

# Tuberculosis and social networks: a narrative review on how social network data and metrics help explain tuberculosis transmission

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**Social network data of tuberculosis (TB) patients could explain the source and pattern of disease spread. A review of the published literature highlights that social network data could identify hidden social or epidemiological links among TB patients and improved TB case finding. Index and betweenness position of patients explained TB transmission. Social networks of TB cases were centred in the hotspots of alcohol, substance uses, sexual activities and hospitals. Multiple sources of TB infection in the community were identified. The findings highlight the potential of social network methods for understanding TB spread in high-burden countries like India.**

**Keywords:** Epidemiological links, hotspots, social network matrices, transmission, tuberculosis.

SOCIAL network as a novel research discipline has been utilized for diverse purposes in the health research and intervention domains<sup>1-3</sup>. Social network exploration of individuals and groups results in unconventional data which provide insights into the relationship dynamics between members within the same group and between members of different groups<sup>4</sup>. Social network has been widely understood and used for explaining the nature of social relationship in terms of relationship status, duration, frequency, closeness, etc. However, the social network as a quantitative discipline exploring the underlying social structure contextualizing various social interactive processes has not been well understood<sup>5-9</sup>.

Social network has been utilized to understand a variety of health issues with its exploratory metrics, which is not otherwise possible with the descriptive or inferential statistics which normally is used to test associations. Social network analysis is a promising research method, which along with clinical, epidemiological, genetic, sociological and geo-spatial tools has provided valuable evidence on the source of tuberculosis (TB) transmission and its pathways of spread in communities not known earlier<sup>10</sup>.

There is a need to review studies which have utilized social network analysis as a primary or secondary method to complement the understanding of TB spread at population level in different countries. This article aims to assess and explain the scientific findings of the scattered and scarcely available social network research findings in TB transmission context as well as the related diagnosis and treatment aspects. It would help researchers who seek to understand TB transmission from a multidisciplinary and novel perspective and on the utilization of social network methods in enhancing our knowledge of disease spread. It could also help understand treatment and care aspects in TB.

Social network studies of TB patients have been conducted in different settings, among different populations and involving varied methodologies, assumptions and definitions. Using this article we explain these differences in the various studies and identify coherences between them. We also assess the social network methods used in these studies, from the backdrop of standard social network principles and summarize the outcomes as quantifiable and comparable indicators and coherent themes. Then we generalize and compare the specific outcomes of different studies through quantitative social network metrics and qualitative informational themes.

## Study design

Pertinent studies which used social network methods to understand TB spread and associated questions were searched in online databases like Google Scholar, PubMed and Embase. The reference list of the searched studies was also reviewed. No time limits were used for this search.

## Method

We conducted a focused study using the keywords 'network', 'social network' and 'tuberculosis', which yielded research papers from Google Scholar, PubMed and Embase. We retrieved publications which have used the

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words ‘network’ related to TB in the social or community context. We conducted a narrative review which focused on TB and social networks along with co-infections like HIV. We have not used the systematic review approach since social network tools have been used very differently in each study and there was absence of a uniform format or metric to bring together all findings for metanalysis. Also the social network research methodologies used in these studies were different and explorative in nature and lacked uniformity in application to understand TB spread, and thus lacked rationale for systematic review. We read the abstract and selected 21 studies which used social network-specific ‘metrics’ or graphs (sociograms) for TB research, which included drug-resistant types. We conducted a narrative review which focused on TB and social networks along with co-infections like HIV. This narrative review included only studies which used social network metrics and excluded those which used merely the term ‘social network’ to refer to the approach, rather than using metrics. Review papers were included based on whether the studies used ‘social network’ as a primary research method or secondary method in their exploration, understanding or intervention of TB-related issues. The study included papers published in peer-reviewed journals, dissertations, and reports published on-line and indexed in PubMed and Google Scholar. No time-frame for the inclusion of a study was considered since social network is a relatively new discipline to be employed in the health domain and especially for TB research. We considered only English publications for our review and synthesized the results from the studies using two table formats under various important findings or themes. We interpreted these results using the findings and themes across the tables.

