Established ways to select a value for the tuning parameter include selection according to an information criterion, such as the Extended BIC (EBIC; Chen & Chen, 2008; Epskamp, 2016; Foygel & Drton, 2010), or via cross-validation (e.g., Krämer, Schäfer, & Boulesteix, 2009). This method has been widely used in psychology[3] (e.g., Beard et al., 2016; Isvoranu et al., 2017; van Borkulo et al., 2015) and, compared to the maximum likelihood estimates of partial correlations, it improves both the accuracy and the interpretability of the results (Tibshirani, 1996), especially if the sparsity of the model matches that of the true data-generating network (Epskamp, Kruis, & Marsman, 2016).

[1] A partial correlation matrix can be computed by standardizing the concentration matrix (each element of the matrix is divided by the square root of the product of the corresponding diagonal elements) and by computing the opposite of the resulting off-diagonal elements (the formula can be found for instance in Lauritzen, 1996, p. 130).

[2] The exact formula of the graphical lasso and the details of the fitting algorithm can be found in the original work by Friedman and colleagues (Friedman et al., 2008).

[3] Other methods for computing a regularized partial correlation matrix are also available (e.g., Krämer et al., 2009; Meinshausen & Bühlmann, 2006). However, in this work we focus exclusively on the glasso, which is more flexible, since it takes as input a correlation matrix instead of the whole dataset. For this reason, the glasso handles ordinal data better, because a polychoric variance-covariance matrix can be used as input (Epskamp, Borsboom, et al., 2017). Furthermore, the glasso has been extended to the case of multiple groups (Danaher et al., 2014; Guo et al., 2011).

Please cite this article as: Costantini, G., et al., Stability and variability of personality networks. A tutorial on recent developments in network psychometrics, *Personality and Individual Differences* (2017), http://dx.doi.org/10.1016/j.paid.2017.06.011

### 1.2. Estimating networks on repeated measures

Recently, Epskamp et al. (2017) have pointed out that repeated-measure data can be used to disentangle networks representing variability between subjects from networks representing variability within subjects. A *between-subject network* can be simply computed by averaging the scores of each participant on each variable across occasions, followed by estimating a network on the person means. Each score gives an estimate of the central tendency of each individual on each dimension, therefore reducing the influence of reporting bias that arguably occurs when a participant is asked to self-rate on a single occasion (Fleeson, 2001; Shiffman et al., 2008). This network tells us if, for example, a person that often is sad might also be a person that often is tired. A *within-subjects* network, encoding the dynamics due to within-person variations from the mean, can then be computed by investigating within-person centered data.

A simple but effective way for estimating fixed effect within-subject networks has been recently proposed by Epskamp et al. (2017). It consists in subtracting the mean of each variable for each participant from each participant's raw scores and then estimating a network on the centered data. The first step removes variance due to between-subject differences across occasions. The second step consists in computing a network on these values using the same methods that are typically used for cross-sectional data, such as the graphical lasso (Friedman et al., 2008). The resulting within-subject network represents contemporaneous relationships: It tells us, for instance, if being sadder than one's typical level is associated to being also more tired than usual. Since the focus is on contemporaneous relationships, as opposed to cross-lagged, this method does not require participants to answer at evenly-spaced time intervals and it can be used to analyze event-based EMA data or time-based EMA data with missing responses (Trull & Ebner-Priemer, 2013). Furthermore, since the graphical lasso takes as input a correlation matrix, the remaining missing values can be handled via listwise deletion or other techniques, such as multiple imputation (Buuren & Groothuis-Oudshoorn, 2011). This method assumes the data are collected in a relatively short timeframe, so that it is legitimate to assume that the model is sufficiently stable during this time (stationarity assumption; Epskamp, Waldorp, et al., 2017). Furthermore, a single within-subject network is estimated across all participants (as opposed to estimating a network separately for each participant), therefore it requires assuming that the underlying processes are similar across individuals. This methodology is particularly useful when the main focus is on contemporaneous relationships, as opposed to cross-lagged, and when one is interested in the overall within-subject network, as opposed to estimating a different network for each individual.[4] This method does not require a very large number of repeated measurements and it is relatively simple to implement, as we will show below.

### 1.3. Multi-group network analysis

It is often useful to estimate networks on the same variables from different classes or groups that could share some similarities but that can present also differences. In this case, it would be desirable to exploit the similarities to improve the network estimates, without masking the true differences among groups. Furthermore, it is often important to compare networks estimates in different groups. The current lack of methods for estimating and comparing networks from different groups has been considered as a challenge to the network methodology (Fried & Cramer, 2017). Although one could choose between estimating a single network or two different networks using an information criterion, such as the BIC (Bringmann et al., 2015), or could explore both the aggregate networks and the separate networks (Rhemtulla et al., 2016), none of these methods would allow simultaneously exploiting the similarities between groups without masking their differences.

The joint estimation of different graphical models (Danaher et al., 2014; Guo, Levina, Michailidis, & Zhu, 2011) provides a solution to these issues. In particular, the Fused Graphical Lasso (FGL) is a valid method that has been recently employed in psychology for comparing the networks of borderline personality disorder patients versus a community sample (Richetin et al., 2017) or to compare situational experience networks from different countries (Costantini & Perugini, 2017). This technique extends the glasso by applying a penalty not only to the sum of the absolute values of the elements of the concentration matrix multiplied by the tuning parameter $\lambda_1$ (as the glasso), but also to the sum of the absolute values of the differences between the corresponding elements of the concentration matrix across groups, multiplied by another tuning parameter, $\lambda_2$. Therefore, this method requires setting two tuning parameters: one ($\lambda_1$) is analogous to the tuning parameter in the graphical lasso and regulates sparsity, whereas the other ($\lambda_2$) affects the similarity of the networks estimates in different groups: The higher $\lambda_2$, the more similar the resulting networks will be.[5] As for the graphical lasso, the values of both tuning parameters can be selected using information criteria or a cross-validation approach.

