Figure 1S. EBICglasso MDD symptom-domain networks at baseline and week 8 (n = 151). Blue and red lines represent, respectively, positive and negative partial correlations, and the thickness of each edge indicates the strength of the association. The gray ring around each MDD symptom-domain represents its predictability. The network layouts were averaged to facilitate visual comparisons.

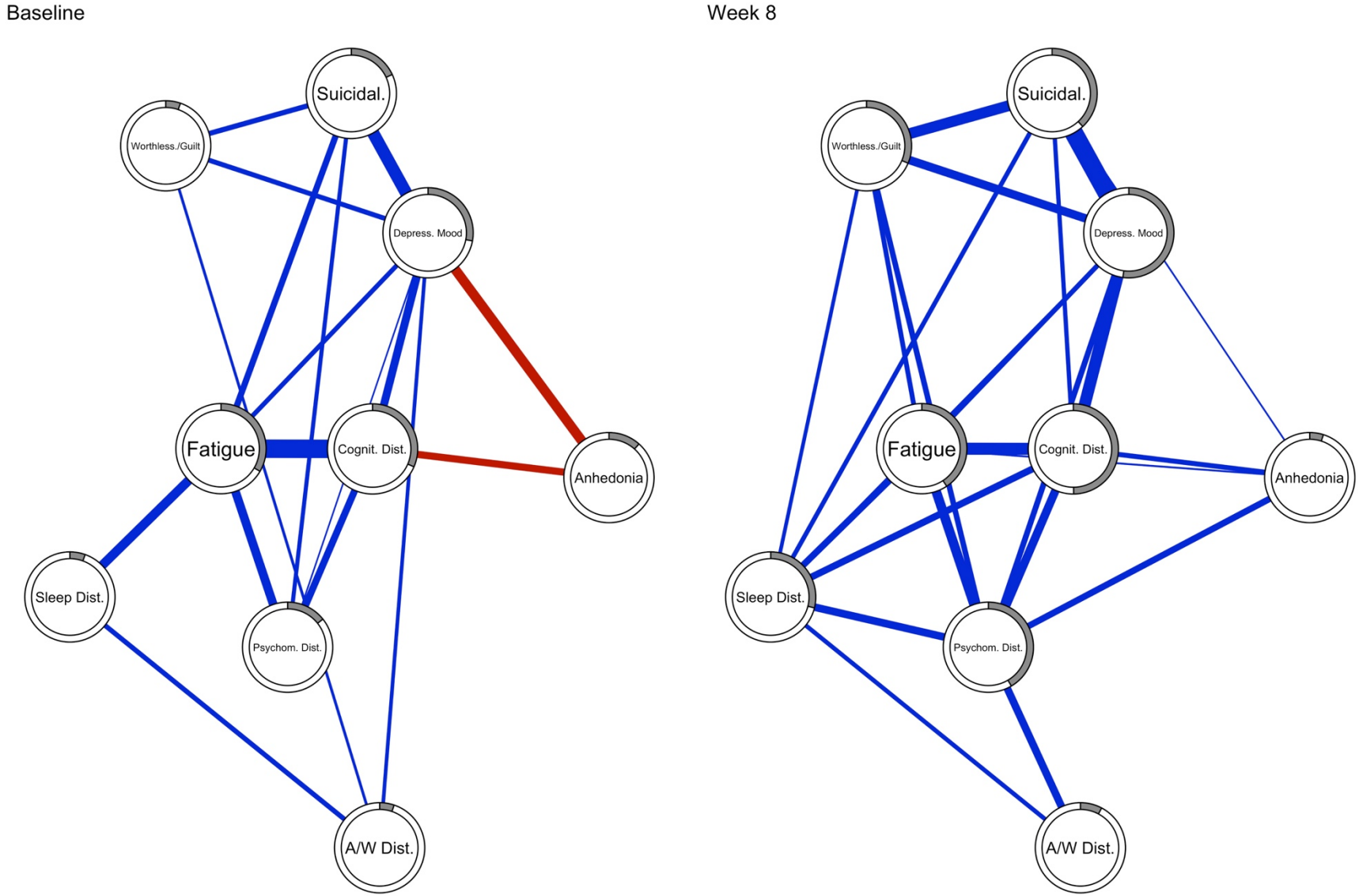


Figure 2S. EBICglasso MDD symptom-domain networks at baseline and following 8 weeks of treatment with desvenlafaxine (n = 74). Blue and red lines represent, respectively, positive and negative partial correlations, and the thickness of an edge indicates the strength of the association. The gray ring around each MDD symptom-domain represents its predictability. The network layouts were averaged to facilitate visual comparisons.

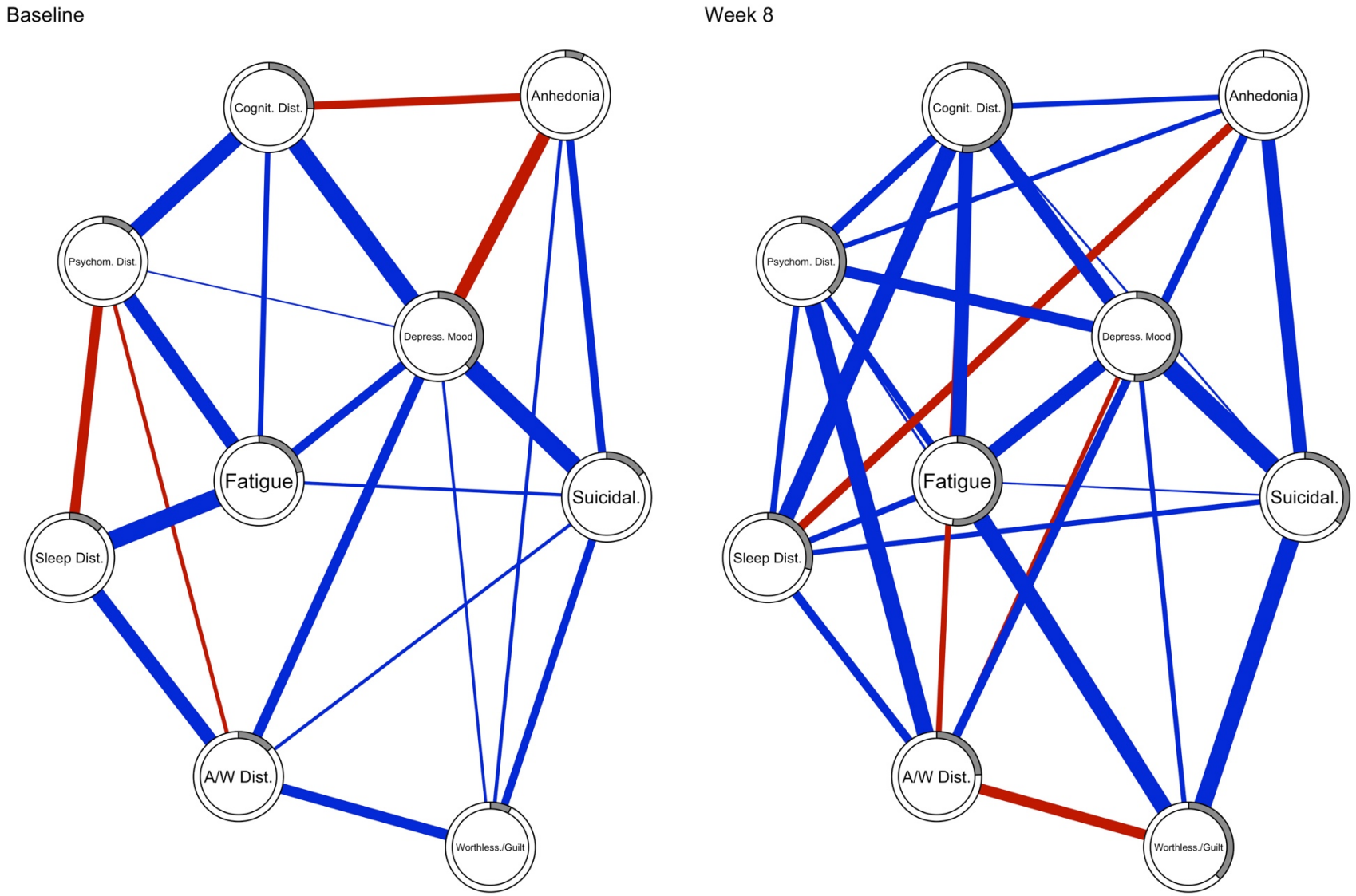


Figure 3S. EBICglasso MDD symptom-domain networks at baseline and following 8 weeks of treatment with escitalopram (n = 77). Blue and red lines represent, respectively, positive and negative partial correlations, and the thickness of an edge indicates the strength of the association. The gray ring around each MDD symptom-domain represents its predictability. The network layouts were averaged to facilitate visual comparisons.

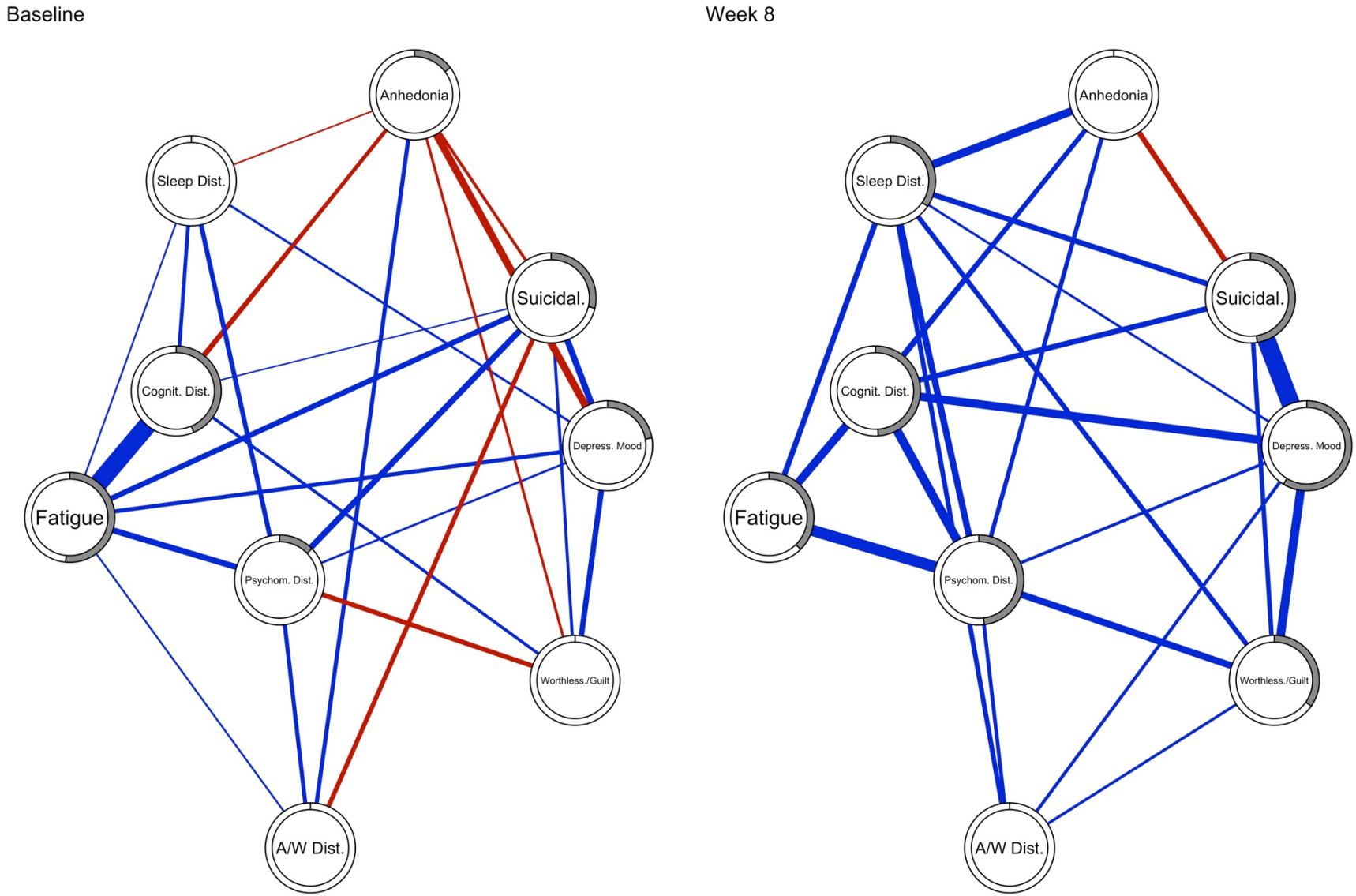
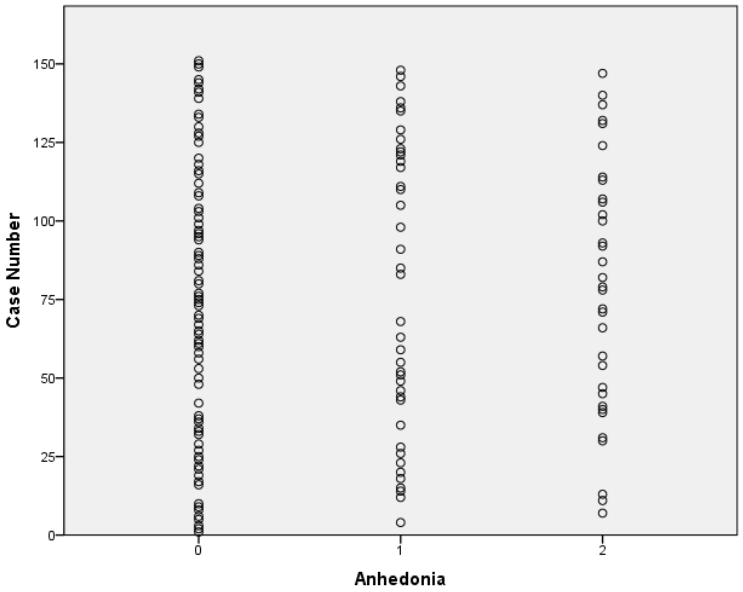
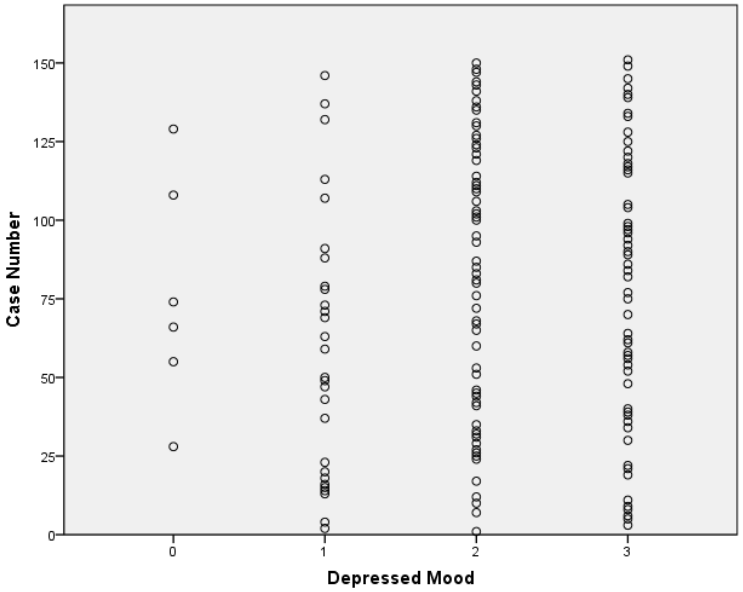


