



## Individual and neighborhood correlates of membership in drug using networks with a higher prevalence of HIV in New York City (2006–2009)

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### ABSTRACT

**Purpose:** To identify individual- and neighborhood-level correlates of membership within high HIV prevalence drug networks.

**Methods:** We recruited 378 New York City drug users via respondent-driven sampling (2006–2009). Individual-level characteristics and recruiter–recruit relationships were ascertained and merged with 2000 tract-level U.S. Census data. Descriptive statistics and population average models were used to identify correlates of membership in high HIV prevalence drug networks (>10.54% vs. <10.54% HIV).

**Results:** Individuals in high HIV prevalence drug networks were more likely to be recruited in neighborhoods with greater inequality (adjusted odds ratio [AOR], 5.85; 95% confidence interval [CI], 1.40–24.42), higher valued owner-occupied housing (AOR, 1.48; 95% CI, 1.14–1.92), and a higher proportion of Latinos (AOR, 1.83; 95% CI, 1.19–2.80). They reported more crack use (AOR, 7.23; 95% CI, 2.43–21.55), exchange sex (AOR, 1.82; 95% CI, 1.03–3.23), and recent drug treatment enrollment (AOR, 1.62; 95% CI, 1.05–2.50) and were less likely to report cocaine use (AOR, 0.40; 95% CI, 0.20–0.79) and recent homelessness (AOR, 0.32; 95% CI, 0.17–0.57).

**Conclusions:** The relationship between exchange sex, crack use, and membership within high HIV prevalence drug networks may suggest an ideal HIV risk target population for intervention. Coupling network-based interventions with those adding risk-reduction and HIV testing/care/adherence counseling services to the standard of care in drug treatment programs should be explored in neighborhoods with increased inequality, higher valued owner-occupied housing, and a greater proportion of Latinos.

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The “HIV risk environment” has been characterized as a dynamic interplay between structural and network factors [1]. Although both structural [1] and network [2–4] factors influence individual-level risk/health behaviors, information flow, and HIV transmission, most HIV prevention research among drug-using populations examines the HIV risk environment from only one of these perspectives.

From a structural perspective, many studies have shown that HIV is disproportionately concentrated in lower income and underserved communities [5,6]. For example, the 2006 U.S. Centers for Disease Control and Prevention HIV prevalence estimates (which did not account for neighborhood characteristics) revealed

significant racial/ethnic disparities (1.7% among blacks, 0.6% among Hispanics, and 0.2% among whites) [7]. Although the 2010 U.S. Centers for Disease Control and Prevention HIV prevalence estimates (which stratified by neighborhood-level poverty) reported no significant racial/ethnic differences in HIV, HIV was significantly more prevalent in low-income areas [8]. Racial and socioeconomic disparities in HIV are argued to be due, in part, to racial residential segregation [6,9], which disproportionately influences poor neighborhoods and results in fewer resources in minority neighborhoods [1,10,11].

Other studies have identified geospatial clusters of HIV and related risk behaviors. For example, one study in the United States identified a cluster of 157 census tracts with a higher prevalence of HIV than the surrounding census tracts. This geospatial cluster was characterized by increased poverty, a lower density of multiracial individuals, and a higher prevalence of HIV-related risk behaviors [12]. In another example, a study among injection drug users (IDUs)

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in Russia reported that HIV and injection risk behaviors were geographically clustered and that clusters frequently overlapped [13]. Another study among IDUs reported that high-risk injection behaviors were more common in census tracts with higher unemployment rates [14]. Other studies among IDUs have reported ecological associations between greater income inequality at the standard metropolitan statistical area-level and increased HIV prevalence [15,16].

Studies using social network-based approaches have demonstrated that network norms are associated with drug-related [17–22] and sex-related HIV risk behaviors. Specifically, among individuals from a drug-using community, self-reported condom use with main partners was associated with communication, proscriptive/injunctive, and descriptive condom use norms [23]. Another study found that female IDUs who reported having peers who exchanged sex were twice as likely to report exchanging sex [24].

