



Can network analysis transform psychopathology?☆



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ABSTRACT

Experimental psychopathology has been the primary path to gaining causal knowledge about variables maintaining mental disorders. Yet a radically different approach to conceptualizing psychopathology promises to advance our understanding, thereby complementing traditional laboratory experiments. In contrast to viewing symptoms as reflective of underlying, latent categories or dimensions, *network analysis* conceptualizes symptoms as constitutive of mental disorders, not reflective of them. Disorders emerge from the causal interactions among symptoms themselves, and intervening on central symptoms in disorder networks promises to foster rapid recovery. One purpose of this article is to contrast network analysis with traditional approaches, and consider its strengths and limitations. A second purpose is to review novel computational methods that may enable researchers to discern the causal structure of disorders (e.g., Bayesian networks). I close by sketching exciting new developments in methods that have direct implications for treatment.

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1. Can network analysis transform psychopathology?

Three years ago the American Psychiatric Association (APA) released the fifth edition of its *Diagnostic and Statistical Manual of Mental Disorders* (DSM-5; APA, 2013) amidst a storm of controversy. Immediately prior to the unveiling of the new manual, the director of the National Institute of Mental Health (NIMH) announced that the DSM would no longer furnish the requisite framework for grant proposals submitted to NIMH (Insel, 2013). The institute, he said, would be “re-orienting its research away from DSM categories” and favoring grant proposals targeting transdiagnostic mechanisms, as embodied in the Research Domain Criteria (RDoC) initiative (Insel et al., 2010). Another former NIMH director had already opined that most DSM disorders are little more than reified labels (Hyman, 2010), not genuine diseases. Even the chair of the DSM-IV (APA, 1994) denounced DSM-5 as “widely regarded as a fiasco” (Frances, 2014, p. 372) for medicalizing normal forms of emotional distress (Frances & Nardo, 2013).

Among the controversies swirling about the development of DSM-5 was the hoary debate over whether disorders should be conceptualized categorically or dimensionally. Should we construe symptoms as reflective of underlying, discrete taxa (e.g., Meehl,

1995) or underlying, continuous dimensions (e.g., Helzer et al., 2008)? That is, do mental disorders differ by kind or degree (McNally, 2011, pp. 184–211)?

Categorical and dimensional approaches attempt to explain a fundamental observation of our field: psychiatric symptoms do not co-occur randomly; some are more likely to co-occur than others are. The categorical account postulates a discrete entity as the common cause of symptom emergence and covariance (e.g., Guze, 1992). Just as a malignant lung tumor explains why a person may experience bloody sputum, chest pain, and chronic cough, so may depression explain the co-occurrence of insomnia, anhedonia, unremitting sadness, and other symptoms (cf. Borsboom & Cramer, 2013).

The alternative dimensional model likewise presupposes a common underlying cause of symptom emergence and coherence. As Reise and Waller (2009, p. 28) emphasized in their discussion of item-response theory approaches to psychopathology, one “must first assume that the item [symptom] covariation is caused by a continuous latent variable (common factor)” (Reise & Waller, 2009).

One reason this debate has persisted is that the strengths and limitations of the categorical model are the mirror images of those of the dimensional model, leaving few psychopathologists fully satisfied with either approach. Yet both assume that symptoms reflect the presence of an unobserved latent entity that causes their emergence and covariance (Bollen & Lennox, 1991; Borsboom, Mellenbergh, & van Heerden, 2003; Edwards & Bagozzi, 2000).

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2. The network approach to psychopathology

The psychometrician, Denny Borsboom, and his colleagues have proposed a radically different explanation for syndromic coherence (e.g., Borsboom & Cramer, 2013; Borsboom, 2008; Borsboom, Cramer, Schmittmann, Epskamp, & Waldorp, 2011; Borsboom, Epskamp, Kievit, Cramer, & Schmittmann, 2011; Cramer, Waldorp, van der Maas, & Borsboom, 2010a; Schmittmann et al., 2013). According to their network¹ model of psychopathology, an underlying latent variable is not the common cause of symptom covariance. Rather, it emerges from the dynamic, causal interactions among symptoms themselves. Accordingly, symptoms are not reflective of underlying mental disorders; they are *constitutive* of them.

Consider an episode of depression in a man whose spouse suddenly leaves him. Ruminating about her departure, he experiences insomnia, and his sleep loss causes fatigue the following day. Too tired to concentrate at work, he becomes irritable at his colleagues. His sleep difficulties persist, and he becomes increasingly sad, anhedonic, and pessimistic about his future. It seems obvious that causal interactions among symptoms abound – an assumption prohibited by the axiom of local independence that justifies inference to a latent variable as their common cause of symptom covariance (Borsboom, 2008). This axiom states that correlations among symptoms must disappear once one conditionalizes on the latent variable.

According to the network perspective, an episode of disorder occurs whenever the requisite number of symptoms becomes activated for a sufficient duration. Recovery from disorder occurs when symptoms deactivate, the links between them dissolve, or both. Hence, a mental disorder constitutes a causal system of dynamically interacting, possibly self-reinforcing, symptoms.