The FGL, coupled with tuning parameters selection via information criteria and cross-validation, has several advantages over independent network estimates in different groups. First, it gives an indication of which edges can be considered as identical in the different groups without worsening the model fit, and which should be better considered as different. The logic behind considering edges as equal or different is the same that is used in the graphical lasso methodology to identify edges that can be shrunk to zero without compromising model fit, therefore this method provides an elegant solution to the issue of network comparison (Danaher et al., 2014). Second, this method makes the networks computed in different groups often more parsimonious, since they involve less unique parameters. Third, the FGL improves network estimates by exploiting similarities among different groups: If two groups have many elements in common, estimating such elements in both groups improves the estimates (Danaher et al., 2014). In cases in which exploiting similarities does not improve model fit, the tuning parameter selection procedure picks a value of the $\lambda_2$ parameter that is very close to zero or zero. In this case, no penalty is imposed to the differences among groups and the FGL reduces to estimating two separate Gaussian Graphical Models, albeit with a shared sparsity parameter. In this way, true differences among groups are not masked. Preliminary simulation results show that this technique improves the accuracy of network estimates in a variety of scenarios (Costantini & Epskamp, manuscript in preparation).

### 1.4. Network indices

Once the network is computed, different tools or indices can be used to summarize the patterns of relations in the network. The visual inspection of a network is always a very useful first step and it conveys relevant information with minimal effort (Cramer et al., 2012). The Fruchterman-Reingold's algorithm (Fruchterman & Reingold, 1991)

[4] If one is interested in cross-lagged effects and in estimating networks for each participant, one could opt for estimating graphical vector autoregressive (VAR) models, which include the lagged variables in the analyses and can be used to describe the pattern of cross-lagged relationships among the individual characteristics of a single participant (Wild et al., 2010). Multilevel extensions of these methods allow describing the typical pattern of cross-lagged relationships across participants (Bringmann et al., 2013, 2016). These methods result in temporal networks, in which temporal dependencies are represented by edge directions. However, they require many data points for each participant and assume that the distance between each data point is fixed (Hamaker, Ceulemans, Grasman, & Tuerlinckx, 2015). Under these conditions, one can estimate not one but two within-person networks: a *temporal network*, encoding the relationships among variables measured at subsequent timepoints, and a *contemporaneous network*, encoding the relationships among variables measured at the same timepoint (Epskamp, Waldorp, et al., 2017).

[5] The formulas and the details of the fitting algorithm of the FGL can be found in the work by Danaher and colleagues (Danaher et al., 2014).

places nodes close to each other or farther apart if they are very connected or not, respectively. Moreover, if the network is very small and sparse, looking at each edge and its weight is sufficient for an interpretation of the network (e.g., Costantini, Richetin, et al., 2015). For larger structures, network analysis provides several formal ways of describing the global and the local properties of a network.

The *topology* of a network that refers to its large-scale organization can provide deeper understanding of the properties of the network and the processes underlying its generation and evolution (e.g., Barabási & Bonabeau, 2003). Psychopathology networks (e.g., Borsboom et al., 2011), attitude networks (Dalege et al., 2015), and personality networks (Costantini & Perugini, 2016a) have been argued to have a small-world topology, implying that the influence of a change in some part of the network can affect other parts of the network as well, despite the presence of clustering in these networks (Watts & Strogatz, 1998). The small-world topology can be formally assessed using the *small-worldness index*, which compares clustering and length of shortest paths in the target network and in comparable random networks (Humphries & Gurney, 2008).

The network approach allows identifying the centrality of the nodes, that is to determine whether some nodes are more influential than others. *Centrality* quantifies the relative importance of a node in the context of other nodes (Borgatti, 2005; Freeman, 1978). However, the concept of centrality is manifold and each index informs on a specific type of centrality. A node can be central because it has strong direct connections with many nodes (*strenght centrality*; Barrat, Barthélemy, Pastor-Satorras, & Vespignani, 2004). Strength is a very stable and widespread index of centrality (Epskamp, Borsboom, et al., 2017) that, for instance, allowed improving the prediction of the onset of depression (Boschloo, van Borkulo, Borsboom, & Schoevers, 2016). A node can be also central because both direct and indirect paths that connect it to other nodes are generally short (*closeness centrality*). A closeness central node will be affected quickly by changes in any part of the network (Borgatti, 2005). A node can be central also because it frequently lies on the shortest path between two other nodes and thus is important in the connection the other nodes have between them (*betweenness centrality*). Finally, the *clustering coefficient* encodes the tendency of a node's neighbors to be directly connected to each other (Saramäki, Kivelä, Onnela, Kaski, & Kertész, 2007; Watts & Strogatz, 1998). The clustering coefficient can be interpreted as an index of local redundancy of a node: If a node's neighbors can affect each other directly, removing a node with a very high clustering coefficient will not have a big effect on the possibility for its neighbors to interact. This property has been recently extended to consider edge weights (Saramäki et al., 2007) and signs (Costantini & Perugini, 2014).