Few studies have assessed the combined influence of structural/neighborhood and network risk factors on HIV. Because individuals who are socially connected may also be in close geographic proximity to one another [25], risk behaviors may cluster among individuals within networks because of their shared structural environment, network norms/relationships, or both. Similarly, geospatial/neighborhood-level clustering of risk behaviors may be partially attributed to network relationships and social norms. For these reasons, it is important to consider network and neighborhood-level factors together to not only account for correlated data, but because there may be different mechanisms through which network-level and neighborhood-level characteristics influence individual-level behaviors.

Other motivations for examining network and structural/neighborhood factors together are (1) those with the greatest disease burden are often more difficult to reach through traditional sampling approaches and (2) poverty and inequality (which structural approaches have identified as leading causes of health disparities) are difficult to modify. Thus, new strategies are needed to recruit subgroups of hidden populations and target them with interventions that more effectively reduce health disparities. Network-based recruitment approaches could target individuals from high-risk structural environments and network-based interventions could be used to disseminate information and build supportive relationships that buffer the influence of structural factors that facilitate HIV transmission. A better understanding of how network and structural factors act independently and/or jointly may better explain racial and socioeconomic disparities in HIV and, in turn, better inform effective strategies to reduce health disparities.

Because infectious disease transmission relies on the presence of both disease and behaviors that facilitate disease transmission, this analysis aims to visualize HIV clustering among a sample of drug users recruited through respondent-driven sampling (RDS) and to identify individual and neighborhood characteristics associated with membership in drug using networks with a higher HIV prevalence (referred to as “high HIV prevalence networks” hereafter). The findings from this analysis are relevant for future research or interventions that aim to target these high-risk, drug-using networks and can inform the development of multilevel intervention approaches that incorporate both network and neighborhood/structural components to reduce HIV transmission among these higher risk, drug-using networks.

## Methods

The data used were from the Social Ties Associated with Risk of Transition into injection drug use (START), a longitudinal study aiming to identify social risk factors for transitioning from

non-injection to injection drug use among young adult heroin, crack, and cocaine users in New York City. START methods have been previously described [26]. In brief, participants were eligible if they were 18 to 40 years old and were active injection or non-injection drug users (NIDU). Although participants were recruited through targeted street outreach and RDS, this analysis was restricted to the respondent-driven sample where social network data were available. RDS participants were given three coupons to recruit drug-using peers. Participants could bring in more than three peers, but were only compensated for the first three. Recruiter–recruit relationships were determined as part of the RDS eligibility screening process. Most participants described their recruiter as a friend or acquaintance (83%); 6% as a relative, 7% as a stranger, and 4% as other. Although peer recruits overlapped with risk network members, RDS recruits tended to be higher risk than the drug using networks reported in the social/risk network inventory [26].

Between July 2006 and June 2009, 621 participants were screened to participate in the respondent-driven sample and 439 were eligible. Of those eligible, 32 were removed from the analysis because they were recruited on the mobile research van, which had changing site locations that made RDS less optimal. Five others (and their six peer recruits) were dropped owing to inconsistencies in self-reported drug use at follow-up visits. Finally, 18 seeds were dropped from this analysis because they did not recruit peers ( $n = 378$ ). All study materials were approved by the institutional review boards at Columbia University and the New York Academy of Medicine.

### *Individual-level variables*

After providing informed consent, individuals completed a 90-minute, interviewer-administered questionnaire, which ascertained demographics, network characteristics and relationships, drug use and sex behaviors, and health service use. Individual-level variables included in the analysis were selected because of the strong association between these characteristics and HIV in the prior literature.