Clinical researchers have applied network methods to elucidate causal interactions among symptoms constitutive of depression (e.g., Cramer, Borsboom, Aggen, & Kendler, 2012; Fried et al., 2015; van de Leemput et al., 2014), posttraumatic stress disorder (PTSD; McNally et al., 2015), obsessive-compulsive disorder (OCD; McNally, Mair, Mugno, & Riemann, 2016), schizophrenia (van Kampen, 2014), childhood disorders (Boschloo, Schoevers, van Borkulo, Borsboom, & Oldehinkel, 2016; Martel, Levinson, Langer, & Nigg, 2016; Saxe et al., 2016), social anxiety disorder (Heeren & McNally, in press), substance abuse and dependence (Rhemtulla et al., 2016; and persistent complex bereavement disorder [PCBD] a.k.a. complicated grief; Robinaugh, LeBlanc, Vuletich, & McNally, 2014). The purpose of this article is to review network analysis of psychopathology, touch upon illustrative recent findings, and to consider the strengths and limitations of the approach.

3. Key concepts in network analysis

Networks consist of nodes and edges. Nodes represent the objects of study, and edges represent the connections between them. In psychopathology networks, nodes represent symptoms, and edges represent associations between symptoms.

Networks can consist of either *weighted* edges or *unweighted* edges. An unweighted edge merely signifies that two symptoms are connected, whereas a weighted edge signifies the magnitude of the

connection (e.g., a Pearson correlation coefficient), represented by thickness of the edge. The association between two symptoms can be either positive or negative, typically signified by the colors green and red, respectively. For example, the nodes *sleep disturbance* and *fatigue* are customarily connected by a green (positive) edge, whereas those for *loss of appetite* and *weight gain* are often connected by a red (negative) edge.

Finally, the edges of networks can be *undirected* or *directed*. Undirected networks consist of edges – single lines – that connect pairs of symptoms. These merely signify an association, but are agnostic about whether activation of symptom X predicts activation of symptom Y, or vice versa. Undirected networks also allow the direction of prediction to go both ways. Directed networks consist of edges with arrow tips at one end of the edge, pointing in the direction of prediction, and perhaps causation.

4. Node centrality metrics

Traditional categorical approaches to psychiatric diagnosis emphasize hallmark symptoms that are strongly associated with a single disorder, but seldom associated with other disorders. Some nosologists have proposed that we purify diagnostic criteria sets of nonspecific symptoms appearing in many disorders, leaving only those strongly associated with the syndrome (e.g., Spitzer, First, & Wakefield, 2007). This recommendation was especially an issue for specialists struggling to make sense of high levels of comorbidity among the supposedly discrete categorical diagnoses of personality disorder.

Network analysis turns this entire enterprise on its head. Indeed, as Cramer et al. (2010a) have persuasively argued, nonspecific symptoms (e.g., concentration impairment) that appear in many diagnostic criteria sets may be especially important. Such symptoms may serve as bridges linking two syndromes (e.g., major depression and generalized anxiety disorder). Activation issuing from a bridge symptom can spread to both syndromes, thereby producing diagnostic comorbidity.

Instead of focusing on hallmark symptoms unique (or nearly so) to a certain disorder, network analysis computes metrics of *node centrality* (Freeman, 1978/1979). Highly central nodes are those of greatest importance in the network, and these need not be unique hallmarks of a specific disorder. Different measures of centrality index different ways of being important. Five measures of centrality are *degree*, *strength*, *expected influence*, *closeness*, and *betweenness*.

4.1. Degree centrality

A node's degree is the number of edges connected to it, and the higher the degree, the more central the node is to the network. This metric is common in unweighted networks. For example, consider a social network comprising individuals (nodes) and the friendship connections (edges) between pairs of individuals. The person who has a lot of friends in the network would appear as a node with many edges, each connected to another node.

4.2. Strength centrality

Weighted networks enable computation of *node strength*, not merely node degree. In such networks edge thickness represents the magnitude of the association and hence the probability that activation of one node will be associated with activation of nodes connected to it. Accordingly, *strength centrality* denotes the sum of the weights (e.g., correlation coefficients) of the edges connected to a node. Strength centrality is especially important for psychopathology networks as it reflects the likelihood that activation of a certain symptom will be followed by activation of other symptoms.

¹ The network approach bears a family resemblance to Boyd's (1991) concept of a *homeostatic property cluster kind*, advanced to provide a nonessentialist interpretation of *species* as a cluster of properties that coheres and exhibits homeostasis despite environmental perturbations. Although Boyd's work caught the attention of clinicians uneasy about essentialist natural kind approaches to mental disorder (McNally, 2011, pp. 203–208; Kendler, Zachar, & Craver, 2011), network analysis possesses powerful computational methods that transcend Boyd's conceptual framework.

For example, in a prospective longitudinal study of healthy adults in The Netherlands, [Boschloo, van Borkulo, Borsboom, and Schoevers \(2016\)](#) found that people reporting subthreshold levels of depression symptoms high on strength centrality (fatigue, depressed mood, anhedonia, and concentration impairment) at baseline were at greater risk for developing an episode of major depressive disorder during the following six years than were people whose baseline subthreshold symptoms were of low strength centrality. These findings suggest that symptoms scoring high on strength centrality may require early intervention to prevent episodes of disorder. Both hallmark symptoms (depressed mood and anhedonia) and nonspecific symptoms (fatigue and concentration impairment) had high strength centrality scores.

Network analysis may enable detection of harbingers of good versus poor response to treatment. After devising a method for comparing network structures, [van Borkulo et al. \(2015\)](#) distinguished two groups of people who had participated in a longitudinal cohort study of depression. One group had remitted by the two-year follow-up, whereas the other group had not. The researchers discovered that at baseline the network of persisters was more densely connected than that of the remitters. Feelings of guilt, fatigue, and loss of energy were especially important in the persister network compared to the remitter network, even after [van Borkulo et al.](#) controlled statistically for differences in overall severity. These data indicate that network analysis can provide novel indicators of risk for recalcitrant depression.

