

Modeling the association between physician risky-prescribing and the complex network structure of physician shared-patient relationships - Tables and Figures

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Table 1: Network statistics of the largest connected component of the shared-patient physician prescribing network (specific to prescriptions of opioids, benzodiazepines, and sedative-hypnotics) for Ohio in 2014.

	Shared-patient physician network		
	Whole net	Prescribing net	LCC of prescribing net
Network statistics			
Number of nodes	35765	22655	17363
Number of ties	494462	265112	261816
Density	0.0008	0.0010	0.0010
Number of components	3002	2056	1
Size of LCC	27503	17363	17363
Degree (mean, IQR, SD)	27.7 (n/a, 44.0) (37.5)	23.4 (n/a, 38.0) (28.7)	30.2 (n/a, 45.0) (29.6)
Global clustering	0.168	0.171	0.171
Average path length	4.663	4.599	4.599
Prescribing statistics			
I_0 (mean, IQR)		0.871 (0.843, 1.0)	0.876 (0.875, 1.0)
I_{OBS} (mean, IQR)		0.009 (0.0, 0.0)	0.009 (0.0, 0.0)
$I_{everOBS}$ (# of 1, # of 0)		(1972, 20683)	(1412, 15951)
$I_{presc2mr}$ (mean, IQR)		0.030 (0.0, 0.0)	0.029 (0.0, 0.0)
$I_{depresc2mr}$ (mean, IQR)		0.017 (0.0, 0.0)	0.016 (0.0, 0.0)
Volume (mean, IQR, SD)	62.7 (n/a, 96.0) (86.3)	70.6 (n/a, 112.0) (87.8)	91.6 (18.0, 136.0) (90.3)

Note: The physician network is constructed based on the overlap of patient care at any point during 2014 between physician pairs treating patients residing in Ohio. The prescribing network is a subset of the whole network where its physicians have prescribed at least one opioid, benzodiazepine, or sedative-hypnotic during 2014. Volume is the number of Ohio Medicare fee-for-service beneficiaries a physician encountered throughout 2014. The values of n/a are suppressed to meet data suppressing rules designed to protect patient privacy by the Center for Medicare and Medicaid Services. LCC = largest connected component.

Table 2: ERGM adjusted homophily effects for models estimated on the largest connected component of the Ohio 2014 shared-patient physician prescribing network.

	Model 1			Model 2			Model 3			Model 4		
	Est.	SE	p	Est	SE	p	Est	SE	p	Est	SE	p
Edges	-5.732	0.012	***	-5.614	0.006	***	-5.609	0.006	***	-5.620	0.006	***
Node attribute												
Prescribing												
Binary												
$I_{everOBS} = 1$	0.327	0.010	***									
Continuous												
I_{OBS}				1.202	0.109	***						
$I_{presc2mr}$							0.492	0.049	***			
$I_{depresc2mr}$										0.337	0.066	***
Specialty (ref. PC)												
EM	-0.584	0.006	***	-0.614	0.006	***	-0.614	0.006	***	-0.611	0.006	***
Neuro	-0.338	0.010	***	-0.358	0.010	***	-0.359	0.010	***	-0.357	0.010	***
Psych	-0.668	0.009	***	-0.654	0.009	***	-0.653	0.009	***	-0.651	0.009	***
Other	-0.396	0.004	***	-0.423	0.005	***	-0.423	0.005	***	-0.420	0.005	***
Prescribing homophily												
Binary												
$I_{everOBS} = 1$	0.037	0.011	***									
Continuous												
$absdiff(I_{OBS})$				-1.200	0.114	***						
$absdiff(I_{presc2mr})$							-0.619	0.054	***			
$absdiff(I_{depresc2mr})$										-0.203	0.068	**
Specialty homophily												
PC	-1.509	0.009	***	-1.509	0.009	***	-1.511	0.009	***	-1.509	0.009	***
EM	0.541	0.019	***	0.541	0.019	***	0.541	0.019	***	0.541	0.019	***
Neuro	-0.190	0.091	*	-0.190	0.091	*	-0.190	0.091	*	-0.190	0.091	*
Psych	0.673	0.050	***	0.670	0.050	***	0.674	0.050	***	0.673	0.050	***

Note: The node attribute term and homophily term associated with the attribute were added one at a time in the model for each of the prescribing or deprescribing indexes, yielding five separate models. In each of the models, physician specialty and homophily of physician specialty (restricted to uniform effects across the different specialties) were included in the model. Absdiff is the ERGM term for examining the homophily of a continuous node attribute, with a negative estimate indicating homophily (smaller differences imply a higher likelihood of a network connection). Abbreviations: PC = primary care, EM = emergency medicine, Neuro = neurology, Psych = psychology. Significance levels: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$.

Table 3: ERGM adjusted homophily effects in HRR shared-patient sub-networks in 2014.