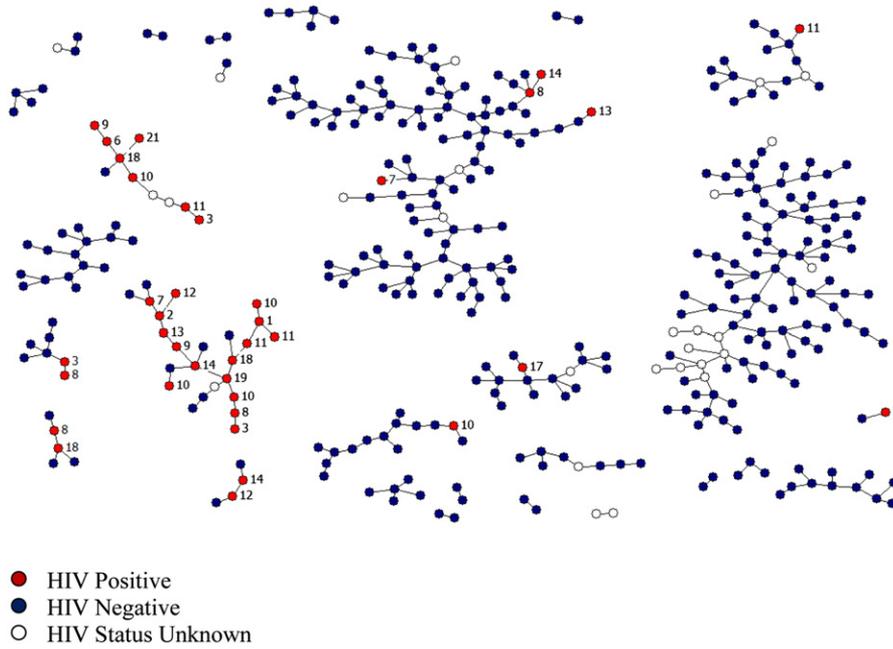
### *Neighborhood-level variables*

Baseline data were merged with tract-level data from the 2000 United States Census via the census tract where he/she was recruited for START. Participants most often described their recruitment neighborhood as the location where they hung out, purchased drugs, and spent most of their time. Previous research comparing street recruitment and neighborhood residence found that the majority of illicit drug users in urban settings (85%) lived in the neighborhoods where they were recruited [27].

Neighborhood covariates selected for inclusion in this analysis were selected based on findings from prior literature on health disparities in HIV prevalence and incidence. The following categories of tract-level neighborhood attributes were used for this analysis: Minority composition, educational attainment, unemployment, income/poverty, inequality, and crowding. Inequality was measured using the index of concentration at the extremes (ICE), which conceptualizes the concentration of affluence and poverty as falling along a continuum ranging from  $-1.0$  to  $+1.0$  ( $ICE = -1.0$  when all families are poor and  $+1.0$  when all families are affluent) [28].

### *Network analysis*

Because standard statistical models cannot capture the interconnectedness of network data, simulations were used to derive a meaningful measure of HIV clustering within networks. RDS



**Fig. 1.** HIV status among 378 New York City drug users recruited via respondent-driven sampling (2006–2009). Each circle represents an individual (red, HIV positive; blue, HIV negative; white, missing HIV status). Lines between individuals indicate respondent-driven sampling recruiter–recruit relationships. Labels indicate the number of years since his/her first HIV positive diagnosis.

recruit–recruiter ties were displayed visually using NetDraw [29] (Fig. 1). To determine whether clustering by HIV status could be explained by chance, the observed network was compared with a null distribution (1000 randomly generated networks with the same network topology and overall prevalence of HIV, but with HIV status distributed randomly) [30]. If HIV clusters more than what would be expected by chance, the probability that an ego is HIV positive given that his/her alter is HIV positive would be higher in the observed network than in the null distribution and would not be included within the 95% confidence interval for the null distribution ( $P < .05$ ; Table 1).

Degree of separation is defined as the social distance, or the smallest number of intermediates, between alter–ego pairs. The association between an ego’s HIV status and his/her alter’s HIV status (for 1–6 degrees of separation) was also examined (risk ratios in Table 1; risk differences in Fig. 2).

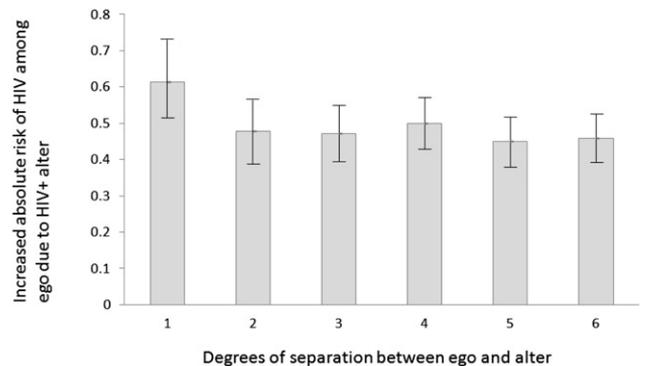
**Table 1**  
Measures of clustering by HIV status (observed and expected risk ratios) among respondent-driven sampling–recruited illicit drug users in New York city, 2006–2009 (n = 378)