Network analysis identifies symptoms having high centrality, and thus ripe as targets for clinical intervention, if we assume that edges reflect potentially causal connections between symptoms. For example, [Fried, Bockting, et al. \(2015\)](#) found that spousal bereavement activated the symptom of loneliness, which in turn, activated other symptoms of depression. This implies that early interventions that successfully reduce loneliness in recently bereaved people should prevent depression from developing. Likewise, successfully targeting a high-centrality symptom among people who already have a disorder (e.g., sleep disturbance in PTSD) should initiate a beneficial therapeutic cascade that turns off other symptoms, thereby hastening recovery. A reanalysis of a large medication trial of people with depression revealed that symptoms having high closeness centrality were most responsive to medication ([Fried, Boschloo, et al., 2015](#)). In our study of complicated grief ([Robinaugh et al., 2014](#)), we found that emotional pain – a symptom that nearly got excluded from the DSM-5 criteria for PCBD – scored very high on three centrality measures. These findings illustrate how network analysis can detect crucial symptoms that clinicians can sometimes miss but need to target therapeutically.

Finally, for directed networks, one can compute the *in-strength centrality* and the *out-strength centrality* of nodes. A node with high out-strength is a source of activation for the nodes receiving its edges, whereas a node with high in-strength is the recipient of activation emanating from other nodes. In clinical treatment, successfully targeting a symptom with high out-strength is likely to result in resolution of other symptoms receiving activation from the target symptom, and hence swift recovery from an episode of disorder.

4.3. Expected influence

Computation of strength centrality concerns a node's incident edges weighted by their *absolute* magnitude. This works fine as long as there are no negative edges between any nodes. However, standard measures of node centrality will provide a progressively inaccurate gauge of a node's influence to the extent that the network has edges depicting negative correlations ([Everett & Borgatti, 2014](#)). Solving this problem, my former Ph.D. student,

Donald J. Robinaugh, devised a new centrality metric called *expected influence* that takes into account both negative and positive edges. Simulations indicated that this new centrality metric matches the performance of strength centrality when networks contain only positive edges, but outperforms it as networks contain increasingly more negative edges ([Robinaugh, Millner, & McNally, in press](#)). Revisiting a longitudinal study on bereaved older adults, we found that decline in the severity of complicated grief symptoms having high expected influence centrality predicted more pronounced clinical improvement in the overall network than did decline in the severity of symptoms having low expected influence centrality.

4.4. Closeness centrality

The *closeness* of a node is the average distance from that node to all other nodes in the network. Closeness is the inverse of *farness* (i.e., the mean shortest weighted path length between a certain node and all other nodes in the network). This metric seems less useful psychopathology than in epidemiology, for example, whereby infection of a person (node) high on closeness centrality will be more likely to incite a rapidly developing epidemic than will infection of a person low on closeness centrality.

4.5. Betweenness centrality

To determine the *betweenness centrality* of a node, one first calculates the shortest path length between each pair of nodes in the network. The betweenness of a node is the number of times that node lies on the shortest path between two other nodes. If the shortest path between node X and node Y has this edge passing through node Z, then node Z has (at least) a betweenness of one. If node Z lies on the shortest path between nodes A and B, then node Z has a betweenness of two, and so forth.

Symptoms shared by two often-comorbid disorders are high on betweenness centrality, and serve as bridges between the two disorders. Activation of a symptom high on betweenness centrality is especially likely to spread to both syndromic clusters, thereby producing a comorbid presentation (e.g., major depression and generalized anxiety disorder; [Cramer et al., 2010a](#)). For example, studying OCD and depression symptoms in patients with severe OCD, we found that one symptom – sadness – connected OCD symptoms to those of depression ([McNally et al., 2016](#)).

5. Types of networks

Psychopathologists have computed several types of networks, most concerning cross-sectional, observational symptom data. Although cross-sectional data cannot alone confirm causality among symptoms, network analysts have devised methods that can bring us closer to characterizing mental disorders as causal systems ([McNally, 2012](#)).

5.1. Association networks

Association networks are the most basic, computable via the R package, *qgraph* ([Epskamp, Cramer, Waldorp, Schmittmann, & Borsboom, 2012](#)). In our study on PTSD symptoms in survivors of the Wenchuan, China earthquake ([McNally et al., 2015](#)), each column corresponded to one of the 17 DSM-IV ([APA, 1994](#)) PTSD symptoms assessed on a 5-point severity/frequency scale ranging from 1 (“Not at all”) to 5 (“Extremely”) on the Posttraumatic Checklist – Civilian (PCL-C; [Weathers, Litz, Herman, Huska, & Keane, 1993](#)). Each node represented one of the 17 PTSD symptoms measured by the PCL-C, and each edge represented the