Figure 4S. Score distribution (0-3) on the QIDS-SR among the MDD symptom-domains with negative partial correlations at baseline (n = 151): (a) Anhedonia, (b) Depressed Mood and (c) Cognitive Disturbance.

(a)



(b)



(c)

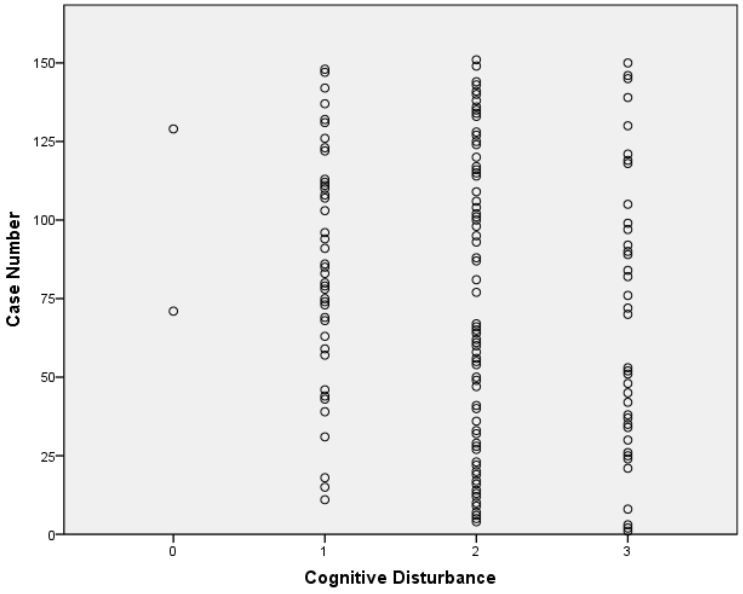


Figure 5S. Permutation test results for comparisons of global strength (top) and structure (bottom) between the MDD symptom-domain networks at baseline and week 8 (n = 151). The *p*-value equals the proportion of network differences from the 5,000 randomly regrouped subsamples at least as extreme as the network differences in the original subsamples. The black triangle on the x-axis represents the estimated difference in the original data.

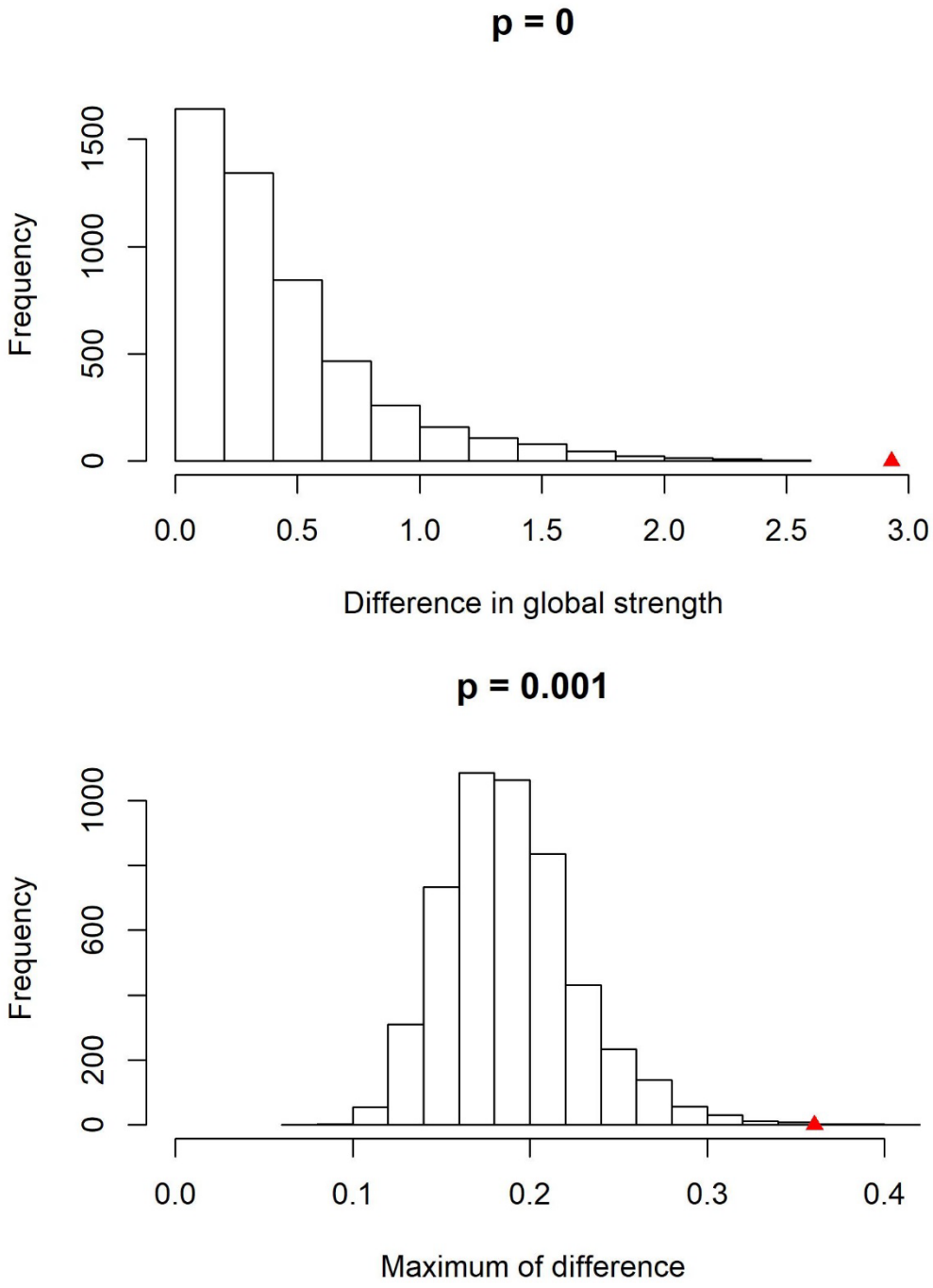


Figure 6S. Maximum proportion of the original sample at baseline (n = 151) that can be dropped (*x* axis) while retaining expected influence (EI) centrality correlation > 0.70 with the original sample. The solid lines indicate the centrality correlations, and the shaded areas indicate the 95% CIs for the centrality correlations.

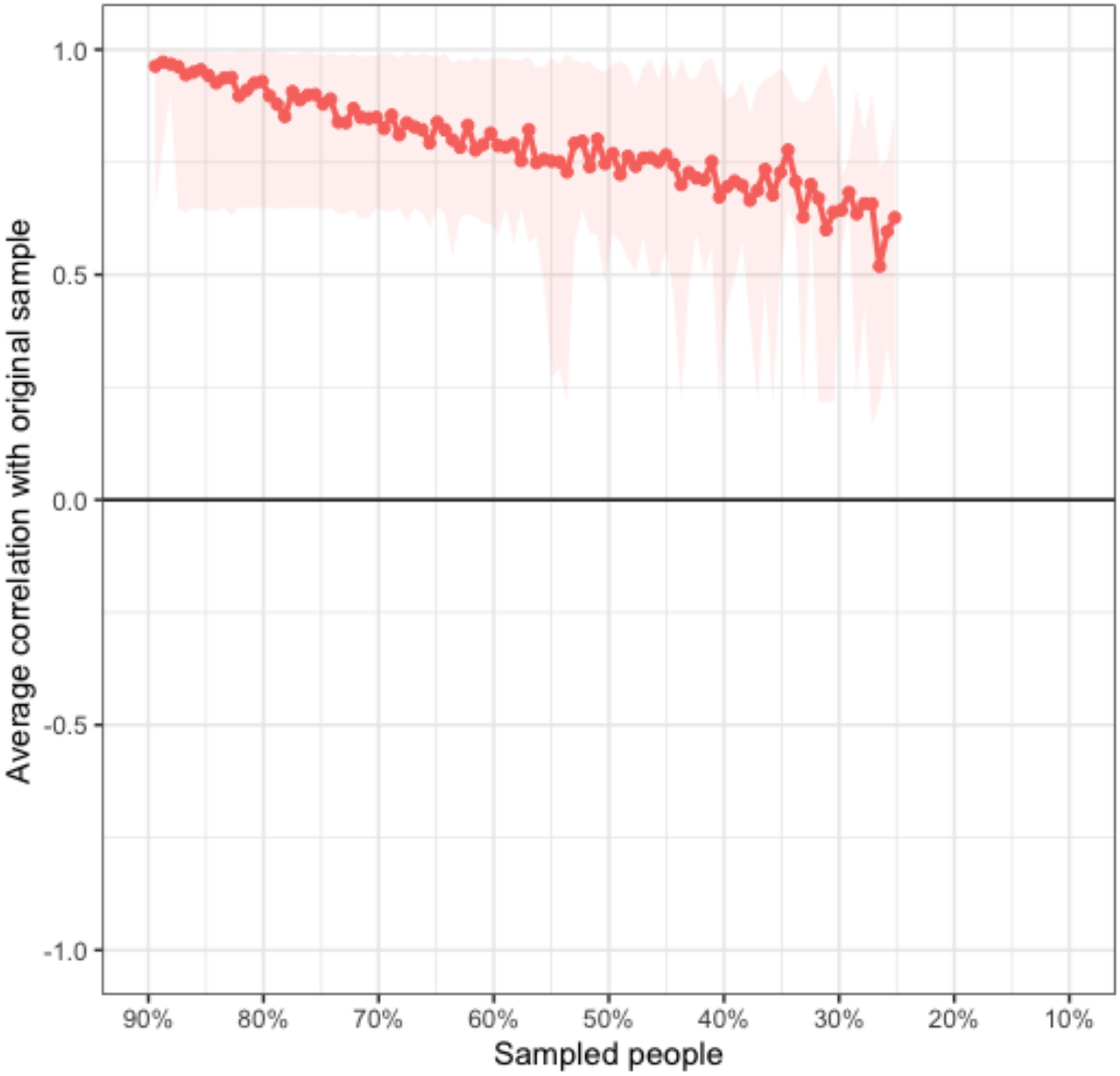


Figure 7S. Maximum proportion of the original sample at week 8 (n = 151) that can be dropped (*x* axis) while retaining an expected influence (EI) centrality correlation > 0.70 with the original sample. The solid lines indicate the centrality correlations, and the shaded areas indicate the 95% CIs for the centrality correlations.