## 2. A tutorial for network analysis on multi-group repeated measures

In the following, we show how different types of networks allow exploring several kinds of dynamics in individual differences research. We present R code (R Core Team, 2017) to compute different networks from repeated-measures data and discuss how each conveys unique information. We also present joint estimation techniques that allow estimating networks on multiple groups simultaneously.

For the examples, we focused on interpersonal perceptions rated in terms of the two orthogonal dimensions of agency and communion (Wiggins, 1991), which are connected to both personality and psychopathological traits (Widiger, 2010). We collected data on one-hundred-twenty-nine participants (78 women, 51 men, $M$ age $= 23.71$, $SD = 4.30$), who were asked to provide ratings of significant face-to-face interactions lasting 5 min or more (event-contingent recording) at least 3 times a day over 7 days via their smartphones.[6] Men and women reported 899 and 1465 interactions overall, respectively. After each social interaction, participants rated their own interpersonal behavior in terms of agency (assured-dominant/unassured-submissive) and communion (cold-quarrelsome/warm-agreeable; self-agency, self-communion) as well as their perception of their interaction partner's interpersonal behavior (other-agency, other-communion). Higher scores indicated greater perceived dominance and communion. Participants also rated their own affect in terms of arousal (active-energized/quiet-passive) and valence (sad-upset/happy-pleased; self-arousal, self-valence) as well as their perception of their interaction partner's affect (other-arousal, other-valence). Higher scores indicated higher perceived arousal (active-energized) and higher perceived valence (happy-pleased). The dataset has been made publicly available in the Supplementary material so that the reader can reproduce the examples presented here.

This dataset constitutes an interesting sample for applying the network techniques we introduced for three reasons. First, it is reasonable to assume that a substantial part of the variance in interpersonal perceptions in social interactions can be explained by relatively stable personality characteristics, such as agreeableness and extraversion (Widiger, 2010), which are not expected to undergo major changes in the time span of the data collection.[7] Second, a portion of variability is likely to be explained by the characteristics of the specific social situation, which are instead expected to vary between measurement occasions. Third, although some dynamics characterizing interpersonal perceptions could be common to all participants irrespective to their gender, one could also expect men and women to show interesting differences in such patterns, for instance they could conform to some gender stereotypes and societal prescriptions (Eagly & Steffen, 1984; Prentice & Carranza, 2002). These dynamics could be in turn part of broader gender differences in personality traits (Costa, & Terracciano, & McCrae, 2001; Schmitt, Realo, Voracek, & Allik, 2008).

### 2.1. Between-subject network with the graphical lasso

In this first part of the tutorial, we use network analysis to explore dynamics that involve stable individual differences between subjects. This type of analysis is performed most frequently on cross-sectional datasets. However, one can aggregate longitudinal data into a one-row-by-subject format by computing the mean value of each participant on each variable (Epskamp, Waldorp, et al., 2017). In this way, one obtains indications on how a participant behaves, feels, and attributes behaviors and feelings to others across different social interactions, using a measure that is less affected by recall biases than retrospective self-reports (Shiffman et al., 2008).

The following command reads the original dataset, which includes one row by occasion.

```
Data <- read.csv("Data.csv")
```

The variables included in the dataset are the following: `subject` and `gender` are the participants' identifier and gender respectively, `warm.S` and `domi.S` indicate the rating of participants' behavior in terms of communion and agency respectively (we used suffix ".S" to indicate that the variable refers to "self"). Variables `happ.S` and `active.S` indicate respectively the valence and arausal ratings of participants' emotions experienced during the social interaction. The same four variables with suffix ".O" indicate the participants' ratings of other's behaviors and emotions.

The following code creates a new dataframe, `Data.m`, which includes for each subject the mean value of each variable across all the reported social interactions (we used suffix "m" to denote that these values are "means"). The first line loads the *dplyr* package (Wickham

[6] Participants completed other measures not used for the tutorial and therefore not discussed further. Some participants stopped reporting social interactions before the seventh day, whereas other participants kept answering the questionnaires a few days after the last day. All responses are considered for the analyses in this tutorial.

[7] Spontaneous changes in personality traits usually occur in relatively long time spans (Roberts, Walton, Viechtbauer, 2006), whereas quicker changes have been observed only as a consequence of interventions (Roberts et al., 2017).

Please cite this article as: Costantini, G., et al., Stability and variability of personality networks. A tutorial on recent developments in network psychometrics, *Personality and Individual Differences* (2017), http://dx.doi.org/10.1016/j.paid.2017.06.011

& Francois, 2016), which includes several functions for manipulating data. In the second line, command `group_by` is used to group data by subject and the dataset is passed through the operator "`%>%`" to command summarize, which computes a custom list of variables for each subject. The first variable computed is "gender", which is simply the gender of the participant. Variables from `warm.Sm` to `acti.Om` correspond to the mean ratings across occasions of the aforementioned eight variables.

```
library("dplyr")

Data.m <- group_by(Data, subject) %>%

  summarize(gender = unique(gender),

            warm.Sm = mean(warm.S),

            domi.Sm = mean(domi.S),

            happ.Sm = mean(happ.S),

            acti.Sm = mean(acti.S),

            warm.Om = mean(warm.O),

            domi.Om = mean(domi.O),

            happ.Om = mean(happ.O),

            acti.Om = mean(acti.O))
```

