Structure and geography of a hospital patient transfer network

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THE STRUCTURE OF CRITICAL CARE TRANSFER NETWORKS

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The data

- Network of transfers of critically ill patients.
- Data derived from 2005 Medicare claims.
- 3308 hospitals with 47820 patient transfers.
- "nearly all hospitals participated in at least one transfer, and 4.5% of all critical care hospitalizations involved such a transfer."
- "Transfer" from hospital A to B defined as patient in A and then in B on the same or next day.
- Transfers are then represented as a directed edge from A to B.

Some general conclusions from the original paper

- Hospitals transfer patients to several other hospitals in a complex network, not a simple hierarchy.
- It is not like a "hub-and-spoke" model explaining secondary and tertiary care.
- Patients seem to move towards better resourced hospitals.

> *While the secondary / tertiary hospital model may have some heuristic value, the implied hierarchy (in which secondary hospitals send but do not receive patients and tertiary hospitals receive but do not send patients) does not appear to be present in our data. Instead, hospitals appear to maintain diverse portfolios of other facilities to which they transfer patients.*

(Iwashyna et al. 2009)

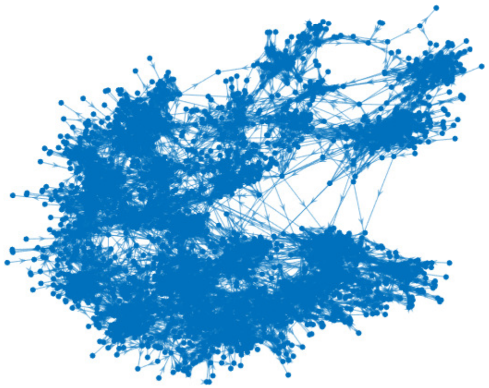
So the simple model is not right. What can we do?

- We can use network models to try to explain the complex observed network structure.
- Network community detection and stochastic block modeling to try to define classes (more complex than the secondary / tertiary model) of hospitals in the network.
- Exponential random graph model (ERGM) to try to find the processes that give rise to the observed network.
- And we will have to account for the effect of geography, as distances between hospitals is clearly likely to be a significant factor.

Community structure and geography

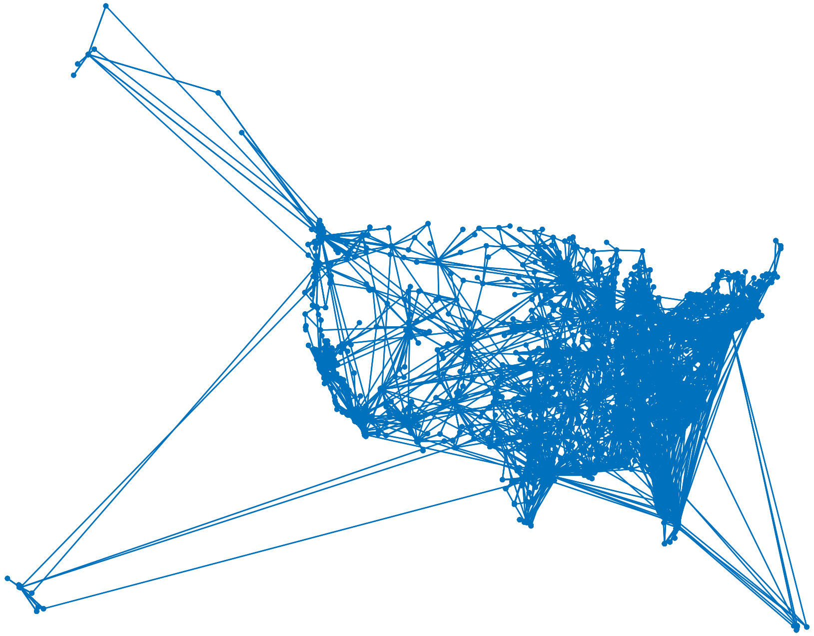
- Network communities are groups of nodes in which the nodes have more connections within the group than to nodes in other groups.
- We can "see" these in the following network plots,
- and there are very many ways to find them algorithmically (we will do some).
- But could the "communities" in this network be mostly be due to geography...?

Network plot by MATLAB "force" (Fruchterman-Reingold)

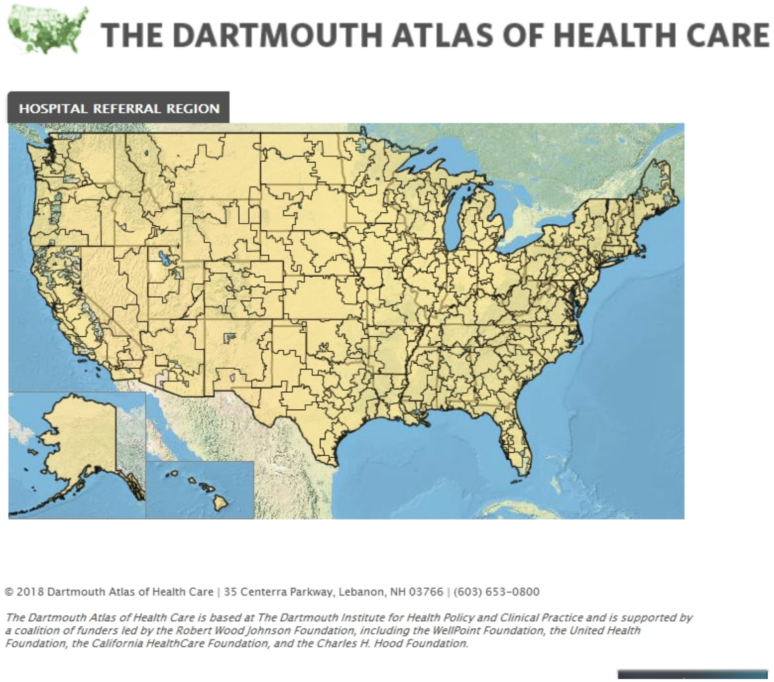


Network plot by MATLAB "subspace" (Koren)

Network plot in MATLAB according to geography



Hospital Referral Regions



THE DARTMOUTH ATLAS OF HEALTH CARE

HOSPITAL REFERRAL REGION

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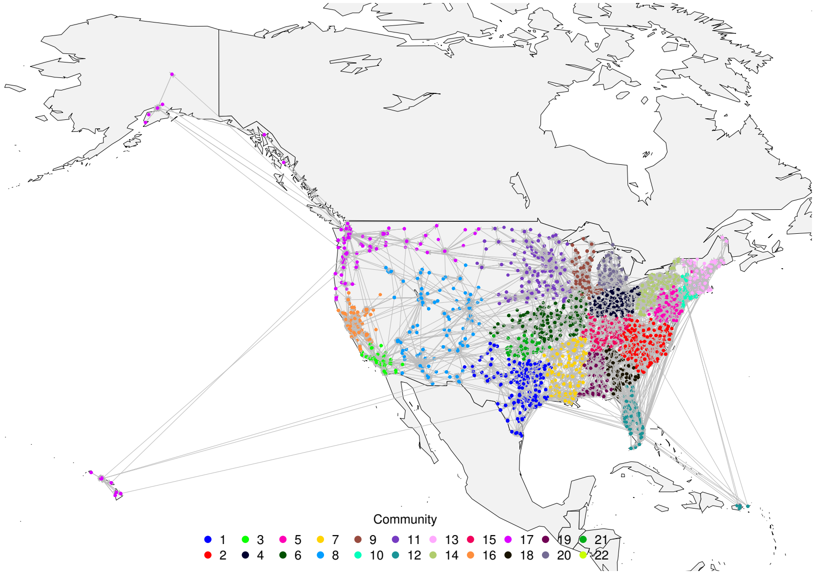
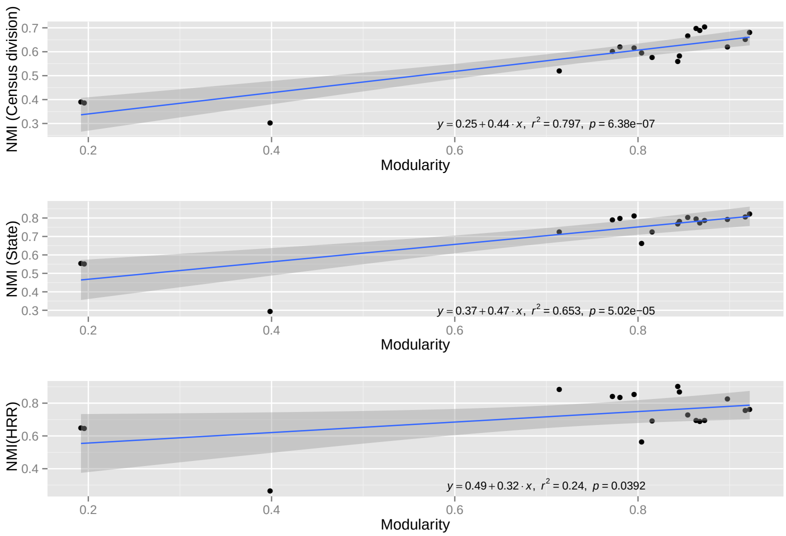
“Hospital Transfer Regions”

- Hu, Y., Wang, F., & Xierali, I. M. (2018). Automated Delineation of Hospital Service Areas and Hospital Referral Regions by Modularity Optimization. *Health Services Research*, 53(1), 236-255.
- This paper describes an automated, data-driven method to define HRRs in order to overcome problems with the existing Dartmouth ones.
- It does this by using community detection (Louvain) on a network of patient-to-hospital flows (hospital and patient ZIP codes as nodes).
- Similarly, by finding network communities in the patient transfer network, we could define “Hospital Transfer Regions” [or perhaps “interhospital referral regions” (Caimo, Pallotti & Lomi, 2017)].

