# Inferred Networks and the Social Determinants of Health

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Abstract. This paper explores the social determinants of health through a network science based approach to analyzing the Latino MSM Community Involvement (LMSM-CI) dataset. Data are clustered to determine identifying characteristics of groups of participants in 3 categories: high self esteem, susceptibility to alcohol abuse, and HIV positive status. A question arises as to the best methodology for inferring a graph from the data, as well as for clustering and analyzing the network. To that end we use 4 different graph inference methods: inverse covariance selection (Glasso), neighborhood selection (MB), Sparse Correlations for Compositional data (SparCC) and the traditional k-Nearest Neighbors (kNN). For each inference we test 4 different clustering methods: Louvain, Leiden, NBR-Clust with VAT, and NBR-Clust with integrity. Surprisingly, the Glasso and MB inference methods produce better clusterings than kNN, as determined by a suite of internal evaluation measures. The most promising clusterings are visualized and their properties are analyzed.

**Keywords:** graph inference, clustering, machine learning, health data analysis

#### 1 Introduction

The desire to find a happy and healthy life has led to the emergence of Social Determinants of Health (SDoH). The Centers for Disease Control (CDC) outlines SDoH as "conditions in the environments where people are born, live, learn, work, play, worship, and age that affect a wide range of health, functioning, and quality-of-life outcomes and risks" [10]. Those conditions can be a catalyst for better health and prosperity. Understanding data on SDoH such as education, income, employment, age, and more can aid in attempts to improve community health. The use of machine learning algorithms such as clustering on graphs inferred from health and medical datasets presents opportunities towards personalized medicine, and a healthier and better quality of life.

There are benefits to inferring a network from existing data and working with it in network form [7]. These include the ability to simplify data to a nodes-and-edges graph representation, the opportunity to employ a wide range of existing algorithms and tools, and the ability to learn from effective visualization of the information. Each of these benefits is put to use in this study.

Due to technical advances in genetic sequencing technologies there has been a large influx of new data. Desire to exploit this data has lead to a variety of new graph inference techniques, including those examined here: inverse covariance selection (Glasso) [14], Meinshausen and Bühlmann (MB) neighborhood selection [23], Sparse Correlations for Compositional data (SparCC) [13], and the traditional k-Nearest Neighbors (kNN). Due to expanded use of electronic medical records, there is a large amount of newly-available medical data. This paper seeks to determine the applicability of these graph inference methods to applications with health and medical data. Surprisingly, Glasso and MB give strong results, which is a contrast with previous papers that preferred kNN graphs [17].

Social determinant data used here are from Jesus Ramirez-Valles' *Latino MSM Community Involvement: HIV Protective Effects* (LMSM-CI) survey [27], the original purpose of which was to determine whether community involvement reduced the risk of HIV in male Latino populations. We examine social determinants leading to target variables of high self esteem, alcohol abuse risk, and positive HIV status via graph inference methods and clustering on the LMSM-CI dataset. The data are available online through application with the National Addiction & HIV Data Archive Program <sup>1</sup>. This research was approved by the SIUE Institutional Review Board.

## 2 Related Work

In this study we have inferred Glasso, MB, SparCC, and kNN graphs. The Glasso method is based on graphical lasso regression, which has been widely used in diverse applications like financial interpretation [4] and facial recognition [32]. KNN is a popular network inference method, with previous medical data applications including predicting sleep disorders [26] and analyzing stroke biomarkers [11]. In [18] the graph methods that we see in this paper are tested with microbial associations. They have also have been applied to other domains, such as metagenomics and inflammatory bowel disease [1], ribosomal and micro RNA [13], and spoilage of food [25].

Machine learning approaches have been employed in the study of social determinants of health [16], such as in [28], where social and economic factors are used to predict medical data like blood pressure and body mass index. In other examples, social and economic factors have been used to study the causes of addiction [2] and to evaluate mental disorders [3].

This paper focuses on four network-based methods of community detection: Louvain, Leiden, and NBR-Clust with VAT and integrity. The best clusterings are chosen by cluster evaluation methods, in accordance with work previously done in [17]. Machine learning tools like clustering have been used on graphs inferred from medical data to analyze and understand conditions such as autism spectrum disorder [22]. Clustering has been used to predict drug-drug reactions [30] and analyze DNA sequences [15]. In this study we rigorously analyze graph inference and machine learning techniques as applied to the LMSM-CI dataset.