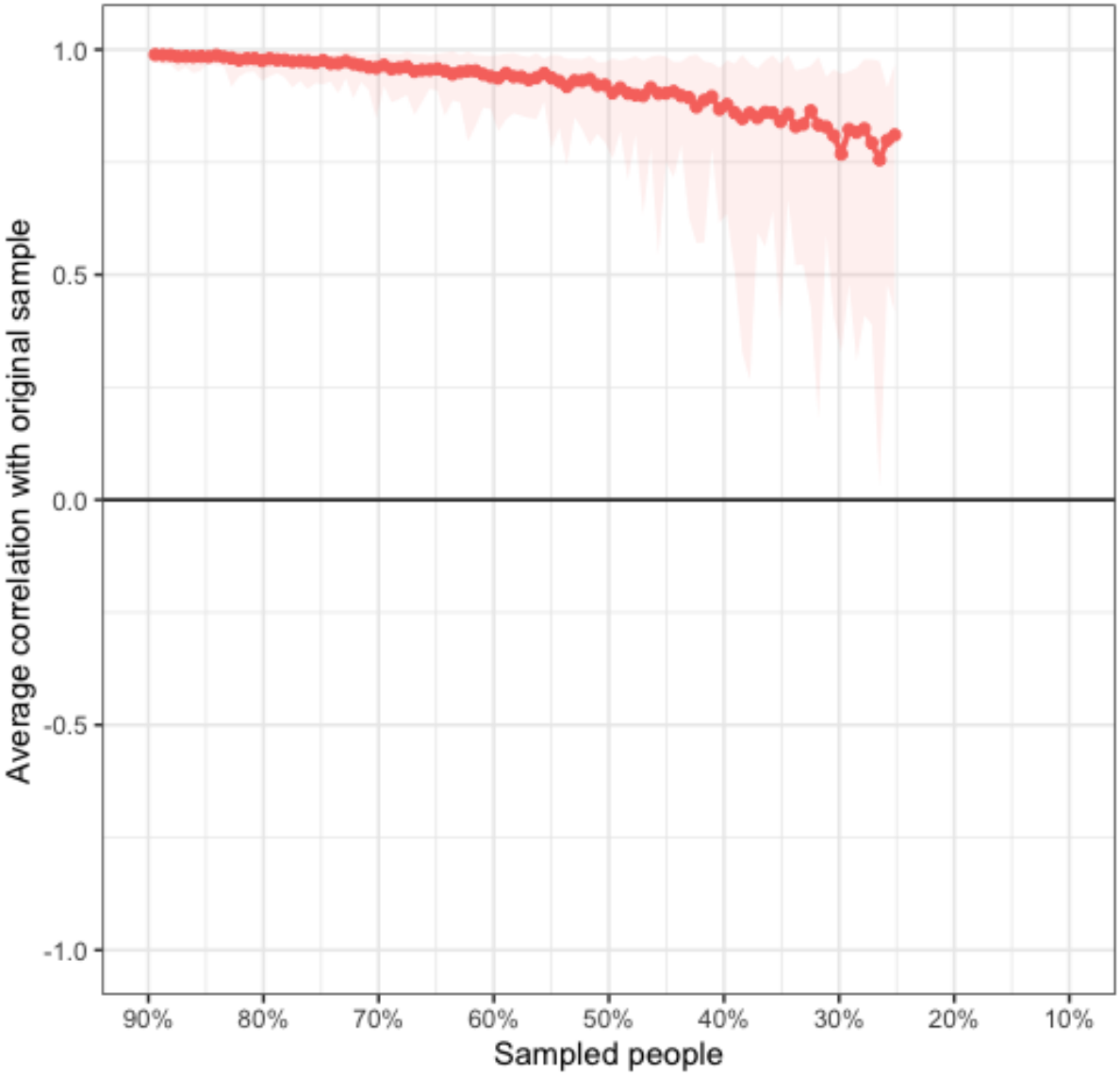


Figure 8S. Bootstrapped difference tests (α = 0.05) for centrality within the MDD symptom-domain network at baseline (n = 151). Nodes are presented in descending order of centrality. Values on the diagonal indicate the unstandardized centrality estimates for each node. Black boxes indicate significant centrality differences, meaning that the bootstrapped difference 95% CI does not span 0. Gray boxes indicate non-significant centrality differences, meaning that the bootstrapped difference 95% CI spans 0.

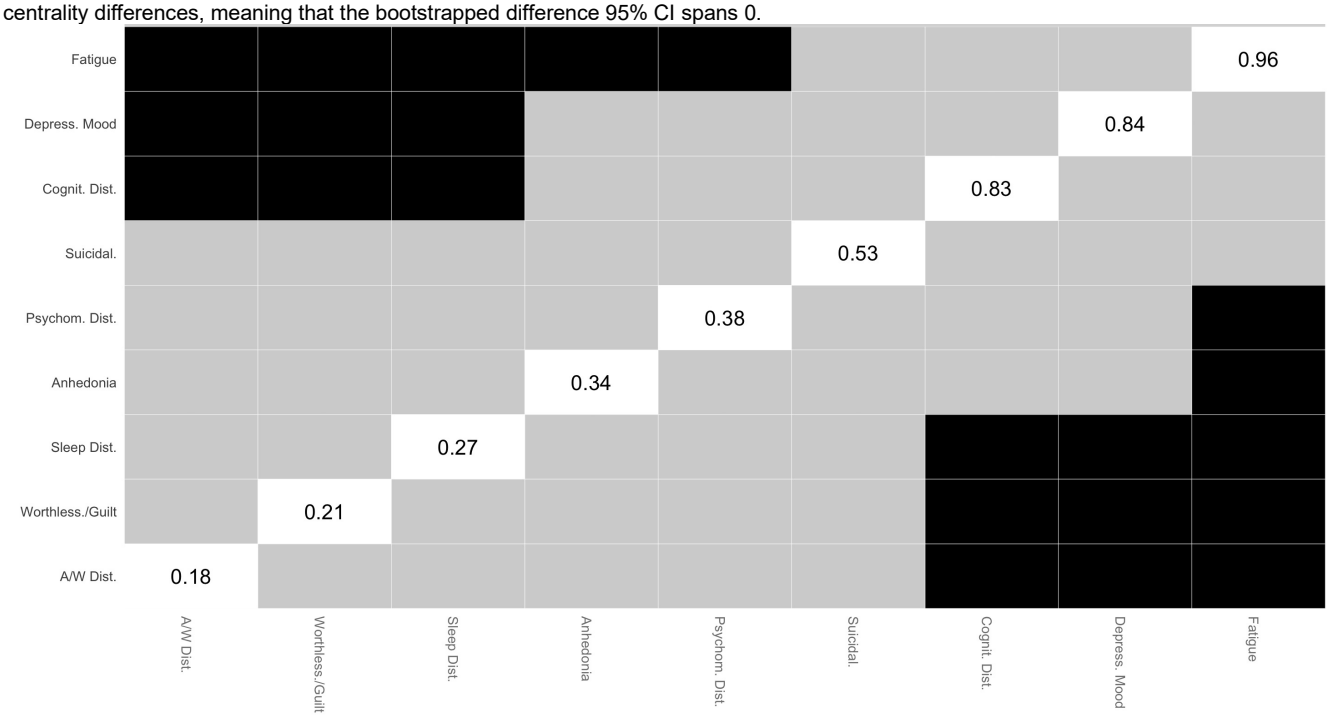


Figure 9S. Bootstrapped difference tests (α = 0.05) for centrality estimates within the MDD symptom-domain network at week 8 (n = 151). Nodes are presented in descending order of centrality. Values on the diagonal indicate the unstandardized estimates for each node. Black boxes indicate significant centrality differences, meaning that the bootstrapped difference 95% CI does not span 0. Gray boxes indicate non-significant centrality differences, meaning that the bootstrapped difference 95% CI spans 0.

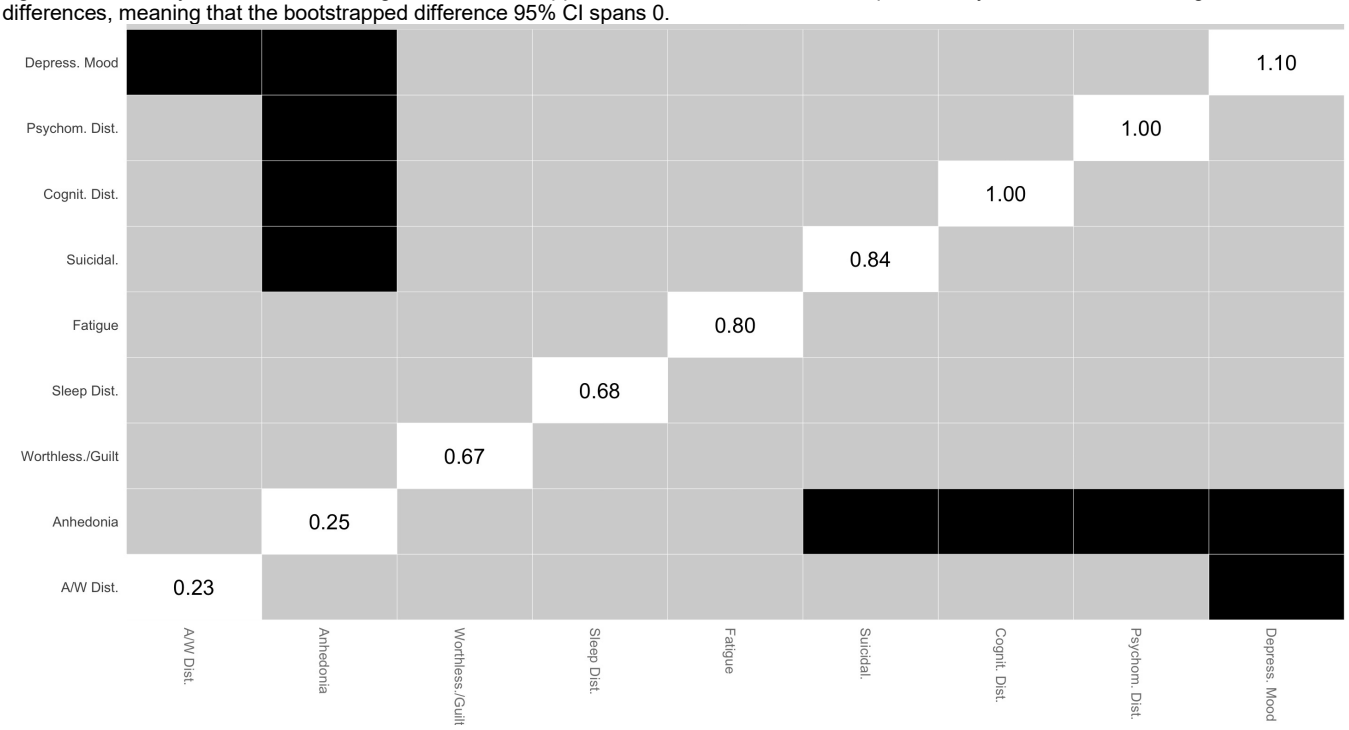


Figure 10S. Bootstrapped 95% confidence intervals (CIs) of estimated edge weights for the MDD symptom-domain network at baseline (n = 151). The red line indicates the sample values and the gray area the bootstrapped 95% CIs. Each horizontal line represents one edge of the network, ordered from the edge with the highest to the lowest weight.

