Supplementary Materials for:

Network analysis of substance abuse and dependence symptoms

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Bootstrapped substance class networks

The Ising model applies $l1$-regularized logistic regressions that constrains many of the small coefficients to zero (Ravikumar *et al.* 2010). The penalty parameter, which determines the extent to which coefficients are shrunk to zero, is selected using the extended Bayesian Information Criterion. The smaller the sample size, the stronger the penalty and the more 'sparse' the resulting network will be (i.e., the fewer edges it will have).

Because the sample sizes were so variable across the six substance classes (cannabis, $N = 2216$; sedatives, $N = 352$; stimulants, $N = 670$; cocaine, $N = 628$; opioids, $N = 195$; hallucinogens, $N = 345$), there was a concern that the resulting networks (referred to as G1 in the remainder of the supplementary materials) would not be comparable due to differential sparsity. To address this concern, we used a bootstrapping procedure to draw 500 samples of size $N = 500$ each, with replacement, from the dataset for each substance class (this means certain participants appear more than once in substance categories with $N < 500$). We produced a network for each bootstrapped sample and averaged across these to create a set of substance class networks based on the same size sample data (G2). G1 is visualized in supplementary Figure S1, whereas G2 is presented as Figure 2 in the main report.

To determine the degree of similarity, we correlated the edge weights of each substance class within G1 with the edge weights of the same substance class of G2 (i.e. the original networks directly obtained from the data with the bootstrapped networks). Correlations ranged from .90 to .99 (on average .95), documenting that the different sample sizes in G1 are not a major concern (in detail, the correlations between the edges of G1 and G2 were: .95 for cannabis, .96 for sedatives, .94 for stimulants, .99 for cocaine, .90 for opioids, and .93 for hallucinogens). We therefore decided to report the conceptually simpler network models based on the data (G1) instead the bootstrapped networks (G2) in the main manuscript of this report.

Of note, one particular edge is D4 – D6 for opioids stands out as very different between G1 and N2. We believe this edge to be a false positive association. With 11 nodes per network, 55 edges are

estimated per network, leading to the overall estimation of 55*6=330 edges. It is not unlikely that one of

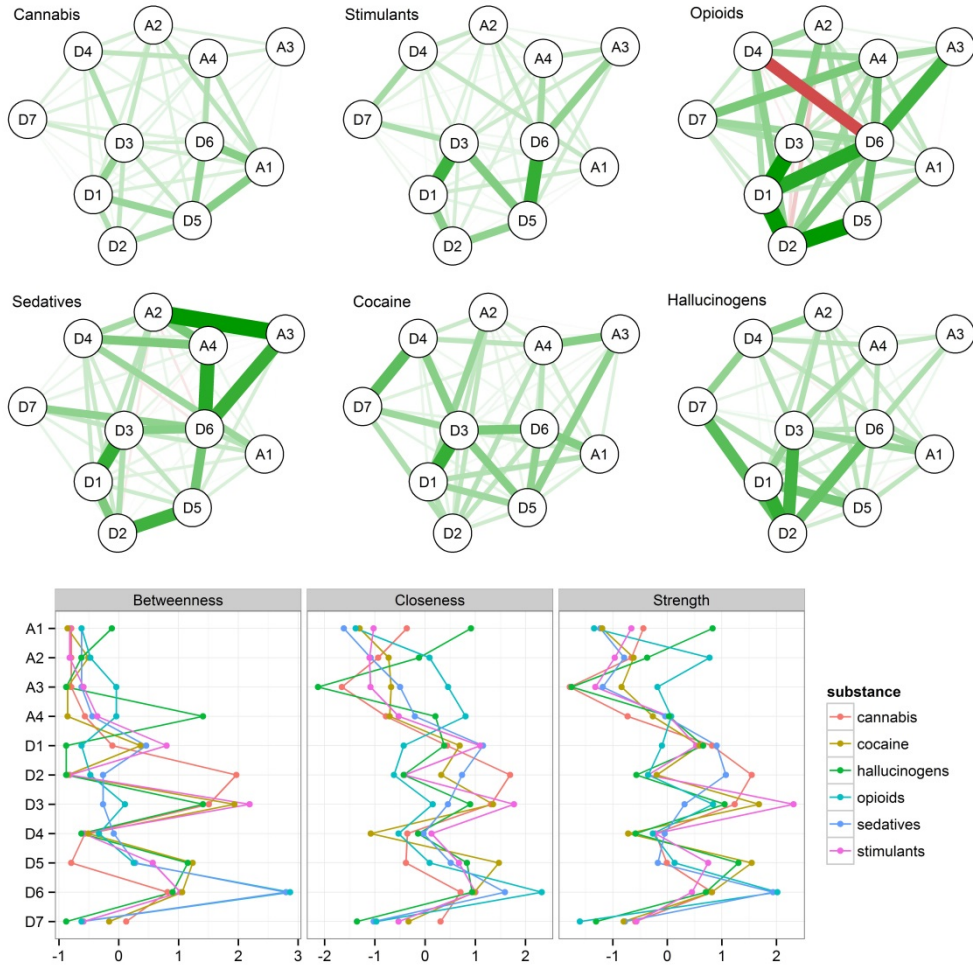these will result in a parameter very different from the original networks.

Figure S1. Symptom networks for individual substances based on the bootstrapping procedure.

Upper: Line thickness indicates the strength of pairwise connections. All six networks use the same

graphical standardization, which means that the strength of the edges can be compared across

networks. Lower: standardized centrality measures for each symptom within each substance

network.