<sup>&</sup>lt;sup>1</sup> https://www.icpsr.umich.edu/web/pages/NAHDAP/index.html

#### 3 Methods

#### 3.1 The LMSM-CI Dataset

The data used in this study are from the Latino MSM Community Involvement: HIV Protective Effects survey (LMSM-CI) [27]. The data were collected in 2003-2004 and consist of 323 samples of Latino men who have sex with men (MSM) in the Chicago, Illinois, USA metro area and 320 samples in the San Francisco, California, USA area. The study consists of over 900 variables, with many variables related to the social determinants of HIV in the Latino MSM community. The foremost aim of the survey is to determine if Latino MSMs are more likely to take precautions against HIV if they are involved in community activities. The large amount of data collected makes this dataset relevant not just to HIV, but to other determinants as well.

#### 3.2 Data Curation

Many of the variables contained in the LMSM-CI dataset were meta-data, such as the IDs of the recruiter and subsequent recruitees of the sample. Also, the survey contained many questions involving participation in specific charities or social groups. To simplify analysis, these variables were removed. The remaining multi-valued variables were converted to binary variables using one-hot encoding. As an example of one-hot encoding, a variable such as employment-status with possible answers employed, unemployed, and on-disability, is changed to three variables with yes/no answers: employment-status:employed, employment-status:unemployed, and employment-status:on-disability.

The National Institute on Alcohol Abuse and Alcoholism (NIAAA) [24] defines heavy alcohol abuse risk for men as binge drinking for more than 4 days in the past month, where binge drinking is defined by the Substance Abuse and Mental Health Services Administration (SAMHSA) as drinking more than 5 alcoholic drinks. We created the target variable Alcohol Risk based on these definitions and the LMSM-CI variables concerning frequency of alcohol consumption and number of drinks on a typical day. The self esteem target we study represents an affirmative answer in the survey to "I have a positive attitude about myself."

Feature selection was performed as described in [11], with stratified testing and training sets. The step forward algorithm was used to select the features giving the best performance as determined by logistic regression. The end result was a list of the most important 70, 20 and 15 variables for each of the 3 target variables being studied.

#### 3.3 Graph Inference

The LMSM-CI data were converted into graph format using four graph inference methods. These inference methods assume sparse networks, so in all cases parameter settings were adjusted to produce a connected graph with the minimum number of edges. The first graph inference method is the widely used k-Nearest Neighbors (kNN), where distances are calculated between each pair of proband vectors  $\overrightarrow{uv}$ , and an edge is placed between node u and its k shortest distance neighbors v. The kNN graphs were created using the CCCD R package [19].

The second graph inference method is Glasso. This is a fast method for "estimating sparse graphs by a lasso penalty applied to the inverse covariance matrix" [14]. The third inference method, Meinshausen and Bühlmann (MB) [23], uses neighborhood selection. It "estimates a sparse graphical model by fitting a lasso model to each variable, using the others as predictors" [14]. The last method is Sparse Correlations for Compositional data (SparCC) [13]. SparCC uses linear Pearson correlations to infer a network of associations. This approach has been shown to ameliorate unreliable results that can occur with correlation analysis methods. Glasso, MB, and SparCC networks were created using Sparse Inverse Covariance Estimation for Ecological Association Inference (SPIEC-EASI) [18].

### 3.4 Clustering

Four clustering methods were used. Louvain [6] is a popular, low-time-complexity algorithm that seeks to produce clusters that maximize modularity, a well-known method of quantifying the goodness of a clustering, as measured against a random clustering. The Leiden algorithm is meant to represent an improvement over Louvain. It "converges to a partition in which all subsets of all communities are locally optimally assigned. The Leiden algorithm is faster than the Louvain algorithm and uncovers better partitions. In addition, it has been proved that the Leiden algorithm yields communities that are guaranteed to be connected" [29]. The NBR-Clust framework [21] uses network resilience measures to partition a graph into clusters. It identifies an attack set of nodes  $S \in V$ , whose removal partitions the network into some number of disconnected components. Resilence measures used with NBR-Clust are integrity, which is defined as

$$I(G) = \min_{S \subset V} \{ |S| + C_{max}(V - S) \},$$
 (1)

and vertex attack tolerance (VAT), which is defined as

$$VAT(G) = \min_{S \subset V} \left\{ \frac{|S|}{|V - S - C_{max}(V - S)| + 1} \right\},\tag{2}$$

where V is the set of vertices, S is the attack set, and  $C_{max}$  is the size of the remaining largest connected component. Resilience measures are approximated using betweenness centrality [20]. For all three clustering methods, the number of clusters is not specified a priori.