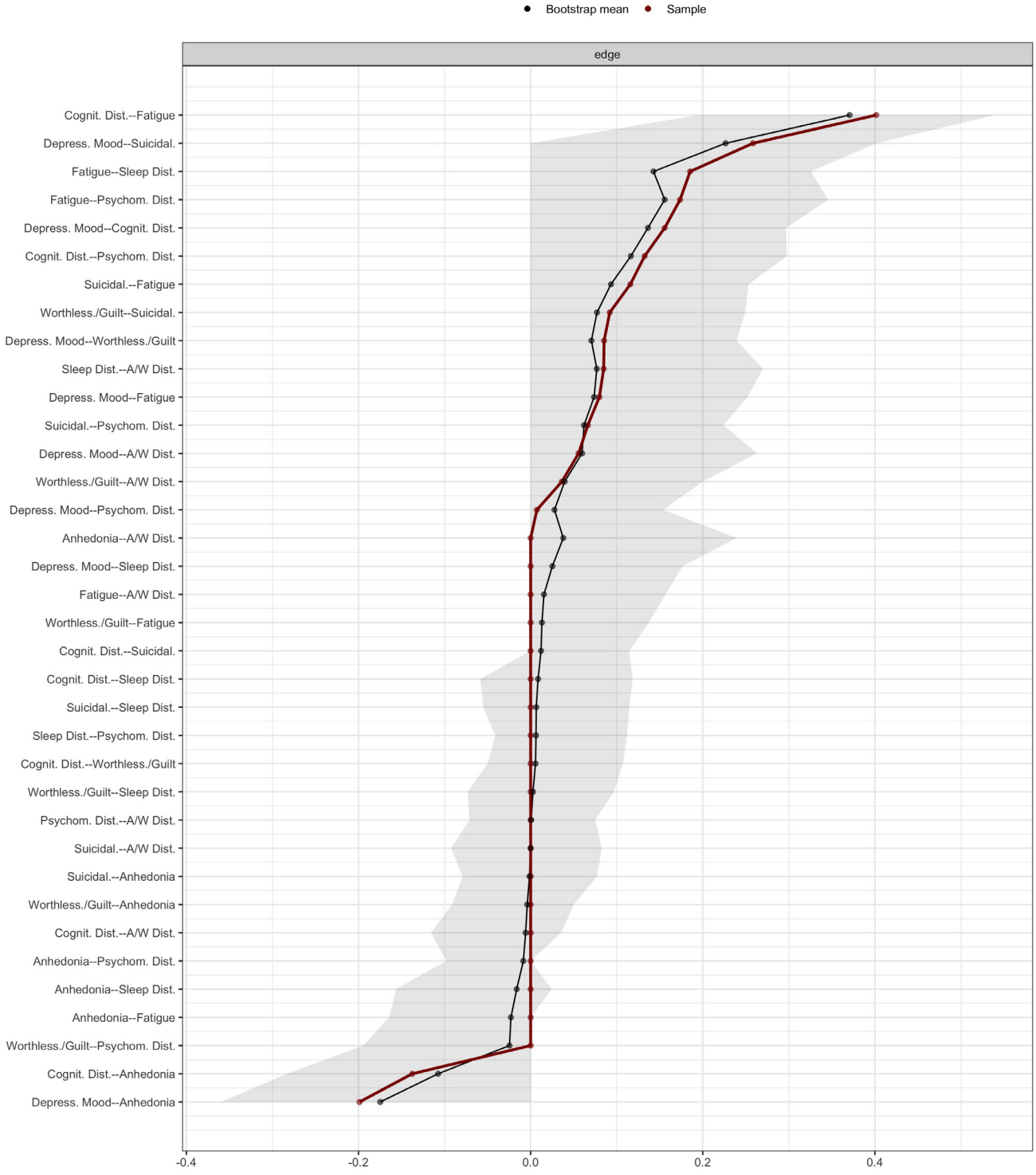


Figure 11S. Bootstrapped 95% confidence intervals (CIs) of estimated edge weights for the MDD symptom-domain network at week 8 (n = 151). The red line indicates the sample values and the gray area the bootstrapped 95% CIs. Each horizontal line represents one edge of the network, ordered from the edge with the highest to the lowest weight.

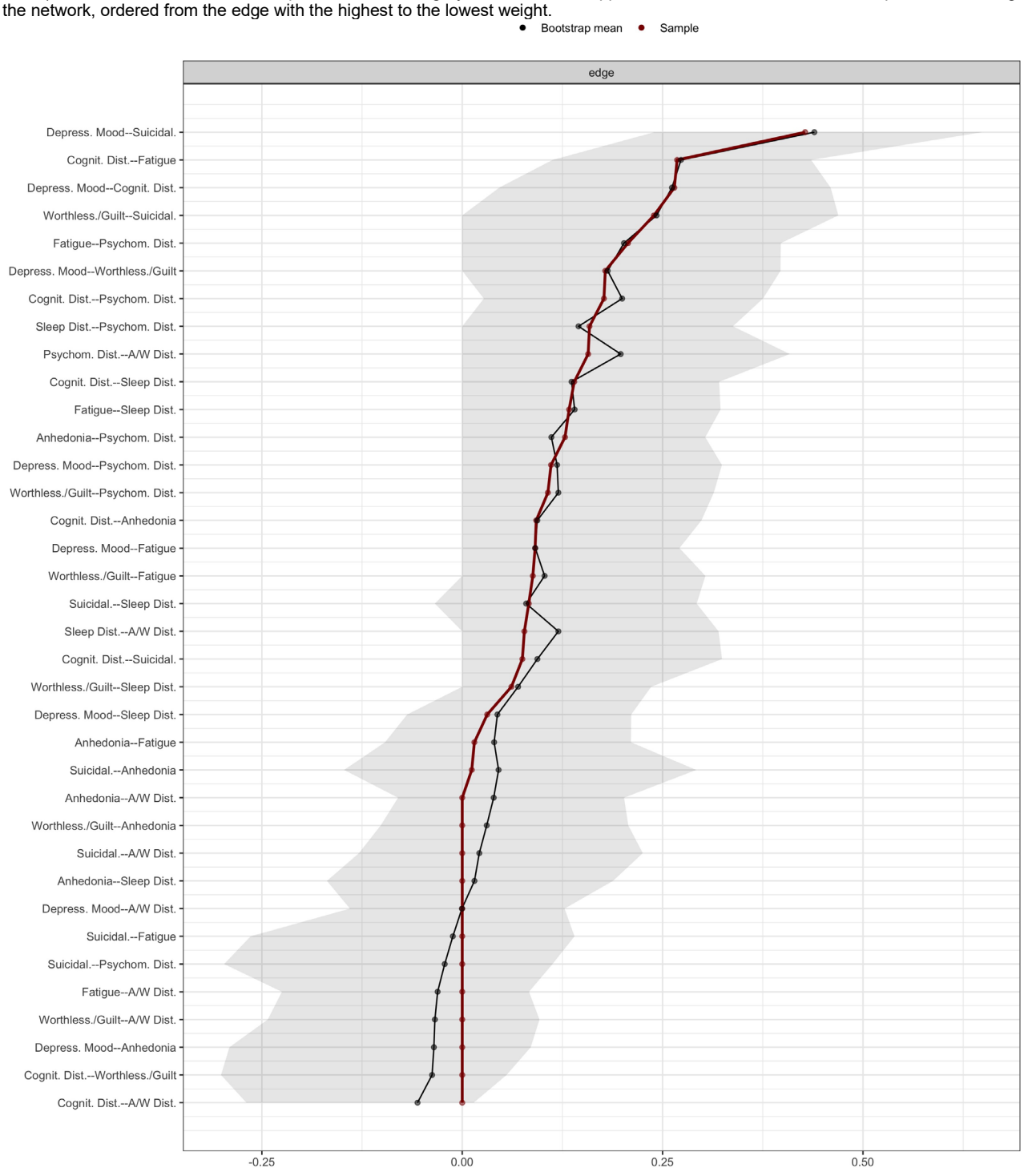


Figure 12S. Bootstrapped difference tests (α = 0.05) between the non-zero edge weights within the MDD symptom-domains network at baseline (n = 151). Grey and black boxes indicate, respectively, edges that do not and do differ significantly from one-another. Colored boxes correspond to the color of the edges in Figure 1 (using the “colorblind” pallete).

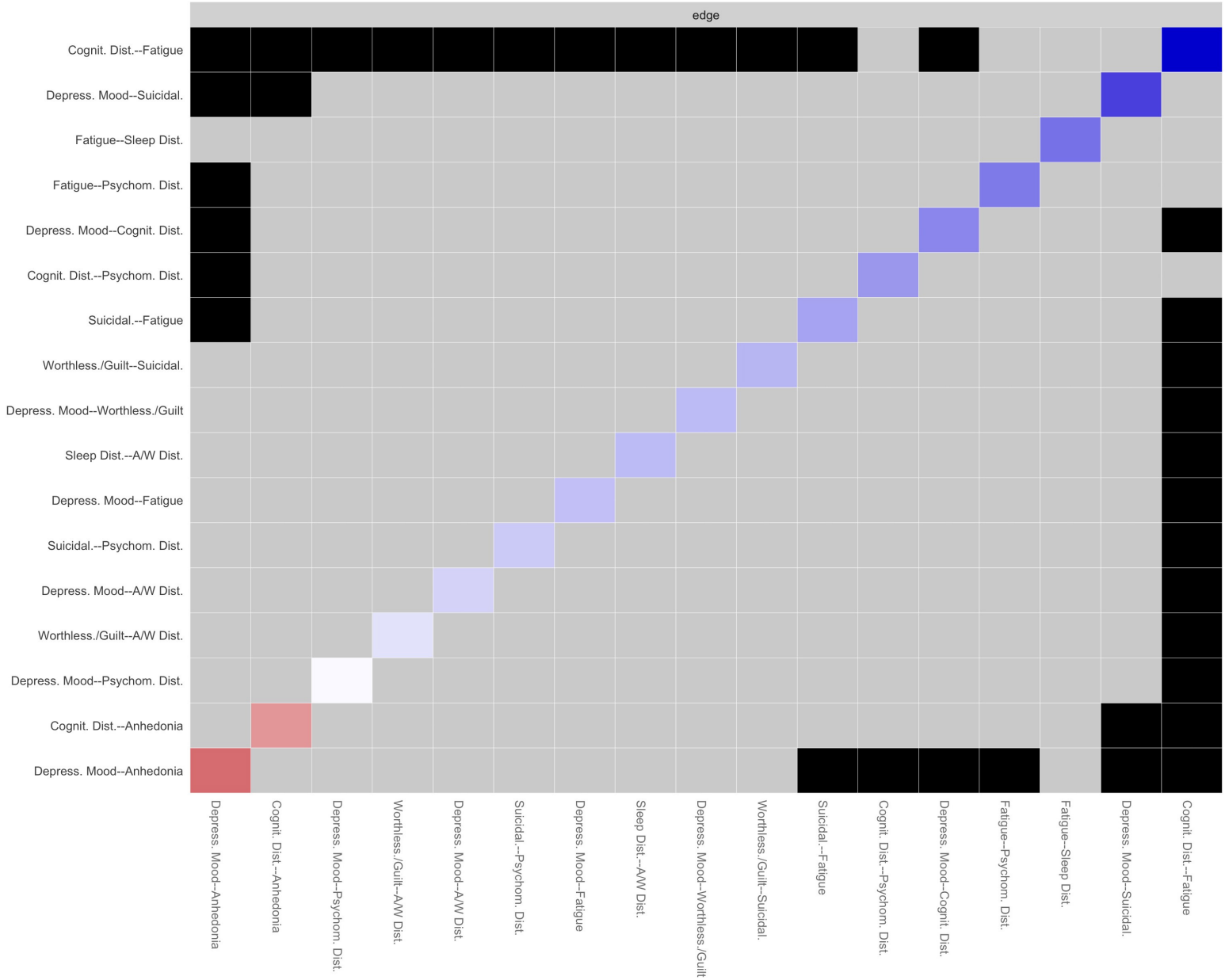


Figure 13S. Bootstrapped difference tests (α = 0.05) between the non-zero edge weights within the MDD symptom-domains network at week 8 (n = 151). Grey and black boxes indicate, respectively, edges that do not and do differ significantly from one-another. Colored boxes correspond to the color of the edge in Figure 1 (using the “colorblind” pallete).