Network communities found with Louvain method



NMI with geographic regions is correlated with modularity



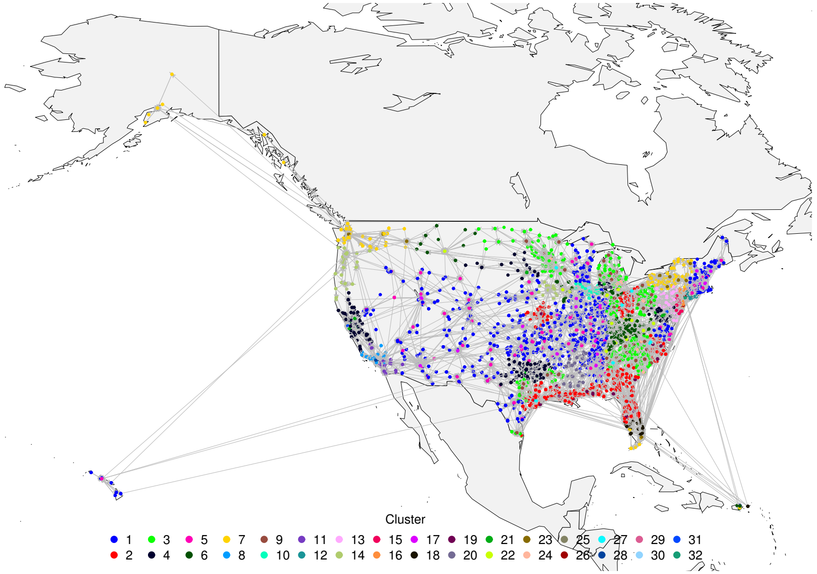
Breaking free of geography

- So it looks like the clusters are highly correlated with geography,
- which means they can be used to define "regions" in a geographically meaningful sense.
- This was assumed implicitly in Hu et al. (2018) for using Louvain method to define HRRs.
- But there is no *a priori* reason to assume network clusters are geographical regions:
- E.g. imagine large hospitals in NY and LA exchanging patients with each other more than any other (closer) hospitals.
- This hypothetical "region" consisting of tiny areas on both coasts makes sense structurally but not geographically.
- The fact that clustering does not find such regions is because in fact geography is a very significant factor: patients are more likely to be transferred to nearby hospitals.
- But what would we find if we tried to exclude geography and look at structural similarities only?

Stochastic Block Model (SBM)

- A model of networks with unobserved classes (blocks) where the probability of a tie between nodes depends only on the classes to which they belong (Nowicki & Snijders, 2001).
- Much more general than community detection, which (by definition) can only find assortative (i.e. community) structure. SBM can also find disassortative, core-periphery, and other structures.
- A large literature on this and the computationally difficult problem of finding the blocks.
- We will use a sophisticated Bayesian method to find the blocks: McDaid, A. F., Murphy, T. B., Friel, N., & Hurley, N. J. (2013). Improved Bayesian inference for the stochastic block model with application to large networks. *Computational Statistics & Data Analysis, 60*, 12-31.

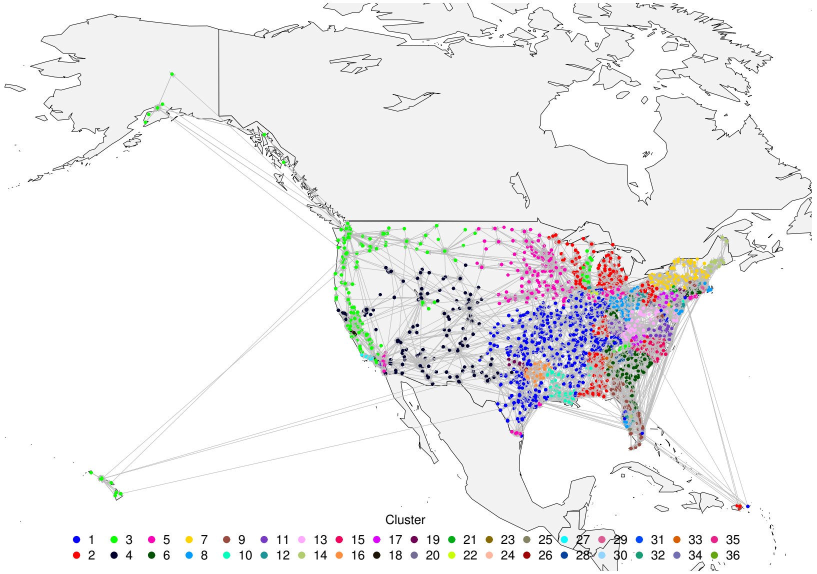
Blocks found by SBM treating edges as undirected



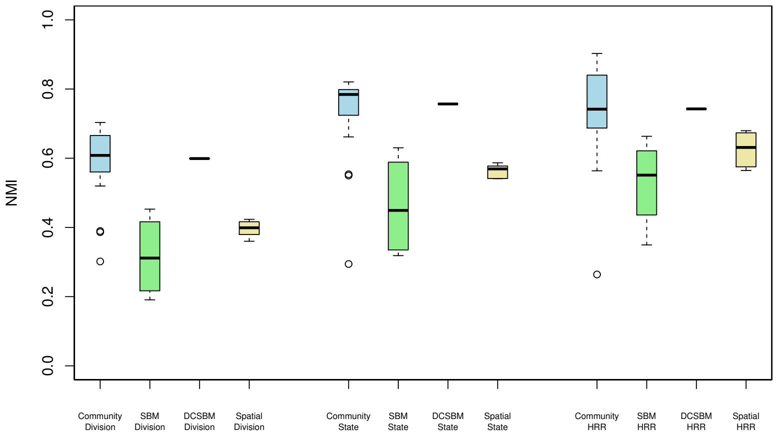
Finding space-independent communities

- Expert et al. 2011 “Uncovering space-independent communities in spatial networks” PNAS 108(19):7663–7668
- Instead of using the Newman-Girvan null model (preserve node degrees on average), use instead a null model that preserves weighted average for an edge to exist at a given distance.
- The null model is similar to a “gravity” model: edge probability between two nodes is proportional to the product of the node “masses” (or importances) over function of the distance between them.
- For “importance” we try both node degree (similar to Newman-Girvan null model) or number of discharges (as a proxy for hospital size).
- For the clustering algorithm we use a generalized Louvain method and implement the Expert et al. (2011) null model in the modularity matrix.

Communities found with degree spatial null model (bin size 100 km)



SBM (but not Degree-Corrected SBM) and spatial null model communities are less related to geographical regions than network communities are



ERGM introduction

- A way of modeling network ties based on structure and attributes.
- Given an observed network, we estimate parameters for local effects, such as reciprocity, closure (clustering), activity (sending more ties), popularity (receiving more ties), preferential attachment, homophily, etc.
- The sign (positive for the effect occurring more than by chance, negative for less than by chance) and significance tell us about these processes, taking dependency into account.
- I.e. it tells us about the process occurring significantly more or less than by chance, *given all the other effects in the model occurring simultaneously*.

Modeling the actual directed network

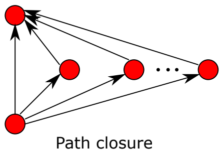
- We were unable to estimate ERGMs for this directed network with existing methods (statnet, PNet, even with snowball sampling).
- We were only able to estimate a simple model treating the network as undirected with the new IFD sampler (Byshkin et al. 2016 *J. Stat. Phys.* 165(4):740–754). But ignoring the edge direction is too limiting as transfers are inherently directional.
- But using the new "Equilibrium Expectation" algorithm (Byshkin et al. 2018 Fast Maximum Likelihood estimation via Equilibrium Expectation for Large Network Data. arXiv preprint arXiv:1802.10311.), extended to apply to directed networks, we can estimate ERGM parameters for this network (in less than an hour).