#### 3.5 Cluster Evaluation

We quantified the success of clustering results with 5 internal evaluation measures, using the methodology presented in [22, 17]. Cluster evaluation measures

Glasso SparCC Cluster Silhou- Calinski-Silhou- Calinski-Algorithm Davies-Baker-Hubert Davies-Baker-Hubert-Bouldin ette Harabasz Hubert Levine Bouldin ette Harabasz Hubert Levine 1.911 0.168 4.376 0.5460.2482.216 -0.021 1.589 0.2400.396 0.199 5.593 0.708 0.155 2.399 1.834 0.223 0.403 20 1.558 0.033 Louvain 2.293 1.841 0.2970.384 2.3540.0540.4260.330 2.275 0.650 0.209 0.031 2.014 0.369 2.402 0.1744.416 2.137 0.2620.708 0.1552.387 0.028 1.820 0.215 0.402 20 1.558 0.1995.593 Leiden 2.648 0.0932.648 0.5260.2812.426 0.0422.038 0.3210.3720.573 0.499 1.974 0.096 3.816 0.2391 711 -0.0841.231 0.008 20 2.130 0.0754.907 0.458 0.2621.718-0.2100.981 -0.1050.563 VAT 2.351 -0.1640.1800.429-0.2260.822 -0.1820.5501.511 15 1.974 0.096 3.816 0.573 0.239 1.794-0.131 1.1940.082 0.467 0.003 2.786 0.228 |201.2630.577 1.718 -0.2100.981 -0.1050.563Integrity 2.086 -0.1740.449 1.598 0.121 0.476

Table 1. Cluster Evaluation Results for Self Esteem

quantify (in different ways) desirable clustering properties, such as maximal separation between clusters combined with minimal separation within a cluster. The following evaluation methods were used: Davies-Bouldin, Silhouette, Calinski & Harabasz, Baker & Hubert, and Hubert & Levine, from the ClusterSim R package [31]. A higher score indicates a better clustering, except with Davies-Bouldin and Hubert & Levine, where a lower score indicates a better clustering.

Each clustering result was given a score, determined by an ensemble method, where the clustering with the best score for each evaluation measure was given a point, and the clustering with the most points was chosen. Ties were broken by comparing individual scores between the tied instances. For example, between two tied clusterings, the clustering with a better score on an evaluation method such as Davies-Bouldain would be assigned 1 point. This would be repeated for all 5 evaluation methods, and the highest-scoring clustering would be chosen.

## 4 Results

#### 4.1 Cluster Evaluation

Results from cluster evaluation are shown in Tables 1, 2, and 3. Each line in a table represents a clustering method in combination with the number of variables used to infer the graph (15, 20, or 70). Highlighted numbers represent the best scores for each clustering algorithm and receive 1 point. Total points determine the best clustering. Due to space limitations, results for some graph types are not shown. For self esteem, the high scoring choice was Glasso-Leiden-20, as shown in Table 1. For alcohol risk, as shown in Table 2, both Glasso and MB clusterings performed well, scoring highest on 3 evaluation measures. The tie between Glasso-Leiden-15 and MB-VAT-20 was broken in favor of MB-VAT-20. For HIV results, the Glasso and MB clusterings performed much better than SparCC and kNN, and are shown in Table 3. The 3-way tie was broken in favor of Glasso-VAT-15. Based on these results, we visualize and analyze the Glasso-

Table 2. Cluster Evaluation Results for Alcohol Risk

Cluster Algorithm		Glasso					MB							
	#	Davies- Bouldin		Calinski- Harabasz	Baker- Hubert	Hubert- Levine	Davies- Bouldin	Silhou- ette	Calinski- Harabasz	Baker- Hubert	Hubert- Levine			
Louvain	15 20 70	1.624 2.623 3.282	0.154 $0.144$ $0.024$	10.203 8.020 3.365	0.700 0.590 0.395	0.164 0.226 0.338	1.867 1.813 2.612	0.011 0.171 0.017	4.919 11.245 2.151	0.484 0.643 0.250	0.272 0.187 0.412			
Leiden	15	1.639	0.113	10.475	0.611	0.216	1.893	0.096	-	0.502	0.277			
	20	2.175	0.117	8.280	0.518	0.253	2.238	0.120	4.967	0.513	0.265			
	70	3.088	-0.030	3.064	0.348	0.369	2.409	0.027	2.282	0.279	0.397			
VAT	15	1.659	-0.017	6.069	0.588	0.218	1.807	-0.013	3.898	0.327	0.341			
	20	2.271	-0.125	4.348	0.332	0.337	1.364	0.190	10.401	0.627	0.196			
	70	2.211	-0.275	1.265	0.095	0.476	2.280	-0.087	1.720	0.186	0.442			
Integrity	15	1.659	-0.017	6.069	0.588	0.218	1.622	0.129	3.511	0.648	0.204			
	20	1.467	-0.095	3.944	0.544	0.257	1.838	0.042	3.315	0.574	0.241			
	70	1.886	-0.251	1.293	0.023	0.514	2.233	-0.104	1.435	0.157	0.467			