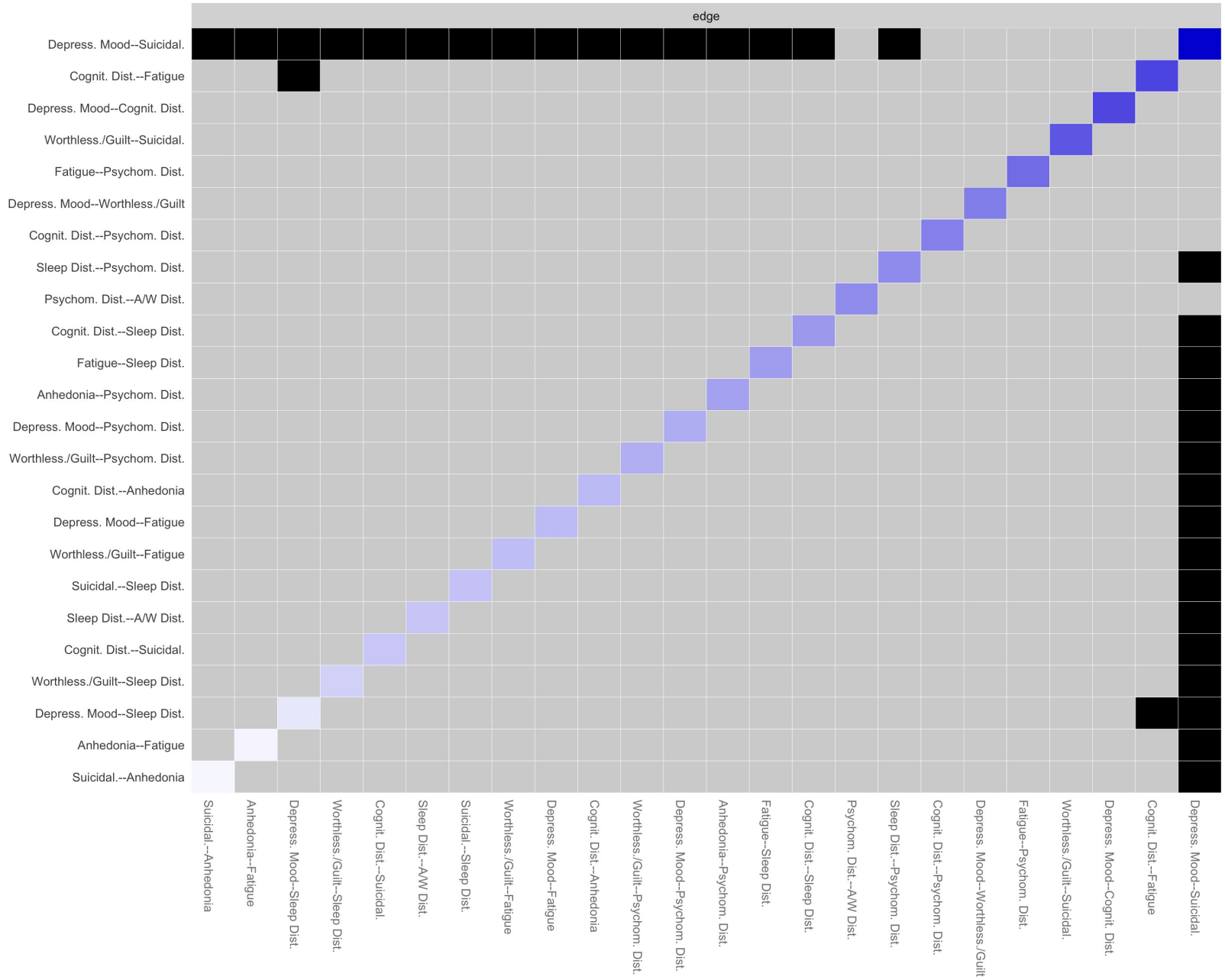
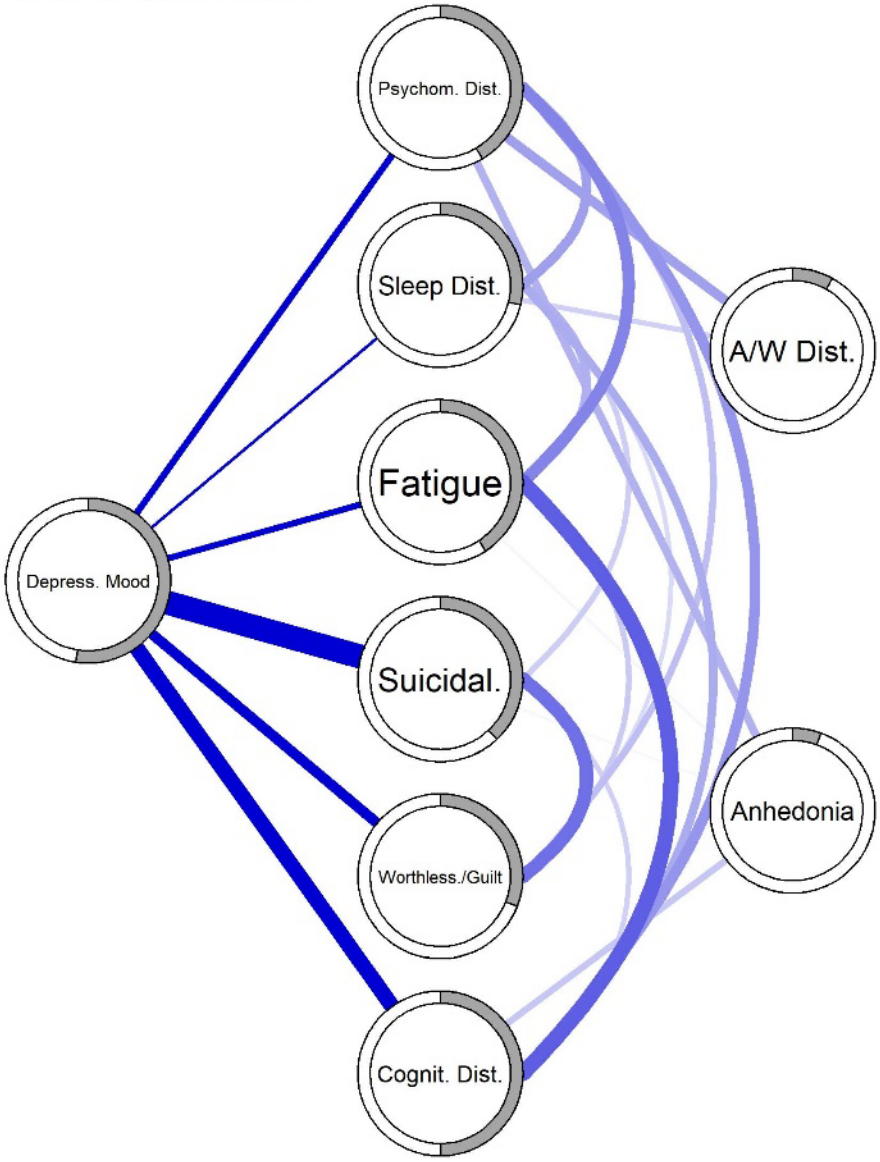


Figure 14S. Flow diagram showing the most predictable MDD symptom-domain at week 8 (i.e., depressed mood) (n = 151). Blue and red lines represent, respectively, positive and negative partial correlations, and the thickness of each edge indicates the strength of the association. The gray ring around each MDD symptom-domain represents its predictability.



EFFICACY ANALYSES – LAST OBSERVATION CARRIED FORWARD (LOCF)

In the analyses including all originally enrolled participants (n = 189) and using the last observation carried forward (LOCF) approach, the mean QIDS-SR score decreased significantly from baseline to week 8 (i.e., 16.10 ± 3.67 *vs*. 11.28 ± 5.60, respectively; *Wilks'* $\lambda = 0.50$, $F_{(1)} = 188.65$, $p < 0.000$) and, at study end, 19% (n = 36) of the participants were considered remitters. Likewise, scores on all MDD symptom-domains (with the exception of anhedonia) also decreased significantly over time.

Additionally, no significant AD*timepoint interaction was found for the nine MDD symptom-domains (*Wilks'* $\lambda = 0.96$, $F_{(9)} = 0.77$, $p = 0.65$) after controlling for the main effect of time (*Wilks'* $\lambda = 0.41$, $F_{(9)} = 28.81$, $p < 0.0001$), thus suggesting that desvenlafaxine and escitalopram were equally effective overall. Finally, there was a statistical trend towards higher remission rates at week 8 among participants who received escitalopram (23/94 [24.5%]) *vs*. desvenlafaxine (13/95 [13.70%]) ($\chi^2 = 3.56$; $p = 0.06$).

General Linear Model

Between-Subjects Factors

		Value Label	N
antidep	1	Escitalopram	94
	2	Desvenlafaxine	95

Descriptive Statistics

	antidep	Mean	Std. Deviation	N
Sleeping Problems	Escitalopram	2.50	.744	94
	Desvenlafaxine	2.64	.617	95
	Total	2.57	.685	189
Sleeping Problems	Escitalopram	2.04	1.067	94
	Desvenlafaxine	2.36	.849	95
	Total	2.20	.974	189
Feeling Sad	Escitalopram	2.12	.774	94
	Desvenlafaxine	2.00	.923	95
	Total	2.06	.852	189
Feeling Sad	Escitalopram	1.15	.892	94
	Desvenlafaxine	1.26	1.002	95
	Total	1.21	.948	189
Weight/Appetite Problems	Escitalopram	2.10	.881	94
	Desvenlafaxine	2.00	1.000	95
	Total	2.05	.941	189
Weight/Appetite Problems	Escitalopram	1.33	1.010	94
	Desvenlafaxine	1.20	.941	95
	Total	1.26	.975	189
Concentration/Decision-Making	Escitalopram	1.90	.817	94
	Desvenlafaxine	2.02	.729	95
	Total	1.96	.774	189
Concentration/Decision-Making	Escitalopram	1.20	.968	94
	Desvenlafaxine	1.49	.944	95
	Total	1.35	.965	189
View of Myself	Escitalopram	1.97	.978	94
	Desvenlafaxine	1.82	1.052	95
	Total	1.89	1.016	189

Descriptive Statistics

	antidep	Mean	Std. Deviation	N
View of Myself	Escitalopram	1.26	1.182	94
	Desvenlafaxine	1.21	1.157	95
	Total	1.23	1.166	189
Thoughts of Death or Suicide	Escitalopram	1.26	.903	94
	Desvenlafaxine	1.01	.881	95
	Total	1.13	.898	189
Thoughts of Death or Suicide	Escitalopram	.66	.874	94
	Desvenlafaxine	.57	.767	95
	Total	.61	.821	189
General Interest	Escitalopram	.78	.844	94
	Desvenlafaxine	.68	.802	95
	Total	.73	.823	189
General Interest	Escitalopram	.68	.819	94
	Desvenlafaxine	.86	1.199	95
	Total	.77	1.029	189
Energy Level	Escitalopram	1.83	.838	94
	Desvenlafaxine	2.07	.688	95
	Total	1.95	.774	189
Energy Level	Escitalopram	1.27	1.007	94
	Desvenlafaxine	1.60	.904	95
	Total	1.43	.969	189
Psychomotor Disturbance	Escitalopram	1.76	.864	94
	Desvenlafaxine	1.75	.743	95
	Total	1.75	.803	189
Psychomotor Disturbance	Escitalopram	1.24	1.013	94
	Desvenlafaxine	1.31	.935	95
	Total	1.28	.972	189

Multivariate Tests[a]

Effect			Value	F	Hypothesis df
Between Subjects	Intercept	Pillai's Trace	.944	337.519[b]	9.000
		Wilks' Lambda	.056	337.519[b]	9.000
		Hotelling's Trace	16.970	337.519[b]	9.000
		Roy's Largest Root	16.970	337.519[b]	9.000
	antidep	Pillai's Trace	.124	2.817[b]	9.000
		Wilks' Lambda	.876	2.817[b]	9.000
		Hotelling's Trace	.142	2.817[b]	9.000
		Roy's Largest Root	.142	2.817[b]	9.000
Within Subjects	time	Pillai's Trace	.592	28.812[b]	9.000
		Wilks' Lambda	.408	28.812[b]	9.000
		Hotelling's Trace	1.449	28.812[b]	9.000
		Roy's Largest Root	1.449	28.812[b]	9.000
	time * antidep	Pillai's Trace	.037	.767[b]	9.000
		Wilks' Lambda	.963	.767[b]	9.000
		Hotelling's Trace	.039	.767[b]	9.000
		Roy's Largest Root	.039	.767[b]	9.000

Multivariate Tests[a]

Effect			Error df	Sig.
Between Subjects	Intercept	Pillai's Trace	179.000	.000
		Wilks' Lambda	179.000	.000
		Hotelling's Trace	179.000	.000
		Roy's Largest Root	179.000	.000
	antidep	Pillai's Trace	179.000	.004
		Wilks' Lambda	179.000	.004
		Hotelling's Trace	179.000	.004
		Roy's Largest Root	179.000	.004
Within Subjects	time	Pillai's Trace	179.000	.000
		Wilks' Lambda	179.000	.000
		Hotelling's Trace	179.000	.000
		Roy's Largest Root	179.000	.000
	time * antidep	Pillai's Trace	179.000	.647
		Wilks' Lambda	179.000	.647
		Hotelling's Trace	179.000	.647
		Roy's Largest Root	179.000	.647

a. Design: Intercept + antidep
Within Subjects Design: time

b. Exact statistic

Tests of Within-Subjects Effects

Multivariate[a,b]

Within Subjects Effect		Value	F	Hypothesis df	Error df	Sig.
time	Pillai's Trace	.592	28.812[c]	9.000	179.000	.000
	Wilks' Lambda	.408	28.812[c]	9.000	179.000	.000
	Hotelling's Trace	1.449	28.812[c]	9.000	179.000	.000
	Roy's Largest Root	1.449	28.812[c]	9.000	179.000	.000
time * antidep	Pillai's Trace	.037	.767[c]	9.000	179.000	.647
	Wilks' Lambda	.963	.767[c]	9.000	179.000	.647
	Hotelling's Trace	.039	.767[c]	9.000	179.000	.647
	Roy's Largest Root	.039	.767[c]	9.000	179.000	.647

a. Design: Intercept + antidep
Within Subjects Design: time

b. Tests are based on averaged variables.

