

Polio Vaccine Hesitancy in the Networks and Neighborhoods of Malegaon, India

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Abstract

Objectives: Eradication and control of childhood diseases through immunization can only work if parents allow their children to be vaccinated. To learn about social network factors associated with polio vaccine hesitancy, we investigated social and spatial clustering of households by their vaccine acceptance status in Malegaon, India, an area known for vaccine refusal and repeated detection of polio cases.

Methods: We interviewed family heads from 2,452 households in 25 neighborhoods in July 2012 and constructed social networks based on advice seeking from other households. The vaccine acceptance status was known for the surveyed households.

Results: Surveyed households made 2,012 nominations to 830 households. Vaccine-refusing households had fewer outgoing ties than vaccine-accepting households. Notably, vaccine-refusing households had 93% more nominations to other vaccine-refusing households compared to vaccine-accepting households, revealing that vaccine-refusing households cluster in the social network. Since roughly half of all ties connect households within neighborhoods, vaccine-refusing clusters lie in spatially localized "pockets."

Conclusions: The finding on social and spatial clustering of vaccine-refusing households could be leveraged to tailor communication strategies to improve vaccine acceptance and community perceptions of immunization programs for polio and other vaccine preventable diseases.

Introduction

The Global Polio Eradication Initiative (GPEI), a partnership between national governments and five core agencies, including the World Health Organization (WHO), Rotary International, the US Centers for Disease Control and Prevention (CDC), the United Nations Children's Fund (UNICEF), and the Bill and Melinda Gates Foundation (BMGF) is striving to eradicate polio worldwide. Polio incidence in the developing world, especially among underserved and hard-to-reach populations, has been reduced through increased rates of vaccination supported by sustained media campaigns and by mobilizing community leaders². Since its launch, the number of polio cases has been reduced from an estimated 350,000in 1988 to 358 in 2014 (Data in WHO HQ as of 27 January 2015). In addition, the number of countries endemic for polio has been reduced from 125 to three, namely Pakistan, Afghanistan and Nigeria. India had its last case in 2011 and the whole South-East Asia region was certified polio-free in 2014.

In spite of these achievements, polio remains an international concern. In May 2014, renewed outbreaks led the WHO's International Health Regulations Emergency Committee to declare the situation a Public Health Emergency of International Concern¹. In particular, segments of susceptible populations continue to resist having their children vaccinated for a variety of reasons. Rumors and misinformation are likely to propagate through social connections, and they might amplify the rates of vaccine refusal. GPEI supported the present study in order to understand better vaccine refusing behavior.

That vaccine acceptance might be related to social connections should not be surprising.

People are connected, and so their health is connected³. Social networks play an important role in human health and disease, through mechanisms such as provision of social support, social engagement, and access to resources, as well as through the dissemination of information and

behaviors^{2,5}. We would expect the structure of social networks to play a critical role in funneling both information and misinformation, including that related to vaccines.

Our goal was to investigate whether the resistance of households to having their young children vaccinated against polio might be related to similar resistance in households to which they are socially connected. If children of unvaccinated households interact frequently, they might reinforce inaccurate beliefs and be substantially more likely to contract and propagate the disease, as herd immunity is reduced within these clusters. Learning about the possible existence of such clusters is therefore critical for eradicating infectious diseases like polio in developing countries by identifying "social pockets" of vaccine hesitancy. Moreover, to the extent that such clusters can be identified, public health officials might be able to use more targeted approaches to overcoming vaccine resistance. We also investigated differences in vaccine acceptance across the surveyed neighborhoods and the geographic distribution of nominations across neighborhoods. This enabled us to distinguish between network and neighborhood effects; in short, does your behavior depend on whom you know, where you live, or both?

Methods

Data Collection

We carried out a population-based study of 2,452 households in contiguous high-risk (by polio planning definitions) neighborhoods in Malegaon Municipal Corporation in the Nashik district of Maharashtra state in the western region of India, about 280km northeast of Mumbai. The study protocol was reviewed and approved by Research Ethics Review Committee of WHO Geneva and the Haffekine Research Institute Mumbai.

Twenty-five teams each consisting of a professional surveyor (recruited through Nielsen Private Limited) and a female volunteer student from a local medical school (Mohammadia Tibbia College) collected data through in-person household surveys in all of the 25 neighborhoods. These household interviews were linked to data on household vaccine acceptance maintained by the WHO. The interviews took place over a three-week period in July 2012. The targeted respondents were household heads, and each household was categorized as vaccine accepting, reluctant, or refusing based on whether the household initially accepted the vaccine, accepted the vaccine after up to two attempts were made, or refused the vaccine. The vaccine status data were collected by the WHO as part of the supplementary immunization campaign concluded just prior to the study. On completing the paper questionnaires, survey teams handed them over for linking with oral polio vaccine (OPV) vaccination status and a quality crosscheck. The questionnaires were then transmitted to the market research firm for coding and anonymous entry into the study database.