No. of degrees of separation	No. of N-degree paths	No. of individuals separated by N degrees	Observed risk ratio (HIV + ego   HIV + alter)/(HIV + ego   HIV– alter)	95% confidence interval for the expected risk ratio (HIV + ego   HIV + alter)/(HIV + ego   HIV– alter) from 1000 random samples*
1	700	378	13.63	–1.00, 1.25
2	1406	356	9.29	–0.79, 0.98
3	1330	336	10.84	–0.76, 0.91
4	1500	321	15.67	–0.66, 0.84
5	1672	306	13.82	–0.66, 0.76
6	1788	283	16.81	–0.70, 0.76

\* The 95% confidence intervals for the null distribution reflect the range of risk ratios that were produced by the middle 950 randomly generated networks when all 1000 estimates were ranked numerically. Observed risk ratios not included in the 95% confidence interval for the expected risk ratio are significantly different from what we would expect by chance ( $p < .05$ ).

*Statistical analysis*

As mentioned, network simulations were used to derive a meaningful measure of HIV clustering. In the Framingham Heart Study, the association between an ego’s attribute and his/her alter’s attribute was no different from that expected by chance after three degrees of separation [31–33]. Because (1) the increased risk of HIV observed for egos with an HIV positive alter was significantly different from that expected by chance for alter–ego pairs separated by one to six degrees ( $P < .05$ ) and (2) the increased risk of HIV among those with HIV positive alters did not vary in strength or significance for alter–ego pairs separated by one to six degrees (Table 1; Fig. 2), individuals were classified based on their membership in an RDS recruitment network with greater than expected HIV (>10.54%) versus less than expected HIV (<10.54%). The expected prevalence assuming random assignment of HIV status



**Fig. 2.** Absolute increased risk of HIV among egos associated with having an HIV-positive alter separated by one to six degrees. Absolute risk is calculated as the difference between the observed risk and the risk from the null distribution (1000 random samples with HIV status randomly distributed). Error bars denote 95% confidence intervals for the observed risk of HIV for alter–ego pairs separated by one to six degrees.

across the sample was 10.54%. Of note, the highest HIV prevalence among the low-prevalence networks was 7.14% and the lowest HIV prevalence among the high-prevalence networks was 28.57%.

Because network clusters included individuals from multiple neighborhoods and individuals within networks were not confined to specific neighborhoods, a multilevel model with two levels of clustering was not possible. We also considered a hierarchical model with two random intercepts (one for network clusters and a second for neighborhood clusters); however, the models did not converge. Therefore, we selected the clustering level most relevant to this analysis (networks) and clustered individuals belonging to the same RDS recruitment network. To account for correlation between observations from individuals within the same RDS recruitment network, we clustered on RDS recruitment network membership using a generalized estimating equations approach and calculated Huber–White robust standard errors using STATA 10 [34]. Neighborhood variables (except ICE) were standardized by z-score in the bivariate and multivariable regressions. Descriptive statistics and logistic regression (with the generalized estimating equation and Huber–White robust standard errors) were used to identify individual- and neighborhood-level factors associated with membership in RDS recruitment networks with a higher HIV prevalence.

## Results

Our sample includes 378 individuals, 28 RDS recruitment networks and 350 one-degree ties (Table 1). The median number of individuals per RDS recruitment network was 4.5 (minimum, 2; maximum, 103; interquartile range, 2–11.75). Sample characteristics are presented in Table 2. The absolute increased risk of HIV associated with having an HIV positive alter ranged from 45% to 61%, was significant for alter–ego pairs separated by one to six degrees, and did not vary by the number of degrees of separation (Fig. 2;  $P < .05$ ). The relative increased risk of HIV associated with having an HIV-positive alter ranged from a relative risk of 9.29 to 16.81 (Table 1;  $P < .05$ ).

Members of high HIV prevalence networks were more likely to report (1) a prior sexually transmitted disease test (herpes, gonorrhea, syphilis, chlamydia), (2) recent drug treatment enrollment, (3) crack use, (4) exchanging sex for money/drugs, and (5) at least a high school diploma or GED. They were less likely to report homelessness, injection drug use, and cocaine use (Table 3).