ERGM results (no geography, and with HRR and state)

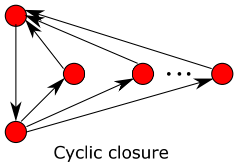
Effect	Model 1	Model 2
Arc	−6.175 (−6.316, −6.034)	−14.914 (−15.058, −14.771)
AltInStars	0.371 (0.351,0.391)	0.244 (0.222,0.265)
AltOutStars	−2.035 (−2.117, −1.954)	−2.364 (−2.444, −2.285)
Reciprocity	5.257 (5.189,5.326)	6.659 (6.569,6.748)
AltKTrianglesT	1.977 (1.955,1.999)	0.937 (0.919,0.956)
AltKTrianglesC	−0.640 (−0.654, −0.626)	−0.383 (−0.395, −0.371)
ContinuousSender log discharges	−0.142 (−0.149, −0.135)	0.309 (0.297,0.321)
ContinuousReceiver log discharges	0.317 (0.312,0.322)	0.837 (0.830,0.843)
Diff log discharges	−0.287 (−0.300, −0.275)	0.124 (0.104,0.144)
Sender teaching hospital	−0.293 (−0.351, −0.234)	−0.472 (−0.531, −0.413)
Receiver teaching hospital	0.506 (0.487,0.526)	0.621 (0.596,0.645)
Interaction teaching hospital	−0.071 (−0.135, −0.006)	−0.150 (−0.223, −0.078)
Matching hrr	—	2.353 (2.330,2.376)
MatchingReciprocity hrr	—	−1.929 (−1.989, −1.869)
Matching state	—	3.705 (3.660,3.751)
MatchingReciprocity state	—	−3.767 (−3.857, −3.678)
logGeoDistance	—	—

Model interpretation (1,2) – structural

- Some hospitals receive patients from many hospitals, but there tend not to be hospitals that send patients to many hospitals.
- There is a tendency for reciprocity.
- There is a tendency for transitive closure, but against cyclic closure:
  - If hospital A sends patients to hospitals B and C, then it is likely that hospital B also sends patients to C (or C to B).
  - But if hospital A sends patients to hospital B, and B to C, then it is unlikely that C also sends patients to A: i.e. generalized exchange is unlikely.



Path closure
AT-T



Cyclic closure
AT-C

Model interpretation (1,2) — attributes and regions

- Teaching hospitals are less likely to send patients and more likely to receive them. And patients are less likely to be transferred between teaching hospitals (than from a teaching to a non-teaching hospital).
- (Using number of discharges as proxy for hospital size), larger hospitals are much more likely to receive transferred patients.
- When geography included, larger hospitals are also more likely to send patients. But this is reversed if geography is not taken into account: it looks like larger hospitals are *less* likely to send patients!
- Similarly transfers are more likely between hospitals of different sizes, but this is reversed if no geographical information is included.
- Transfers are more likely within states and within HRRs.
- However reciprocity within (rather than between) states or HRRs is less likely.

ERGM results (include geographical distance)

Effect	Model 3	Model 4
Arc	−10.711 (−10.869, −10.554)	−6.122 (−6.245, −5.999)
AltInStars	0.161 (0.136,0.187)	0.103 (0.083,0.122)
AltOutStars	−2.918 (−2.989, −2.847)	−4.057 (−4.125, −3.989)
Reciprocity	5.464 (5.364,5.564)	1.222 (1.183,1.261)
AltKTrianglesT	0.715 (0.697,0.732)	0.925 (0.905,0.946)
AltKTrianglesC	−0.441 (−0.453, −0.429)	−0.556 (−0.572, −0.541)
ContinuousSender log discharges	0.501 (0.491,0.511)	0.723 (0.719,0.727)
ContinuousReceiver log discharges	1.052 (1.047,1.057)	1.039 (1.037,1.041)
Diff log discharges	0.296 (0.277,0.315)	0.387 (0.378,0.395)
Sender teaching hospital	−0.558 (−0.611, −0.505)	−0.665 (−0.710, −0.620)
Receiver teaching hospital	0.493 (0.465,0.521)	0.316 (0.295,0.337)
Interaction teaching hospital	−0.439 (−0.505, −0.373)	−0.569 (−0.628, −0.511)
Matching hrr	1.313 (1.281,1.344)	—
MatchingReciprocity hrr	−1.781 (−1.844, −1.717)	—
Matching state	2.164 (2.116,2.213)	—
MatchingReciprocity state	−3.435 (−3.536, −3.333)	—
logGeoDistance	−0.982 (−0.993, −0.971)	−1.529 (−1.536, −1.521)

Model interpretation (3,4)

- Now the (logarithm of) geographical distance between hospitals is included.
- This parameter is negative: patient transfers are less likely between more distant hospitals.
- This is in addition to patient transfers being more likely within the same state and within the same HRR.
- But now it seems that the negative interaction parameter for teaching hospitals is no longer significant (not well converged): we can no longer conclude that transfers between teaching hospitals are less likely than those between teaching and non-teaching hospitals.

Limitations and future work

- The validity of "hospital transfer regions" should be assessed with various indices as in Hu et al. (2018) for HRRs (but would need different ones for transfers not referrals).
- We do not have thorough Goodness-of-Fit tests when using the new ERGM estimation algorithm on large (directed) networks. More method development is required here.
- We are also subject to all the limitations of the original data: it is derived from Medicare only, for a single year, and only includes transfers between critical care hospitalizations (see Iwashyna et al. 2009).
- Some more information about hospital organization form, ownership, size, and performance may be available by matching this data to publicly available US Government Medicare data, which would allow models with more attributes to be constructed.

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- This research was supported by Melbourne Bioinformatics at the University of Melbourne, grant number VR0261.
- This work was partly funded by PASC project "Snowball sampling and conditional estimation for exponential random graph models for large networks in high performance computing" and was supported by a grant from the Swiss National Supercomputing Centre (CSCS) under project ID c09.
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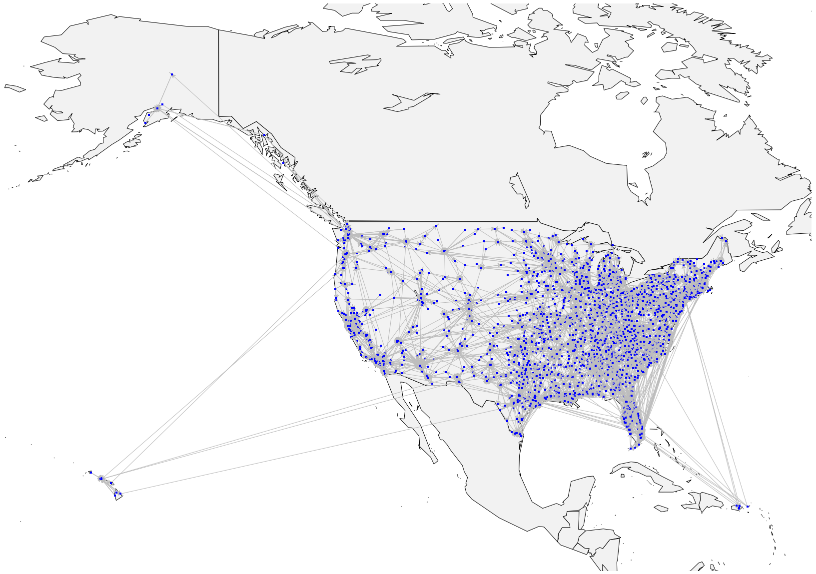
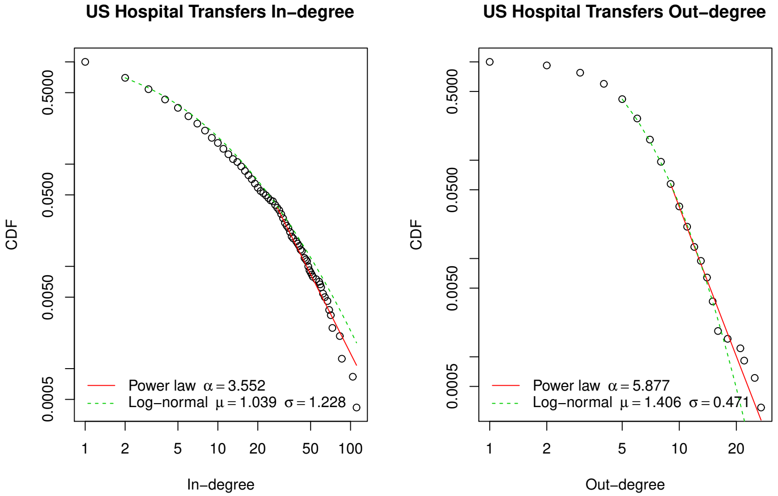
- We thank Aaron McDaid for making his SBM source code available, Brian Karrer and Mark Newman for making the DCSBM source code available, and Lucas Jeub, Marya Bazzi, Inderjit Jutla, and Peter Mucha for making their generalized Louvain method source code available.