Table 3. Cluster Evaluation Results for HIV

Cluster		Glasso					MB							
Algorithm	#	Davies-	Silhou-	Calinski-	Baker-	Hubert-	Davies-	Silhou-	Calinski-	Baker-	Hubert-			
		Bouldin	ette	${\bf Harabasz}$	Hubert	Levine	Bouldin	ette	${\bf Harabasz}$	Hubert	Levine			
Louvain	15	3.755	-0.065	1.039	0.016	0.547	1.554	0.306	10.891	0.700	0.167			
	20	2.387	0.154	10.297	0.578	0.215	2.132	0.164	6.135	0.514	0.270			
	70	3.657	0.003	3.146	0.250	0.414	2.637	0.012	2.145	0.202	0.434			
Leiden	15	1.600	0.226	20.264	0.747	0.155	1.673	0.292	11.231	0.637	0.189			
	20	2.350	0.162	10.774	0.606	0.203	2.150	0.168	6.123	0.481	0.280			
	70	3.635	0.016	2.952	0.229	0.431	2.702	0.009	2.151	0.184	0.444			
VAT	15	1.422	0.373	37.268	0.783	0.092	1.412	0.098	9.461	0.127	0.353			
	20	2.764	-0.214	5.092	0.160	0.405	1.474	0.078	6.408	0.154	0.344			
	70	2.952	-0.291	1.332	-0.105	0.576	2.168	-0.156	1.201	-0.100	0.577			
Integrity	15	1.364	0.052	12.457	0.732	0.163	1.511	0.246	7.239	0.737	0.155			
	20	1.871	-0.142	4.400	0.354	0.328	1.595	0.163	4.405	0.663	0.202			
	70	2.713	-0.278	1.304	0.008	0.539	2.168	-0.156	1.201	-0.100	0.577			

Leiden-20 graph for self esteem, the MB-VAT-20 graph for alcohol risk, and the Glasso-VAT-15 graph for HIV status. The clusterings are described below.

#### 4.2 Cluster Properties

For the top three clusterings, the composition of each cluster for 40 variables, or attributes, is shown in Table 4. The color at the top of the column corresponds to the node color in the network's visualization. Each line of the table represents an attribute, and numbers shown are the percentages of cluster members displaying that attribute. Some variables, like *Income: 0 to 19999* and *In a Relationship* have similar percentages across most of the clusters. On the other hand, the percentage of cluster members who were previously diagnosed with syphilis (*STD: Syphilis*) varies greatly across clusters from 0 to 35%.

**Self-Esteem** Results for the high self esteem cohort are visualized in Fig 1. Here probands are divided into 5 clusters, displayed in violet, orange, green,

Table 4. Cluster composition for 40 variables. Numbers represent the percentage of cluster members exhibiting the described attribute. Alc. represents alcohol abuse risk.