c. Exact statistic

Univariate Tests

Source	Measure		Type III Sum of Squares	df	Mean Square
time	Sleep_Dist	Sphericity Assumed	12.995	1	12.995
		Greenhouse-Geisser	12.995	1.000	12.995
		Huynh-Feldt	12.995	1.000	12.995
		Lower-bound	12.995	1.000	12.995
	Sad	Sphericity Assumed	68.671	1	68.671
		Greenhouse-Geisser	68.671	1.000	68.671
		Huynh-Feldt	68.671	1.000	68.671
		Lower-bound	68.671	1.000	68.671
	Weight_Appet	Sphericity Assumed	57.932	1	57.932
		Greenhouse-Geisser	57.932	1.000	57.932
		Huynh-Feldt	57.932	1.000	57.932
		Lower-bound	57.932	1.000	57.932
	Cognit_Dist	Sphericity Assumed	35.651	1	35.651
		Greenhouse-Geisser	35.651	1.000	35.651
		Huynh-Feldt	35.651	1.000	35.651
		Lower-bound	35.651	1.000	35.651
	Worthless	Sphericity Assumed	41.369	1	41.369
		Greenhouse-Geisser	41.369	1.000	41.369

Univariate Tests

Source	Measure		F	Sig.
time	Sleep_Dist	Sphericity Assumed	25.226	.000
		Greenhouse-Geisser	25.226	.000
		Huynh-Feldt	25.226	.000
		Lower-bound	25.226	.000
	Sad	Sphericity Assumed	153.490	.000
		Greenhouse-Geisser	153.490	.000
		Huynh-Feldt	153.490	.000
		Lower-bound	153.490	.000
	Weight_Appet	Sphericity Assumed	75.744	.000
		Greenhouse-Geisser	75.744	.000
		Huynh-Feldt	75.744	.000
		Lower-bound	75.744	.000
	Cognit_Dist	Sphericity Assumed	91.737	.000
		Greenhouse-Geisser	91.737	.000
		Huynh-Feldt	91.737	.000
		Lower-bound	91.737	.000
	Worthless	Sphericity Assumed	63.452	.000
		Greenhouse-Geisser	63.452	.000

Univariate Tests

Source	Measure		Type III Sum of Squares	df	Mean Square
		Huynh-Feldt	41.369	1.000	41.369
		Lower-bound	41.369	1.000	41.369
	Suicidal	Sphericity Assumed	25.447	1	25.447
		Greenhouse-Geisser	25.447	1.000	25.447
		Huynh-Feldt	25.447	1.000	25.447
		Lower-bound	25.447	1.000	25.447
	Anhedonia	Sphericity Assumed	.164	1	.164
		Greenhouse-Geisser	.164	1.000	.164
		Huynh-Feldt	.164	1.000	.164
		Lower-bound	.164	1.000	.164
	Fatigue	Sphericity Assumed	25.430	1	25.430
		Greenhouse-Geisser	25.430	1.000	25.430
		Huynh-Feldt	25.430	1.000	25.430
		Lower-bound	25.430	1.000	25.430
	Psychom_Dist	Sphericity Assumed	21.444	1	21.444
		Greenhouse-Geisser	21.444	1.000	21.444
		Huynh-Feldt	21.444	1.000	21.444
		Lower-bound	21.444	1.000	21.444
time * antidep	Sleep_Dist	Sphericity Assumed	.709	1	.709
		Greenhouse-Geisser	.709	1.000	.709
		Huynh-Feldt	.709	1.000	.709
		Lower-bound	.709	1.000	.709
	Sad	Sphericity Assumed	1.263	1	1.263
		Greenhouse-Geisser	1.263	1.000	1.263
		Huynh-Feldt	1.263	1.000	1.263
		Lower-bound	1.263	1.000	1.263
	Weight_Appet	Sphericity Assumed	.027	1	.027
		Greenhouse-Geisser	.027	1.000	.027
		Huynh-Feldt	.027	1.000	.027
		Lower-bound	.027	1.000	.027
	Cognit_Dist	Sphericity Assumed	.730	1	.730
		Greenhouse-Geisser	.730	1.000	.730
		Huynh-Feldt	.730	1.000	.730
		Lower-bound	.730	1.000	.730

Univariate Tests

Source	Measure		F	Sig.
		Huynh-Feldt	63.452	.000
		Lower-bound	63.452	.000
	Suicidal	Sphericity Assumed	75.490	.000
		Greenhouse-Geisser	75.490	.000
		Huynh-Feldt	75.490	.000
		Lower-bound	75.490	.000
	Anhedonia	Sphericity Assumed	.218	.641
		Greenhouse-Geisser	.218	.641
		Huynh-Feldt	.218	.641
		Lower-bound	.218	.641
	Fatigue	Sphericity Assumed	61.439	.000
		Greenhouse-Geisser	61.439	.000
		Huynh-Feldt	61.439	.000
		Lower-bound	61.439	.000
	Psychom_Dist	Sphericity Assumed	35.978	.000
		Greenhouse-Geisser	35.978	.000
		Huynh-Feldt	35.978	.000
		Lower-bound	35.978	.000
time * antidep	Sleep_Dist	Sphericity Assumed	1.376	.242
		Greenhouse-Geisser	1.376	.242
		Huynh-Feldt	1.376	.242
		Lower-bound	1.376	.242
	Sad	Sphericity Assumed	2.824	.095
		Greenhouse-Geisser	2.824	.095
		Huynh-Feldt	2.824	.095
		Lower-bound	2.824	.095
	Weight_Appet	Sphericity Assumed	.036	.850
		Greenhouse-Geisser	.036	.850
		Huynh-Feldt	.036	.850
		Lower-bound	.036	.850
	Cognit_Dist	Sphericity Assumed	1.879	.172
		Greenhouse-Geisser	1.879	.172
		Huynh-Feldt	1.879	.172
		Lower-bound	1.879	.172

Univariate Tests

Source	Measure		Type III Sum of Squares	df	Mean Square
	Worthless	Sphericity Assumed	.247	1	.247
		Greenhouse-Geisser	.247	1.000	.247
		Huynh-Feldt	.247	1.000	.247
		Lower-bound	.247	1.000	.247
	Suicidal	Sphericity Assumed	.558	1	.558
		Greenhouse-Geisser	.558	1.000	.558
		Huynh-Feldt	.558	1.000	.558
		Lower-bound	.558	1.000	.558
	Anhedonia	Sphericity Assumed	1.783	1	1.783
		Greenhouse-Geisser	1.783	1.000	1.783
		Huynh-Feldt	1.783	1.000	1.783
		Lower-bound	1.783	1.000	1.783
	Fatigue	Sphericity Assumed	.192	1	.192
		Greenhouse-Geisser	.192	1.000	.192
		Huynh-Feldt	.192	1.000	.192
		Lower-bound	.192	1.000	.192
	Psychom_Dist	Sphericity Assumed	.111	1	.111
		Greenhouse-Geisser	.111	1.000	.111
		Huynh-Feldt	.111	1.000	.111
		Lower-bound	.111	1.000	.111
Error(time)	Sleep_Dist	Sphericity Assumed	96.328	187	.515
		Greenhouse-Geisser	96.328	187.000	.515
		Huynh-Feldt	96.328	187.000	.515
		Lower-bound	96.328	187.000	.515
	Sad	Sphericity Assumed	83.663	187	.447
		Greenhouse-Geisser	83.663	187.000	.447
		Huynh-Feldt	83.663	187.000	.447
		Lower-bound	83.663	187.000	.447
	Weight_Appet	Sphericity Assumed	143.026	187	.765
		Greenhouse-Geisser	143.026	187.000	.765
		Huynh-Feldt	143.026	187.000	.765
		Lower-bound	143.026	187.000	.765
	Cognit_Dist	Sphericity Assumed	72.672	187	.389
		Greenhouse-Geisser	72.672	187.000	.389

Univariate Tests

Source	Measure		F	Sig.
	Worthless	Sphericity Assumed	.379	.539
		Greenhouse-Geisser	.379	.539
		Huynh-Feldt	.379	.539
		Lower-bound	.379	.539
	Suicidal	Sphericity Assumed	1.654	.200
		Greenhouse-Geisser	1.654	.200
		Huynh-Feldt	1.654	.200
		Lower-bound	1.654	.200
	Anhedonia	Sphericity Assumed	2.380	.125
		Greenhouse-Geisser	2.380	.125
		Huynh-Feldt	2.380	.125
		Lower-bound	2.380	.125
	Fatigue	Sphericity Assumed	.464	.497
		Greenhouse-Geisser	.464	.497
		Huynh-Feldt	.464	.497
		Lower-bound	.464	.497
	Psychom_Dist	Sphericity Assumed	.186	.667
		Greenhouse-Geisser	.186	.667
		Huynh-Feldt	.186	.667
		Lower-bound	.186	.667
Error(time)	Sleep_Dist	Sphericity Assumed		
		Greenhouse-Geisser		
		Huynh-Feldt		
		Lower-bound		
	Sad	Sphericity Assumed		
		Greenhouse-Geisser		
		Huynh-Feldt		
		Lower-bound		
	Weight_Appet	Sphericity Assumed		
		Greenhouse-Geisser		
		Huynh-Feldt		
		Lower-bound		
	Cognit_Dist	Sphericity Assumed		
		Greenhouse-Geisser		

Univariate Tests

Source	Measure		Type III Sum of Squares	df	Mean Square
		Huynh-Feldt	72.672	187.000	.389
		Lower-bound	72.672	187.000	.389
	Worthless	Sphericity Assumed	121.917	187	.652
		Greenhouse-Geisser	121.917	187.000	.652
		Huynh-Feldt	121.917	187.000	.652
		Lower-bound	121.917	187.000	.652
	Suicidal	Sphericity Assumed	63.035	187	.337
		Greenhouse-Geisser	63.035	187.000	.337
		Huynh-Feldt	63.035	187.000	.337
		Lower-bound	63.035	187.000	.337
	Anhedonia	Sphericity Assumed	140.048	187	.749
		Greenhouse-Geisser	140.048	187.000	.749
		Huynh-Feldt	140.048	187.000	.749
		Lower-bound	140.048	187.000	.749
	Fatigue	Sphericity Assumed	77.401	187	.414
		Greenhouse-Geisser	77.401	187.000	.414
		Huynh-Feldt	77.401	187.000	.414
		Lower-bound	77.401	187.000	.414
	Psychom_Dist	Sphericity Assumed	111.460	187	.596
		Greenhouse-Geisser	111.460	187.000	.596
		Huynh-Feldt	111.460	187.000	.596
		Lower-bound	111.460	187.000	.596

Tests of Within-Subjects Contrasts

Source	Measure	time	Type III Sum of Squares	df	Mean Square	F
time	Sleep_Dist	Linear	12.995	1	12.995	25.226
	Sad	Linear	68.671	1	68.671	153.490
	Weight_Appet	Linear	57.932	1	57.932	75.744
	Cognit_Dist	Linear	35.651	1	35.651	91.737
	Worthless	Linear	41.369	1	41.369	63.452
	Suicidal	Linear	25.447	1	25.447	75.490
	Anhedonia	Linear	.164	1	.164	.218
	Fatigue	Linear	25.430	1	25.430	61.439
	Psychom_Dist	Linear	21.444	1	21.444	35.978
time * antidep	Sleep_Dist	Linear	.709	1	.709	1.376
	Sad	Linear	1.263	1	1.263	2.824
	Weight_Appet	Linear	.027	1	.027	.036
	Cognit_Dist	Linear	.730	1	.730	1.879
	Worthless	Linear	.247	1	.247	.379
	Suicidal	Linear	.558	1	.558	1.654
	Anhedonia	Linear	1.783	1	1.783	2.380
	Fatigue	Linear	.192	1	.192	.464
	Psychom_Dist	Linear	.111	1	.111	.186
Error(time)	Sleep_Dist	Linear	96.328	187	.515	
	Sad	Linear	83.663	187	.447	
	Weight_Appet	Linear	143.026	187	.765	
	Cognit_Dist	Linear	72.672	187	.389	
	Worthless	Linear	121.917	187	.652	
	Suicidal	Linear	63.035	187	.337	
	Anhedonia	Linear	140.048	187	.749	
	Fatigue	Linear	77.401	187	.414	
	Psychom_Dist	Linear	111.460	187	.596	

Tests of Within-Subjects Contrasts

Source	Measure	time	Sig.
time	Sleep_Dist	Linear	.000
	Sad	Linear	.000
	Weight_Appet	Linear	.000
	Cognit_Dist	Linear	.000
	Worthless	Linear	.000
	Suicidal	Linear	.000
	Anhedonia	Linear	.641
	Fatigue	Linear	.000
	Psychom_Dist	Linear	.000
time * antidep	Sleep_Dist	Linear	.242
	Sad	Linear	.095
	Weight_Appet	Linear	.850
	Cognit_Dist	Linear	.172
	Worthless	Linear	.539
	Suicidal	Linear	.200
	Anhedonia	Linear	.125
	Fatigue	Linear	.497
	Psychom_Dist	Linear	.667
Error(time)	Sleep_Dist	Linear	
	Sad	Linear	
	Weight_Appet	Linear	
	Cognit_Dist	Linear	
	Worthless	Linear	
	Suicidal	Linear	
	Anhedonia	Linear	
	Fatigue	Linear	
	Psychom_Dist	Linear	