Hidden bonus slides

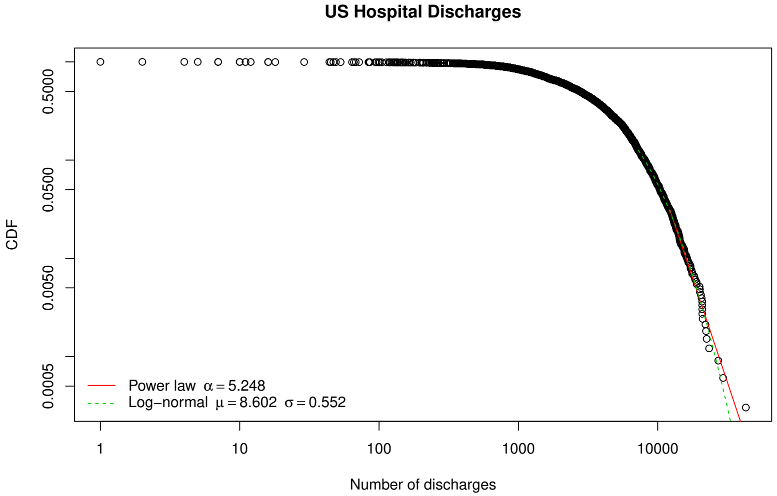
Network plot on map of North America (using R)



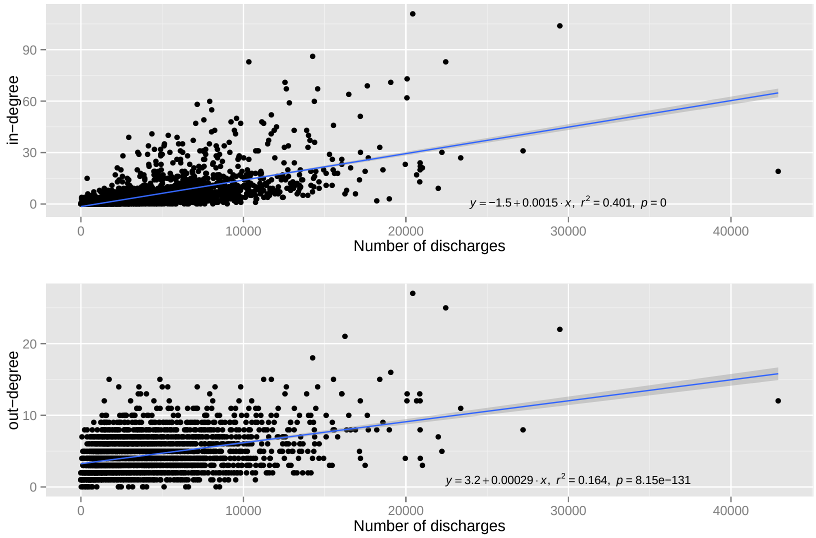
In- and out-degree distributions are consistent with both power law and log-normal distributions



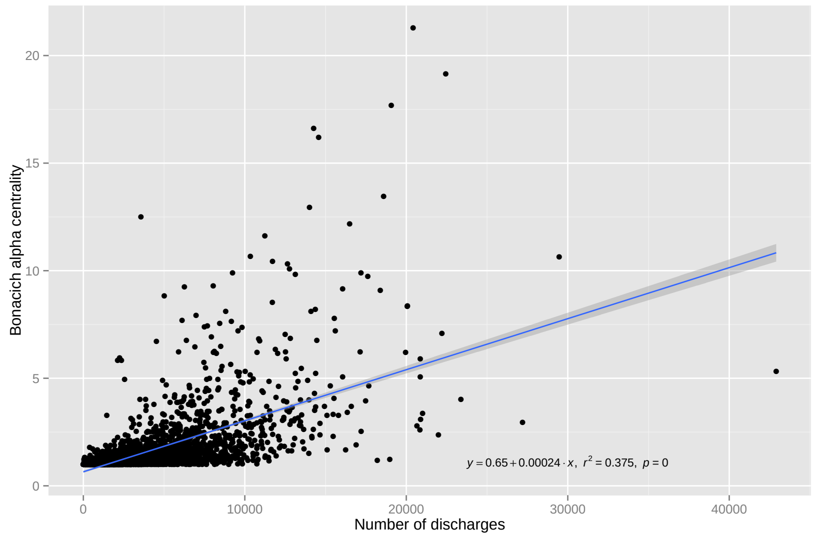
Distribution of the number of discharges is consistent with both power law and log-normal distributions



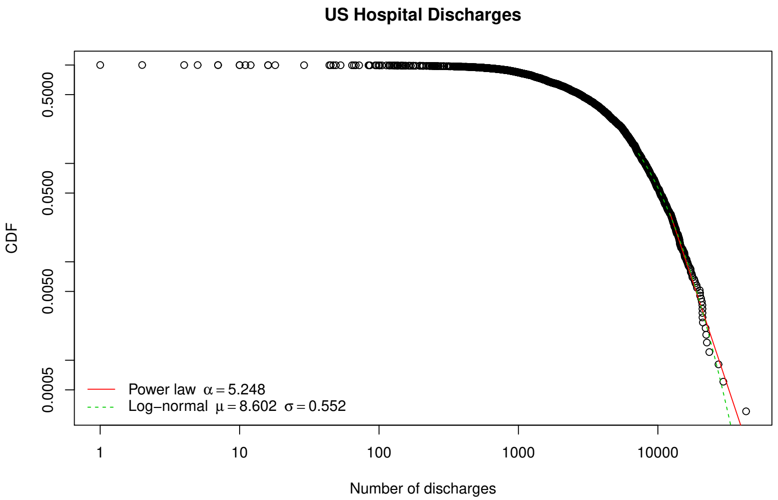
Degree is correlated with number of discharges (in- more so than out-degree)



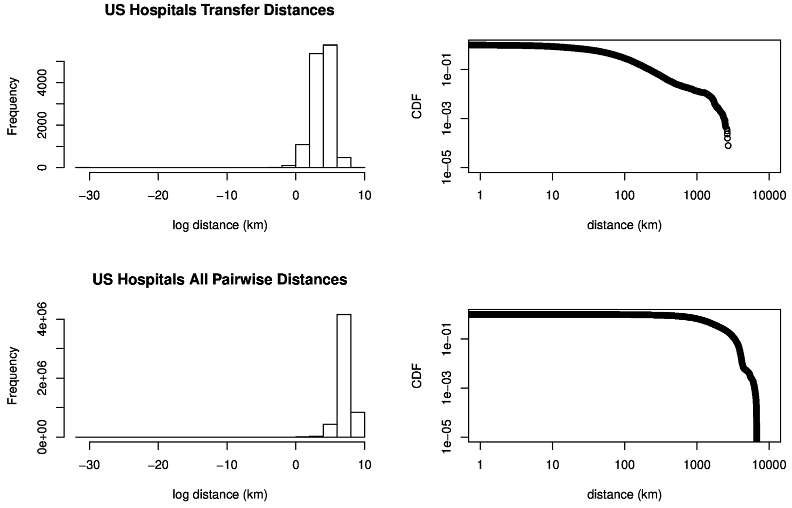
Bonacich alpha Centrality is correlated with number of discharges



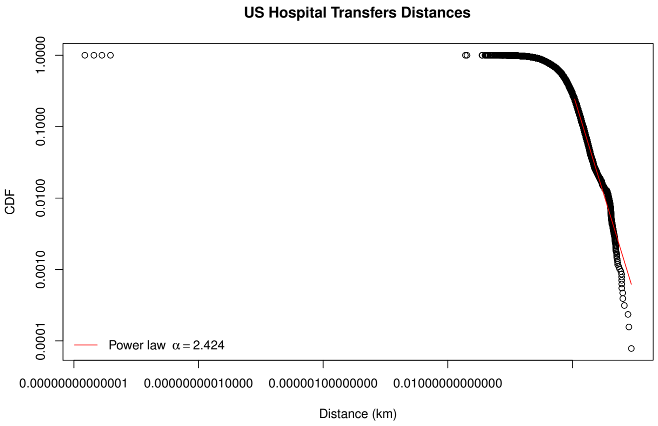
Distribution of the number of discharges is consistent with both power law and log-normal distributions



Distribution of transfer distances and hospital distances



Patient transfer distances are not power law



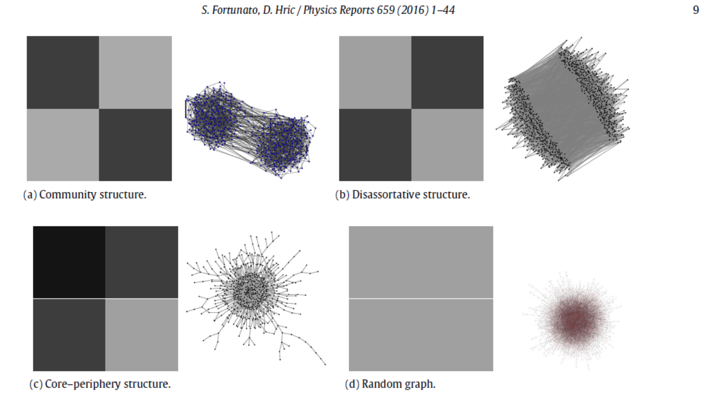
Using the statistical tests described by Clauset et al. (2009) this distribution is not consistent with a power law distribution ($p < 0.01$).