	A	lc.	н	HIV+			Self Esteem				
Variables / Cluster Number	0	1	0	1	2	0	1	2	3	4	
Age: 18 to 30	53	100	17	3	5	36	31	28	15	50	
Age: 31 to 45	43	0	58	71	82	65	62	46	86	50	
Age: 46 to 99	6	0	24	26	14	0	8	28	0	0	
Income: 0 to 19999	65	89	84	55	100	58	54	82	72	75	
Income: 35000 to 75000	6	11	5	3	0	15	8	10	15	0	
Living State: Relatives	8	22	5	3	14	15	24	10	0	0	
Living State : Alone	18	22	33	58	5	22	24	10	29	25	
Living State: Hotel	3	0	7	0	23	8	8	28	15	0	
Living State: Roommates (Friends)	34	0	29	14	36	29	23	9	29	25	
Education: Did Not Finish High School	57	56	50	60	77	37	48	65	87	50	
Education: At Least Some College	36	46	43	34	18	59	47	29	15	50	
In A Relationship	48	67	40	47	55	29	54	64	43	25	
Talks To Friends: At Least Monthly	15	12	13	14	22	16	31	38	15	25	
Talks To Friends: Yearly	38	11	41	37	27	29	54	37	43	25	
Talks To Friends: Never	45	78	44	45	41	50	16	28	43	50	
Talks To Family: At Least Monthly	29	24	43	46	27	23	16	19	29	25	
Talks To Family: Yearly	26	23	12	29	14	43	31	37	29	0	
Talks To Family: Never	29	56	18	11	32	8	31	19	29	75	
Feels There Is No One To Turn To: Most Time	16	0	12	20	19	36	39	10	58	0	
Feels There Is No One To Turn To: Sometimes	53	78	53	46	41	36	47	55	15	25	
Feels There Is No One To Turn To: Never	21	22	25	29	23	0	0	10	15	50	
Feels Left Out: Always	5	0	6	15	10	8	8	37	29	25	
Feels Really Understood: At Least Most Time	56	0	49	40	49	87	78	83	58	50	
Feels Really Understood: Never	14	0	21	23	19	0	0	10	0	0	
Has Trusted Friend: At Least Most Time	54	0	41	41	47	87	62	83	86	25	
Has Trusted Friend: Never	19	33	31	26	32	0	0	0	0	25	
Has A Person To Lend Money: Always	8	0	16	5	5	29	8	28	0	0	
Has A Person To Lend Money: Sometimes	24	56	22	15	23	22	16	10	15	50	
Feels Part Of A Group: At Least Most Time	34	12	39	26	41	58	62	65	58	0	
Feels Part Of A Group: Never	34	67	28	40	15	8	0	19	29	50	
Feels Lack Of Companionship: Always	11	22	3	6	5	36	16	10	15	0	
Feels Lack Of Companionship: Never	18	33	26	26	10	15	16	10	0	75	
STD: Syphilis	13	0	39	12	5	0	24	19	15	0	
STD: Gonorrhea	15	11	40	3	5	15	31	19	0	25	
STD: Genital warts	15	11	36	3	5	22	16	28	0	25	
STD: Genital Herpes	8	0	28	3	5	36	0	0	0	25	
STD: HIV	17	0	100	100	100	50	31	28	29	25	
STD: None	46	67	1	84	100	22	47	46	58	50	
Unprotected Sex (last 2 months)	13	22	13	3	0	22	24	10	29	50	
Unprotected Sex (last 12 months)	41	67	30	20	24		62			50	
Size Of The Cluster (number of nodes)	119	9	113	35	22	14	13	11	7	4	

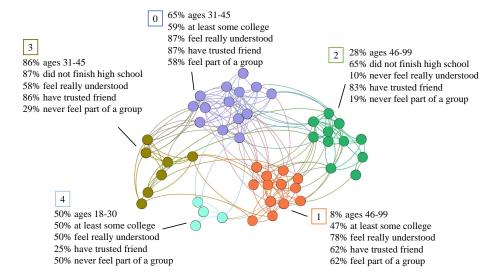


Fig. 1. Probands with high self-esteem are clustered.

brown, and arctic blue. Cluster 0 is 65% middle-aged, and is well-educated, with 59% of its members having at least some college. This cluster is distinguished by the prevalence of members who feel really understood and have a trusted friend (87%). More than half (58%) of its members feel part of a group of friends at least most of the time. Cluster 1 is somewhat older. 62% of members have a trusted friend and feel part of a group at least most of the time. 47% of its members have at least some college.

Cluster 2 is dominated by 83% of members who have a trusted friend; at the same time, 10% of its members never feel really understood, and 19% never feel part of a group of friends. This cluster is less educated, with 65% not finishing high school. Cluster 3 is distinguished by the middle-aged group, and a large percentage of members who have a trusted friend. More than half (58%) feel really understood, but 29% never feel of part of a group. Cluster 4 is the youngest group, half of whose members have at least some college and feel really understood.

Risk of Alcohol Abuse The results for risk of alcohol abuse are visualized in Fig 2 with two clusters in violet and orange. The clustering method is VAT, which produces an attack set, members of which are shown in yellow. Cluster 0 represents the majority of members, most of whom have a low income level. The group is older than cluster 1, with only 53% ages 18-30. 48% are in a relationship. Almost half of the members never talk to friends. Additionally, 17% of members are HIV positive, and 41% have had unprotected sex in the previous year.