Survey Instrument

Using suitable "name generators"⁶, household heads were asked to identify up to four contacts with whom they discuss general issues (e.g., business, sports, personal matters, or issues that affect their community) and up to four contacts with whom they discuss health-related issues. Although the surveyed households were located within a defined geographic region, there were no restrictions on whom the respondents could name. Consequently, many of the identified contacts were outside the surveyed area with unknown vaccination status, and these contacts are omitted from most of our analyses below. Such limitations are unavoidable in social network studies⁷.

In addition, respondents were asked their name and occupation, the highest level of education attained, and the number of people (both adults and children) living in the household. Finally,

socioeconomic status was measured by a series of questions asking about the number of rooms in the house, whether there was a separate toilet in the home, and whether they owned a television, mobile phone, or cooking gas cylinder. See Supplemental Material for survey details.

Network Measures and Concepts

When the responses to name generator questions are represented as a network, nodes (or vertices) correspond to individuals and ties (or edges) correspond to nominations between any two individuals. We call this network the *nomination network* or *nomination graph*. A pair of nodes, connected or not, is called a *dyad*. The person doing the nomination is often called the ego and the person(s) nominated the alter(s). In this case, the responses of subjects to name generator questions gives rise to a directed network, where, by convention, the direction of the edges is from the person doing the nomination to the person(s) nominated. The number of outgoing edges is called that person's out-degree; in this case it is bound by the study design to be less than or equal to eight, the maximum number of allowed nominations in the two categories combined. The number of in-coming edges is called that person's *in-degree*; the size of network minus 1 is the natural upper limit on its value given that any person in the study could be nominated by any number of other persons. Network neighbors of a node refer to the set of nodes to which any given node is connected to by ties where the direction of ties is usually ignored (unless stated otherwise). Nodes with a disproportionately high in-degree (large number of nominations) are called hubs. There is no universally accepted definition of what constitutes a hub, and here we settled for a definition that a hub is any node with an in-degree that is four standard deviations above the mean in-degree. A connected component refers to a piece of the network that has no ties whatsoever with the rest of the network. Most empirical networks consist of several components, but even then it is typical that one component is much larger than the others. This component is called the *largest connected component* (LCC) and its size is measured as the number of nodes that it contains. Finally, an induced subgraph refers to a

subset of the network that consists of a specified set of nodes and all edges that fall between these nodes in the underlying network.

Construction of the Polio Vaccine Network

Connected individuals within a social network tend to resemble each other⁸. There are at least three different mechanisms that can produce clustering of individuals by their attributes: influence, selection, and confounding. Briefly, influence refers to a person inducing a behavior on another person, thereby making their attributes similar; selection refers to the tendency of people to seek out others who are like them but implies no influence; and confounding refers to an external factor that has an effect on the attribute(s) of both individuals, typically such that they resemble each other even if influence and selection are absent. Cross-sectional data like ours do not allow for disentangling these potential mechanisms behind the observed similarity of connected individuals, but it is nevertheless important from the perspective of targeted interventions, to learn about potential clustering of nodes by their attributes.

The network representing all nominations (without any exclusions) consisted of 804 components with the LCC containing 6,113 of the 11,828 (51.7%) network nodes and 6,647 of the 11,655 (57.0%) network ties. All of the other components are substantially smaller, for example, the 2nd largest component had only 59 nodes. All network nodes had at least one tie (incoming or outgoing); 1,600 nodes had no incoming ties and 9,400 had no outgoing ties. We constructed the *vaccine network* by first extracting the LCC of the nomination graph and then extracted a subgraph of the LCC induced by the set of nodes with known polio vaccination status, i.e., for nodes within the geographic area we are studying. The vaccine network therefore retains nodes of the LCC with known vaccination status only and any edges that fall between these nodes in our area.

Although study subjects could nominate anyone in the region, the vaccine status of households was known for only those people in the surveyed neighborhoods. The percentage of nominations into the sampled neighborhoods was 14.2% for vaccine accepting households, 16.2% for vaccine reluctant households, 12.7% for vaccine refusing households, and 15.0% for households with no vaccine eligible children. These sample proportions were not statistically significantly different from one another ($\chi^2 = 5.11$, p=0.16), which supported the extraction of the vaccine network from the larger underlying nomination network without potentially introducing a bias across households by their vaccine status.