Those in high HIV prevalence networks were more likely to have been recruited in neighborhoods characterized by greater inequality, a higher percentage of residents with at least a bachelor's degree, higher median household incomes, higher valued owner-occupied housing (a higher median value for owner-occupied housing in that census tract), and greater residential crowding.

The final multivariable model (Table 4) assessed individual- and census tract-level correlates of membership in high HIV prevalence networks. Members of high HIV prevalence networks were more likely to be recruited in neighborhoods characterized by greater inequality (adjusted odds ratio [AOR], 5.85), higher valued owner-occupied housing (AOR, 1.48), and a higher proportion of Latinos (AOR, 1.83). Individuals in high HIV prevalence networks were more likely to have exchanged sex for money/drugs in the past year (AOR, 1.82), to have used crack (past 6 months; AOR, 7.23), and to have been enrolled in drug treatment (past 6 months; AOR, 1.62). They were less likely to have used cocaine (AOR, 0.40) or to report homelessness in the past 6 months (AOR, 0.32).

## Discussion

In this sample, membership in high HIV prevalence networks was not random; individuals who recruited (or were recruited by)

HIV-positive individuals were much more likely to be HIV positive and the strength and significance of this association did not diminish with increasing degrees of separation. Our data highlight an association between exchanging sex, crack use, and increased HIV prevalence in these drug-using networks. Additionally, high HIV prevalence network members were more likely to be recruited in neighborhoods characterized by increased inequality, higher valued owner-occupied housing, and a greater proportion of Latinos.

Prior studies examining the “reach” of attributes (e.g., smoking, obesity, happiness, and loneliness) have consistently reported a threshold of three degrees of influence. There are several possible explanations for the difference in the degree to which networks exhibit clustered behavior. First, because HIV is infectious, its “reach” is likely greater, particularly among networks connected by drug use and in most instances drug/sex behaviors that directly facilitate HIV transmission. In this sample, these data suggest HIV was predominately acquired through sexual transmission, which is consistent with literature that suggests the HIV epidemic among drug users is primarily sustained through sexual transmission [35]. Members of high HIV prevalence networks were more likely to report exchanging sex and crack use, which has been well established in the literature [36,37].

Second, because the data were cross-sectional, we cannot determine whether high HIV prevalence network members knew each other before seroconversion or whether they met after being diagnosed. However, the number of years since first HIV diagnosis (median, 10) did not differ by group. In either case, HIV-negative individuals and others with unknown HIV status within these high HIV prevalence networks are at increased risk for HIV through high-risk sex behaviors (i.e., 94% and 51% of individuals in high HIV prevalence networks reported crack use and exchanging sex, respectively). Although it is possible that HIV-positive individuals in high HIV prevalence networks acquired HIV from high-risk behaviors with others not in these networks, their current HIV status and risk behaviors still pose a risk of transmission to their current sex and/or injecting network members (some of whom are in this dataset). The diffusion of a network-driven intervention would likely reach additional at-risk network members (including those not captured here).

Also of note, the reach of HIV more than three degrees of separation in this sample may reflect limitations in our network data. Rather than sociometric data, our data reflect RDS recruitment ties. Because individuals could only be recruited by one other person, it is possible that the number of one-degree ties is underestimated and the number of several-degree links is overestimated. Thus, individuals separated by more than one degree may be directly connected to one another, but because of the way in which network links were generated, we were unable to discern these ties. The impact of this limitation on our subsequent findings is reduced because we analyzed individuals in the same recruitment network together, rather than focusing on the relationship between social distance and HIV status. Additionally, it is possible that individuals in distinct networks knew one another, but that this was not captured in our data. This could result in misspecification of the clustering variable and consequently artificially narrow confidence estimates.

Despite the limitations of our network data, the networks in this study represent actual recruitment linkages, similar to those that would be generated with a network-driven intervention used in the field. Consequently, our findings demonstrate the feasibility of reaching HIV-positive NIDUs and HIV-at-risk NIDUs using a network-driven approach (such as RDS) and could potentially increase uptake of (1) HIV care and treatment adherence among HIV positive NIDUs, and (2) HIV testing services among at-risk

**Table 2**

Individual and neighborhood correlates of membership in a drug network with greater than expected HIV versus less than expected HIV in New York City, 2006–2009