Tests of Between-Subjects Effects

Transformed Variable: Average

Source	Measure	Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Sleep_Dist	2151.240	1	2151.240	2443.034	.000
	Sad	1007.090	1	1007.090	854.527	.000
	Weight_Appet	1037.053	1	1037.053	964.392	.000
	Cognit_Dist	1036.002	1	1036.002	921.082	.000
	Worthless	924.298	1	924.298	529.210	.000
	Suicidal	288.381	1	288.381	254.088	.000
	Anhedonia	213.302	1	213.302	216.271	.000
	Fatigue	1082.589	1	1082.589	994.757	.000
	Psychom_Dist	865.462	1	865.462	863.761	.000
antidep	Sleep_Dist	4.944	1	4.944	5.614	.019
	Sad	.000	1	.000	.000	.990
	Weight_Appet	1.202	1	1.202	1.117	.292
	Cognit_Dist	3.960	1	3.960	3.521	.062
	Worthless	.869	1	.869	.498	.481
	Suicidal	2.666	1	2.666	2.349	.127
	Anhedonia	.191	1	.191	.194	.660
	Fatigue	7.891	1	7.891	7.251	.008
	Psychom_Dist	.065	1	.065	.065	.799
Error	Sleep_Dist	164.665	187	.881		
	Sad	220.386	187	1.179		
	Weight_Appet	201.089	187	1.075		
	Cognit_Dist	210.331	187	1.125		
	Worthless	326.607	187	1.747		
	Suicidal	212.239	187	1.135		
	Anhedonia	184.433	187	.986		
	Fatigue	203.511	187	1.088		
	Psychom_Dist	187.368	187	1.002		

Crosstabs

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
response * antidep	189	100.0%	0	0.0%	189	100.0%
remission * antidep	189	100.0%	0	0.0%	189	100.0%

response * antidep

Crosstab

			antidep		
			Escitalopram	Desvenlafaxine	Total
response	Yes	Count	32	21	53
		% within antidep	34.0%	22.1%	28.0%
	No	Count	62	74	136
		% within antidep	66.0%	77.9%	72.0%
Total		Count	94	95	189
		% within antidep	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3.337[a]	1	.068		
Continuity Correction[b]	2.771	1	.096		
Likelihood Ratio	3.355	1	.067		
Fisher's Exact Test				.076	.048
Linear-by-Linear Association	3.319	1	.068		
N of Valid Cases	189				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 26.36.

b. Computed only for a 2x2 table

remission * antidep

Crosstab

			antidep		
			Escitalopram	Desvenlafaxine	Total
remission	Yes	Count	23	13	36
		% within antidep	24.5%	13.7%	19.0%
	No	Count	71	82	153
		% within antidep	75.5%	86.3%	81.0%
Total		Count	94	95	189
		% within antidep	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3.563[a]	1	.059		
Continuity Correction[b]	2.898	1	.089		
Likelihood Ratio	3.601	1	.058		
Fisher's Exact Test				.066	.044
Linear-by-Linear Association	3.545	1	.060		
N of Valid Cases	189				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 17.90.

b. Computed only for a 2x2 table

WEIGHT MATRIX - BASELINE

	Depress. Mood	Cognit. Dist.	Worthless./Guil	Suicidal.	Anhedonia	Fatigue	Sleep Dist.	Psychom. Dist.	A/W Dist.
Depress. Mood	0	0.155747553	0.085314777	0.258334204	-0.198820668	0.079826398	0	0.00728831	0.055714944
Cognit. Dist.	0.155747553	0	0	0	-0.137525038	0.401533941	0	0.132452681	0
Worthless./Guilt	0.085314777	0	0	0.091922638	0	0	0	0	0.036230037
Suicidal.	0.258334204	0	0.091922638	0	0	0.115843454	0	0.066377637	0
Anhedonia	-0.198820668	-0.137525038	0	0	0	0	0	0	0
Fatigue	0.079826398	0.401533941	0	0.115843454	0	0	0.185309278	0.173618224	0
Sleep Dist.	0	0	0	0	0	0.185309278	0	0	0.084847888
Psychom. Dist.	0.00728831	0.132452681	0	0.066377637	0	0.173618224	0	0	0
A/W Dist.	0.055714944	0	0.036230037	0	0	0	0.084847888	0	0

WEIGHT MATRIX - WEEK 8

	Depress. Mood	Cognit. Dist.	Worthless./Guilt	Suicidal.	Anhedonia	Fatigue	Sleep Dist.	Psychom. Dist.	A/W Dist.
Depress. Mood	0	0.264625351	0.178469299	0.427805448	0	0.090939734	0.031149126	0.1108089	0
Cognit. Dist.	0.264625351	0	0	0.075022065	0.092269116	0.268093244	0.139738439	0.176811221	0
Worthless./Guilt	0.178469299	0	0	0.239191045	0	0.088071168	0.061369208	0.106856701	0
Suicidal.	0.427805448	0.075022065	0.239191045	0	0.011862386	0	0.082998711	0	0
Anhedonia	0	0.092269116	0	0.011862386	0	0.015156297	0	0.128189582	0
Fatigue	0.090939734	0.268093244	0.088071168	0	0.015156297	0	0.133342705	0.206790607	0
Sleep Dist.	0.031149126	0.139738439	0.061369208	0.082998711	0	0.133342705	0	0.158776209	0.077513293
Psychom. Dist.	0.1108089	0.176811221	0.106856701	0	0.128189582	0.206790607	0.158776209	0	0.157120618
A/W Dist.	0	0	0	0	0	0	0.077513293	0.157120618	0