Statistical Analyses: Tie Prediction

We constructed a simple statistical model to predict the existence of a tie in the polio vaccine network between two households based on the observed household attributes in order to detect which attributes are most highly predictive of ties. We modeled the binary status of each dyad using logistic regression where differences of nodal attributes across the dyad were used as predictors. In other words, we formed the predictors by considering all node pairs in the network, connected or not, and regressed them on the differences in nodal attributes across all pairs. The observed outcome for each node pair was set to 0 if the nodes were not connected and to 1 if they were connected.

The nodal attributes we considered were vaccine status, neighborhood, sum and difference of degree (taken as undirected, combining general and health categories), education, and mobile phone ownership (ownership of other items, such as cooking cylinder, were dropped because of their limited predictive power). When analyzing vaccine acceptance, we combined the reluctant and refuser groups and then set the vaccine status indicator to one if the vaccine statuses of the two nodes were identical. The pooling is justified from the substantive perspective in that both reluctant and refusing households exhibit some level of vaccine non-acceptance. For

neighborhood, a bivariate indicator predictor was set to one if the two neighborhoods were the same; otherwise it was set to zero.

Statistical Analyses: Clustering of Households by their Polio Vaccination Status

To investigate the statistical significance of the clustering of households in the vaccine network, we developed a simple non-parametric resampling procedure to generate the distribution of the test statistic under the null. We first identified all nodes in a given category (say, accepting) and then examined them one at a time. For each such node, we identified its network neighbors but instead of using their observed vaccine statuses, we sampled those statuses with replacement from the observed distribution of all vaccine statuses in the vaccine network. We applied this

from the observed distribution of all vaccine statuses in the vaccine network. We applied this procedure to every node in each of the four categories, thus covering all nodes in the vaccine network, and computed the proportion of neighboring accepting, reluctant, refusing, and vaccine ineligible households for them. We repeated this procedure 10,000 times. The observed value

of the test static was obtained by using the actual vaccine status of each node.

Results

The number of household respondents included in the study (after excluding 24 respondents due to incomplete data) was 2,452, which represented 99.0% of the households approached for the interview. Of these, 1,355 included a child between the ages of 0 and 5 eligible for the vaccine for whom we had data on vaccine status. Among eligible households, 1,074 accepted the vaccine, 137 were reluctant, and 144 refused the vaccine. Respondents identified a total of 10,228 unique alters (some of whom were also egos) who were nominated a total of 13,819 times (some alters being nominated multiple times). A total of 2,012 of the nominations, or 14.6%, were to the 830 households located within the sampled neighborhoods.

Households varied in terms of their possessions and level of education. From less common to more common items: 519 (21.6%) had a cooking cylinder, 710 (29.6%) a toilet, 1080 (45.0%) a TV, and 1752 (72.9%) had a mobile phone. Education was coded as a categorical variable, and the categories and the number of people in them were as follows: 1 = no school (459), 2 = primary school (1,220), 3 = middle school (369), 4 = high school (173), 5 = intermediate or post high school diploma (63), 6 = graduate or post graduate (42), 7 = profession or honors (22), 8 = religious (Islamic) education (54).

Nominations

Figure 1 shows the estimated mean out-degree and associated standard errors for general nominations, health nominations, and both combined. Combining general and health nominations, vaccine-accepting households made on average 4.93 nominations, vaccine-reluctant households 4.92 nominations, and vaccine-refusing households 4.41 nominations. The differences of the means were statistically significant (ANOVA F = 5.97, p < 0.001). The mean out-degree of 4.77 for households without an eligible child was somewhat lower than that for accepting households (t-test t = -2.40, p = 0.02). There was also a statistically significant difference in the mean out-degrees for general ties (ANOVA F = 4.60, p < 0.001) and health ties (ANOVA F = 3.19, p = 0.02) between vaccine accepting and vaccine refusing households. There were no significant differences (ANOVA F = 0.22, p = 0.88) among the mean in-degrees combining general and health categories (0.60 for vaccine accepting, 0.64 for vaccine-reluctant, 0.57 for vaccine refusing, and 0.64 for vaccine-ineligible households).

Using an in-degree cut-off value of 6 for hubs (see Methods), a total of 13 nodes (0.5%) in the vaccine network qualified as hubs. Hub households had 0.72 rooms more than non-hub households (p=0.01), had 1.5 fewer people living per room (p=0.01), and appeared to be more educated than non-hub households (0.95 units higher on the education scale, p=0.09). In

addition, 92% of hub households had a mobile phone compared to the 73% of non-hub households (p=0.03). (The p-values for hubs are based on a two-tailed variant of the Welch 2-sample test). There was no evidence of different neighborhoods having different proportions of hub households ($\chi^2 = 20.4$, d=24, p=0.68). We found that 6 out of 13 hub households were vaccine accepting, and the remaining 7 households had no vaccine eligible children. No hub was vaccine reluctant or vaccine refusing.