Once the new dataset is created, one can easily compute a graphical lasso network with function `EBICglasso` from package *qgraph* (Epskamp, Costantini, et al., 2017; Epskamp, Cramer, Waldorp, Schmittmann, & Borsboom, 2012). This function performs tuning parameter selection for the graphical lasso using the EBIC and returns the corresponding network. The following code loads package *qgraph*, computes a correlation matrix, and then calls function `EBICglasso` to compute the network, which is stored in the variable `network1`. The first argument of `EBICglasso` is `S`, a correlation matrix of the variables of interest. In this case, the variables of interest are the participants' mean ratings of behavior and affect for themselves and for their interaction partners. The second argument is `n`, the number of observations on which the correlation matrix was computed, in this case 129. Function `EBICglasso` allows setting several other arguments: Type `help("EBICglasso")` in the R console for a complete description of such arguments.

```
library("qgraph")

S <- select(Data.m, warm.Sm:acti.Om) %>% cor()

network1 <- EBICglasso(S = S, n = 129)
```

The values of each edge are reported in Supplementary Table S1. If the network computed is sufficiently small and sparse (with few nodes and few edges) its graphical representation can immediately convey a large amount of information. The `qgraph` function in package *qgraph* includes several options to visualize the network, the "spring" layout corresponding to the Frutherman-Reingold visualization algorithm (Fruchterman & Reingold, 1991). The following code visualizes the network (the corresponding plot is reported in Fig. 1A).

```
plot1 <- qgraph(network1,

                layout = "spring",

                labels = colnames(network1))
```

It is important to notice that the network computed and presented in Fig. 1A is a between-subject network, which does not convey information on variability across occasions. However, between-subject networks provide information on how the differences between participants are structured and they can be also informative on important processes and dynamics (Epskamp, Waldorp, et al., 2017). From the network in Fig. 1A, one can immediately see that warmth and happiness of self and others cluster together, and that activation and dominance, both referred to self and others, form a second relatively separate cluster. Participants who behave more warmly across social interactions tend to experience more happiness and to attribute more warmth to others compared to participants who behave more coldly. In turn, participants who are generally happier and attribute more warmth to others tend to attribute also more happiness to others. Similarly, participants who on average behave in a more dominant way, tend also to feel more activated and attribute more dominance to others, compared to participants who typically behave in a more submissive way. In turn, self-attributed activation and other-attributed dominance are on average connected to perceiving more activation in others. It is also worth noticing that the two clusters are not completely separate, but are connected with weaker links than the within-cluster links. These relationships in mean levels echo somehow previous research showing that individuals tend to hang out with individuals whom they perceive as similar to themselves (e.g., Selfhout et al., 2010).

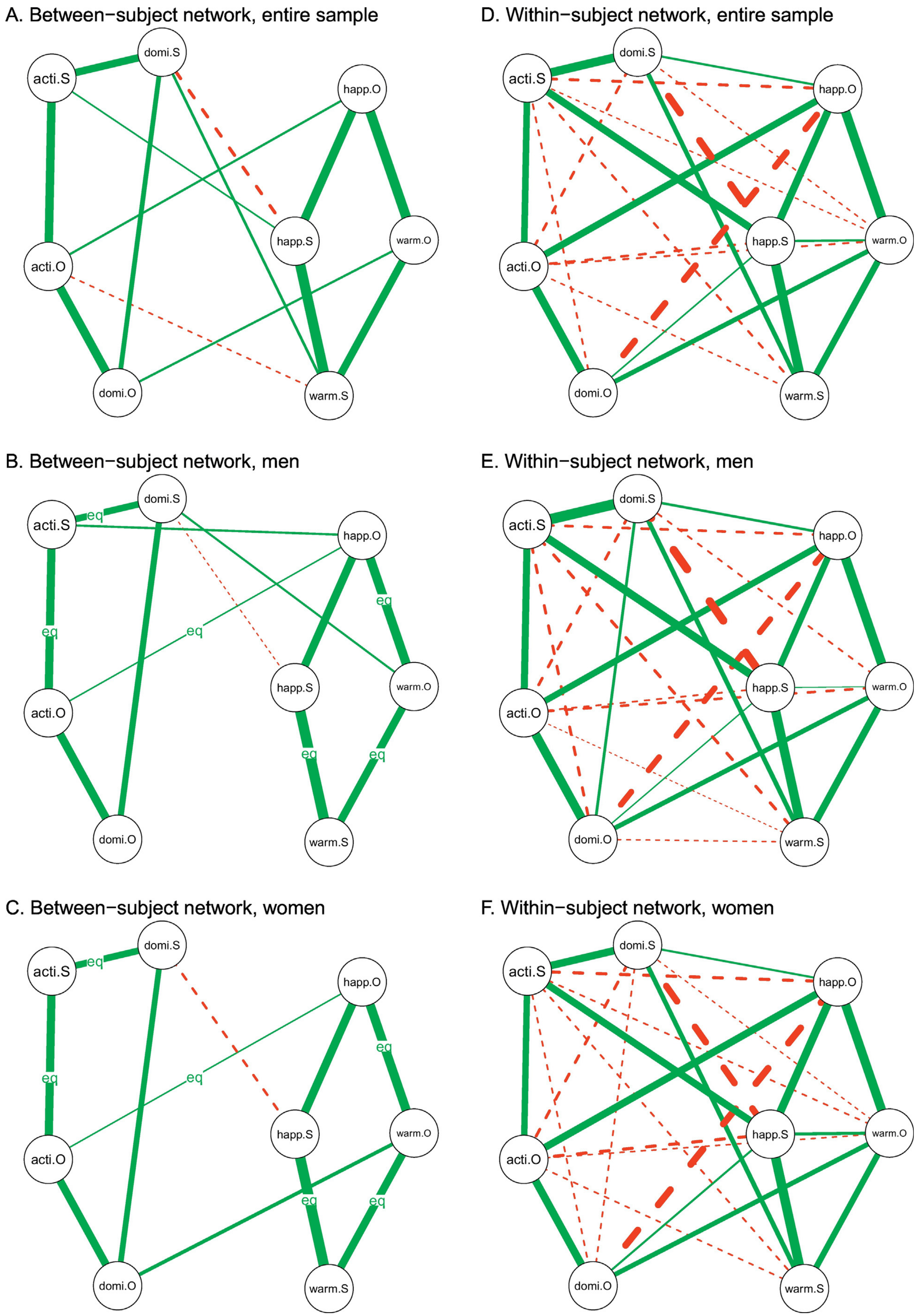
### 2.2. Joint estimation of multiple between-subject networks with Fused Graphical Lasso

