**Data analysis**

*Network estimation*

We estimated the network structure of anxiety and depression symptoms as a multilevel vector auto-regression model (MVAR) with orthogonal random effects (Bringmann et al., 2013; Epskamp et al., 2018), using the mlVAR (Epskamp et al., 2021) package in R (R Core Team, 2022), version 0.5. In multilevel VAR models, variables at time point t are sequentially regressed on the lagged version of themselves and all other variables at time point t-1, assuming a random intercept and a random slope for every predictor. The mlVAR function in R automatically applies within-person centring for all predictors. We estimated the network with different sets of symptoms and compared them by AIC and BIC fit indices to select the best fitting model. Finally, we applied a False Discovery Rate controlling procedure described in (Benjamini & Hochberg, 1995, see also Bringmann et al., 2013).

The initially envisioned model with 17 variables on the complete data set returned convergence issues. We addressed this by removing participants with low variance in too many variables. As we collected psychopathological data from a community sample and did not apply any selection criteria in this sense, some participants had little to zero variance in most of the symptoms. We counted the zero variances for each participant and removed those whose number of zero variance variables was greater than the 3rd quartile (Q3 = 4). We also addressed the convergence issues by reducing the complexity of the model, averaging the scores of the two items regarding “Concentration difficulties” and the two items regarding „Fatiguability” (see Table 1). Because these items had very close conceptual similarity, this resulted in very strong edges between the two, affecting the fading of other edges and leading to artificially inflated centrality indices for the two symptoms.

Additionally, “Sleep difficulties” were not included in the analysis because this symptom cannot vary within the day. We aimed for the best possible DSM-5 symptoms’ representations in our network, and initially measured this symptom. However, plotting the model revealed a very strong auto-regressive effect for “Sleep difficulties”, which biased the fading of other edges and inflated this symptom’s centrality. Additionally, some edges pointed towards this symptom, which does not have any relevant logical interpretation as it suggests a prediction of past night “Sleep difficulties” by future daytime symptoms.

*Centrality analyses*

 We used version 1.4.0 of R package *networktools* (Jones, 2021) to estimate *bridge strength, bridge indegree*, and *outdegree* (Jones et al., 2021). *Bridge strength* indicates how strongly a node from a predefined community is related to other communities and is calculated by summing the absolute value of weights attributed to edges weights that lead from one node to nodes from other communities. We can separate *bridge strength* into *bridge indegree* and *outdegree[[1]](#footnote-1)* to take the direction of edges into account. For a more extensive description of bridge centrality indices see Jones et al. (2021). Because depression and anxiety have both shared and unique symptoms, we explored bridge centrality twice: 1) first time considering shared symptoms as part of the anxious community and 2) second time considering them as part of the depressive community of nodes.

Regular centrality measures were also investigated, namely *instrength* and *outstrength* (Bringmann et al., 2019). Outstrength will indicate how much a node overall predicts other nodes at subsequent timepoints, and instrength will indicate how much a node is predicted by other nodes at previous timepoints. For the contemporaneous network we analysed strength centrality. All data analyses were carried out in R version 4.1.3 (R Core Team, 2022).

*Community analysis*

To identify sub-graphs of nodes that are more densely connected to each other than with the rest of the network, we performed a community structure analysis using the Walktrap algorithm with different lengths of random walks (Pons & Latapy, 2006). The Walktrap algorithm is based on the idea that short random walks tend to stay in the same vicinity and can be used to identify groups of nodes in a network. To identify communities, we used *cluster\_walktrap* function from package *igraph*, version 1.2.11 (Csardi & Nepusz, 2006). The function requires the number of walks to be specified prior to calculations. We estimated the communities with a different number of steps, ranging from 1 to 10000. To identify the best community structure, we plotted and compared the modularity of each version of the community structure that was obtained. Modularity is a quantification of how densely connected are nodes within communities as opposed to connections between communities (Newman, 2006). Therefore, we selected the solution with the highest modularity values, indicating more strongly connected communities.

**Empirically derived communities of nodes**

 In some networks, certain nodes tend to be more correlated with each other and form communities of nodes (Golino & Epskamp, 2017). Community detection in network analysis has a similar purpose to exploratory factor analysis: to identify groups of observed variables that are more tightly related to each other. The difference between the two is the explanation of why the observed variables group together. According to factor analysis, the covariance of several observed variables is explained by an underlying latent variable that functions as their common cause. In network community detection, the grouping of variables is explained solely by the strong relationships between certain variables.

Community detection was applied in several studies on cross-sectional networks of depression and anxiety. In two past studies, authors identified almost identical communities to the scale’s factor structure (Bergh et al., 2021; Gauld et al., 2021). However, Cramer et al. (2010) have reported no separate communities in their network, all depression and anxiety symptoms being strongly connected and forming only one community. Kaiser et al. (2021) used the Clique Percolation Method for detecting communities in network of MDD and GAD DSM-5 diagnostic criteria. Unlike the aforementioned studies, this method yielded four communities which they labelled: withdrawal, psychomotor, anxiety, and auto-aggression.

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1. Regular degree centrality doesn’t consider the weight of edges and is a mere counter of the number of edges that are associated with a node (Bringmann et al., 2019). However, bridge indegree and bridge outdegree does consider the weights of edges (Jones, 2021), and is a counterpart for instrength and outstrength centrality indices, but in the bridge framework. If we were to sum bridge indegree and bridge outdegree, we will get bridge strength values. [↑](#footnote-ref-1)