Neighborhoods

The neighborhoods varied considerably in terms of their vaccine status. The mean percentage of (i) vaccine accepting households was 44.0% (range 33.3%–54.4%), (ii) vaccine reluctant households was 5.6% (range 0%–12.7%), and (iii) vaccine refusing households was 5.8% (range 0%–12.1%). The vaccine status composition of neighborhoods varied more than chance alone could explain (χ^2 -test p < 0.001).

We also investigated the proportion of nominations to households located in the same neighborhood as the nominating household, and we aggregated these household-level results to the neighborhood level. Note that we only consider nominations within and across the sampled neighborhoods, not those outside the surveyed neighborhoods. Taken over all neighborhoods, 48.9% (range 23.8% –66.7%) of nominations were to households in the same neighborhood. The fact that about half of all ties were located within neighborhoods suggests strong spatial clustering of network ties. (Note that by spatial clustering we refer to clustering with respect to defined boundaries of neighborhoods, not to clustering with respect to physical distance).

Clustering of Nodes by Vaccine Status

The vaccine network had mean out-degree of 2.34 for accepting households, 2.13 for reluctant households, and 2.06 for refusing households, thus retaining the trend for out-degrees by vaccine status observed in the full nomination network. An undirected version of the vaccine network, obtained from the directed vaccine network by ignoring edge directions, is shown in Figure 3. The visualization suggests that nodes of a given vaccine status might cluster together. Using the resampling approach described in Methods, we found that reluctant households had more reluctant alters and more refusing alters than accepting households did. Furthermore, the proportion of refusing alters was higher for refusing households than for reluctant households. These findings can be summarized in two ways. First, the percentage of neighboring households that were either reluctant or refusing was 17.1% for refusing households but only 10.8% for accepting households, resulting in a difference of 17.1% - 10.8% = 6.3% [p-value: 0.08; 95% CI: -6.4%, 7.2%]. Second, and more important, the observed difference between refusing and accepting households in the percentage of neighboring refusing households was 11.4% - 5.9% = 5.5% [p-value: 0. 05; 95% CI: -5.0%, 5.5%]. Phrased differently, vaccinerefusing households had 93% more ties to vaccine-refusing households than vaccine-accepting households did.

Predicting Ties based on Network and Neighborhood Effects

The statistically significant predictors of dyadic similarity were bivariate degree sum, bivariate degree difference, and residence in the same neighborhood (Table 1). Because a relatively high fraction of ties were within neighborhoods, knowing that two households were located in the same neighborhood substantially increased the log-odds for them to be connected. All else equal, high-degree individuals were more likely to be connected to one another than predicted based on their individual degrees. Note that difference in degree decreased the probability of the two households being connected. The degree difference predictor informs us that the probability for two households being connected is higher in the former case, even though in both

cases the degree sum is the same. This finding is consistent with the notion of dyadic similarity, i.e., households tend to connect to other households that are similar to them, and, in this case, that similarity manifests itself by the households being close in degree.

Discussion

Using a population-based, household-level survey in Malegaon, India, we find that vaccine-refusing households have fewer outgoing ties than vaccine-accepting households and that they had fewer health ties than vaccine-accepting households. Moreover, the surveyed neighborhoods varied significantly by their vaccine status composition, and, on average, 49% of network nominations were to households in the same neighborhood. This suggests that social ties are spatially localized. Finally, when analyzing the vaccine network, vaccine-refusing households nominated on average 93% more vaccine-refusing households than vaccine-accepting households did, meaning that vaccine refusers clustered in the social network and not just within neighborhoods. Thus, there was both social and geographic clustering. These findings parallel recent findings regarding the clustering of latrine use in India^{9,10}.

Influence, selection, and confounding are difficult to disentangle in observational studies, especially if there are pertinent unmeasured factors^{11–14}. However, if longitudinal data were available, it would be possible to use a model-based approach to get a sense of the extent to which each the mechanism might be driving the behavior. Here, given the cross-sectional nature of the study, these types of approaches are not feasible. In addition, other methods, such as those involving the directionality of ties¹¹ or instrumental variables¹⁵ are not possible here either.

The present study has a number of further limitations. First, a large number of households nominated households outside the surveyed neighborhoods and vaccine status was only

available for the households in the surveyed neighborhoods. Second, because the study is cross-sectional, it was not possible to disentangle selection and influence processes as potential causes of the observed clustering. Third, the network model used to predict the existence vs. non-existence of ties assumes dyadic independence, which is likely to be violated. However, because the networks studied here were relatively sparse, we believe this approach was reasonable.