## Results

### *Study designs*

We identified a total of 21 studies which have used ‘social network’ as a primary or secondary research method in the TB research context. Among these, two were review articles<sup>11,12</sup> and one study utilized social network for exploring TB-related research published online<sup>13</sup>. This Brazilian study used a retrospective longitudinal design to reconstruct institutional networks in tuberculosis research<sup>13</sup>. The rest 18 were studies which collected primary social network data and information directly from the study population. All these were observational studies, either prospective or retrospective in design. Case control – social network design<sup>14</sup>, longitudinal social network study design<sup>15</sup> and qualitative social network design have been used in these studies<sup>16</sup>. Eleven of the studies collected retrospective social network data<sup>11,16–25</sup> and six of them collected prospective

social network data<sup>10,15,26–29</sup>. Two studies involved hypothesis-based statistical tests for social network data and the rest did not use any hypothesis<sup>14,15</sup>. Both these studies were not published in any journal, but were part of outcomes of doctoral studies in the field of social work (Table 1)<sup>14,15</sup>.

One study was used to understand the importance of social network in leading the TB patients to reach correct diagnosis at the right time. This was the only study which utilized social network concept to understand social support related to TB diagnosis rather than TB transmission dynamics (Table 1)<sup>24</sup>.

### *Study settings*

Nineteen studies were conducted in different countries across the globe having diverse disease burden and socio-economic status. Of the 18 studies involving primary social network data, seven studies were done in United states<sup>10,11,15,18–20,22</sup> two studies in Canada<sup>14,26</sup>, two studies in Europe<sup>16,17</sup> one study in Australia<sup>27</sup>, one study in Japan<sup>25</sup>, and five in Africa<sup>21,23,24,28,29</sup>. One study was done in both countries including both US and Canada<sup>10</sup>. Of the five African studies, three were conducted in South Africa<sup>23,28,29</sup> and two were conducted in Uganda<sup>21,24</sup>. Only one study was conducted in South America, in Brazil (Table 1)<sup>13</sup>.

### *Period of studies*

All the studies were published in the past 17 years from 2000 to 2017. The earliest of studies were published in the US between 2000 and 2001 (refs 18, 19, 22). The last published studies were in South Africa and Brazil in 2017 (refs 13, 29).

Studies have utilized social network data over a period of time, which involved collection of data across years. The study in Scotland utilized social network data of ten years<sup>16</sup>, followed by the Canadian study which utilized eight years of social network data or information of TB patients from 1992 to 1999 (ref. 14). There were studies which used 4–5 years of social network data from TB patients in the US and Africa<sup>20,29</sup>, United Kingdom<sup>17</sup> and South Africa<sup>29</sup>. Other studies utilized social network data which spanned for 2–3 or less years or months. The study in Brazil retrospectively collected ten years of data on TB (Table 1)<sup>13</sup>.

### *Study populations*

Three of the above-mentioned eighteen studies involved collection or utilization of social network data from aboriginal populations with TB<sup>14,27</sup>. Two studies were conducted in rural settings<sup>21,23</sup>, one among Transgender

**Table 1.** Major characteristics of studies that have used social network analysis in tuberculosis (TB) research

First author (ref. no)	Study period	Publication year	Study place	Population involved	Study design	Other methodologies used in the study	Study setting and TB burden
Fitzpatrick, L. K. <sup>18</sup>	1996–99	2001	Industry-based urban city in north western Indiana, USA	34,000 (white black and Asian)	Retrospective reconstruction/index case predicted	Secondary records/contact network information/DNA fingerprinting IS6110-/epidemiological investigation	Outbreak setting 6–8 cases per 100,000 populations in 1996 to 57 per 100,000 in 1998.
Andre, M. <sup>20</sup>	1996–2000	2007	Four locales in three contiguous counties in southwestern Oklahoma, USA	Prison, hospital and other community settings	Retrospective reconstruction/index case lead	Secondary case data, contact network information/DNA fingerprinting IS6110-/epidemiological investigation	Outbreak setting 3 per 100,000
Chamie, G. <sup>21</sup>	2012–2013	2015	Tororo, Uganda, Africa over one year	Rural town: 44,800	Retrospective construction of social network	Social network/molecular epidemiology/geo-spatial	304 per 100,000 person-years
Jackson, A. D. <sup>16</sup>	1994–2004	2009	Scotland, UK	Not specified	Retrospective reconstruction/qualitative mixed method	Contact investigation/molecular epidemiology and semi-structured patient interviews for social network enquiry	Outbreak setting incidence 10 per 100,000 population per annum since 2000.
Munang, M. L. <sup>17</sup>	2010–2014	2016	Birmingham, United Kingdom, Europe	1.2 million	Retrospective observational cohort study	Contact tracing/social network information/strain typing with 15- or 24-locus MIRU-VNTR	51 per 100 000 population in 2009
Shah, N. S. <sup>29</sup>	2011 and 2014	2017	KwaZulu, Natal Province, South Africa	10.3 million persons. HIV cases involved	Prospective observational	Clinical/social network information/DNA fingerprinting IS6110-/investigation/Geographic information system	1076 cases per 100,000 population prevalence and 2.8XDR cases per 100,000 population
CDC <sup>22</sup>	June 1998–December 1999	2000	Baltimore, Maryland/New York City area, USA	Transgender HIV TB	Retrospective/index case lead	Contact investigation and social network information/DNA fingerprinting IS6110-/epidemiological investigation	Not specified
Kawatsu, L. <sup>25</sup>	2010 and 2012	2015	Shinjuku City, Tokyo, Japan	330,000	Index case lead/retrospective	Contact tracing/social network information/DNA fingerprinting IS6110-/epidemiological investigation	Outbreak setting. 48.2 per 100 000 population