The network and all census division subnetworks are small-world

Network	N	L_g	L_r	L_l	C^*_g	C^*_r	C^*_l	SWI
USA	3308	5.15	3.74	189.95	0.438	0.003	0.653	0.664
EastSouthCentral	285	3.91	2.68	17.31	0.510	0.029	0.646	0.713
Pacific	428	4.26	3.09	30.15	0.377	0.017	0.627	0.566
Mountain	204	3.93	2.86	15.88	0.440	0.031	0.612	0.646
WestSouthCentral	437	3.69	2.92	27.17	0.462	0.018	0.643	0.687
NewEngland	156	2.80	2.38	9.37	0.516	0.053	0.648	0.733
SouthAtlantic	572	4.03	2.92	32.63	0.492	0.015	0.653	0.719
EastNorthCentral	519	3.98	2.94	30.90	0.464	0.016	0.649	0.681
WestNorthCentral	284	3.82	3.00	21.54	0.402	0.023	0.616	0.611
MidAtlantic	413	3.25	2.62	20.73	0.495	0.024	0.666	0.709

- All networks are small-world according to the S^{Δ} significance test of Humphries & Gurney (2008).
- Small World Index (SWI) (Neal 2017) ranges from 0 to 1.
- L_g is the average shortest path length of the network
- C^*_g is its clustering coefficient.
- L_r and C^*_r are, respectively, the average shortest path length and clustering coefficient for an Erdős-Renyi random graph with same size and mean degree.
- L_l and C^*_l are, respectively, the mean path length and clustering coefficient for a ring lattice graph with the same size and mean degree.

SBM structure examples



(a) Community structure.

(b) Disassortative structure.

(c) Core–periphery structure.

(d) Random graph.

Fig. 8. Stochastic block model. We show the schematic adjacency matrices of network realisations produced by the model for special choices of the edge probabilities, along with one representative realisation for each case. For simplicity we show the case of two blocks of equal size. Darker blocks indicate higher edge probabilities and consequently a larger density of edges inside the block. (a) Illustrates community (or assortative) structure: the probabilities (link densities) are much higher inside the diagonal blocks than elsewhere. (b) Shows the opposite situation (disassortative structure). (c) Illustrates a core–periphery structure. (d) Shows a random graph à la Erdős and Rényi: all edge probabilities are identical, inside and between the blocks, so there are no actual groups.
Source: Adapted figure with permission from [19].
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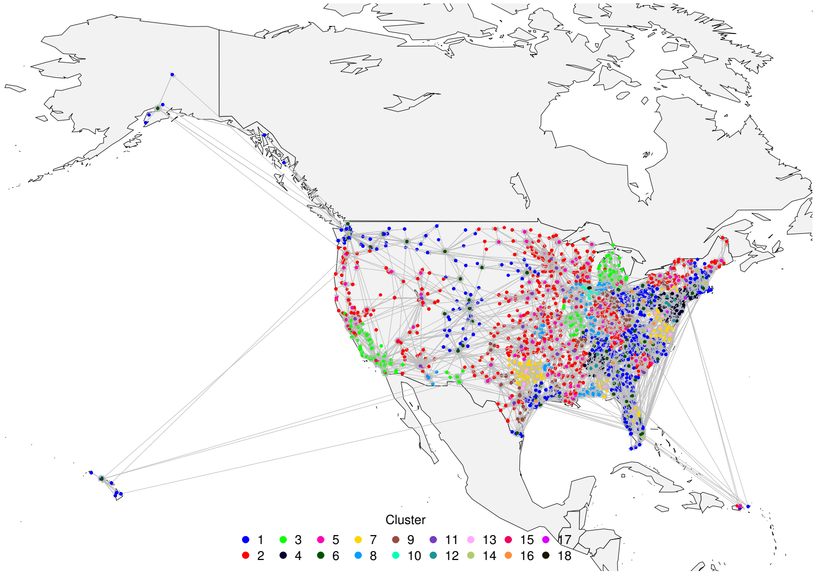
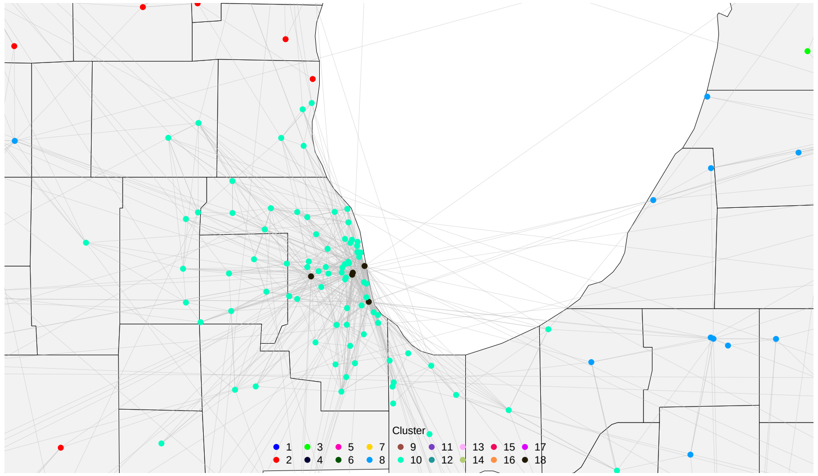
Community detection results (nodes with no HRR removed)

Method	Dir.	We.	# com.	Modularity	State NMI	Div. NMI	HRR NMI	Time (m)
Louvain	N	Y	45	0.92	0.82	0.68	0.76	0.00
Fast greedy	N	Y	46	0.92	0.81	0.65	0.76	0.00
Walktrap	N	Y	118	0.90	0.79	0.62	0.83	0.01
Edge betweenness	N	Y	35	0.87	0.79	0.70	0.69	29.16
Louvain	N	N	31	0.87	0.77	0.69	0.69	0.00
Edge betweenness	N	N	33	0.86	0.79	0.70	0.69	15.03
Walktrap	N	N	52	0.85	0.80	0.67	0.73	0.01
Infomap	Y	Y	197	0.85	0.78	0.58	0.87	0.02
Infomap	N	Y	251	0.84	0.77	0.56	0.90	0.02
Leading eigenvector	N	Y	57	0.82	0.72	0.58	0.69	0.03
Fast greedy	N	N	24	0.80	0.66	0.59	0.56	0.00
Infomap	N	N	121	0.80	0.81	0.62	0.85	0.03
Label propagation	N	N	120	0.78	0.80	0.62	0.84	0.00
Infomap	Y	N	145	0.77	0.79	0.60	0.84	0.02
Label propagation	N	Y	465	0.71	0.72	0.52	0.88	0.00
Leading eigenvector	N	N	16	0.40	0.29	0.30	0.26	0.00
Edge betweenness	Y	N	1629	0.20	0.55	0.39	0.65	4.25
Edge betweenness	Y	Y	1656	0.19	0.55	0.39	0.65	6.29

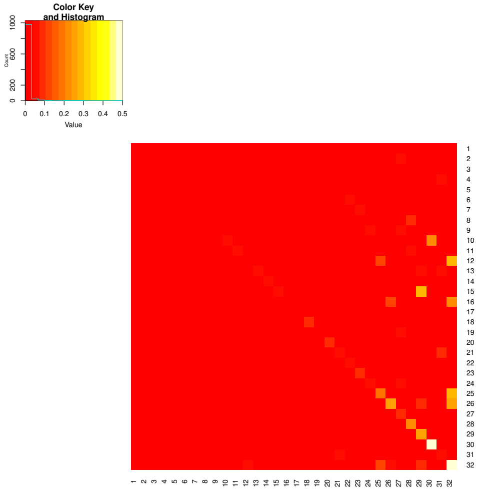
Blocks found by SBM with directed arcs



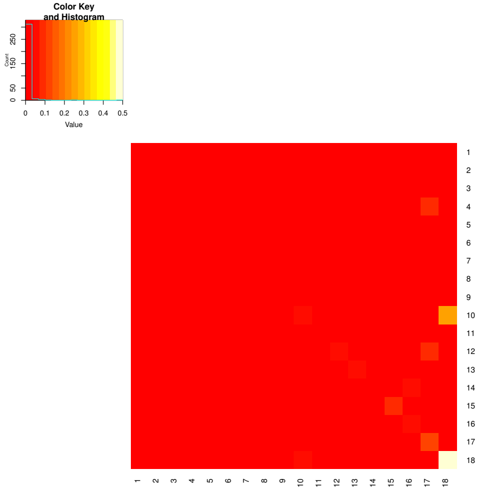
SBM (directed) block 18 consists of 5 high in-degree hospitals in the Chicago area



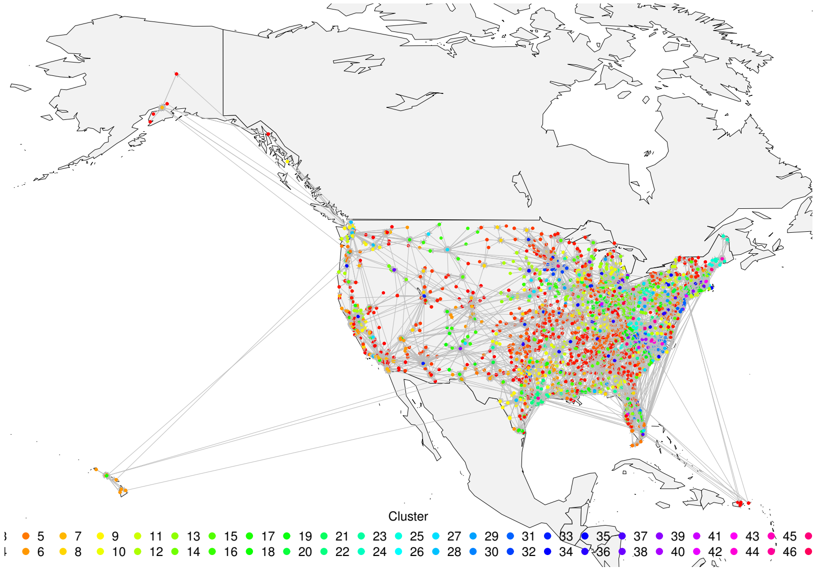
Empirical block matrix for SBM with undirected edges