Joint network estimation techniques such as the FGL (Danaher et al., 2014) provide an appropriate solution to inspect the patterns of similarities and differences among groups of individuals. Based on the data we collected, we will focus on the similarities and differences between men and women in the networks of the self-attributed and other attributed behaviors and emotions during interactions.

The Fused Graphical Lasso has been implemented in the R package *JGL* (Danaher, 2013) but it does not include tuning parameter selection. A recently developed package, *EstimateGroupNetwork* (Costantini & Epskamp, 2017), implements automatic tuning parameter selection both via information criteria and via k-fold cross validation (Guo et al., 2011). The main function of the package, `EstimateGroupNetwork`, requires as input a list of covariance or correlation matrices plus a vector of sample sizes for each group, in this case 51 men and 78 women. Other inputs, such as a dataframe or a list of dataframes, are accepted as well. The function supports two main strategies for tuning parameters selection, by information criterion and by k-fold cross validation. In the following examples, we use tuning parameter selection via EBIC, which is the default option, for consistency with package *qgraph*'s function `EBICglasso`. Several other arguments supported by this package are described in the help file, which can be accessed by typing `help("EstimateGroupNetwork")` in the R console window. The following code loads package *EstimateGroupNetwork*, computes correlation matrices separately for men and women, and performs simultaneous estimation of two networks, one for men and one for women.

```
library("EstimateGroupNetwork")

S.males <- filter(Data.m, gender == "male") %>%

          select(warm.Sm:acti.Om) %>% cor()

S.females <- filter(Data.m, gender == "female") %>%

            select(warm.Sm:acti.Om) %>% cor()

network2 <- EstimateGroupNetwork(list("males" = S.males,

                                      "females" = S.females),

                                 n = c(51, 78))
```

The output networks are saved in the object `network2`, which is a list of two elements, one (`network2$males`) includes the network for men and the other (`network2$females`) includes the network for


A. Between−subject network, entire sample
D. Within−subject network, entire sample
B. Between−subject network, men
E. Within−subject network, men
C. Between−subject network, women
F. Within−subject network, women
acti.S
domi.S
happ.O
happ.S
warm.O
acti.O
domi.O
warm.S
eq

women. Function qgraph can be used to visualize these graphs as well. In this example, we used the same layout as in Fig. 1A to facilitate comparison with the solution obtained on the whole sample. In the plots, we included a label "eq" to denote edges that are identical for men and women (the code for drawing these edge labels is available in the Supplementary material).

```
qgraph(network2$males,
        layout = plot1$layout,
        labels = colnames(network2$males))
qgraph(network2$females,
        layout = plot1$layout,
        labels = colnames(network2$males))
```

The results are presented in Fig 1B and C, whereas the exact values of each edge are presented in Supplementary Table S2. It is immediately clear that the two clusters that emerge in the full sample are present for both men and women, the pattern of present and absent edges within each cluster being identical. Furthermore, identical weights are assigned to most of the within-cluster edges in both groups, the other within-cluster edges presenting only minor differences (see Table S2).

The most important gender differences emerged in the connections between the two clusters. Men who in general rated themselves as more active throughout social interactions attributed more happiness to the other and men who considered themselves as generally more dominant attributed more warmth to the other, whereas this was not true for women. Conversely, women who typically attributed more dominance to others considered them as warmer, whereas this was not true for men. These results echo gender differences in agreeableness and assertiveness (Costa et al., 2001; Schmitt et al., 2008), and in societal prescriptions (Prentice & Carranza, 2002).

### 2.3. Within-subject networks

The methods we have examined until now refer to the typical behaviors of individuals across different social interactions. Such methods do not allow inspecting the dynamics that involve the transient variability of individual differences within different social interactions. For instance, from a link between self-rated and other-attributed dominance in the between-subject networks one can infer that individuals who perceive themselves as generally more dominant tend also to perceive the interlocutor as more dominant. However, for investigating dynamics that characterize interactions, one needs to compute networks on variables representing variance between different occasions and not between individuals. Here we present how to implement in R a method to infer such "within-subject" networks that was proposed by Epskamp et al. (2017). This method has several advantages. First, it is very simple to apply since it uses the same techniques typically used for computing between-subject networks. Second, it allows separating relationships due to differences between occasions from between-subject relationships even if the number of time points is small (it can be applied even in cases in which only two repeated measures per participant are available; Epskamp et al., 2017). Finally, it can be extended to different groups using the Fused Graphical Lasso.