(Contd)

Table 1. (Contd)

First author (ref. no)	Study period	Publication year	Study place	Population involved	Study design	Other methodologies used in the study	Study setting and TB burden
Cook, V. J. <sup>10</sup>	February–August 2004	2007	Contra Costa County, California, USA (2000 population), DeKalb, County, Georgia, USA (2000 population) and the Downtown Eastside area of Vancouver, Canada (2000 population)	Asian, black, and Aboriginal, and foreign-born HIV and TB patients	Prospective construction of social network	Contact investigation and social network information/DNA fingerprinting IS6110-/epidemiological investigation	Not specified
Wood, R. <sup>28</sup>	2010	2012	Cape Town, Africa	18,000 residents of low socio-economic status	A diary-based community social mixing survey-prospective	Diary/social network	386 per/100,000 population
Al-Azem, A. A. <sup>14</sup>	1992–1999	2006	Manitoba, Canada	Aboriginal population	Case control	Contact racing/social network case control/DNA fingerprinting IS6110-/investigation	48.4 per 100,000 population per year overall, with rates as high as 496 per 100,000 population per year in some communities
Rothenberg, R. B. <sup>30</sup>	Not specified	2003	Not specified	Not specified	Review	Not specified	Not specified
Klov Dahl, A. S. <sup>19</sup>	Not specified	2001	Texas, Houston, USA	Not specified	Retrospective reconstruction	Social network information/DNA fingerprinting IS6110-/epidemiological investigation	Outbreak setting
Cook, V. J. <sup>12</sup>	Not specified	2011	Not specified	Not specified	Review	Not specified	Not specified
McElroy, P. D. <sup>11</sup>	2001	2003	Wichita, Sedgwick County, USA	Not specified	Retrospective reconstruction	Contact investigation/social network information/DNA fingerprinting IS6110-/epidemiological investigation	Outbreak setting
Fonseca, B. P. F. <sup>13</sup>	2005–2014	2017	Brazil, South America	Not specified	Retrospective longitudinal mapping	Not specified	Not specified

(Contd)

Table 1. (Contd)

First author (ref. no)	Study period	Publication year	Study place	Population involved	Study design	Other methodologies used in the study	Study setting and TB burden
Cozatt, D. M. <sup>17</sup>	2010, 2011 and 2012	2014	Clark County, Nevada, USA	Pediatrics	Prospective longitudinal study	Contact investigation and social network information/DNA fingerprinting IS6110-/epidemiological investigation	5.7 cases per 100,000 among 1-4 year-old; 5-14 cases per 100,000 among 5-14 year-old during 2008-12
Gandhi, N. R. <sup>23</sup>	January 2005 through December 2006	2013	Tugela Ferry, South Africa	Rural area with 160,000 population with high HIV prevalence	Retrospective, observational study	Secondary data/social network information/DNA fingerprinting IS6110-/epidemiological investigation	52 XDR-tuberculosis cases per 100,000 population during 2005-09.
Sekandi <sup>24</sup>	March to July 2014	2015	Kampala, Uganda, Africa	Not specified	Retrospective study design	Social network analysis/diary methods	Not specified
Gardy, J. L. <sup>26</sup>	May 2006 and December 2008	2011	British Columbia, Canada	Not specified	Prospective observational	Clinical/contact tracing/social network information/DNA fingerprinting IS6110-whole genome sequencing/epidemiological investigation	Outbreak setting 6.4 cases per 100,000 population
Devlin, S. <sup>27</sup>	October 2000-July 2012	2013	New South Wales, Australia	Aboriginal communities	Prospective study design	Clinical/epidemiological/social network analysis	4.8 cases per 100,000 population