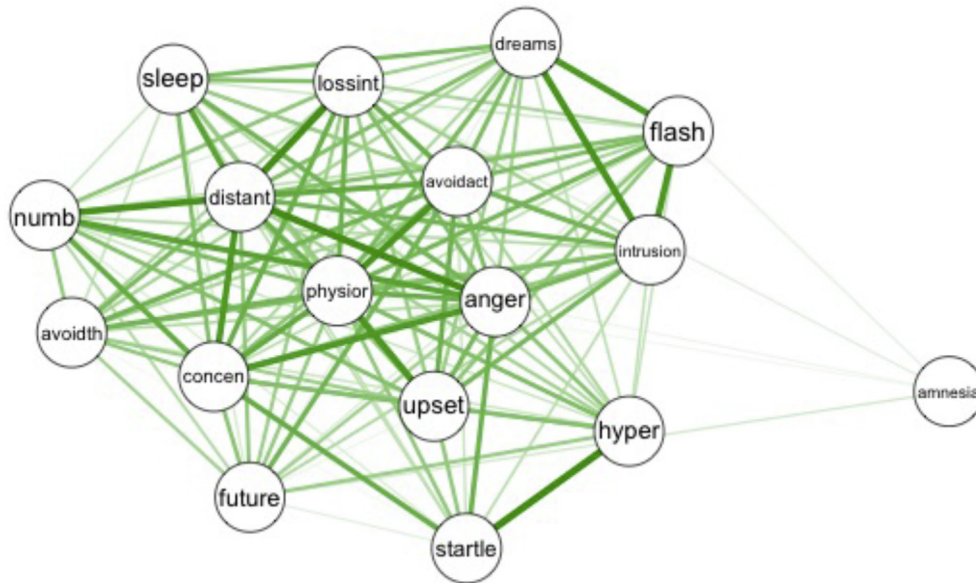


Fig. 1. Association network ($r \geq 0.3$) depicting zero-order correlations among PTSD symptoms in adults reporting histories of childhood sexual abuse.

strength of association between two symptoms connected by an edge (i.e., zero-order correlation).

In the original article (McNally et al., 2015), Fig. 2 presented an association graph of these data, depicting zero-order correlations between pairs of symptoms reaching threshold (i.e., $r > 0.3$). Here, Fig. 1² presents an association network depicting PCL-C PTSD symptoms reported by adults reporting histories of childhood sexual abuse (McNally, 2015). The network is weighted and undirected (i.e., no arrows at the tips of edges, and the threshold for depiction is $r > 0.3$). Implementing Fruchterman and Reingold's (1991) algorithm, *qgraph* places nodes with stronger correlations near the center of the network, and those with weaker correlations near the outskirts of the network. Strong edges appear between numbness and feeling distant from others; between hypervigilance and startle; and between flashbacks and traumatic dreams and intrusive thoughts about the trauma. Difficulty remembering aspects of the abuse ("amnesia") is least central to the network.

5.2. Partial correlation networks

The ultimate purpose of network analysis is to discern the causal relations among symptoms, not merely the correlations among them. As correlations constitute a necessary, but insufficient basis for causal inference, association networks can count as only the first step in this process.

Partial correlation networks rectify a limitation integral to association networks. For example, in an association network, an edge connecting symptom X with symptom Y may signify that activation of X activates Y (or vice versa) or that the association between X and Y arises partially or entirely from the influence of other symptoms. Partial correlation networks take us one step closer to discerning causal relations by computing the partial correlation between symptom X and symptom Y after adjusting for the influence of all other symptoms in the network. Accordingly, edges appearing in an association network that remain after adjustment

are plausible candidates for counting as causal connections.

Network researchers have computed partial correlation networks in two ways. Concentration networks depict partial correlations that exceed some specified threshold (e.g., $r \geq 0.1$; Fig. 3 in McNally et al., 2015). Alternatively, one can run the graphical lasso (i.e., Least Absolute Shrinkage and Selection Operator) algorithm (Friedman, Hastie, & Tibshirani, 2010).

Using the R packages *qgraph* and *glasso*, I computed a partial correlation network on PTSD symptoms from survivors of the Wenchuan earthquake. Applying an L1 penalty, the graphical lasso estimates a sparse inverse covariance matrix that shrinks small partial correlations, setting them to zero such that they do not appear in the final partial correlation network. That is, it eliminates trivial partial correlations that are likely "false alarms." Hence, only the most robust partial correlations remain visible following this iterative procedure.

Fig. 2 presents a partial correlation network depicting edges that survived the graphical lasso after appearing in the association network (Fig. 2 in the original article; McNally et al., 2015). For example, strong edges remained between hypervigilance and exaggerated startle responses, and between intrusive thoughts and traumatic dreams. The analysis also uncovered other associations less obvious to clinical observation. Strong associations remained between anger and concentration impairment; emotional numbness and future foreshortening; and loss of interest in previously enjoyed activities and feeling distant from other people.

5.3. Relative importance networks

Partial correlation networks depict only direct associations between pairs of symptoms, but the network itself is not directed. Hence, X could influence Y, Y could influence X, or both.

In a relative importance network, each edge depicts the relative importance of a symptom as a predictor of another symptom (Johnson & LeBreton, 2004). Relative importance concerns both the direct effect of node X on node Y and the effect of node X on node Y after one has adjusted for all other nodes in the network. These networks are both weighted and directed. Hence, the graph depicts both the magnitude of the association and the direction of prediction, with arrows originating from the predictor node and

² To obviate reprinting published figures in this article, I computed conventional networks on new data sets (McNally, 2015) or novel networks on old data sets (McNally et al., 2015).