As an initial step, it is necessary to center the variables around every participant's mean. The following code merges the raw values and the mean values (already stored in the Data.m dataframe) by subject, using function merge. Variable gender is removed from the Data.m dataframe, since this information is already present in the first dataset and it would result in a duplicated variable. The centered values (denoted by the suffix "c") are then computed by subtracting the mean from the raw values with function mutate from package *dplyr*.

```
Data.c <- merge(Data, select(Data.m, -gender), by = "subject")
Data.c <- mutate(Data.c,
                          warm.Sc = warm.S - warm.Sm,
                          domi.Sc = domi.S - domi.Sm,
                          happ.Sc = happ.S - happ.Sm,
                          acti.Sc = acti.S - acti.Sm,
                          warm.Oc = warm.O - warm.Om,
                          domi.Oc = domi.O - domi.Om,
                          happ.Oc = happ.O - happ.Om,
                          acti.Oc = acti.O - acti.Om)
```

In the resulting dataset, Data.c, a score on a variable represents the participant's deviation from his or her central tendency. For instance, a positive score on variable happ.Sc means that a participant is happier than his or her usual level, and a positive score on warm.Oc indicates that a participant's interlocutor is behaving in a warmer fashion than the usual interlocutor.

The code for computing the networks on the centered values is then analogous to the code showed earlier for between-subject networks. The only difference is that now n is the number of occasions, which are 2364 overall, 899 for men and 1465 for women. The following code computes networks both on all participants together using graphical lasso and separately by gender using FGL.

```
S <- select(Data.c, warm.Sc:acti.Oc) %>%
     cor()
S.males <- filter(Data.c, gender == "male") %>%
           select(warm.Sc:acti.Oc) %>%
           cor()
S.females <- filter(Data.c, gender == "female") %>%
             select(warm.Sc:acti.Oc) %>%
             cor()
network3 <- EBICglasso(S = S, n = 2364)
network4 <- EstimateGroupNetwork(list("males" = S.males,
                                      "females" = S.females),
                                 n = c(899, 1465))
```

The code for visualizing the data is nearly identical as for the cross-sectional analysis and is reported in the Supplementary material. The three networks are reported in Fig. 1D, E, and F, whereas edge values are reported in Supplementary Tables S3 and S4. The first thing immediately apparent is that the within-subject networks are denser than the between-subject networks. In the within-subject networks, variables characterizing interactions seem to be more connected to each other, to a point that the clusters that emerged in the between-subject networks are not clearly separated in the within-subject networks. Second, although the structure of the networks estimated separately by gender is similar, there are no edges estimated to be identical for men and women. This means that in this case both sparsity (i.e., regularizing edges to zero) and similarity (i.e., regularizing edges to be identical in the two groups) did not improve model fit according to the EBIC (Epskamp, 2016).

Another interesting result is that the most important connections are present in both the between-subject network and in the within-subject networks. There are however a few exceptions. Whereas in the between-subject networks there was a positive connection between self and others' dominance, in the within-subject network this connection is positive for men, negative for women, and absent when men and women are pooled. Individuals who are typically dominant tend to

**Fig. 1.** Between-subject and within-subject networks of eight variables. Green (full) lines represent positive connections and red (dashed) lines represent negative connections. Thicker lines represent stronger connections and thinner lines represent weaker connections. Edges that are identical in the Panels B and C are indicated with the label "eq". The node placement of all graphs is based on the network in Fig. 1A to facilitate comparison. warm.S = self-rating of behavior in terms of communion, domi.S = self-rating of behavior in terms of agency; happ.S = self-rating of affect in terms of valence; acti.S = self-rating of affect in terms of arousal. Variables warm.O, domi.O, happ.O, and acti.O respectively indicate the same ratings of other's behavior and affect. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

perceive others as more dominant in general. However, in a situation in which another person is perceived more dominant than their usual interlocutor, men tend to behave in a more dominant way, whereas women tend to be less dominant. This is the only edge characterized by a different sign for men and women in the within-subject network and this difference is consistent with prescriptions regarding gender roles (Prentice & Carranza, 2002).

### 2.4. Network indices

The within-subject networks are denser and grasping the patterns of relationships is more difficult than for the sparse between-subject networks. Network indices, such as centrality and clustering coefficient indices, can be used to summarize broader patterns of relationships (for a more detailed tutorial on such techniques, see Costantini et al., 2015).