population<sup>22</sup> and one among pediatric population<sup>15</sup>. Rest of the studies involved general population or were not specified accurately (Table 1).

### *Methodologies involved*

Of the 18 studies, only three utilized social network method independently without being complemented by molecular epidemiology data<sup>24,27,28</sup>. All other studies used social network data and information along with contact investigation data, epidemiological data, and molecular DNA fingerprinting data. The study in British Columbia utilized a maximum of investigation methods, including clinical, contact tracing, social network, DNA fingerprinting IS6110, whole genome sequencing and epidemiological to understand TB transmission<sup>26</sup>. A study in South Africa utilized all, except the contact tracing information<sup>29</sup>. Only one study utilized geo-spatial analysis to identify clusters of TB transmission in real-time geographical settings<sup>29</sup>, and two studies used diary methods to collect social network information<sup>24,28</sup>. The Brazilian study used bibliographic mapping and clustering together with social network analysis to explore the web database (Table 1)<sup>13</sup>.

### *Context of studies*

Seven studies were implemented to understand the outbreak of TB epidemic at the community level<sup>11,16,18–20,25,26</sup>, which were all TB low incidence settings ranging from less than 10 cases per 100,000 population to 50 per 100,000 population. Other studies were conducted in non-outbreak related context and TB burden was as high as 1076 cases per 100,000 population (Table 1)<sup>29</sup>.

### *Sample size of studies*

Three studies used less than 10 TB patients as the sample for social network survey<sup>12,22,25</sup>, five studies used less than 50 TB patients as sample<sup>18–20,27,30</sup>, three studies used between 50–100 TB patients<sup>10,16,21</sup>, four studies used 100 to 300 TB patients as sample<sup>15,17,23,24</sup> and three studies used more than 400 TB patients (Table 2)<sup>14,29,28</sup>.

### *Social network metrics used*

Among all the studies, 12 used social network metrics to characterize and explain the social network relationships and structures of TB patients in their settings, and one study used metrics to characterize institutional and research networks<sup>13</sup>. The most commonly used social network metrics were: ‘degree’ measure<sup>18,20,21,25,27</sup>, ‘cen-

trality’ measure<sup>13–15,29</sup>, ‘betweenness’ measure<sup>15,19,20,25</sup>, ‘reach’ measure<sup>12,13,15,20</sup>, ‘density’ measure<sup>14,15,17,23</sup>, ‘*k*-plex’ measure<sup>10,14</sup>, ‘degree of cohesion’<sup>14,31</sup>, and ‘Median daily contacts’<sup>28,29</sup> and ‘clustering coefficient’<sup>15</sup>. External–internal tie index (EI index) was used in one study<sup>13</sup>. Except for three studies<sup>22,24,28</sup> all the studies have used socio grams (network graphs) to explain the social network structure and patterns.

### *Social network analysis packages used*

The most widely used software packages for analysing the social network data were UCINET<sup>10,11,13–16,23,25,29–31</sup> and Pajek<sup>10,11,14,23,30</sup>. Other software which were used in the studies included R, STATA, Cytoscape, Gephi and InFlow (Table 2).

### *Major findings of the studies*

All the studies provided new knowledge or information on the social network patterns, structures, characteristics, which either involved individuals or places or behaviours. Few studies helped in understanding how TB patients were connected to one another, which could not be explained by conventional epidemiological or contact tracing methods. The quantitative findings show that social network analysis leads to the identification of social or epidemiological links in at least 30% of TB patients with their contacts or index patients<sup>16–18,20,21,29</sup>. Studies have also established that index cases have a prominent role in TB transmission network with high centrality scores<sup>20</sup>. A study identified that it was not centrality measure of TB patient, but betweenness measure which defined the importance of transmission<sup>25</sup>.