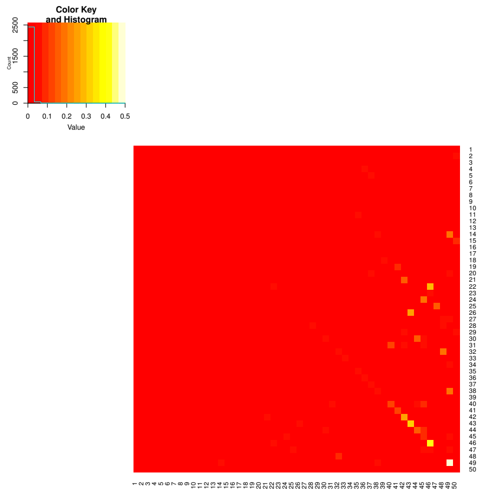
Empirical block matrix for SBM with directed arcs



Blocks found by SBM with directed and weighted arcs



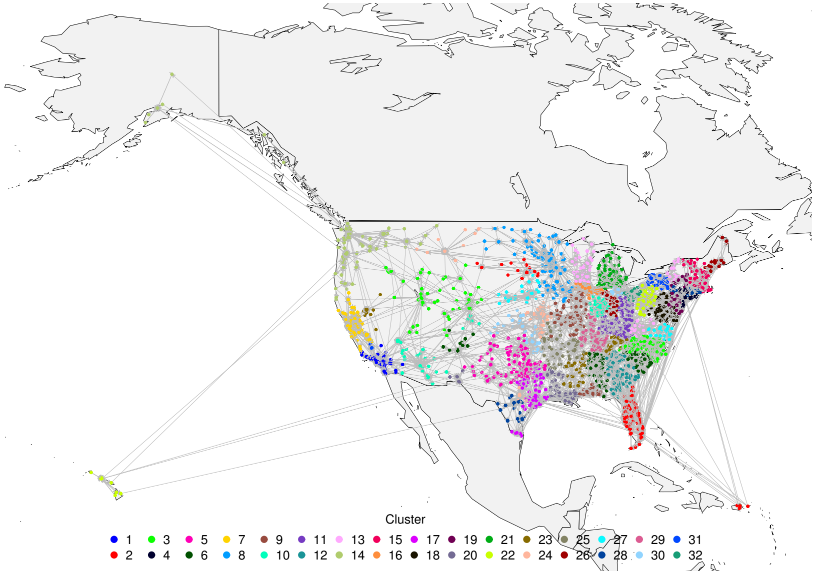
Empirical block matrix for SBM with directed weighted arcs



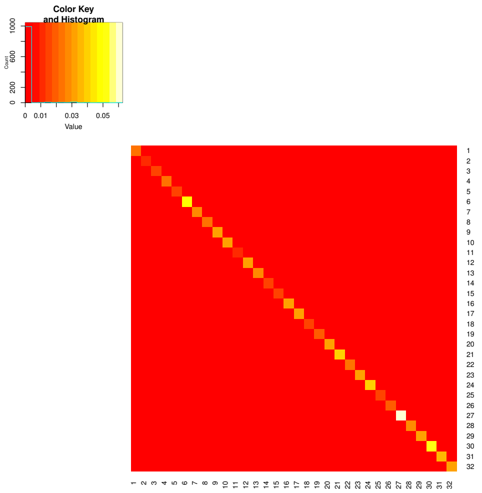
Degree-Corrected Stochastic Block Model

- We used a “standard” SBM (albeit with a very sophisticated Bayesian estimation method). But perhaps a “degree-corrected” SBM (Karrer & Newman 2011) would give (more) interesting results, by using empirical degree distribution as null model so blocks are not created based on node degree.
- So we used the DCSBM (implemented for undirected networks only) with $k = 32$, the same number of blocks found by the Bayesian SBM (DCSBM does not estimate the number of blocks).
- It looks like the DCSBM basically finds community structure similar to modularity maximization, corresponding to geography...

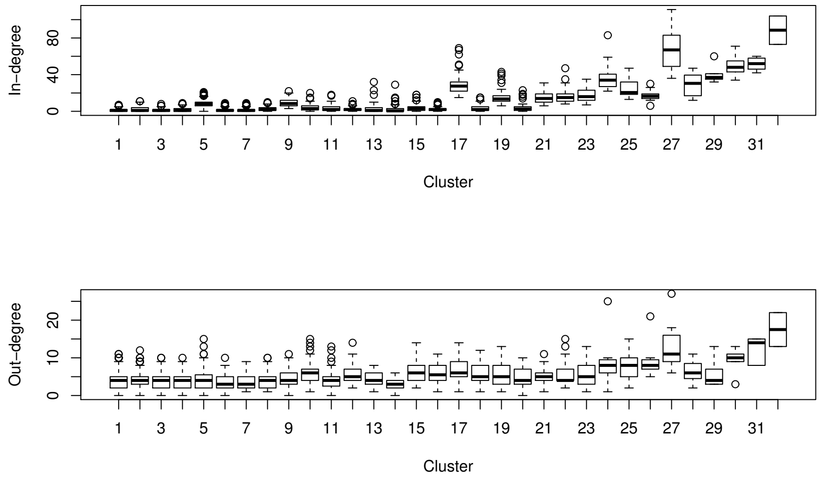
Blocks found by Degree-Corrected SBM with $k = 32$



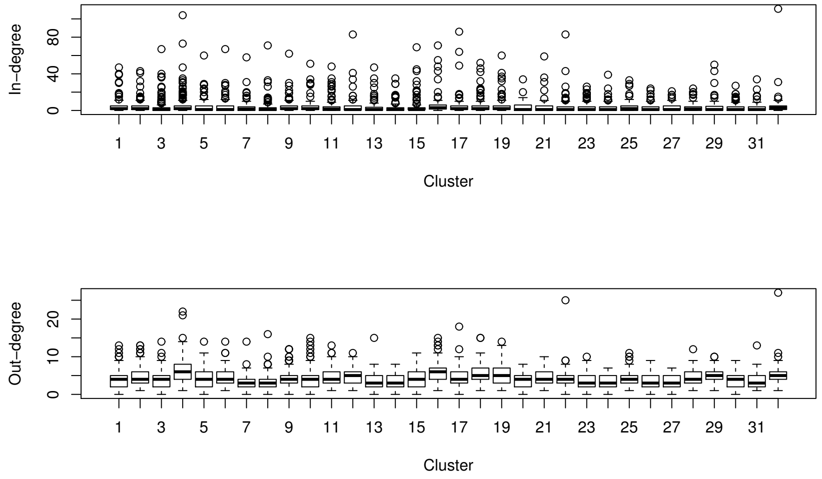
DCSBM block matrix shows assortative (community) structure



SBM assigns some blocks apparently according to degree heterogeneity



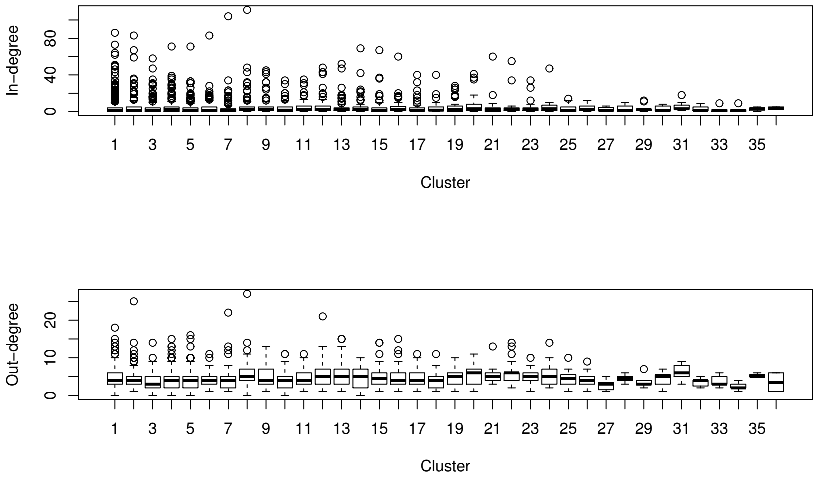
DCSBM by construction assigns blocks independent of node degrees



Spatial null model generalized Louvain method results

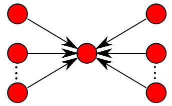
Importance	Binsize (km)	Modularity	# communities
Size	5	0.63	181
Size	10	0.63	182
Size	50	0.65	159
Size	100	0.66	143
Degree	5	0.70	43
Degree	10	0.70	38
Degree	50	0.71	38
Degree	100	0.72	36