Centrality estimates need to be sufficiently accurate to be interpretable: Recently, the *correlation stability coefficient* (*CS*-coefficient) has been proposed as an index of accuracy for centrality and it has been implemented in the R package *bootnet* (Epskamp, Borsboom, et al., 2017). It is the proportion of cases that can be dropped such that the resulting centrality estimate correlates more than 0.7 with the original centrality estimate with 95% probability in case-dropping bootstrap resamples. A centrality index should not be interpreted if the CS-coefficient is below 0.25, whereas a value of 0.5 indicates sufficient stability. This technique has not been implemented yet for FGL, but the analysis performed on the entire sample provides a proxy of the stability of the results also for the FGL. The largest CS-coefficients in the between-subjects network was 0.093 and therefore warned against considering centrality in this network. Conversely, CS-coefficients in the within-subject network ranged between 0.74 and 0.75, indicating very high stability.[8]

Centrality estimates can be easily computed using the `centrality_auto` function and they can be visualized using function `centralityPlot`. Similarly, clustering coefficients can be computed and visualized using the `clustering_auto` and `clusteringPlot` functions respectively. These functions are all implemented in package *qgraph*. Centrality estimates for the within-subject network are presented in Fig. 2 and are standardized to facilitate comparison among networks. We choose not to present centrality estimates for the between-subject networks since the results regarding such indices do not seem to be accurate enough to be interpretable. The code below shows how to compute and visualize centrality and the Zhang clustering coefficient for signed networks (Costantini & Perugini, 2014; Zhang & Horvath, 2005) in the within-subject network estimated on all participants. The code for obtaining similar estimates for men and women is very similar and is presented in the Supplementary material, together with the code for generating Fig. 2, which combines centrality and clustering coefficient indices.

```
centrality_auto(network3)

centralityPlot(network3)

clustcoef_auto(network3)

clusteringPlot(network3, include = "Zhang", signed = TRUE)
```

Fig. 2 reports the centrality and clustering coefficients estimated on the within-subject networks, for the entire sample and for men and women separately. All centrality indices converge in indicating that self-rated happiness is the most central nodes in all networks. This means that, all else being equal, the self-reported happiness is more connected with other characteristics of the social interactions, both directly (strength centrality) and indirectly (closeness centrality), and is more relevant for characteristics of social interactions to influence each other (betweenness centrality; Costantini, Epskamp, et al., 2015). This seems to be true irrespective of participants' gender. Happiness attributed to others results as the second most central node according to all indices, with the exception of betweenness centrality for men, according to which other nodes, such as self-reported warmth and activity are more central than others' attributed happiness. This means that, although the perception of others' happiness plays a very important role in shaping social interactions, the role of other's happiness in affecting the possibility for other nodes to interact seems to be more marked for women than for men.

The clustering coefficients both for all participants and for men and women separately converge in indicating that warmth attributed to others is the most locally redundant node, because its neighbors tend to be strongly connected with each other (Costantini & Perugini, 2014). Also for this reason, this node occupies a peripheral position in the network according to all centrality indices.

The code presented below shows how the small-worldness index (Humphries & Gurney, 2008) can be easily computed in R using function `smallworldness` in package *qgraph*. Since the computation of this index requires generating random networks, to ensure the exact replicability of the results we set the random seed to a fixed value of 1. The code presented below is for the within-subject network of all participants, the code for estimating small-worldness on other networks is analogous and is presented in the Supplementary material.

```
set.seed(1)

smallworldness(network3)
```

A value of the small-worldness index larger than 3 indicates that a network has the small world property, whereas *t* values computed on the networks presented here ranged between 0.00 and 1.00, indicating that none of the networks presented here had the small-world property. This could be simply because the variables presented here have been selected to conform to a precise structure (Wiggins, 1991), whereas the small-world property seems to emerge more easily when the nodes reflect broader patterns of individual characteristics (Costantini & Perugini, 2016a).

## 3. Conclusions

In this contribution, we have introduced different techniques connected to network analysis and we have shown how such techniques can be used to examine self- and other-attributed behaviors and emotions dynamics in social interactions. We discussed how to use network analysis to disentangle dynamics that involve stable components of personality (between-subject network) from dynamics that involve the transient variability in such personality features across occasions (within-subject networks; Epskamp et al., 2017). We also showed how the Fused Graphical Lasso (Danaher et al., 2014) allows examining patterns of stability and variability in such dynamics among different groups. For each of these techniques, we presented a guided example of application in a simple setting, in which men and women rated themselves and their interlocutors across different occasions on four dimensions: agency, communion, arousal, and valence. The results obtained in this very simple setting echo well established results regarding gender differences in personality and different descriptive and prescriptive gender stereotypes (Costa et al., 2001; Eagly & Steffen, 1984; Schmitt et al., 2008).

It is important to notice that the methods that we have presented here are not the only ways in which network analysis can be used in psychological research. For instance, we estimated within-subject networks that focus only on fixed effects and do not include estimates of different network structures for each subject, neither they include estimates of cross-lagged relationships among nodes (Epskamp, Waldorp, et al., 2017). One could focus on cross-lagged dynamics using a

[8] We do not present a tutorial on these techniques, since they have been thoroughly described elsewhere (Epskamp, Borsboom, et al., 2017). The code for performing these analyses can be found in the Supplementary material.