Median number of contacts or frequency of contacts with social network members was used to define the increasing TB infection among contacts in three studies<sup>10,14,28</sup>. One study identified specific behaviours of subgroups underlying the social network of the TB patients and their contacts that otherwise were homogeneous in characteristics<sup>30</sup>.

All the studies provided insights about the key role of public and private places in the transmission of TB within the social networks. Common places of importance which were shared by TB patients and their contacts in these studies were similar across settings. Places of alcohol consumption, drug sharing, bars, places of sexual activities and prisons were repeatedly recorded by these studies<sup>16,18,19,21,22,26,29,30</sup>. Hospital settings also consistently emerged as the place where the social network of TB patients and their contacts overlapped<sup>20,23,29</sup>. Only one study found that no public or private place was named by two or more participants, and thus there was no direct link between them<sup>29</sup>.

**Table 2.** Major characteristics, research findings and outcomes of studies that have used social network (SN) analysis in TB research

First author (ref. no.)	Sample size of TB cases/infected	Metrics/sociograms used in study	Software used	Major findings	Social network places identified and activities involved which are important in TB transmission	Major outcomes of public health importance
Fitzpatrick, L. K. <sup>18</sup>	31	Sociogram	Not specified	29 (94%) outbreak-related cases socially connected either directly or indirectly. Epidemiological links for 18 cases (58%) were discovered through complex social networks. Also, networks for HRGs would be useful in outbreak settings.	Apartment complex, a junkyard, a local bar and a liquor store. Common activities underlying networks were use of drugs and alcohol, and prostitution.	24 (77%) of 31 known outbreak-related cases may have been prevented if social network survey was used.
Andre, M. <sup>20</sup>	35	Reach, degree, betweenness and sociogram	InFlow software (orgnet.com, Cleveland, Ohio, USA)	Index patient (1) was directly linked to 19 (56%) and indirectly linked to 6 (18%) of the first 34 secondary cases in the community respectively. Index had the highest reach, degree and betweenness scores.	Prison, hospital and other community settings.	Contacts prioritized and screened by network analysis were more likely to have LTBI than non-prioritized contacts (odds ratio (OR) = 7.8; 95% confidence interval = 1.6, 36.6).
Chamie, G. <sup>21</sup>	54	Relative network 'degree' (which is number of TB cases reporting or visiting specific location)	Gephi software (Gephi.org, version 0.8)	18/54 (33%) of TB cases could be socially linked to one another. Using a combination of molecular epidemiological, social network and GIS data could lead to large number of community-based cases and reduce TB incidence in high-prevalence settings.	134 locations, including clinic, bar, church, market, shop, hotel, school, restaurant, video hall, mosque, garage, farm, transportation vehicles, factory, drinking venues, workplaces, shops and marketplaces. The largest proportion of time (22.4%) was spent at drinking venues.	Social network lead, location-based active TB case findings and infection control interventions could be used as tools to interrupt TB transmission in rural east Africa.
Jackson, A. D. <sup>16</sup>	64	Socio gram	UCINET 6.0 (Analytic Technologies, Harvard, MA, USA)/ NetDraw	One-third (n = 14, 32.6%) of the 43 epidemiological links detected was discerned as a result of patient social network interviews, and not previously identified.	These included 11 public houses, a village centre with several closely situated public houses, a nursing home, an apartment and the home of one cluster patient, where people gathered regularly to consume alcohol.	Rather than a single-source outbreak, eight pockets of transmission were identified, the largest involving UK-born persons.
Munang, M. L. <sup>17</sup>	139	Density and Sociogram	R package I graph	Social network information of 139/431 clustered cases found new epidemiological links in 11/19 clusters (≥5 members). Using a social network approach, unexpected transmission was a frequent finding occurring in 11/16 medium or large clusters.	Not specified	98 additional contacts were assessed, with one case of active TB and 24 with latent tuberculosis infection diagnosed. Social network approach increased knowledge of likely transmission events, but few additional TB cases were diagnosed. Systematic molecular cluster investigation supplemented by social network data could improve understanding of occasional micro-epidemics.