	Greater than expected HIV (n = 52; 13.76%)	Less than expected HIV (n = 326; 86.24%)	All (n = 378)	Two-sided P
	n (%)	n (%)	n (%)	
<b>Individual-level variables</b>				
HIV positive	30 (61.22)	7 (2.32)	37 (10.54)	.000
HIV status unknown	3 (5.80)	24 (7.40)	27 (7.14)	.679
Total income >\$10,000	7 (15.22)	47 (15.11)	54 (15.13)	.985
Homeless in past 6 months	24 (46.15)	235 (72.09)	259 (68.52)	.000
<b>Race/ethnicity</b>				
Hispanic	11 (21.15)	119 (36.5)	130 (34.39)	
Black	40 (76.92)	171 (52.45)	211 (55.82)	
Other	1 (1.92)	36 (11.04)	37 (9.79)	
HIV test in the past 6 months	14 (66.67)	213 (70.07)	227 (69.85)	.743
Ever tested for an STD (herpes, gonorrhea, syphilis, chlamydia)	46 (88.46)	221 (70.83)	267 (73.15)	.008
Drug treatment in the past 6 months	26 (50)	116 (35.58)	142 (37.57)	.046
Inject	2 (3.85)	30 (9.2)	32 (8.47)	.198
Any cocaine past 6 months	31 (59.62)	257 (79.32)	288 (76.6)	.002
Any crack past 6 months	49 (94.23)	273 (84)	322 (85.41)	.052
Any heroin past 6 months	22 (42.31)	156 (48.6)	178 (47.72)	.400
Exchange sex in the past year	26 (50.98)	95 (30.06)	121 (32.97)	.003
Male	41 (78.85)	241 (74.8)	282 (74.8)	.469
High school education or more	32 (61.54)	165 (50.61)	197 (52.12)	.143
Always use condoms	16 (31.17)	98 (30.82)	114 (30.89)	.937
Ever done city time or gone to jail (short stay of ≤1 year)	34 (69.39)	234 (69.64)	268 (79.76)	.051
Ever done time upstate or gone to a state or federal prison	17 (34.69)	125 (43.55)	142 (42.26)	.246
Age, median (IQR)	35.50 (32.00, 38.50)	34.00 (29.00, 38.00)	34.50 (29.00, 38.00)	.034
Number of drug using networks, median (IQR)	1 (0, 2)	1 (0, 2)	1 (0, 2)	.429
Number of people he/she uses, Median (IQR) drugs with	1 (0, 1)	1 (0, 1)	1 (0, 1)	.452
Years HIV positive, median (IQR)	9.80 (7.43, 12.86)	11.31 (7.89, 14.25)	10.02 (7.61, 13.12)	.4983
<b>Neighborhood-level variables</b>				
	Median (IQR)	Median (IQR)	Median (IQR)	Two-sided P
<b>Minority composition</b>				
Percent Latino	20.09 (13.68, 67.27)	27.73 (13.81, 49.77)	23.64 (13.68, 49.77)	.183
Percent black	44.76 (17.56, 76.93)	55.92 (44.44, 75.78)	55.92 (44.44, 75.78)	.040
Percent white	2.50 (1.11, 3.52)	2.34 (1.13, 11.69)	2.34 (1.13, 11.67)	.362
Percent foreign born	19.85 (16.58, 30.86)	16.58 (14.51, 22.57)	16.58 (14.51, 22.87)	.339
<b>Educational attainment</b>				
Percent with bachelor's degrees and beyond (25+)	9.04 (6.01, 17.21)	6.29 (3.03, 9.87)	6.70 (3.74, 10.77)	.003
<b>Unemployment</b>				
Percent unemployed	18.32 (5.56, 19.37)	19.28 (14.98, 22.55)	19.25 (14.19, 21.10)	.012
<b>Income/poverty</b>				
Median household income	19,434 (16,148, 24,091)	15,900 (9829, 19,434)	15,900 (9829, 20,816)	.000
Percent poverty—individuals	38.54 (29.39, 47.31)	43.91 (31.19, 49.12)	43.91 (30.92, 49.12)	.039
Percent housing units vacant	10.25 (4.56, 21.06)	9.82 (5.36, 13.74)	9.86 (4.91, 13.74)	.414
Percent owner-occupied housing	7.95 (2.86, 12.99)	4.20 (1.40, 12.99)	5.38 (1.40, 12.99)	.003
Median value of owner-occupied housing	350,000 (176,250, 410,400)	177,750 (17,500, 363,200)	186,200 (17,500, 363,200)	<.001
<b>Inequality</b>				
ICE*	−0.12 (−0.28, 0.28)	−0.21 (−0.31, −0.08)	−0.21 (−0.31, −0.02)	.019
<b>Crowding</b>				
Percent crowding (>1 res/room) <sup>†</sup>	15.35 (12.82, 20.62)	14.41 (12.82, 16.25)	14.41 (12.82, 17.62)	.030