One lesson that was recently put forward to help tailor strategies to communities to counter vaccine resistance was to find out what is driving rumors and resistance by identifying key influencers of vaccine acceptance and refusal in communities¹⁶. In the US, discredited claims about the safety of the MMR vaccine have contributed to immunizations rates in some areas falling short of the targeted rate of 90% for children 19–35 months¹⁷. A randomized trial concluded that pro-vaccine messages, however, do not always work as intended and, for some parents, may actually increase misperceptions or reduce vaccination intention¹⁷.

Convincing vaccine-refusing households of the benefits of the polio vaccine is likely to remain a difficult challenge. However, identification of these clusters is an important step in that it enables better targeting of subsequent interventions and, furthermore, establishes the relevant units of study, the clusters, for future investigations into different vaccine adoption strategies. Moreover, taking into account people's social network position can enhance the effectiveness and efficiency of public health messaging and interventions: the effectiveness because people are more likely to change their perceptions and behavior if their friends do, and the efficiency because perceptions and behavioral changes can spread out from the primary targets of interventions, creating spillovers that may benefit whole populations.

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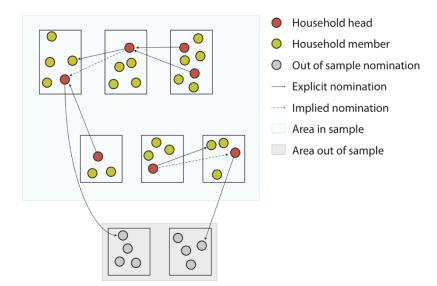


Figure 1. Schematic of sampling design. The rectangles correspond to households and the circles inside the rectangles to household members. One of the household members is the Household Head (HH). In this study, Household Heads were asked to nominate households by naming either Household Heads or other household members in response to the name generator questions. If the nominated person was not a Household Head, we implicitly re-directed the nomination to the Household Head of the corresponding household. This means that all households in the network can be treated the same way; in particular, we do not distinguish between households based on whether the corresponding Household Head or household member was the target of the nomination.

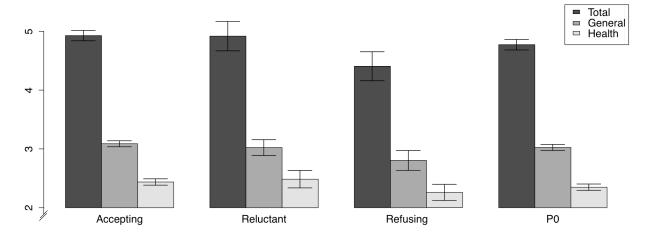


Figure 2. Mean out-degrees (total, general, health), and the corresponding 95% confidence intervals, stratified by vaccine status of the recipient. Note that the vertical axis starts at 2.

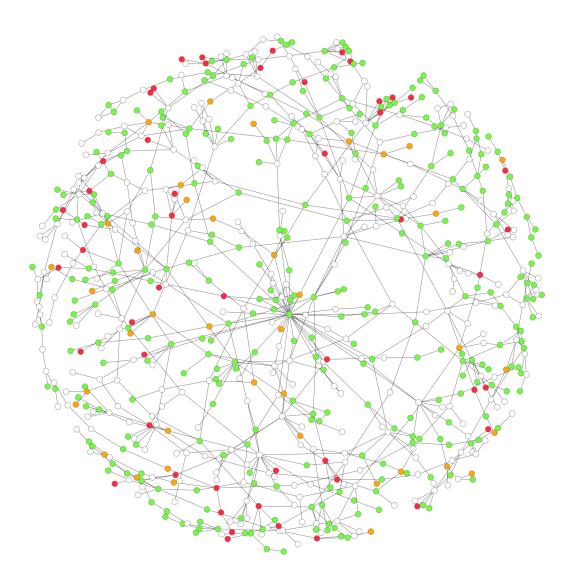


Figure 3. Largest connected component (LCC) of the vaccine network. Node colors: green = accepting (1), orange = reluctant (2), red = refusing (3), and white = P0 household (4).

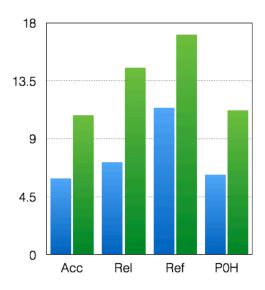


Figure 4. Mean proportion of refusing alters (blue) and reluctant or refusing alters (green) stratified by the vaccine status of the ego nodes.

Table 1. Estimated regression coefficients for a logistic regression model, where tie status is regressed on the difference in the attributes for the corresponding pair of individuals (dyad). The model was estimated on the largest connected component (LCC) of the vaccine network.