(Contd)

Table 2. (Contd)

First author (ref. no.)	Sample size of TB cases/infected	Metrics/sociograms used in study	Software used	Major findings	Social network places identified and activities involved which are important in TB transmission	Major outcomes of public health importance
Shah, N. S. <sup>29</sup>	404	Median contacts	UCINET software	Person-to-person or hospital-based epidemiologic links were identified in 30% patients. A person-to-person link was identified in 59 of 404 participants (15%) who formed 25 social networks.	61% of TB patients had a hospital-based link with another study participant. A total of 177 other locations where TB patients spent substantial time – like churches, bars, beauty salons, prisons, restaurants, nightclubs, and other locations. No locations were named by two or more participants to suggest a direct link.	A total of 2901 contacts were named. Among these, 293 had tuberculosis (10%) and 25 had XDR tuberculosis.
CDC <sup>22</sup>	4	Not specified	Not specified	105 social network contacts identified. Screening of 83 mobile contact members resulted in 7% TST-positive rate lower ( $P < 0.01$ ) than in the social network screening.	Membership in a house, attendance at particular nightclubs or balls.	Of the 105 social network contacts, 96 (91%) had a TST, 65 (68%) tests were read, and 24 (37%) were TST-positive.
Kawatsu, L. <sup>25</sup>	8	Degree and betweenness centrality scores sociogram	UCINET, version 6 (Analytic Technologies, Harvard, MA, USA)	Centrality scores did have statistically significant association with the risk of contacts being diagnosed with LTBI. Contacts with high betweenness scores were more likely to be diagnosed with LTBI than contacts with lower scores (OR 2.88, 95% CI 1.31–5.83, $P = 0.007$ ).	Household, room, building, floor, smoking room.	Betweenness score could be useful in prioritizing contacts during TB contact investigation.
Cook, V. J. <sup>10</sup>	87	Case contact dyads/sociogram K-plex modelling, degree of cohesion Seidman z-plexes	UCINET, version 6.101 (Analytic Technologies), Harvard, MA, USA and Pajek, version 1.09	A total of 453 case-contact dyads were recorded. Median number of recorded contacts per TB patient was 5.	1056 places of social aggregation. A greater number of daytime places were elicited.	A positive correlation between contacts with TST positive and location in denser portions of the person-place network was observed ( $P.01$ ). Combining SNA with genotyping should help improve the specificity of molecular genotyping methods.
Wood, R. <sup>28</sup>	571	Median daily contacts	Stata	Median daily contacts within household and in transport facilities changed over age.	Five locations contributed 97.2% of total indoor time and 80.4% of total indoor contact, which are own household, other households, transport, creche/school and work.	Increase in non-home socialization corresponds to increasing TB infection rates during childhood and young adulthood.

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**Table 2.** (Contd)

First author (ref. no.)	Sample size of TB cases/infected	Metrics/sociograms used in study	Software used	Major findings	Social network places identified and activities involved which are important in TB transmission	Major outcomes of public health importance
Al-Azem, A. A. <sup>14</sup>	504	Network size, contact size, closeness, network type, cohesion, core collapse sequence and <i>k</i> -score/sociogram	UCINET (138) and Pajek	Three significant variables played a key role in transmission :: contact size, network type, and frequency of contacts. The whole network approach identified boundaries of the outbreaks in a community networks.	Nursing station, general store, and school were attended by index nodes and contacts. Control group network attended general store, school and community recreational hall.	Addition of centrality measures and centralization of the network or cohesion of the network nodes around focal nodes helped in identifying public places conducive for TB transmission. Network members exposed to 7 or more TB cases had a 100% probability of being TB cases themselves. Network members with more than two TB patients had more chances of contracting the disease.
Rothenberg, R. B. <sup>30</sup>	Not specified	Not specified	Not specified	Social network-informed methods to understand community dynamics of transmission will be useful.	Not specified	Not specified
Klovdahl, A. S. <sup>19</sup>	37	Betweenness and centrality	Not specified	Not specified	Over 40 places (including many gay bars).	Network methods were used to reconstruct outbreak network and to quantify the relative importance of network members in transmitting TB.
Cook, V. J. <sup>12</sup>	Not specified	Not specified	Not specified	Standards and guidelines for SN methods to use during TB outbreaks and in routine follow-up need to be developed, as evidences show their usefulness.	Not specified	Need to enhance systematic collection, analysis, and interpretation of contact investigation data using novel methodologies like social network survey, especially in high-risk communities.
McElroy, P. D. <sup>11</sup>	45	Sociogram	UCINET-V <sup>13</sup> and Pajek14	Crack cocaine use behaviour by TB cases and TST positive contacts distinguished the network against TST-negative network members.	Exotic dance clubs	Social network analysis can help discern behaviour al variations or relationship differences in a homogenous group, that may explain transmission in a way not possible by conventional methods.
Fonseca, B. P. F. <sup>15</sup>	Size of the giant component, average degree, average clustering coefficient, average path length, connectivity and fragmentation and E-I index	Gephi and UCINET	Top three most influential Brazilian institutions and researchers in the national TB research network were identified. Top areas of TB research were identified.	Not specified	SN analysis identified key central institutions maintaining network connectivity; most influential researchers; synergy between internal research groups working in complementary areas.	