ICE = index of concentration at the extremes; IQR = interquartile range; STD, = sexually transmitted disease.

\* ICE =  $\frac{(\# \text{households in a census tract with incomes} > \$100,000) - (\# \text{households in a census tract with incomes} < \$20,000)}{\# \text{households in the census tract with income data}}$  [50].

† Occupied housing units with &gt;1 person/room are considered crowded.

HIV-negative NIDUs, particularly in neighborhoods that are most vulnerable.

We also observed an association between homelessness and membership in high HIV prevalence networks; however, it was not in the expected direction. In prior studies among IDUs, homelessness was associated with increased HIV prevalence and HIV-related risk behaviors; this relationship is thought to result from fewer socioeconomic resources, inadequate access to medical care, and reduced treatment adherence [38,39]. The fact that individuals with HIV/AIDS in New York are provided with housing services by the HIV/AIDS Services Administration (HASA) may in part explain the observed inverse association between homelessness and HIV prevalence [40]. HASA, which is within the New York City Human Resource Association, is among the most comprehensive government programs serving people living with HIV/AIDS in the world.

However, in November 2011, HASA started to enforce mandatory drug treatment for drug users applying for and living in HASA housing. Thus, data collected after 2011 should be explored with respect to homelessness.

Members of high HIV prevalence networks were also more likely to have been recruited in neighborhoods with a greater proportion of Latino residents. To better understand these findings, we mapped the data using ArcGIS and the association between being recruited in a neighborhood with a higher percent Latino population and membership in a drug using network with a higher prevalence of HIV seemed to be driven by those individuals who were recruited in the Bronx, which has a greater concentration of Latino residents than other New York City boroughs where participants were recruited. Although there were fewer participants recruited in the Bronx than in other New York City boroughs, most were members

**Table 3**  
Individual and neighborhood correlates of membership in a drug network with greater than expected HIV versus less than expected HIV in New York City, 2006–2009

	Odds ratio	95% Confidence interval
Individual-level variables		
Total income >\$10,000	1.01	0.48, 2.11
Homeless in past 6 months	0.33	0.20, 0.55
Race/ethnicity		
Hispanic	3.33	0.32, 35.14
Black	8.42	0.96, 73.85
Other	Ref	Ref
HIV test in the past 6 months	0.85	0.44, 1.65
Ever tested for an STD (herpes, gonorrhea, syphilis, chlamydia)	3.16	1.67, 5.98
Drug treatment in the past 6 months	1.81	1.18, 2.79
Injection	0.39	0.16, 0.99
Any cocaine past 6 months	0.38	0.17, 0.85
Any crack past 6 months	3.11	1.23, 7.84
Any heroin past 6 months	0.78	0.35, 1.73
Exchange sex in the past year	2.42	1.42, 4.11
Male	1.30	0.50, 3.38
High school education or more	1.56	1.04, 2.35
Always use condoms	1.03	0.56, 1.89
Age	1.07	0.99, 1.15
Neighborhood-level variables		
Minority composition		
Percent Latino*	1.29	0.98, 1.69
Percent black*	0.60	0.30, 1.19
Percent white*	1.35	0.64, 2.83
Percent foreign born*	0.95	0.72, 1.25
Educational attainment		
Percent with bachelor's degrees and beyond (25+)*	1.85	1.31, 2.63
Unemployment		
Percent unemployed*	0.80	0.58, 1.10
Income/poverty		
Median household income*	2.36	1.48, 3.77
Percent poverty—individuals*	0.81	0.57, 1.14
Percent housing units vacant*	1.07	0.84, 1.36
Percent owner-occupied housing*	0.75	0.58, 0.97
Median value of owner-occupied housing*	1.40	1.13, 1.76
Inequality		
ICE†	3.68	1.33, 10.20
Crowding		
Percent crowding (>1 res/room)*‡	1.49	1.02, 2.19

ICE = index of concentration at the extremes; IQR = interquartile range; STD, = sexually transmitted disease.