Variable	Coefficient	SE	z-score	p-value
Intercept	-7.316	0.066	-110.693	0.000
Vaccine status equal	0.007	0.052	0.131	0.896
Neighborhood ID equal	2.711	0.053	51.392	0.000
Degree sum	0.265	0.010	25.804	0.000
Degree difference	-0.179	0.011	-15.917	0.000
Education difference	0.010	0.017	0.574	0.566
SES difference	-0.039	0.053	-0.730	0.466

Polio Vaccine Refusal in the Networks and Neighborhoods of Malegaon, India SUPPLEMENTAL MATERIAL

Survey

Social ties were solicited in two different categories, the general category and health category. In the general issues category, respondents were asked: "Looking back over the past 12 months, think of up to four people (ages 16 and over) outside of your own household with whom you discuss things important to you such as business, sports, personal matters, or issues that affect your community. By household, we mean people who live in the same house and share a kitchen. You may provide none, some or up to four names. The four people can live in separate households or be members of the same households." Similarly, in the "health issues" category, respondents were asked: Looking back over the past 12 months, think of up to four people (ages 16 and over) outside of your own household with whom you discuss your family health issues. This can include doctors, but also try to think of friends or coworkers from whom you ask advice. By household, we mean people who live in the same house and share a kitchen. You may provide none, some or up to four names. The four people can live in separate households or be members of the same households." The actual survey is reproduced below.

Social Network Analysis of Households in Malegaon: Survey Questionnaire					
1. Survey Team ID:	2. Date of First Visit:	D M M 2012	3. Time of Visit: H H M M		
4. Surveyor Name:	-	5. Unani Medical Gradu	uate Name:		
6. Household Serial No:	7. House is (circle): Open	/ Locked 8. Vaccin	ne acceptance status (Accepting / Reluctant / Refusing) (Code to be filled by NPSP at the end of survey)		
9. If Locked (Expected dates & timing of return) (For subsequent visits)	D D M M 2012	D D M M 201	D D M M 2012		
	H H M M	H H M M	H H M M		
10. If House Open; Head of Household Available for I	nterview (Y/N)				
11. If No, expected date/time of availability for intervious (For subsequent visits)	ew D D M M 2012	D D M M 201	D D M M 2012		
	H H M M	H H M M	H H M M		
12. Consent Given (Y/N)	13. If Yes: Assign Household ID		Household Identification		
	Stop procedure if consent	denied			
14. Details of Head of Household:					
(i) Name of Head of household:		(ii) Name of father of head of house	hold:		
(iii) Occupation of Head of Household (circle):	Loom Industry Labourer Other: Text	Service Business Re	tired Unemployed		
(iv) Head of Household's Workplace: (v) Head of Household's Telephone Number					
15. Date of interview D D M M 2012	Starting time:	H H M M	Completion time:		

Social Network Analysis of Households in Malegaon: Name Generator Questions 1. Looking back over the past 12 months, think of up to four people (ages 16 and over) outside of your own household with whom you discuss things important to you such as business, sports, personal matters, or issues that affect your community. By household, we mean people who live in the same house and share a kitchen. You may provide none, some or up to four names. The four people can live in separate households or be members of the same households. ID Code Person 1 Person 2 Person 3 Person 4 1(a) Name (write): 1(b) Relationship (write): 1(c) Sex (circle): 1(d) Age (write): VERY CLOSE MODERATELY CLOSE NOT AT ALL CLOSE VERY CLOSE VERY CLOSE VERY CLOSE 1(e) Closeness (circle): MODERATELY CLOSE NOT AT ALL CLOSE MODERATELY CLOSE NOT AT ALL CLOSE MODERATELY CLOSE NOT AT ALL CLOSE 1(f) Days of Interaction per Week (circle): 0 1 2 3 4 5 6 7 0 1 2 3 4 5 6 7 0 1 2 3 4 5 6 7 0 1 2 3 4 5 6 7 1(g) Location (circle; select from key below): 1 2 3 4 5 1 2 3 4 5 1 2 3 4 5 1 2 3 4 5 1(h) Is Head of Household N Υ N Υ N Ν (HOH)? (circle): 1(i) If No to 1(h), Name of HOH (write): 1(j) HOH Occupation 1(k) HOH Father's Name 1(I) HOH Telephone Key to 1(g): 1: Next Door 2: On Same Lane/Mohalla 3: Within 2-3 km 4: In Maleagon 5: Outside Maleagon For all Questions, enter the following codes when appropriate: 77: Don't Know 88: None 99: Refuse to Give

Social Network Analysis of Households in Malegaon: Name Generator Questions

2. Looking back over the past 12 months, think of up to four people (ages 16 and over) outside of your own household with whom you discuss your family health issues. This can include doctors, but also try to think of friends or coworkers from whom you ask advice. By household, we mean people who live in the same house and share a kitchen. You may provide none, some or up to four names. The four people can live in separate households or be members of the same households.