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Table 2. (Contd)

First author (ref. no.)	Sample size of TB cases/infected	Metrics/sociograms used in study	Software used	Major findings	Social network places identified and activities involved which are important in TB transmission	Major outcomes of public health importance
Cozatt, D. M. <sup>15</sup>	252	Sociogram/degree centrality, reach centrality, betweenness, density, clustering coefficient	UCINET version 6	Group-level network analysis identified history of incarceration of a contact as a risk factor for pediatric TB cases.	Prison, household and contacts with specific countries of birth.	Betweenness score and two-step reach could be the best metrics for surveillance network.
Gandhi, N. R. <sup>23</sup>	148	Component size, network density, and centrality and sociogram	UCINET, and Pajek	Social network analysis explained multi-generational TB transmission within a highly interconnected network. Patients with highest centrality (1 man with 11 contacts and 6 women with 6 to 10 contacts) were central transmitting infection.	Hospitalization, extended length of stay, combined with the congregate design of wards.	High degree of interconnectedness leading to multiple generations of nosocomial transmission. Rather than a point-source outbreak.
Sekandi <sup>24</sup>	294	Network size	Not specified	58% of patients first contacted persons in their social network for seeking TB-related information. Those who first contacted a non-TB health provider had a significantly lower likelihood of a timely final diagnosis when compared to those who contacted a social network member (HR: 0.72, 95% CI: 0.55, 0.95). The most probable source case leading to an epidemic was identified and validated.	Not specified	Network analysis provides insights about the nature of contacts made during diagnostic cascade.
Gardý, J. L. <sup>26</sup>	9	Transitivity/sociogram	Cytoscape software		Transient living arrangements, crack cocaine use and alcohol use.	SN analysis and location-based surveillance could have prevented outbreak.
Devlin, S. <sup>27</sup>	30	Sociogram	Not specified	The cases have extensively overlapped social networks.	Overcrowded households and persons highly mobile during their long infectious period.	More than 1000 TSTs provided for social network contacts.

A study was unique in identifying the most influential research institution, researchers and research clusters in the Brazilian tuberculosis field, which has strong policy implications (Table 2)<sup>13</sup>.

### *Public health impact of social networks*

Utilization of social network analysis led to increased finding of TB cases or tuberculin skin test (TST) positives, with maximum positivity of 37% reported in a high-risk group setting<sup>22</sup>, to 10% TB infection in a high-burden extensively drug resistance (XDR) setting of South Africa<sup>29</sup>. Social network prioritization leads to increased probability of identifying latent TB in contacts in an outbreak setting<sup>20</sup>.

A study quantified the importance of social network approach in averting TB transmission in an outbreak setting<sup>18</sup>. Two studies highlighted the importance of social network in identifying highly vulnerable individuals or index patients for TB infection<sup>14,26</sup>. The importance of location-based screening and of public places in increasing the cohesion or linking of TB patients in larger communities was underscored by two studies and three references<sup>11,14</sup>.

Two studies highlighted the concept of multiple sources of TB infection in a community, through complex social and epidemiological networks rather than the conventionally specified single-source concentric circle approach<sup>16,23</sup>. The importance of network metrics in TB surveillance and new case identification were highlighted in a few studies<sup>14,15,25</sup>. Munang *et al.*<sup>17</sup> reported that there was only one additional case of TB identified by social network approach and highlighted its minimal use in identifying new cases (Table 2).