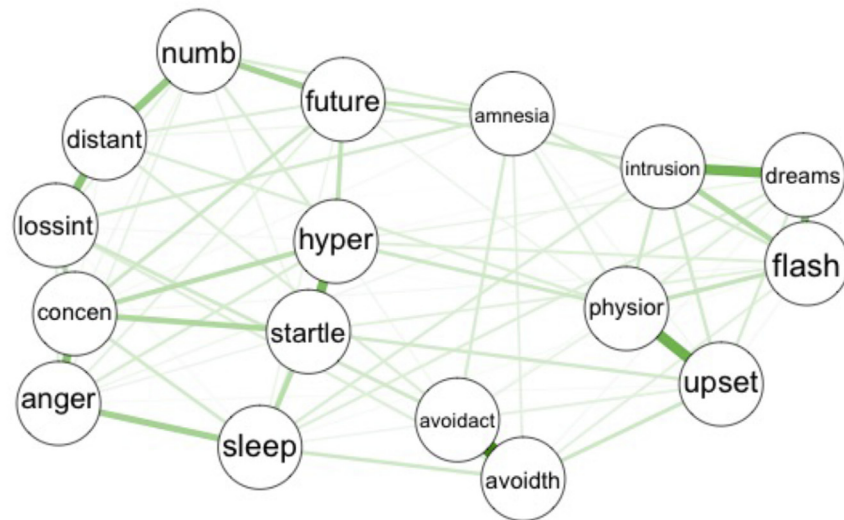


Fig. 2. Partial correlation network constructed via the graphical lasso depicting PTSD symptoms in adult survivors of the Wenchuan, China earthquake.

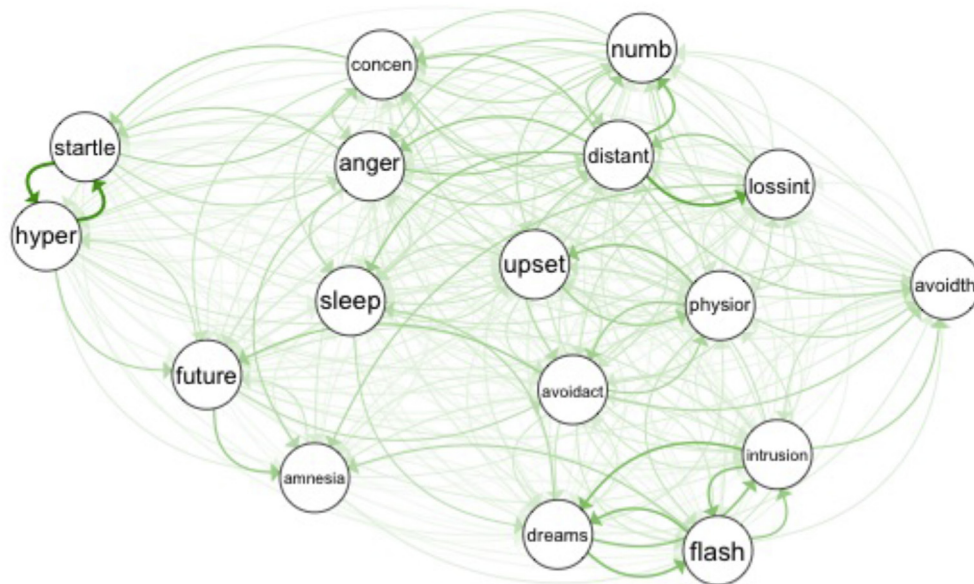


Fig. 3. A directed relative importance network depicting the strength of a PTSD symptom as a predictor of another symptom PTSD in adults reporting histories of childhood sexual abuse.

terminating on the predicted node. To compute relative importance, we have used the *lmg* metric in the R package *relainpo* (Grömping, 2006).

Relative importance networks resemble partial correlation networks in that they control for the effects of other nodes when one is attempting to ascertain the magnitude of prediction between node X and node Y. However, these networks describe the strength and direction of prediction, not causation. For example, in our network analysis of symptoms of complicated grief among subjects who had experienced spousal bereavement (Fig. 2; Robinaugh et al., 2014), we found that emotional pain had a high level of relative importance as a predictor of thoughts about the deceased person, difficulty envisioning a future, yearning for the deceased, and avoidance of reminders of the death.

Fig. 3 presents a relative importance network depicting PTSD symptoms among adults reporting a history of childhood sexual abuse (McNally, 2015). Feeling distant from others is a strong

predictor of loss of interest in previously enjoyed activities and a strong predictor of numbness; the strength of prediction in the opposite direction is much weaker for these edges. In contrast, being hypervigilant is a strong predictor of startle responses and vice versa. Traumatic dreams, intrusive thoughts, and flashbacks are all strong predictors of one another.

5.4. Bayesian networks

Network research in psychopathology has hitherto been mainly a descriptive enterprise. In contrast, Bayesian network analysis is a parametric method that produces directed acyclic graphs (DAGs). A DAG is a directed network whereby each edge has an arrow tip on one end, signifying the direction of prediction and possibly causation. A DAG lacks cycles (i.e., activation emanating from one node does not flow through the network and return to its node of origin).

Bayesian network analysis emerged from an interdisciplinary

program comprising electrical engineers, statisticians, philosophers specializing in causation, computer scientists, and mathematicians specializing in graph theory. The aspiration of Bayesian network analysis is to discern causality, even from cross-sectional, observational data. However, causal inference does require additional assumptions (Pearl, 2011).

