**Supplementary Material**

**Data Analysis**

**Network analysis*.*** *The CAPS+MADRS-items network (PTSD sample only)*. Network models estimating the associations between symptoms were constructed using the Graphical Gaussian Model (GGM; Epskamp and Fried, 2016), through the R-package *qgraph* (Epskamp *et al.*, 2012). In computing the network, we controlled for false positives from statistical noise and multiple testing, by using L1-regularization, balancing sparsity and goodness of fit (Tibshirani, 1996), thus allowing for better approximation of the population network (Boschloo *et al.*, 2016, Costantini *et al.*, 2015). Next, using the LASSO procedure (Friedman *et al.*, 2008, Friedman *et al.*, 2014), we applied regularized model selection, estimating a maximum likelihood solution by minimizing the extended Bayesian information criterion. This criterion relies on a hyper-parameter, λ, which was assigned a value of 0.5 based on prior research (Costantini *et al.*, 2015). For the PTSD-MDD network visualization, we used the multidimensional scaling approach (Jones *et al.*, 2018).

*The CPAS-items networks (PTSD and TE samples)*. In addition to including a penalty on density (as in the graphical lasso) regulated by the tuning parameter λ1 (i.e. the lasso parameter), the FGL also includes a penalty on differences among corresponding edge weights in networks computed in different samples, regulated by a tuning parameter λ2 (Fried *et al.*, 2018). Because we did not know whether the true networks of the PTSD and trauma-exposed (TE) treatment-seeking patients not meeting full criteria for PTSD samples are similar or different, we chose both λ1 and λ2 is through *k*-fold cross-validation, as implemented in the R-package Estimate Group Network (Costantini and Epskamp, 2017). For visualization of these networks we used a circular layout to make it easier to discern the differences in densities between the two networks. Recent work suggests that the Fruchterman-Reingold (FR) algorithm, commonly used for the visualization of psychological networks, can be misleading when directly comparing two networks (Jones *et al.*, 2018).

Within the resultant graphical networks, each node depicts a specific symptom as measured by the CAPS/MADRS. Edges connecting nodes represent an association between two symptoms while controlling for all other symptoms, with line thickness representing association strength. Blue and red edges represent positive and negative associations, respectively. In our network estimations, we plotted the network structure for the treatment-seeking PTSD and TE samples, using the 17 symptom items of the CAPS (CAPS-items network). We then plotted the network structure for the PTSD sample while incorporating both the CAPS 17-symptom-items and the MADRS depressive symptom-items (CAPS+MADRS-items network). Due to the use of ordinal variables from the MADRS, polychoric correlations were used for network estimation.

**Node centrality measures*.*** The relevance or importance of symptoms (nodes) within networks was characterized by using the expected influence measure of node centrality, as standard centrality measures provide a progressively inaccurate gauge of a node’s influence when a network has edges depicting negative correlations (Everett and Borgatti, 2014).

Expected influence analysis were done using the R package *bootnet* (Epskamp *et al.*, 2018) and included the one-step expected influence (Robinaugh *et al.*, 2016, Wang *et al.*, 2018), which reflects the summed weight, including positive and negative values, of a node’s edges with the neighboring nodes in the network, and as such assess the node’s more direct influence (Heeren *et al.*, 2018). Higher values denote greater centrality indicative of greater importance of a node/symptom to the network/disorder (Freeman, 1979, Opsahl *et al.*, 2010)

Expected influence was computed for all presented networks. For the CAPS+MADRS-items network, EI was also computed considering only bridge nodes, namely, nodes which have symptom-level connections with nodes of the opposite disorder, reflecting between-disorder symptom associations (Jones *et al.*, 2019).

**Network Robustness (Accuracy and Stability).** *Network accuracy* was computed using the R-package *bootnet* (Epskamp *et al.*, 2018) employing a non-parametric bootstrap approach. We estimated edge weights accuracy at a 95% confidence intervals (CIs) by sampling the data 1,000 times (with replacement), thereby generating a distribution of edge weights. *Network stability* was assessed using a bootstrap person-dropping procedure (Costenbader and Valente, 2003) in which centrality metrics of the original data set are repeatedly correlated with those calculated for subsamples of progressively fewer participants, yielding a correlation stability (CS-coefficient) coefficient for each centrality measure. CS-coefficients quantify the maximum proportion of cases that can be dropped from the original dataset while retaining a correlation with the original centrality measure higher than 0.7. Network structure stability is indicated by a CS-coefficient, that should not be below 0.25 and preferably be above 0.50 (Epskamp *et al.*, 2018). Network robustness measures were computed for all three networks. While reporting all robustness measures, interpretation of findings was based primarily on node strength, as recent research has shown node strength to be more reliably estimated (Epskamp *et al.*, 2018, Fried *et al.*, 2018).

**Network Comparison*.*** *The Network Comparison Test* (NCT R-package; van Borkulo and Millner, 2016), a permutation-based algorithm that evaluates the null hypothesis of equal connectivity between networks across randomly regrouped permutations of individuals, was used to compare the CAPS-items and TE-CAPS-items networks. First, we randomly sampled 306 PTSD patients from the original PTSD sample to ensure an even number of participants in the PTSD and TE samples. Next, we used an omnibus test evaluating invariance of the *network structure* across groups. Then, we tested the differences in *global strength* (i.e., connectivity) between the networks by comparing the sum of absolute edge weight values.

**Directed acyclic graph (DAG) analysis*.*** We used a Bayesian network analysis, applying the R-package, *bnlearn* (Scutari, 2010, Scutari and Denis, 2014), to produce directed acyclic graphs (DAGs). The aim of Bayesian network analysis, including DAG, is to discern causality (Pearl, 2011). By submitting symptom data to the hill-climbing algorithm furnished by the *bnlearn* R-package, a DAG adds edges, removes them, and reverses their direction until a goodness-of-fit target score (e.g., Bayesian Information Criterion; BIC) is reached, indicating how damaging it would be to model fit if one were to remove the edge from the network.

This first step determines whether an edge between two symptoms exists (it does not determine its weight). To determine edge existence across the network, it uses an iterative procedure where it randomly restarts the procedure with various candidate edges potentially linking different pairs of symptoms, perturbing the system, and so forth, till the system learns the network structure. We bootstrapped 1,000 samples to stabilize the network, computing a network for each sample (McNally *et al.*, 2017). In the second step, these networks were averaged to obtain the final network. To this end, edge retention was set to determine the frequency an edge appeared in the 1,000 bootstrapped networks, using a statistically-driven method retaining edges with high sensitivity and specificity (Scutari and Nagarajan, 2013). Thus, edges that are almost certainly genuine appear in the DAG, with “false alarm” edges eliminated. Finally, BIC value was computed for each edge, with higher values signifying higher importance of an edge within the network structure. The magnitude of the BIC value is visualized through the edge thickness.

For the present study, we used the completed partially DAG (CPDAG) which accounts for some of the shortcomings of equivalent separate DAGs (Scutari and Denis, 2014). Thus, in the DAG estimating procedure in which DAGs are bootstrapped we used the equivalence class instead of the network structure itself. The bootstrapping procedure we applied also attempts to account for the possibility of multiple DAGs fitting the data, by computing an average. We also took similar precautions as (McNally, 2016) and (Heeren *et al.*, 2018) to ensure network stability by accepting only the edges that appeared in a specified proportion of the models based on an optimal significance threshold for inclusion.

To clarify the directionality between PTSD specific symptoms and depression and functioning levels, we computed the DAG network including the 17 CAPS single items, the 10 MADRS single items, and POAMS-TV total score.

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