### **Discussion**

The important finding of this study is that 'social network' methodology can be successfully employed to understand the transmission of TB in any community across a small number of countries with diverse TB burden, geography and socio-economic status. All the studies considered in this review have shown that social network data and information hold the potential to either complement TB case detection, or explain the complexity of TB transmission along with conventional methods like contact tracing methods, epidemiological methods, molecular epidemiological methods, clinical diagnosis, secondary analysis of records and geo-spatial methods. Social network methods have been predominantly used in the developed country settings with low TB prevalence and incidence (like the US), especially to help explain the local epidemic outbreak. Very few studies in TB high burden countries like South Africa have tested the potential of social network data in assessing and understanding

the TB transmission dynamics. There is no study which has tested the usefulness of social network data in very high burden countries like India, where there is a great necessity for novel approaches to improve case detection and understand TB transmission patterns<sup>32</sup>.

Also, except for one study conducted in Uganda, the role of social network in enabling and supporting TB patients with information, services and resources to access and avail diagnosis, treatment care and support has not been analysed in any country. This is a lacuna considering the numerous studies which have so elaborately assessed the role of social network members and social relationships in determining the health-care behaviour, health access, treatment care and prevention of people living with HIV (PLHIVs) and key populations<sup>33,34</sup>.

With regard to the methodologies, many studies have relied on sample size less than 50 and have mostly retrospectively reconstructed the social network of TB patients. Only few studies have prospectively collected primary data on social network which would be of real use for public health practice.

While most studies used common social network metrics, there is an evident lack of common methodology to implement social network studies in the TB context. While this is inevitable considering the exploratory nature of social network methods, a common standard and research logics should be followed in implementing social network surveys. For example, none of the studies justified the sample size which was used for generating the social network of TB patients. Also, the definitions used in all the studies to understand the nature of social relationships are very different and arbitrary. Only two studies utilized and published the full-fledged social network questionnaire that they used and the rest did not have any material to refer but had only descriptions about the questions<sup>16,29</sup>.

The lack of hypothesis-led studies involving social network data in published journals shows paucity in the focus and interest in this discipline by researchers in the TB field. Two of the doctoral dissertation studies done in a gap of 15 years utilized elaborate social network methodologies and tested the hypothesis based on social network data, which highlights the rare academic pursuits shown in this discipline<sup>14,15</sup>. Also the doctoral research must have provided the needed time and liberty for these researchers to pursue a more focused and rigorous hypothesis-based social network research in TB settings, which is not easily possible in real-world outbreak driven studies that use social network data as a complementary approach.

The importance of public places or hotspots of transmission has been elaborately recorded in almost all studies. Common public places (like drinking bars) have been consistently documented to have played a key role in the transmission of TB in all countries, where these studies have been implemented. This would be one real

contribution of social network analysis in filling in the research gap in understanding TB transmission in largely populated countries like India, Africa and China. The innumerable public and private places of social congregation, where people come together could be effectively short-listed using social network-based approaches, which would greatly help save resources and time by prioritizing preventive and treatment measures in the selected localities<sup>35</sup>. Similarly, social network metrics would be of use in effectively shortlisting key susceptible and at risk individuals, which would greatly help save resources and time by prioritizing them for preventive and treatment measures.

Overall the present study highlights social network data and information as a methodological innovation in addressing TB epidemic across the globe. Social network methods along with novel genomic and geo-spatial tools could play a major role in understanding the much complex TB transmission dynamics. More studies which follow a common standard and operational definitions should be implemented and tested in different TB prevalence settings for the usefulness of social network data and information. The so far unknown dimensions of social network in determining the health behaviour of TB patients need to be explored by studies which could lead to develop effective intervention models. The application of social network in other aspects of TB such as system-patient communication, health-care delivery, networking of intervention partners, community networks, etc. needs to be studied.

## Conclusion

The present study explains how social network analysis involving TB patients and their contacts helps in understanding disease transmission in a way which is not possible with routine clinical, epidemiological and contact investigation methods. It highlights how social networks of TB patients have opened up new opportunities in identifying key network members who have transmitted infections, and in identifying susceptible and infected contacts in larger communities. The study lists the ‘hotspots’ of TB transmission in community settings outside family spaces, identified through social network analysis. It summarizes research findings to guide future conceptualization of social network studies in other countries and regions. The study also provides an outlook on how social network analysis could especially help address challenges in countries with high population and high TB burden in terms of door-to-door screening and prioritizing ‘susceptible contacts’ and ‘hotspots’ for implementing prevention interventions.

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