Our research group has been exploring Bayesian psychopathology networks (McNally et al., 2016). Our approach involves submitting symptom data to the *hill-climbing* algorithm furnished by the R package, *bnlearn* (Scutari, 2010). This algorithm adds edges, removes them, and reverses their direction until a goodness-of-fit target score (e.g., Bayesian Information Criterion [BIC]) is reached. Standard procedure calls for randomly restarting the process with different candidate edges between different symptom pairs, perturbing the system, and so forth. Via this iterative procedure, the system learns the structure of the network. One can stabilize the network by extracting many bootstrap samples (e.g., 500), and averaging the resultant network. Also, one can set a criterion for edge retention in the averaged network (e.g., an edge must appear in at least 85% of the bootstrapped networks). This produces a “sparse” network whereby only edges appear that are almost certainly genuine (i.e., “false alarm” edges disappear). Moreover, not only does the DAG compute the direction of edges, it reveals the percentage of the bootstrapped samples in which the edge appeared in the direction depicted in the final, averaged

Bayesian network. Finally, it computes a BIC value for each edge. The BIC value indicates how damaging it would be to model fit if one were to remove the edge from the network. Accordingly, high absolute BIC values reflect how important the edge is to the model that best captures the structure of the data.

Revisiting the data from the Wenchuan earthquake study, Patrick Mair, my departmental statistics colleague, and I computed Bayesian networks. We did this in two ways. First, I provided “hints” to the algorithm by excluding (“blacklisting”) edges that made no clinical sense. That is, I directed it not to bother testing for certain edges that are unlikely to embody causal connections between pairs of PTSD symptoms (e.g., avoidance of thoughts about the trauma seems unlikely to cause exaggerated startle; emotional numbness is unlikely to cause hyperarousal). Second, we let the algorithm learn the structure of the network on its own without any hints from me. Strikingly, both the restricted and unrestricted networks were identical (Fig. 4). According to the network, the trauma of the earthquake incited anger, and anger triggered sleep problems, hypervigilance, concentration impairment, and loss of interest in previously enjoyed activities. Emotional numbing and feeling distant from other people are among the downstream symptoms.

But what, precisely, is flowing through this network? Aspirationally, it depicts the direction of causation (Pearl, 2011). Conservatively, it depicts the direction of “probabilistic dependencies”

Unrestricted Network

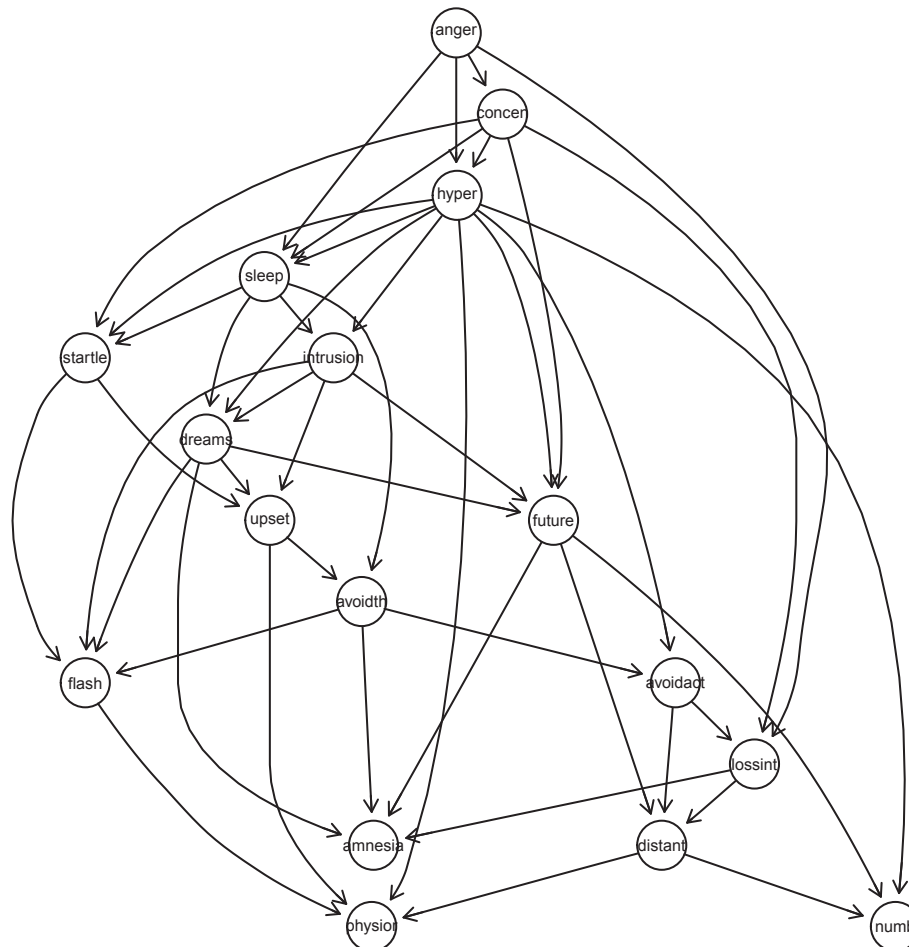


Fig. 4. A Bayesian network (Directed Acyclic Graph [DAG]) depicting PTSD symptoms in adult survivors of the Wenchuan, China earthquake.

(Scutari, 2010, p. 2) or prediction. That is, the presence of anger is associated with an increased likelihood that the earthquake survivor will experience difficulty sleeping, for example.

Leaders in the field of causal inference and Bayesian network analysis agree that correlation (*alone*) does not signify causation. Nevertheless, they argue that under a certain set of assumptions one can reasonably make causal inferences from correlational, observational data (e.g., Pearl, 2011). First, there cannot be any unobserved variables influencing those in the network. That is, if there is another variable (e.g., unmeasured symptom of another disorder) that produces a strong causal effect on symptoms modeled by the DAG, then spurious associations between symptoms will be wrongly be interpreted as causal connections. Second, the causal Markov assumption must be met. That is, given its causes, each symptom must be independent of its direct and indirect non-effects. Third, certain assumptions about the probability distribution of each symptom must be met. Fourth, sometimes it is difficult to identify the single best causal Bayesian network. Sometimes computation returns several plausible causal DAGs, especially when the number of subjects is relatively small. Sometimes the direction of the edges varies among these DAGs.