ID Code	Person 1	Person 2	Person 3	Person 4
a) Name (write):				
b) Relationship (write):			1	
(c) Sex (circle):	M F	M F	M F	M F
(d) Age (write):	YRS	YRS	YRS	YRS
e(e) Closeness (circle):	VERY CLOSE MODERATELY CLOSE NOT AT ALL CLOSE	VERY CLOSE MODERATELY CLOSE NOT AT ALL CLOSE	VERY CLOSE MODERATELY CLOSE NOT AT ALL CLOSE	VERY CLOSE MODERATELY CLOSE NOT AT ALL CLOSE
2(f) Days of Interaction per Week (circle):	0 1 2 3 4 5 6 7	0 1 2 3 4 5 6 7	0 1 2 3 4 5 6 7	0 1 2 3 4 5 6 7
(g) Location (circle; elect from key below):	1 2 3 4 5	1 2 3 4 5	1 2 3 4 5	1 2 3 4 5
(h) Is Head of Household HOH)? (circle):	Y N	Y N	Y N	Y N
(i) If No to 2(h), Name of HOH (write):		1	 	
(j) HOH Occupation write)				
2(k) HOH Father's Name				
(I) HOH Telephone lumber		 	 	

For all Questions, enter the following codes when appropriate: 77: Don't Know 88: None 99: Refuse to Give

Social Network Analysis of Households in Malegaon: Socio-demographic Information						
Please tell me about the person in your household health and well-being of children. By household, we house and share a kitchen. (Respondent may name him/herself of the children in the	mean people who live in the san		Name:			
2. This person is the child's (circle one):	Father Mother Paternal Grandfather Other:	Paternal Uncle Paternal Grandmothe	Paternal Aunt r	Maternal Uncle Maternal Grandfa	Maternal Aunt ther Maternal Grandfather	
The highest level of school the head of household has completed (circle one):	No School High School Certificate (Class	•	Certificate (Class V) Post-High School Diploma		Aiddle School Certificate (Class VIII) Profession or Honours	
4. Do you own a	(a) Television (Y/N)?	(b) Mobile Phon	e (Y/N)?	(c) Cooking Gas Cylinder?	
5. How many rooms do you have in your household	(excluding kitchen)? Text					
6. Is there a separate toilet in the household (Y/N)?						
7. How many people live in this household?						
8. How many children under age 5 live in this household?						
What is the name and age of the youngest child in	this household? Name:		Age:		YRS	
Result of Survey: 1) Completed S	successfully 2)	Partially Complet	ed 3) Refu	sal		
Survey Successfully Completed Toam to Thank the Family and Unani Medical Graduate to Hand Over the Gift to the Family						

Results

Nominations and vaccine status

Subjects typically nominated more individuals in the general category than in the health category, suggesting that the study subjects had fewer friends and acquaintances with whom they discuss health-related issues. We note however that could have been cased by respondent fatigue since respondents were asked for nominations in the general category first. Total number of nominated alters and unique alters are listed in Table 1. Table 2 shows the estimated mean out-degree and associated standard errors for general nominations, health nominations, and both combined.

Table 1. Number of alters nominated and number of unique alters in the study for each name generator.

Name generator	Number of alters	Number of unique alters
General contact 1	2,421	2,213
General contact 2	2,353	2,225
General contact 3	1,979	1,892
General contact 4	1,112	1,079
Health contact 1	2,396	2,263
Health contact 2	2,108	2,021
Health contact 3	1,082	1,058
Health contact 4	368	363

Table~2.~Mean~out-degrees~(total, general, health), and~the~corresponding~95%~confidence~intervals, stratified~by~vaccine~status~of~the~recipient.

Variable / Status	Accepting	Reluctant	Refusing	P0
Out-degree (T)	4.93 (4.84, 5.02)	4.92 (4.67, 5.17)	4.41 (4.16, 4.65)	4.77 (4.68, 4.86)
Out-degree (G)	3.09 (3.04, 3.14)	3.02 (2.89, 3.16)	2.80 (2.63, 2.97)	3.03 (2.97, 3.08)
Out-degree (H)	2.44 (2.38, 2.49)	2.49 (2.34, 2.63)	2.26 (2.12, 2.40)	2.35 (2.29, 2.40)

We also examined to what extent the general and health nominations from each respondent overlapped. Overlap here is defined for each household as the number of common alters across the two categories divided by the total number of alters. An overlap value of 1 indicates that the respondent nominated the same set of households in the health category as in the general category, whereas an overlap of 0 means that nominations across the two categories were completely distinct (disjoint). Table 3 gives the means, standard deviations, and 95% confidence intervals (CI) for households in each of the vaccine categories. Overall, general and health nominations overlapped on average 15.8% of the time, suggesting that the extent of overlap between the two categories was non-trivial but relatively low. After stratifying by vaccine status of the household, overlap ranged from 15.5% to 17.9%, with refusing households having higher overlap rates.