			Homophily effects of indexes							
Descriptive Stats			absdiff(I_{OBS})		absdiff($I_{presc2mr}$)		absdiff($I_{depresc2mr}$)		$I_{everOBS}$	
HRR	N	Density	Coef.	SE	Coef.	SE	Coef.	SE	Coef.	SE
180	129	0.116	-3.998	3.662	0.004	1.623	1.052	1.898	0.026	0.133
357	193	0.106	0.810	2.707	-1.541*	0.714	0.467	0.775	-0.268	0.149
331	256	0.128	-5.156	2.675	-1.792*	0.697	-0.325	0.773	0.047	0.117
332	415	0.048	-1.765*	0.745	-0.863***	0.250	0.299	2.410	0.056	0.079
335	550	0.060	-1.887*	0.920	-0.881**	0.305	-0.545	0.416	0.063	0.070
326	648	0.050	-1.281	0.795	-1.066***	0.306	44.210	280.321	-0.080	0.056
325	750	0.030	-0.469	0.814	-0.917**	0.279	0.496	0.699	0.0002	0.089
334	1039	0.029	-0.532	0.416	-1.190***	0.226	-0.301	0.209	0.018	0.045
330	1164	0.024	-1.205**	0.419	-0.339	0.196	-0.071	0.319	0.0002	0.037
327	1760	0.015	-1.711**	0.584	-0.783***	0.179	-0.362*	0.171	0.120**	0.044
328	2623	0.010	-1.603***	0.370	-0.897***	0.142	-0.193	0.227	0.060	0.034
329	3101	0.008	-1.181***	0.234	-0.754***	0.109	-0.327*	0.157	-0.018	0.025

Note: The HRR sub-networks were partitioned from the largest connected component of the Ohio 2014 shared-patient physician prescribing network and the HRR sub-networks were not restricted to their respective largest connected components thus they may not be fully connected. Significance levels:

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$.

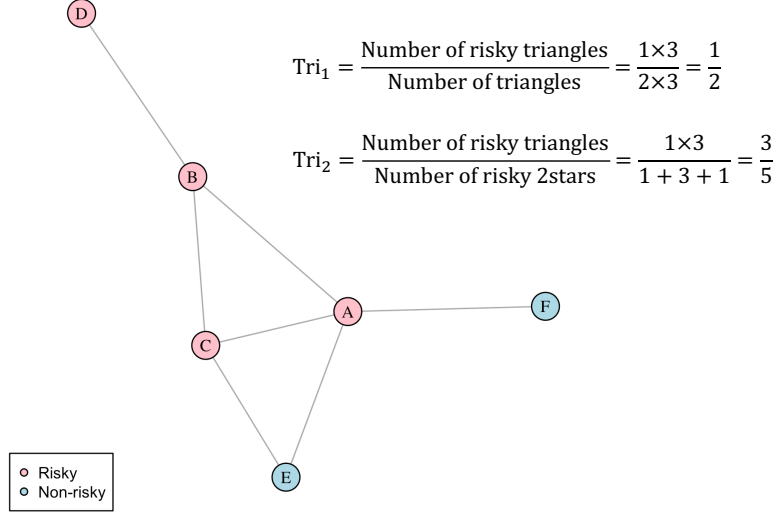
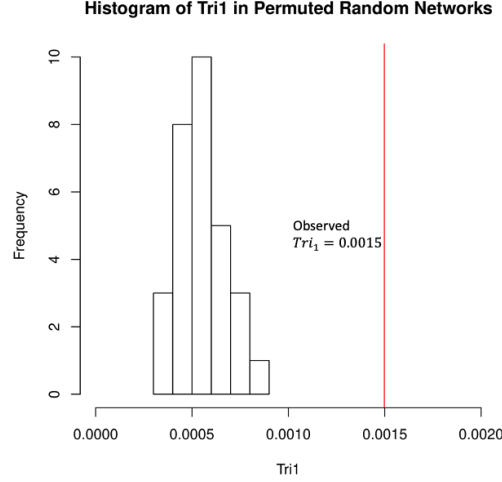
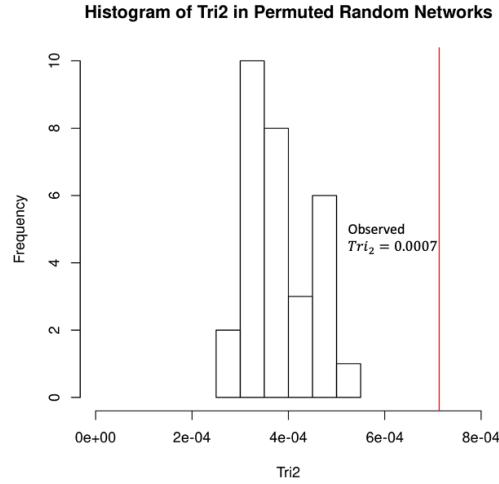


Figure 1: Diagram of computing triadic homophily statistics Tri_1 and Tri_2 in an example network. Suppose nodes A, B, C, and D are physicians who have contributed to risky prescribing, and nodes E and F are non-risky-prescribing physicians. The number of risky 2-stars with nodes A, B, C, and D being the center vertex is 1, 3, 1, and 0, respectively. Therefore, the total number of 2-stars among risky prescribing physicians is five.



(a) Triadic homophily statistic Tri_1



(b) Triadic homophily statistic Tri_2

Figure 2: Histogram of triadic homophily network statistics generated by the triadic homophily non-parametric test. The triadic homophily statistic Tri_1 is the proportion of closed triangles with the $I_{everOBS}$ node attribute (whether a physician has ever contributed to bringing patients to the riskiest prescription state OBS) in the network. The triadic homophily statistic Tri_2 is the proportion of open two-paths with all nodes having the same attribute that are closed in the network. Panel (a) is the histogram of Tri_1 and panel (b) is the histogram of Tri_2 calculated from 30 networks with randomly shuffled node attributes under the null hypothesis of no homophily with respect to the given prescribing index. The red vertical lines denote the values in the observed network.