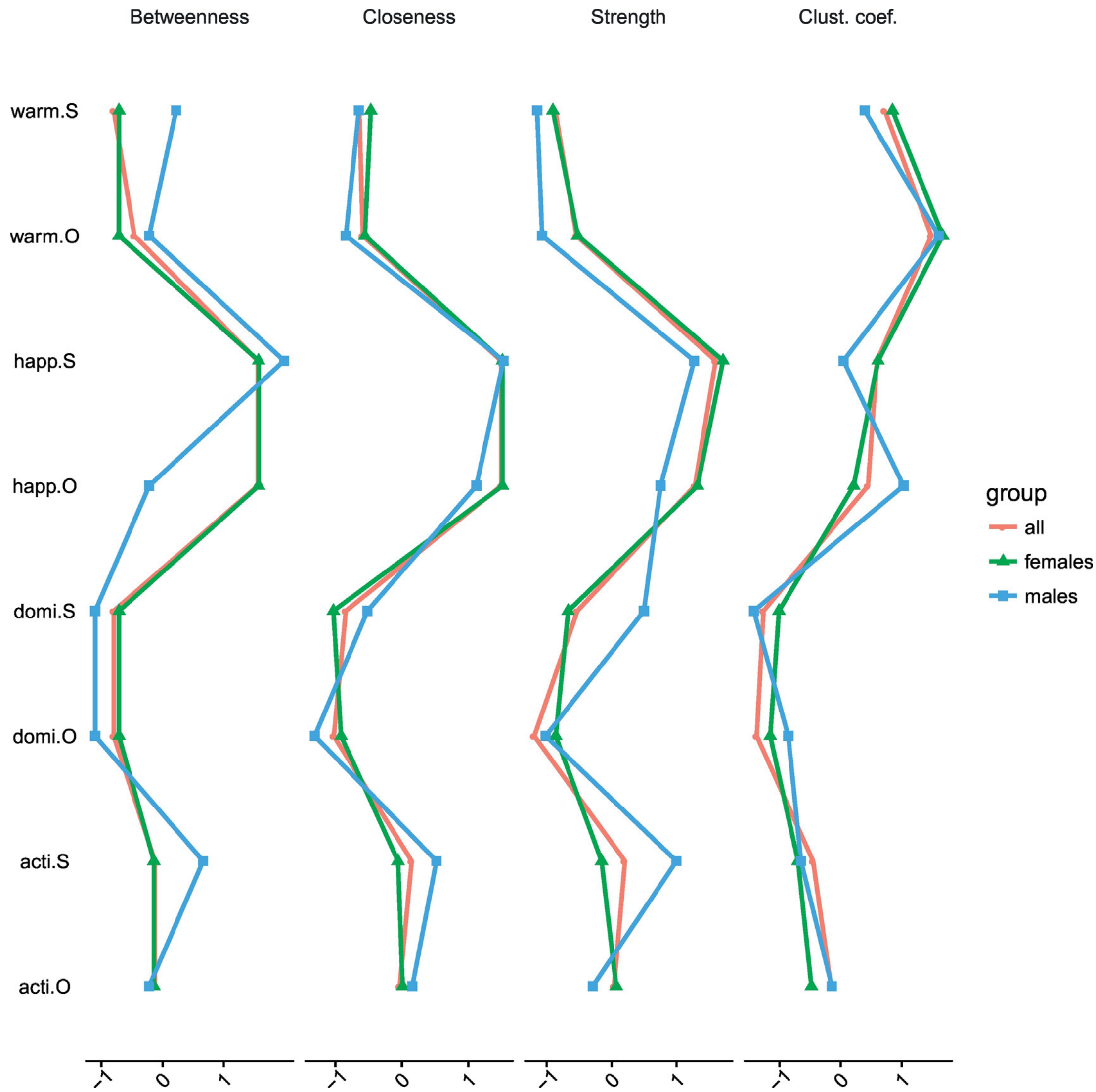



**Fig. 2.** Centrality and clustering coefficient estimates in the within-subject networks. The clustering coefficient reported here is the Zhang signed clustering coefficient (Costantini & Perugini, 2014). The indices have been standardized, to make it easier to compare results in different networks. warm.S = self-rating of behavior in terms of communion, domi.S = self-rating of behavior in terms of agency; happ.S = self-rating of affect in terms of valence; acti.S = self-rating of affect in terms of arousal. Variables warm.O, domi.O, happ.O, and acti.O respectively indicate the same ratings of other's behavior and affect.

combination of autoregressive models and mixed models (Bringmann et al., 2013, 2016). One could also focus on combining network analysis and structural equation modeling (Epskamp, Rhemtulla, & Borsboom, 2017). Furthermore, networks can be also estimated from alternative sources of data, such as participants' evaluations of causal associations among objects of interest (e.g., their own symptoms; Frewen, Schmittmann, Bringmann, & Borsboom, 2013), or data extrapolated directly from diagnostic manuals (Borsboom et al., 2011). In the last few years, the applications of network techniques within psychology are becoming more and more widespread and this has led to the development of many new techniques that are tailored to the needs of this field. Providing a complete overview of the entire spectrum of network techniques is out of the scope of a single contribution. In this work, we focused on a subset of network techniques that allow investigating the between-subjects and within-subject dynamics in personality and psychopathology, across different groups. Methods for simultaneous network estimation and methods for disentangling between-subject and within-subject network have been implemented only very recently in psychology and proved important to understand how personality varies among groups (Costantini & Perugini, 2017; Epskamp, Waldorp, et al., 2017). These methods can be essential to further the understanding of patterns of heterogeneity in individual differences both in personality and in psychopathology (Fried & Cramer, 2017; Mõttus et al., 2015; Østergaard, Jensen, & Bech, 2011).

## Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.paid.2017.06.011.

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Please cite this article as: Costantini, G., et al., Stability and variability of personality networks. A tutorial on recent developments in network psychometrics, *Personality and Individual Differences* (2017), http://dx.doi.org/10.1016/j.paid.2017.06.011

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Please cite this article as: Costantini, G., et al., Stability and variability of personality networks. A tutorial on recent developments in network psychometrics, *Personality and Individual Differences* (2017), http://dx.doi.org/10.1016/j.paid.2017.06.011