In light of these constraints, what can we conclude? As causal, actionable knowledge, not merely associational, correlational knowledge, is the goal of mental health professionals (indeed, of everyone!), how often can we say that the direction of prediction in a Bayesian network occurs because of causality? Our confidence in causality grows when computation converges on a stable DAG whose edges reliably occur in one direction, when the model makes sense clinically, and when we are reasonably confident that we did not miss any important variables that could produce spurious associations in the DAG. Intervening on symptoms can provide additional information bearing on causality. Treating a symptom that appears in the DAG should turn off activation in its “descendant” symptoms. For example, successfully reducing anger in the earthquake victims should yield swifter therapeutic benefits than reducing flashbacks (Fig. 4).

6. Strengths and limitations of network analysis?

A potentially fatal objection to latent variable approaches to psychopathology, whether construed categorically or dimensionally, is their failure to satisfy the axiom of local independence requisite for justifying an inference to an underlying entity as the common cause of symptom emergence and covariance (Borsboom & Cramer, 2013; Borsboom, 2008). Indeed, it seems obvious that causal connections abound between symptoms (e.g., sleep loss causing fatigue; phobic fear causing avoidance behavior; obsessional distress causing rituals).

Yet some critics object that network theorists overstate the seriousness of this problem (e.g., Ashton & Lee, 2012; Terracciano & McCrae, 2012), arguing that one can, indeed, accommodate residual correlations among items (symptoms) independent of their association with the latent variable. In reply, network theorists note that when one relaxes assumptions to enable such model-tweaking, “factor analysis ceases to be a credible tool for identifying unobserved causes because that [causal] interpretation is crucially dependent on the assumption of local independence” (Cramer, van der Sluis, et al., 2012b, p. 452). Moreover, direct interactions between symptoms appear to be the rule, not the exception. Accordingly, accommodating many residual correlations would seemingly undermine the plausibility of any latent variable approach.

Most network studies rely on single self-report measures of specific symptoms, raising concerns that such measures may imperfectly capture the clinical phenomena. To address this

concern, network theorists could integrate multiple measures of a symptom. For example, the PTSD symptom of psychophysiological reactivity to reminders of the trauma could be assessed via self-report, electromyographic, electrodermal, and cardiac measures (Orr, McNally, Rosen, & Shalev, 2004). Yet, critics ask, does this not reintroduce latent variables, one for each node so measured (e.g., Krueger, DeYoung, & Markon, 2010)? In reply, network theorists have distinguished latent variables that have a natural referent versus abstract ones that do not. For example, Cramer, Waldorp, van der Maas, and Borsboom (2010b) observe that the symptom of insomnia could be assessed with multiple indicators (e.g., self-report, electroencephalographic, and observational). Yet latency to fall asleep has a natural referent whose effects on the three measures are known and that accounts for correlations among the indicators (i.e., satisfies the axiom of local independence). Latent variables having a natural referent within the person comport well with network analysis. However, other latent categorical variables (e.g., depression) or latent dimensional ones (e.g., neuroticism) do not have such natural referents.

Ontological distinctions are relevant (Borsboom, 2008; McNally, 2012). Both the network and latent variable perspectives are ontologically realist about symptoms as these have existential referents. However, the network perspective denies the existential status of the diagnostic latent variable. Depression, for example, is not a separate thing that causes symptoms in the manner of a lung tumor that causes symptoms. In the case of cancer, the tumor is identifiable independent of its symptoms – the cause is logically and empirically distinct from its effects. Accordingly, a person can have cancer yet be currently asymptomatic, whereas it makes no sense to say that an asymptomatic person has depression. In the case of most psychiatric disorders,³ the relation to symptoms to disorder is mereological (Borsboom & Cramer, 2013) – part(s) to whole – in the same manner as the relation of the 50 states to the USA is mereological.

Focusing on symptoms – “*symptomics*” (Fried, Boschloo, et al., 2015, p. 1) – than conjectured latent variables yields additional benefits, as work on depression shows (Fried, 2015). Symptoms of depression vary in their risk factors (e.g., female sex, childhood stress; Fried, Nesse, Zivin, Guille, & Sen, 2014), the kinds of life stressors triggering them (Cramer, Borsboom, Aggen, & Kendler, 2012; Keller & Nesse, 2006; Keller, Neale, & Kendler, 2007), and their impact on different aspects of psychosocial functioning (e.g., Fried & Nesse, 2014). For example, Keller et al. (2007) found that bereavement and romantic breakups were strongly associated with sadness, appetite loss, and anhedonia, whereas chronic stress and failure were associated with fatigue and hypersomnia.

Finally, although some theorists believe that latent variable research is revelatory of “core psychopathological processes” (Krueger, 1999, p. 921), it is questionable whether latent variables, such as internalizing or externalizing, tell us anything about the processes operating within individuals. Just as psychometric *g* does not itself signify a process or module within an individual person (Borsboom & Dolan, 2006), nor do other between-subjects variables, such as neuroticism or heritability (Lewontin, 1974), within people. Indeed, many psychological variables do not possess *ergodicity* (Borsboom, Kievit, Cervone, & Hood, 2009; Molenaar & Campbell, 2009; Molenaar, 2004a, 2004b). That is, they do not

³ Occasionally, a realist ontology works for a DSM disorder (e.g., Down syndrome; Borsboom, Epskamp, et al., 2011). The British physician, John Langdon Down, described a syndrome characterized by intellectual deficiency, protruding tongue, slanted palpebral fissures, and short stature in 1866, and in 1959 geneticists discovered its characteristic common cause – a third copy of chromosome 21 (Hickey, Hickey, & Summar, 2012).

exist or function *within* individuals as they do *between* or *among* individuals.