Dec18-2019.r

```
#1 LOADING R PACKAGES

library(haven)
library(ggplot2)
library(qgraph)
library(mgm)net)
library(EstimateGroupNetwork)
library(NetworkComparisonTest)
library(psych)
library(networktools)
library(NetworkToolbox)
options(scipen = 999)
#####

#2 READING THE FILES

dataqids_biomarkers_pre <- read_sav("...")
dataqids_biomarkers_pre <- na.omit(dataqids_biomarkers_pre)
View(dataqids_biomarkers_pre)

dataqids_biomarkers_post <- read_sav("...")
dataqids_biomarkers_post <- na.omit(dataqids_biomarkers_post)
View(dataqids_biomarkers_post)

#####

#3 NAMING THE VARIABLES

names(dataqids_biomarkers_pre) <- c("Depress. Mood", "Cognit. Dist.",
"Worthless./Guilt", "Suicidal.", "Anhedonia", "Fatigue", "Sleep Dist.",
"Psychom. Dist.", "A/W Dist.", "QIDS-SR Pre", "Gender")
View(dataqids_biomarkers_pre)
names(dataqids_biomarkers_post) <- c("Depress. Mood", "Cognit. Dist.",
"Worthless./Guilt", "Suicidal.", "Anhedonia", "Fatigue", "Sleep Dist.",
"Psychom. Dist.", "A/W Dist.", "QIDS-SR Post", "Antidepressant", "Response",
"Remission")
View(dataqids_biomarkers_post)

#####

#4 SELECTING THE VARIABLES

biomarkers_qids_pre <- dataqids_biomarkers_pre[c(1:9)]
biomarkers_qids_post <- dataqids_biomarkers_post[c(1:9)]

################

#5 CALCULATING NODEWISE PREDICTABILITY

p <- ncol(biomarkers_qids_pre)

nodepredict_biomarkers_qids_pre <- mgm(data = biomarkers_qids_pre, type =
rep('g', p), level = rep(1, p), lambdaSel = "CV", ruleReg = "OR")
predictabil_biomarkers_qids_pre <- predict(object =
nodepredict_biomarkers_qids_pre, data = biomarkers_qids_pre, errorCon = "R2")
predictabil_biomarkers_qids_pre$errors

nodepredict_biomarkers_qids_post <- mgm(data = biomarkers_qids_post, type =
rep('g', p), level = rep(1, p), lambdaSel = "CV", ruleReg = "OR")
predictabil_biomarkers_qids_post <- predict(object =
nodepredict_biomarkers_qids_post, data = biomarkers_qids_post, errorCon =
```

```
"R2")
predictabil_biomarkers_qids_post$errors

#5.1 Calculating mean predictability per node

mean_predict_biomarkers_qids_pre <- mean(predictabil_biomarkers_qids_pre$error
$R2)
round(mean_predict_biomarkers_qids_pre, digits = 2)

mean_predict_biomarkers_qids_post <- mean(predictabil_biomarkers_qids_post
$error$R2)
round(mean_predict_biomarkers_qids_post, digits = 2)

################

#6 CALCULATING THE CORRELATION MATRICES (BASELINE & WEEK 8)

cormatrix_biomarkers_qids_pre <- cor_auto(biomarkers_qids_pre, detectOrdinal =
T, forcePD = T, missing = "pairwise")

cormatrix_biomarkers_qids_post <- cor_auto(biomarkers_qids_post, detectOrdinal
= T, forcePD = T, missing = "pairwise")

#####

#7 CALCULATING THE EBICGLASSO NETWORKS WITH PREDICTABILITY (BASELINE & WEEK 8)

ebicglasso_biomarkers_qids_pre <- qgraph(cormatrix_biomarkers_qids_pre, graph
= "glasso", gamma = 0.5, layout = "spring", sampleSize =
nrow(biomarkers_qids_pre), legend = F, details = F, vsize = 10, edge.labels =
F, edge.label.cex = 1, border.width = 1, fade = F, labels =
colnames(biomarkers_qids_pre), theme = "colorblind", pie =
as.numeric(as.character(predictabil_biomarkers_qids_pre$errors[,2])), pieColor
= rep('gray65', p), title = "Baseline")

ebicglasso_biomarkers_qids_post <- qgraph(cormatrix_biomarkers_qids_post,
graph = "glasso", gamma = 0.5, layout = "spring", sampleSize =
nrow(biomarkers_qids_post), details = F, legend = F, vsize = 10, edge.labels =
F, border.width = 1, fade = F, labels = colnames(biomarkers_qids_post), theme
= "colorblind", pie = as.numeric(as.character(predictabil_biomarkers_qids_post
$errors[,2])), pieColor = rep('gray65', p), title = "Week 8")

#####

#8 CALCULATING THE CENTRALITY ESTIMATES (BASELINE & WEEK 8)

centrality_biomarkers_qids_plot <- centralityPlot(list(Baseline =
ebicglasso_biomarkers_qids_pre, "Week 8" = ebicglasso_biomarkers_qids_post),
weighted = T, signed = T, scale = "z-scores", labels =
colnames(biomarkers_qids_pre), include = "ExpectedInfluence", orderBy =
"ExpectedInfluence")

################

#9 CALCULATING THE FUSED GRAPHICAL LASSO NETWORK FOR EACH ANTIDEPRESSANT
(BASELINE & WEEK 8)

#9.1 Calculating the correlation matrices

cormatrix_biomarkers_qids_escital_pre <-
cor_auto(dataqids_biomarkers_pre[dataqids_biomarkers_pre$Antidepressant == 1,
c(1:9)], detectOrdinal = T, forcePD = T, missing = "pairwise")
```

```
cormatrix_biomarkers_qids_escital_post <-
cor_auto(dataqids_biomarkers_post[dataqids_biomarkers_post$Antidepressant ==
1, c(1:9)], detectOrdinal = T, forcePD = T, missing = "pairwise")

cormatrix_biomarkers_qids_desvenla_pre <-
cor_auto(dataqids_biomarkers_pre[dataqids_biomarkers_pre$Antidepressant == 2,
c(1:9)], detectOrdinal = T, forcePD = T, missing = "pairwise")
cormatrix_biomarkers_qids_desvenla_post <-
cor_auto(dataqids_biomarkers_post[dataqids_biomarkers_post$Antidepressant ==
2, c(1:9)], detectOrdinal = T, forcePD = T, missing = "pairwise")

#9.2 Calculating the EBICGLASSO networks for each antidepressant

fgl_biomarkers_qids_AD_pre <- EstimateGroupNetwork(list(Escitalopram =
cormatrix_biomarkers_qids_escital_pre, "Desvenlafaxine" =
cormatrix_biomarkers_qids_desvenla_pre), n = c(sum(dataqids_biomarkers_pre
$Antidepressant == 1), sum(dataqids_biomarkers_post$Antidepressant == 2)),
covfun = cor_auto, method = "InformationCriterion", criterion = "ebic", gamma
= 0, optimize = T, penalty = "fused", weights = "sample.size", ncores = 2,
simplifyOutput = T)

fgl_biomarkers_qids_AD_post <- EstimateGroupNetwork(list(Escitalopram =
cormatrix_biomarkers_qids_escital_post, "Desvenlafaxine" =
cormatrix_biomarkers_qids_desvenla_post), n = c(sum(dataqids_biomarkers_pre
$Antidepressant == 1), sum(dataqids_biomarkers_post$Antidepressant == 2)),
covfun = cor_auto, method = "InformationCriterion", criterion = "ebic", gamma
= 0, optimize = T, penalty = "fused", weights = "sample.size", ncores = 2,
simplifyOutput = T)

#9.3 Calculating node predictability for each antidepressant (baseline)

p <- ncol(biomarkers_qids_pre)

nodepredict_biomarkers_qids_fgl_escital_pre <- mgm(data =
dataqids_biomarkers_pre[dataqids_biomarkers_pre$Antidepressant == 1, c(1:9)],
type = rep('g', p), level = rep(1, p), lambdaSel = "CV", ruleReg = "OR")
predictabil_biomarkers_qids_fgl_escital_pre <- predict(object =
nodepredict_biomarkers_qids_fgl_escital_pre, data =
dataqids_biomarkers_pre[dataqids_biomarkers_pre$Antidepressant == 1, c(1:9)],
errorCon = "R2")

nodepredict_biomarkers_qids_fgl_desvenla_pre <- mgm(data =
dataqids_biomarkers_pre[dataqids_biomarkers_pre$Antidepressant == 2, c(1:9)],
type = rep('g', p), level = rep(1, p), lambdaSel = "CV", ruleReg = "OR")
predictabil_biomarkers_qids_fgl_desvenla_pre <- predict(object =
nodepredict_biomarkers_qids_fgl_desvenla_pre, data =
dataqids_biomarkers_pre[dataqids_biomarkers_pre$Antidepressant == 2, c(1:9)],
errorCon = "R2")

predictabil_biomarkers_qids_fgl_escital_pre$error
predictabil_biomarkers_qids_fgl_desvenla_pre$error

#9.4 Calculating node predictability for each antidepressant (week 8)

p <- ncol(biomarkers_qids_post)

nodepredict_biomarkers_qids_fgl_escital_post <- mgm(data =
dataqids_biomarkers_post[dataqids_biomarkers_post$Antidepressant == 1,
c(1:9)], type = rep('g', p), level = rep(1, p), lambdaSel = "CV", ruleReg =
"OR")
predictabil_biomarkers_qids_fgl_escital_post <- predict(object =
nodepredict_biomarkers_qids_fgl_escital_post, data =
```

```
dataqids_biomarkers_post[dataqids_biomarkers_post$Antidepressant == 1,
c(1:9)], errorCon = "R2")

nodepredict_biomarkers_qids_fgl_desvenla_post <- mgm(data =
dataqids_biomarkers_post[dataqids_biomarkers_post$Antidepressant == 2,
c(1:9)], type = rep('g', p), level = rep(1, p), lambdaSel = "CV", ruleReg =
"OR")
predictabil_biomarkers_qids_fgl_desvenla_post <- predict(object =
nodepredict_biomarkers_qids_fgl_desvenla_post, data =
dataqids_biomarkers_post[dataqids_biomarkers_post$Antidepressant == 2,
c(1:9)], errorCon = "R2")

predictabil_biomarkers_qids_fgl_escital_post$error
predictabil_biomarkers_qids_fgl_desvenla_post$error

################

#10 COMPARING NETWORK PROPERTIES

#10.1 Baseline vs Week 8

nct_biomarkers <- NCT(biomarkers_qids_pre, biomarkers_qids_post, gamma = 0.5,
it = 5000, binary.data = F, paired = T, weighted = T, test.edges = T, edges =
"all", p.adjust.methods = "holm", make.positive.definite = T, progressbar = T,
test.centrality = T, centrality = "expectedInfluence")

#10.1.1 To obtain the difference in "global strength" between the networks
nct_biomarkers$glstrinv.real

#10.1.2 To obtain the "global strength values" of the individual networks
nct_biomarkers$glstrinv.sep

#10.1.3 To obtain the p-value from the permutation test concerning the
difference in "global strength"
nct_global_strength_pvalue_biomarkers_qids_pre_post <- nct_biomarkers
$glstrinv.pval
round(nct_biomarkers$glstrinv.pval, digits = 3)

#10.1.4 To obtain the value of the maximum difference in edge weights
nct_biomarkers$nwinv.real

#10.1.5 To obtain the p-value from the permutation test concerning the maximum
difference in edge weights
nct_max_diff_edgeweights_pvalue_biomarkers_qids_pre_post <- nct_biomarkers
$nwinv.pval
round(nct_biomarkers$nwinv.pval, digits = 3)

#10.1.6 To obtain the value of the difference in edge weights of networks
nct_biomarkers$einv.real

#10.1.7 To obtain the Holm-Bonferroni corrected p-values per edge from the
permutation test concerning differences in edge weights
nct_biomarkers$einv.pvals

#10.1.8 To obtain the values of the difference in centralities of the networks
nct_biomarkers$diffcen.real

#10.1.9 To obtain the p-values per node from the permutation test concerning
differences in centrality
nct_biomarkers$diffcen.pval

#####
```

```
#10.2 Escitalopram (baseline vs week 8)

# Reading the files

escital_pre <- read_sav("...")
escital_post <- read_sav("...")

# Selecting the variables

biomarkers_qids_escital_pre <- escital_pre[c(1:9)]
biomarkers_qids_escital_post <- escital_post[c(1:9)]

nct_biomarkers_escital <- NCT(biomarkers_qids_escital_pre,
biomarkers_qids_escital_post, gamma = 0, it = 5000, binary.data = F, paired =
T, weighted = T, test.edges = F, make.positive.definite = T, progressbar = F,
test.centrality = F)

#10.2.1 To obtain the difference in "global strength" between the networks
nct_biomarkers_escital$glstrinv.real

#10.2.2 To obtain the global strength values of the individual networks
nct_biomarkers_escital$glstrinv.sep

#10.2.3 To obtain the p-value from the permutation test concerning the
difference in "global strength"
round(nct_biomarkers_escital$glstrinv.pval, digits = 3)

#10.2.4 To obtain the value of the maximum difference in edge weights
nct_biomarkers_escital$nwinv.real

#10.2.5 To obtain the p-value from the permutation test concerning the maximum
difference in edge weights:
round(nct_biomarkers_escital$nwinv.pval, digits = 3)

#####

#10.3 Desvenlafaxine (baseline vs week 8)

# Reading the files

desvenla_pre <- read_sav("...")
desvenla_post <- read_sav("...")

# Selecting the variables

biomarkers_qids_desvenla_pre <- desvenla_pre[c(1:9)]
biomarkers_qids_desvenla_post <- desvenla_post[c(1:9)]

nct_biomarkers_desvenla <- NCT(biomarkers_qids_desvenla_pre,
biomarkers_qids_desvenla_post, gamma = 0, it = 5000, binary.data = F, paired =
T, weighted = T, test.edges = F, make.positive.definite = T, progressbar = F,
test.centrality = F)

#10.3.1 To obtain the difference in global strength between the networks
nct_biomarkers_desvenla$glstrinv.real

#10.3.2 To obtain the "global strength" values of the individual networks
nct_biomarkers_desvenla$glstrinv.sep

#10.3.3 To obtain the p-value from the permutation test concerning the
difference in "global strength"
```

```
round(nct_biomarkers_desvenla$glstrinv.pval, digits = 3)

#10.3.4 To obtain the value of the maximum difference in edge weights
nct_biomarkers_desvenla$nwinv.real

#10.3.5 To obtain the p-value from the permutation test concerning the maximum
difference in edge weights
round(nct_biomarkers_desvenla$nwinv.pval, digits = 3)

#####

#10.4 Escitalopram vs Desvenlafaxine (baseline)

nct_biomarkers_escital_desvenla_pre <- NCT(biomarkers_qids_escital_pre,
biomarkers_qids_desvenla_pre, gamma = 0, it = 5000, binary.data = F, paired =
F, weighted = T, test.edges = F, make.positive.definite = T, progressbar = F,
test.centrality = F)

#10.4.1 To obtain the difference in "global strength" between the networks
nct_biomarkers_escital_desvenla_pre$glstrinv.real

#10.4.2 To obtain the "global strength" values of the individual networks
nct_biomarkers_escital_desvenla_pre$glstrinv.sep

#10.4.3 To obtain the p-value from the permutation test concerning the
difference in "global strength"
round(nct_biomarkers_escital_desvenla_pre$glstrinv.pval, digits = 3)

#10.4.4 To obtain the value of the maximum difference in edge weights
nct_biomarkers_escital_desvenla_pre$nwinv.real

#10.4.5 To obtain the p-value from the permutation test concerning the maximum
difference in edge weights
round(nct_biomarkers_escital_desvenla_pre$nwinv.pval, digits = 3)

#####

#10.5 Escitalopram vs Desvenlafaxine (week 8)

nct_biomarkers_escital_desvenla_post <- NCT(biomarkers_qids_escital_post,
biomarkers_qids_desvenla_post, gamma = 0, it = 5000, binary.data = F, paired =
F, weighted = T, test.edges = F, make.positive.definite = T, progressbar = F,
test.centrality = F)

#10.5.1 To obtain the difference in "global strength" between the networks
nct_biomarkers_escital_desvenla_post$glstrinv.real

#10.5.2 To obtain the global strength values of the individual networks
nct_biomarkers_escital_desvenla_post$glstrinv.sep

#10.5.3 To obtain the p-value from the permutation test concerning the
difference in "global strength"
round(nct_biomarkers_escital_desvenla_post$glstrinv.pval, digits = 3)

#10.5.4 To obtain the value of the maximum difference in edge weights
nct_biomarkers_escital_desvenla_post$nwinv.real

#10.5.5 To obtain the p-value from the permutation test concerning the maximum
difference in edge weights
round(nct_biomarkers_escital_desvenla_post$nwinv.pval, digits = 3)

################
```

```
#11 CALCULATING THE ACCURACY & STABILITY OF THE NETWORKS (BASELINE & WEEK 8)

#11.1 To perform a case-dropping bootstrap

casedrop_boot_biomarkers_qids_pre <- bootnet(biomarkers_qids_pre, default =
"EBICglasso", nCores = 2, nBoots = 5000, statistics = c("edge",
"expectedInfluence"), labels = names(biomarkers_qids_pre), type = "case",
model = "GGM", verbose = T, caseN = 150)
casedrop_boot_biomarkers_qids_post <- bootnet(biomarkers_qids_post, default =
"EBICglasso", nCores = 2, nBoots = 5000, statistics = c("edge",
"expectedInfluence"), labels = names(biomarkers_qids_post), type = "case",
model = "GGM", verbose = T, caseN = 150)

plot(casedrop_boot_biomarkers_qids_pre, statistics = "expectedInfluence") +
theme(legend.position = "none")
plot(casedrop_boot_biomarkers_qids_post, statistics = "expectedInfluence") +
theme(legend.position = "none")

summary(casedrop_boot_biomarkers_qids_pre)
summary(casedrop_boot_biomarkers_qids_post)

#11.2 To obtain the correlation stability coefficients for the centrality
estimates

corStability(casedrop_boot_biomarkers_qids_pre, cor = 0.7, statistics =
"expectedInfluence", verbose = T)
corStability(casedrop_boot_biomarkers_qids_post, cor = 0.7, statistics =
"expectedInfluence", verbose = T)

#11.3 To perform a nonparametric bootstrap

nonpar_boot_biomarkers_qids_pre <- bootnet(biomarkers_qids_pre, default =
"EBICglasso", nCores = 2, nBoots = 5000, weighted = T, signed = T, type =
"nonparametric", model = "GGM", verbose = T, labels =
names(biomarkers_qids_pre))
nonpar_boot_biomarkers_qids_post <- bootnet(biomarkers_qids_post, default =
"EBICglasso", nCores = 2, nBoots = 5000, weighted = T, signed = T, type =
"nonparametric", model = "GGM", verbose = T, labels =
names(biomarkers_qids_post))

plot(nonpar_boot_biomarkers_qids_pre, order = "sample", plot = "area", verbose
= T)
plot(nonpar_boot_biomarkers_qids_post, order = "sample", plot = "area",
verbose = T)

summary(nonpar_boot_biomarkers_qids_pre)
summary(nonpar_boot_biomarkers_qids_post)

#11.4 To plot significant differences in nodes and edges

plot(nonpar_boot_biomarkers_qids_pre, "edge", plot = "difference", onlyNonZero
= T, order = "sample", labels = T, verbose = T)
plot(nonpar_boot_biomarkers_qids_post, "edge", plot = "difference",
onlyNonZero = T, order = "sample", labels = T, verbose = T)

plot(nonpar_boot_biomarkers_qids_pre, "strength", order = "sample", labels =
T, verbose = T, plot = "difference")
plot(nonpar_boot_biomarkers_qids_post, "strength", order = "sample", labels =
T, verbose = T, plot = "difference")
```