Spatial null model community degree distributions

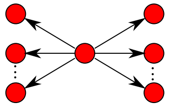


Model configurations — structural

Alternating *k*-stars: useful for capturing degree distribution

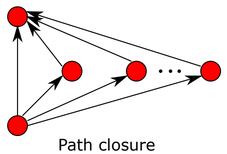


Popularity spread
Alt. in-star
AinS

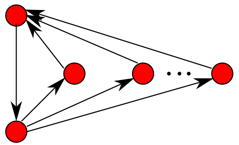


Activity spread
Alt. out-star
AoutS

Alternating *k*-triangles (AT): useful for modeling social circuit dependence

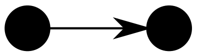


Path closure
AT-T

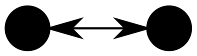


Cyclic closure
AT-C

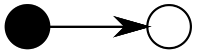
Model configurations — categorical attributes



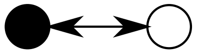
Matching



Matching reciprocity



Mismatching



Mismatching reciprocity

ERGM results (removing unconverged Interaction teaching)

Effect	Model 5	Model 6
Arc	−10.730 (−10.873, −10.586)	−6.147 (−6.282, −6.012)
AltInStars	0.167 (0.141,0.192)	0.115 (0.093,0.137)
AltOutStars	−2.921 (−2.988, −2.854)	−4.037 (−4.103, −3.970)
Reciprocity	5.499 (5.396,5.601)	1.236 (1.197,1.276)
AltKTrianglesT	0.713 (0.696,0.731)	0.919 (0.899,0.938)
AltKTrianglesC	−0.432 (−0.444, −0.420)	−0.543 (−0.558, −0.527)
ContinuousSender log discharges	0.499 (0.490,0.509)	0.720 (0.716,0.724)
ContinuousReceiver log discharges	1.053 (1.049,1.058)	1.040 (1.038,1.042)
Diff log discharges	0.306 (0.287,0.325)	0.401 (0.392,0.409)
Sender teaching hospital	−0.771 (−0.808, −0.734)	−0.961 (−0.997, −0.924)
Receiver teaching hospital	0.391 (0.373,0.408)	0.195 (0.170,0.219)
Interaction teaching hospital	—	—
Matching hrr	1.306 (1.288,1.325)	—
MatchingReciprocity hrr	−1.762 (−1.816, −1.707)	—
Matching state	2.175 (2.130,2.221)	—
MatchingReciprocity state	−3.467 (−3.565, −3.370)	—
logGeoDistance	−0.975 (−0.980, −0.971)	−1.523 (−1.536, −1.509)

ERGM estimation attempts

- Could not estimate network at all using PNet.
- Also could not get estimations to work with snowball samples.
- Using statnet (even new “stepping” algorithm), could not estimate whole network, and only ended up with converged estimations for 4/9 census divisions with MCMC.burnin=1e07 and took between 17 and 78 hours.
- The first successful estimation for whole network was using IFD sampler, but only implemented for undirected networks so limited usefulness.

statnet model for New England census division

Effect	Estimate	std. errror	p-value	
A2P-T(2.00) [gwdsp(ln(2))]	0.0054	0.0141	0.70125	
AKT-T(2.00) [gwesp(ln(2))]	0.6699	0.0631	$< 1 \times 10^{-04}$	***
Edge	-6.3790	0.2442	$< 1 \times 10^{-04}$	***
gwidegree	-1.6636	0.2357	$< 1 \times 10^{-04}$	***
gwodegree	4.2110	0.4939	$< 1 \times 10^{-04}$	***
mutual	4.7064	0.5091	$< 1 \times 10^{-04}$	***
mutual.hrr	-1.5377	0.3317	$< 1 \times 10^{-04}$	***
mutual.state	-1.6585	0.5294	0.00174	**
mutual.teaching_hospital	-1.6400	0.3935	$< 1 \times 10^{-04}$	***
nodeicov.teaching_hospital	1.2164	0.1443	$< 1 \times 10^{-04}$	***
nodematch.hrr	1.1058	0.1149	$< 1 \times 10^{-04}$	***
nodematch.state	1.7341	0.1475	$< 1 \times 10^{-04}$	***
nodematch.teaching_hospital	0.1075	0.1532	0.48279	
nodeocov.teaching_hospital	-0.7591	0.1907	$< 1 \times 10^{-04}$	***

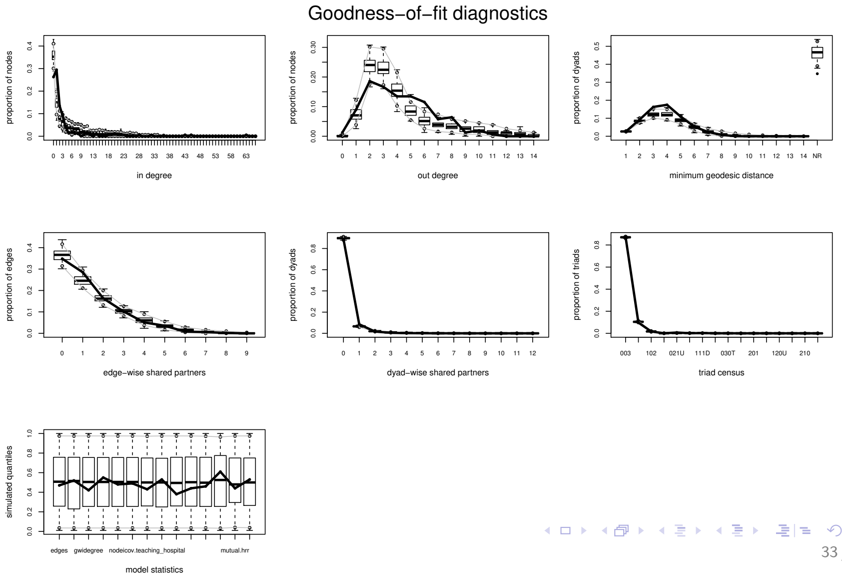
Interpretation of statnet results

- There is centralization on in-degree and not on out-degree, consistent with the overall model. (See Hunter 2007 Soc. Netw. 29:216–230 and Levy 2016 J. Open Source Softw. 1(3):36 for interpretation of gwidegree and gwodegree parameters).
- Consistent with models 2–4 (geographical information included), positive overall reciprocity parameter, but negative within HRR and state.
- And also homophily on region (HRR and state) i.e. transfers more likely within than between these regions.
- Consistent with overall models, teaching hospitals are less likely send patients and more likely to receive them.

Statnet models for other census divisions

- The other 3 census divisions that we obtained converged models for (Mountain, WestNorthCentral, EastSouthCentral) have similar results.
- Only significant differences:
  - Mountain, EastSouthCentral and WestNorthCentral have significant negative A2P-T (not significant in New England).
  - Mountain teaching hospital reciprocity is significant and negative (consistent with overall models); not significant in the other converged statnet census division models.

statnet goodness-of-fit for New England



Lomi & Pallotti (2012) "Relational collaboration among spatial multipoint competitors."

- Interhospital patient transfer network of 13 178 patients between 91 hospitals in Lazio region of Italy (includes Rome) in 2003.
- Model includes:
    - Patient pool overlap, "diffuse competition", geographical distance, LHU.
    - size, occupancy rate, case mix index, complementarity, performance index, organizational form.
- Estimation using MCMLE.

Lomi & Pallotti 2012 ERGM results

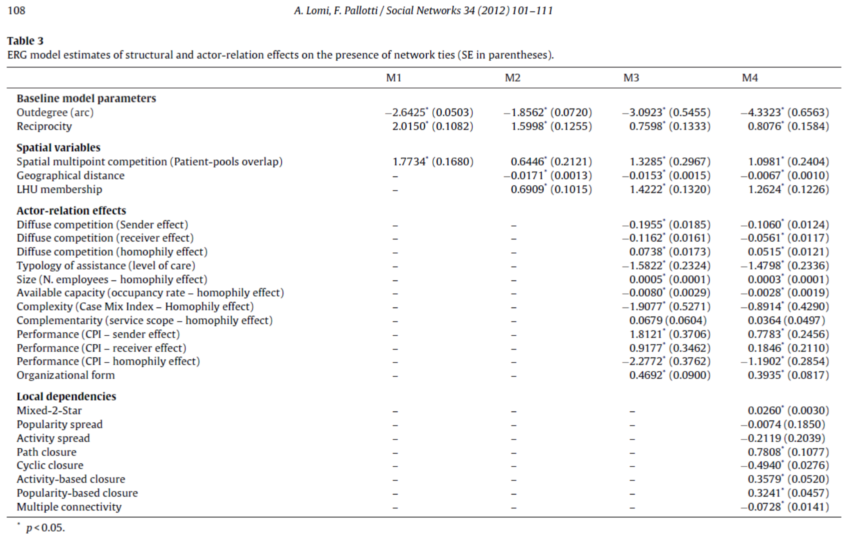


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Table 3
ERG model estimates of structural and actor-relation effects on the presence of network ties (SE in parentheses).