For a clinical example, consider two approaches to the “fear of fear,” anxiety sensitivity (Reiss & McNally, 1985) and catastrophic misinterpretation of bodily sensations (Clark, 1986). The former, measured by the Anxiety Sensitivity Index (ASI; Reiss, Peterson, Gursky, & McNally, 1986), denotes individual differences *among* people, whereas the latter denotes a process occurring *within* individuals. Accordingly, differences among people in their ASI scores can explain why people vary in their propensity to panic in response to a carbon dioxide inhalation, but they are silent about the psychological processes unfolding within a person who panics after inhaling carbon dioxide. In contrast, catastrophic misinterpretation of certainly bodily sensations induced by carbon dioxide inhalation can accomplish this.

Finally, despite its causal promissory note, Bayesian network analysis has potential limitations. First, as Shrouf (2011) observed, DAGs “tend to emphasize causal relations as if they occur all at once” (p. 12) akin to a diagram in electrical engineering where a state change in node X immediately causes a change in downstream nodes Y, Z, and so forth. Yet, as he observed, causal relations in psychopathology occur over different time scales (e.g., seconds for panic attacks; weeks for response to medication).

Second, DAGs prohibit looping effects whereby a node early in the chain events activates other nodes that wind up influencing the state of the originating node. That is, cycles cannot occur. But is acyclicity plausible, at least for certain disorders? For example, Clark's (1986) model of panic provides a classic example of an informal network of symptoms > catastrophic misinterpretations > increased fear > increased symptoms constituting a single cycle. On the other hand, such apparent causal cycles may actually signify the unfolding of an autonomous process; assuming a causal loop may amount to falling prey to the *post hoc, ergo propter hoc* fallacy (McNally, 1994, p. 13). But to the extent that genuine causal cycles do occur, DAGs cannot model them.

7. Future directions

The aim of research in abnormal psychology is to discover the causes of mental health problems, thereby enhancing the efficacy of prevention and treatment. The field of experimental psychopathology remains at the forefront of these efforts (van den Hout, Engelhard, & McNally, *in press*). However, for obvious ethical reasons, many questions concerning causality are unanswerable with experimental methods. Complementing experimental approaches, network analysis aims to elucidate the causal processes among symptoms that culminate in episodes of disorder. However, most network studies have involved correlational analyses on cross-sectional symptom reports. Correlation is necessarily consistent with causation, but does not confirm it.

Researchers have begun to introduce a temporal dimension to network analysis that takes us beyond cross-sectional data and moves us one step closer to discerning causality. An important recent development is the application of network analysis to longitudinal time series data whereby subjects use digital devices to record their mood multiple times per day over various periods of time (e.g., Bringmann et al., 2013; Wichers, 2014; van de Leemput et al., 2014).

Indeed, as Molenaar (2004a) has emphasized, for non-ergodic psychological processes, such quantitative, idiographic methods are essential for advancing psychology, including psychopathology, in the 21st century. In one study conducted over seven days revealed that patients with major depression had an especially densely connected emotion network, especially for negative emotions, relative to healthy subjects (Pe et al., 2015).

In another study, Bringmann, Lemmens, Huibers, Borsboom, and Tuerlinckx (2015) submitted weekly depression symptom scores to a vector autoregressive multilevel analysis that estimated the network of depression symptoms as they evolved over 14 weekly assessments. This method revealed the temporal dynamics of a network whereby anhedonia played a central role.

Network analysis has identified markers of impending tipping points whereby people shift suddenly from a healthy to a depressed state (Hofmann, Curtiss, & McNally, *in press*). Using an Experience Sampling Method in a ground-breaking time series study, van de Leemput et al. (2014) had healthy and depressed subjects rate four moods (content, cheerful, sad, and anxious) on digital devices multiple times per day for 5–6 days. Analyzing these time series data, they found that increased temporal autocorrelation of ratings of negative moods and increased variance in the ratings predicted shifts from healthy to depressed states. These metrics reflect a phenomenon called *critical slowing* whereby dynamic networks take increasingly longer to rebound from perturbations, eventually reaching a tipping point.

In conclusion, network analysis may very well transform the field of psychopathology in important ways. Advances in quantitative methods, computational power, and mobile technology will pay if clinical researchers can use idiographic network methods to guide therapeutic intervention in the coming years (Hayes, Yasinski, Barnes, & Bockting, 2015). Progressively sophisticated methods, combined with data from other sources, can support a causal abductive inference (Peirce, 1901/1940) or inference to the best explanation (Harman, 1965), just as they do in epidemiology. Indeed, the discovery that cigarette smoking is a cause of lung cancer did not emerge from longitudinal investigation of people randomly assigned to smoking versus nonsmoking groups. Rather, diverse sources of evidence supported this causal inference (Hill, 1965). No single method in the field of psychopathology is likely to provide answers to all the questions we pose about the origins and treatment of psychological disorders. Yet network analysis holds promise as both a scientific and practical approach to conceptualizing and guiding treatment of these conditions.

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