Table 3. Mean, standard deviation (SD), and 95% confidence interval for nomination overlap stratified by vaccine status of the nominating household.

Respondents	Mean of overlap	SD of overlap	95% CI for the mean
All households	0.158	0.227	0.149 0.168
Vaccine accepting households	0.155	0.217	0.142 0.168
Vaccine reluctant households	0.159	0.245	0.118 0.201
Vaccine refusing households	0.179	0.253	0.136 0.222
P0 households	0.159	0.231	0.145 0.173

Neighborhoods

Vaccine status of each of the studied neighborhoods in shown visually in Figure 1 and tabulated in Table 4.

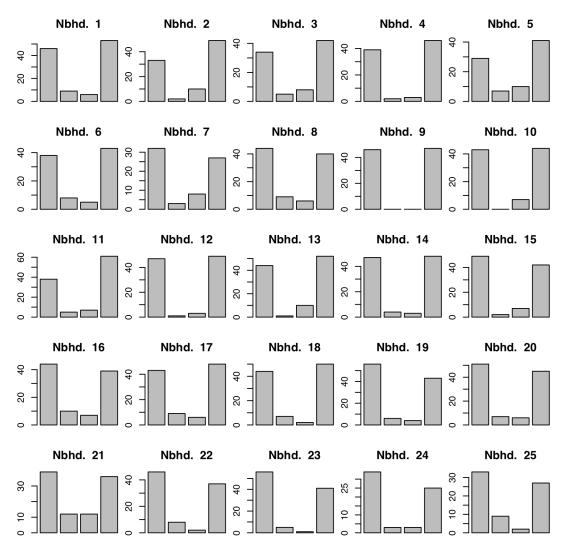


Figure 1. Vaccine status by neighborhood.

Table 4. Vaccine status by neighborhood.

Neighborhood	Accepting	Reluctant	Refusing	P0
1	46 (40.4%)	9 (7.9%)	6 (5.3%)	53 (46.5%)
2	33 (35.1%)	2 (2.1%)	10 (10.6%)	49 (52.1%)
3	34 (38.2%)	5 (5.6%)	8 (9%)	42 (47.2%)
4	39 (43.3%)	2 (2.2%)	3 (3.3%)	46 (51.1%)
5	29 (33.3%)	7 (8%)	10 (11.5%)	41 (47.1%)
6	38 (40.4%)	8 (8.5%)	5 (5.3%)	43 (45.7%)
7	32 (45.7%)	3 (4.3%)	8 (11.4%)	27 (38.6%)
8	44 (44.4%)	9 (9.1%)	6 (6.1%)	40 (40.4%)
9	46 (49.5%)	0 (0%)	0 (0%)	47 (50.5%)
10	43 (45.7%)	0 (0%)	7 (7.4%)	44 (46.8%)
11	38 (34.2%)	5 (4.5%)	7 (6.3%)	61 (55%)
12	47 (47%)	1 (1%)	3 (3%)	49 (49%)
13	44 (41.1%)	1 (0.9%)	10 (9.3%)	52 (48.6%)
14	47 (46.1%)	4 (3.9%)	3 (2.9%)	48 (47.1%)
15	49 (49%)	2 (2%)	7 (7%)	42 (42%)
16	44 (44%)	10 (10%)	7 (7%)	39 (39%)
17	43 (40.6%)	9 (8.5%)	6 (5.7%)	48 (45.3%)
18	44 (42.7%)	7 (6.8%)	2 (1.9%)	50 (48.5%)
19	56 (51.4%)	6 (5.5%)	4 (3.7%)	43 (39.4%)
20	51 (46.8%)	7 (6.4%)	6 (5.5%)	45 (41.3%)
21	39 (39.4%)	12 (12.1%)	12 (12.1%)	36 (36.4%)
22	46 (49.5%)	8 (8.6%)	2 (2.2%)	37 (39.8%)
23	56 (54.4%)	5 (4.9%)	1 (1%)	41 (39.8%)
24	34 (52.3%)	3 (4.6%)	3 (4.6%)	25 (38.5%)
25	33 (46.5%)	9 (12.7%)	2 (2.8%)	27 (38%)