	M1	M2	M3	M4
Baseline model parameters				
Outdegree (arc)	−2.6425* (0.0503)	−1.8562* (0.0720)	−3.0923* (0.5455)	−4.3323* (0.6563)
Reciprocity	2.0150* (0.1082)	1.5998* (0.1255)	0.7598* (0.1333)	0.8076* (0.1584)
Spatial variables				
Spatial multipoint competition (Patient-pools overlap)	1.7734* (0.1680)	0.6446* (0.2121)	1.3285* (0.2967)	1.0981* (0.2404)
Geographical distance	–	−0.0171* (0.0013)	−0.0153* (0.0015)	−0.0067* (0.0010)
LHU membership	–	0.6909* (0.1015)	1.4222* (0.1320)	1.2624* (0.1226)
Actor-relation effects				
Diffuse competition (Sender effect)	–	–	−0.1955* (0.0185)	−0.1060* (0.0124)
Diffuse competition (receiver effect)	–	–	−0.1162* (0.0161)	−0.0561* (0.0117)
Diffuse competition (homophily effect)	–	–	0.0738* (0.0173)	0.0515* (0.0121)
Typology of assistance (level of care)	–	–	−1.5822* (0.2324)	−1.4798* (0.2336)
Size (N. employees – homophily effect)	–	–	0.0005* (0.0001)	0.0003* (0.0001)
Available capacity (occupancy rate – homophily effect)	–	–	−0.0080* (0.0029)	−0.0028* (0.0019)
Complexity (Case Mix Index – Homophily effect)	–	–	−1.9077* (0.5271)	−0.8914* (0.4290)
Complementarity (service scope – homophily effect)	–	–	0.0679 (0.0604)	0.0364 (0.0497)
Performance (CPI – sender effect)	–	–	1.8121* (0.3706)	0.7783* (0.2456)
Performance (CPI – receiver effect)	–	–	0.9177* (0.3462)	0.1846* (0.2110)
Performance (CPI – homophily effect)	–	–	−2.2772* (0.3762)	−1.1902* (0.2854)
Organizational form	–	–	0.4692* (0.0900)	0.3935* (0.0817)
Local dependencies				
Mixed-2-Star	–	–	–	0.0260* (0.0030)
Popularity spread	–	–	–	−0.0074 (0.1850)
Activity spread	–	–	–	−0.2119 (0.2039)
Path closure	–	–	–	0.7808* (0.1077)
Cyclic closure	–	–	–	−0.4940* (0.0276)
Activity-based closure	–	–	–	0.3579* (0.0520)
Popularity-based closure	–	–	–	0.3241* (0.0457)
Multiple connectivity	–	–	–	−0.0728* (0.0141)

* $p < 0.05$.

Comparing results with Lomi & Pallotti 2012 (1)

- No significant centralization effects here; unlike our models of US network which find centralization on in-degree and against centralization on out-degree.
- Both find significant positive path closure but negative cyclic closure, just as we did.
- Both also find overall positive reciprocity.

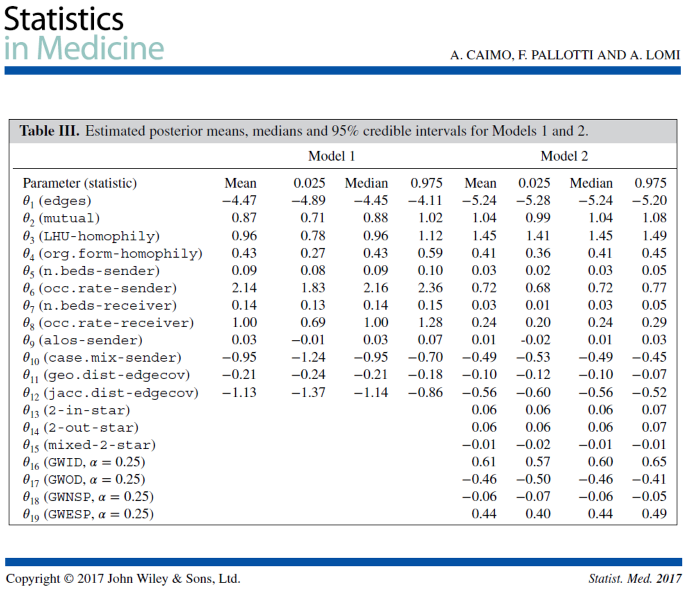
Comparing results with Lomi & Pallotti 2012 (2)

- Hospital attributes:
  - Both show regional homophily effects (HRR and LHU respectively).
  - When geography is included, we find heterophily on size (num. discharges) but Lomi & Pallotti found homophily on size (num. employees).
  - We did not have data on organization form, occupancy rate, case mix, complementarity, performance index or patient pool overlap / competition to compare.

Caimo, Pallotti & Lomi (2017) "Bayesian exponential random graph modelling of interhospital patient referral networks"

- Interhospital patient transfer network of total 16 557 patients between 110 hospitals in Lazio region (12 Local Health Units [LHUs]) of Italy for 2007.
- Model includes:
  - number of beds
  - occupancy rate
  - average length of stay
  - case mix index
  - Organizational form (LHU / trust / research / classified / private)
  - Jaccard distance between all hospitals in space of all clinical specialties
  - geographical distance between hospitals
- Estimation using Bayesian ERGM (Caimo & Friel 2011)

Caimo, Pallotti & Lomi 2017 BERGM results



Statistics
in Medicine

A. CAIMO, F. PALLOTTI AND A. LOMI

Table III. Estimated posterior means, medians and 95% credible intervals for Models 1 and 2.

	Model 1				Model 2			
Parameter (statistic)	Mean	0.025	Median	0.975	Mean	0.025	Median	0.975
θ_1 (`edges`)	−4.47	−4.89	−4.45	−4.11	−5.24	−5.28	−5.24	−5.20
θ_2 (`mutual`)	0.87	0.71	0.88	1.02	1.04	0.99	1.04	1.08
θ_3 (`LHU-homophily`)	0.96	0.78	0.96	1.12	1.45	1.41	1.45	1.49
θ_4 (`org.form-homophily`)	0.43	0.27	0.43	0.59	0.41	0.36	0.41	0.45
θ_5 (`n.beds-sender`)	0.09	0.08	0.09	0.10	0.03	0.02	0.03	0.05
θ_6 (`occ.rate-sender`)	2.14	1.83	2.16	2.36	0.72	0.68	0.72	0.77
θ_7 (`n.beds-receiver`)	0.14	0.13	0.14	0.15	0.03	0.01	0.03	0.05
θ_8 (`occ.rate-receiver`)	1.00	0.69	1.00	1.28	0.24	0.20	0.24	0.29
θ_9 (`alos-sender`)	0.03	−0.01	0.03	0.07	0.01	-0.02	0.01	0.03
θ_{10} (`case.mix-sender`)	−0.95	−1.24	−0.95	−0.70	−0.49	−0.53	−0.49	−0.45
θ_{11} (`geo.dist-edgecov`)	−0.21	−0.24	−0.21	−0.18	−0.10	−0.12	−0.10	−0.07
θ_{12} (`jacc.dist-edgecov`)	−1.13	−1.37	−1.14	−0.86	−0.56	−0.60	−0.56	−0.52
θ_{13} (`2-in-star`)					0.06	0.06	0.06	0.07
θ_{14} (`2-out-star`)					0.06	0.06	0.06	0.07
θ_{15} (`mixed-2-star`)					−0.01	−0.02	−0.01	−0.01
θ_{16} (`GWID`, $\alpha = 0.25$)					0.61	0.57	0.60	0.65
θ_{17} (`GWOD`, $\alpha = 0.25$)					−0.46	−0.50	−0.46	−0.41
θ_{18} (`GWNSP`, $\alpha = 0.25$)					−0.06	−0.07	−0.06	−0.05
θ_{19} (`GWESP`, $\alpha = 0.25$)					0.44	0.40	0.44	0.49

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Comparing results with Caimo, Pallotti & Lomi 2017 (1)

- Both find a limited number of hospitals receive a large number of transfers, but diffuse activity of sending patients.
- Both find tendency for interhospital transfer to be in closed structures of collaborating hospitals:

  > *"This tendency towards network closure is consistent with the idea that patient transfer relations require a considerable level of trust and social control between partner hospitals."*

  (Caimo, Pallotti & Lomi, 2017)
- Both also find overall reciprocity of transfers between hospitals.

Comparing results with Caimo, Pallotti & Lomi 2017 (2)

- Geographical: Both show that transfers are less likely as distance increases.
- Hospital attributes:
  - Both show positive sender and receiver effects for hospital size (num. discharges [when geography included] or num. beds).
  - Both show regional homophily effects: within HRR, state, division; or within LHU (of course this is also related to geographic distance).
- We did not have data on organization form, occupancy rate, case mix, average length of stay, or clinical specialties to compare.
- However an interesting difference is that Caimo et al. find no significant effect of organization form, and we use only the binary "teaching hospital", we actually find heterophily on this attribute: teaching hospitals, while generally more likely to be receivers and less likely to be senders, are also less likely to send patients to each other (although this is only significant in models 1 and 2).

Comparing results with Caimo, Pallotti & Lomi 2017 (3)

- The Bayesian approached used in Caimo et al. allows some more sophisticated analyses than we can do with a non-Bayesian approach, such as incorporating prior information and the greater flexibility and intuitiveness of the posterior distribution, as well as allowing analysis of the posterior correlation matrix.
- It is however, still very computationally expensive: we would not have been able to analyze the 3308 node network with this approach (Caimo et al. use a 110 node network).