Cluster 1 is a younger group, comprised entirely of 18 to 30 years old, 67% of whom are in a relationship. The cluster is more isolated than cluster 0 –

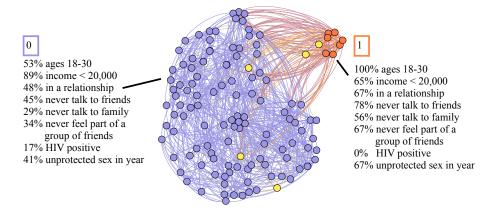


Fig. 2. Probands at risk for alcohol abuse are clustered.

78% never talk to friends and more than half never talk to family. 67% had unprotected sex in the last year, but none were HIV positive.

HIV+ Status The results for HIV positive status are visualized in Fig 3. The attack set nodes provided by VAT clustering (shown in yellow) along with information from the visualization allowed for enhanced analysis by identifying subgroups for clusters 1 and 2. Cluster 0 is the largest and youngest cluster, with 17% of members aged 18-30. Other clusters consist of members aged 31+. This cluster is primarily distinguished by the prevalence of STDs. For example, 39% have had syphilis and 40% have had gonorrhea. The prevalence of unprotected sex in this group is relatively high at 30% in the last year, and the group is sexually very active, with 13% having unprotected sex within the last 2 months.

Cluster 1 is divided into 4 sub-clusters. Cluster 1b, with many edges into cluster 0, is the only sub-cluster not free of STDs, with only 38% never reporting an STD diagnosis. Cluster 1d, which is attached to the graph by a single edge, truly consists of outsiders. None are in a relationship, and 100% live alone. They have very low rates of unprotected sex. Clusters 1a and 1c show no STDs, but have higher rates of unprotected sex at 38% and 29% within the last year.

Cluster 2 is 100% without STDs, and has relatively low rates of unprotected sex. The subclusters are distinguished primarily by living situation, with cluster 2a living in a hotel, and cluster 2b living with relatives, roommates, or friends.

## 5 Discussion and Conclusion

The clustering was able to find meaningful subgroups in the data, and it is particularly interesting that different variable combinations were important for the three targets. It is well-known that feature selection improves machine learning

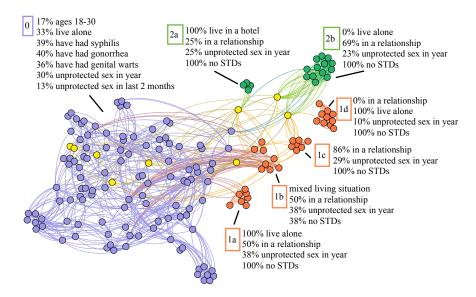


Fig. 3. Probands with HIV positive status are clustered.

performance, and this study confirms that result. Our best performing data was reduced from hundreds of variables to 15 or 20.

It is hard to pinpoint what factors lead to higher self-esteem; however results show that feeling really understood, having trusted friends, and belonging in a group of friends might lead to higher self-esteem. While these variables were relatively consistent, clusters were distinguished by age and education level.

For risk of alcohol abuse, the important variables were relationships and frequency of communication with family and friends. We identified a younger, more isolated group with a less developed social network and a higher propensity to engage in unprotected sex. From a public health perspective, efforts to prevent HIV targeting this group could also productively attempt to curb alcohol abuse. This is substantiated by many studies linking substance abuse and HIV [8].

For HIV+ status, one cluster had previous history of STDs, and two clusters did not. The connection between HIV and other STDs has been widely studied (e.g. see [5]), and this is another example where public health prevention efforts could be combined. The no-STD clusters were further distinguished by living situation and the frequency of unprotected sex.

From a network science perspective, graphs with the best internal evaluation scores were inferred with Glasso and MB. These methods were developed to work with microbial count data, which is similar to the attribute counts of the LMSM-CI dataset. There are previous examples of Glasso networks being used with medical data, such as to study PTSD [9] and frailty in older persons [12], but none that we could find with MB, suggesting that this is an area for further research. This result is also surprising in that Glasso and MB performed bet-

ter than kNN, which is often used to infer graphs in data science applications. For clustering, it is said in [17] that NBR-Clust with VAT is useful for "initial exploratory clustering" and "where the number of desired clusters is low." Our study confirms that result, as the NBR-Clust with VAT clustering was able to find distinctive, useful clusters. Leiden also performed well. Network science based machine learning and analysis techniques were able to produce results of interest to workers in public health and other health-related areas.

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