\* Standardized by z-score.

†  $ICE = \frac{(\#households\ in\ a\ census\ tract\ with\ incomes\ >\ \$100,000) - (\#households\ in\ a\ census\ tract\ with\ incomes\ <\ \$20,000)}{\#households\ in\ the\ census\ tract\ with\ income\ data}$  [50].

‡ Occupied housing units with >1 person/room are considered crowded.

of high HIV prevalence drug-using networks and were recruited in census tracts with a greater concentration of Latino residents. We therefore hypothesized that this association could be partially explained by the New York–Puerto Rico “airbridge” in the Bronx, which is characterized by high-risk illicit drug users from Puerto Rico who migrate to New York and typically reside in Latino neighborhoods. Recent migrants from Puerto Rico typically represent a higher risk group with an increased burden of HIV compared with Latinos and other groups born in New York City and those engaging in high-risk drug and sex behaviors with these individuals are also at increased risk for HIV acquisition [41–44].

Individuals in drug-using networks with a higher prevalence of HIV were also more likely to be recruited in neighborhoods with greater inequality, which is consistent with prior research findings [15,16]. Our data also revealed that members of drug-using networks with a higher prevalence of HIV were more likely to be recruited from neighborhoods with higher valued, owner-occupied property. The association between high HIV prevalence networks and both (1) income inequality and (2) higher valued, owner-occupied property may at first seem paradoxical. However, this is consistent with the impact of the New York–Puerto Rico airbridge and expanding gentrification in low-income, black, and Latino

neighborhoods in New York City [45]. Researchers have suggested that, in the presence of heightened income inequality during periods of gentrification and migration of marginalized Puerto Rican communities into New York City neighborhoods, relatively high rates of property ownership and income inequality could coexist [46,47]. More detailed investigation of HIV network clusters in Latino neighborhoods that focus on aspects of migration are needed to support this explanation and/or elucidate other possible explanations.

Other drawbacks also require some discussion. Because HIV status was measured via self-report, those reporting unknown or negative status may have been HIV positive but unaware of or unwilling to disclose their HIV status. However, self-reported unknown HIV status was not different by group. Additionally, of the 27 individuals who reported unknown HIV status, 12 reported that he/she had never been tested for HIV, 5 had been tested for HIV (but not in the past 6 months), and 11 refused to answer any questions about their HIV testing history. Prior studies suggest that the growing prevalence of HIV among NIDUs may be partially owing to overlapping sexual partnerships between NIDUs and IDUs [35,48,49]. Owing to our eligibility criteria, (1) our findings are generalizable only to the target population and (2) information on

**Table 4**

Final multivariable logistic regression with robust Huber–White standard error estimates clustering on respondent-driven sampling recruitment network membership, New York City (2006–2009)

	Adjusted odds ratio	95% Confidence interval
Individual-level variables		
Exchange sex in the past year	1.82	1.03, 3.23
Any crack past 6 months	7.23	2.43, 21.55
Homeless in past 6 months	0.32	0.17, 0.57
Any cocaine past 6 months	0.40	0.20, 0.79
Drug treatment in the past 6 months	1.62	1.05, 2.50
Neighborhood-level variables		
Percent Latino*	1.83	1.19, 2.80
Median value of owner-occupied housing*	1.48	1.14, 1.92
ICE (Index of concentration at the extremes) <sup>†</sup>	5.85	1.40, 24.42

ICE = index of concentration at the extremes.

\* Standardized by z-score.

$$\dagger \text{ICE} = \frac{(\#\text{households in a census tract with incomes} > \$100,000) - (\#\text{households in a census tract with incomes} < \$20,000)}{\#\text{households in the census tract with income data}} [50].$$

all relevant network relationships may not be captured. For example, study participants may engage in high-risk sex with HIV-positive individuals not recruited/eligible for START; however, this is also likely to be the case in other network-based studies. Finally, individuals may have selectively engaged in high-risk drug and sex practices with individuals of the same serostatus. However, given the high number of HIV-positive individuals observed in the high HIV prevalence networks, the HIV-negative individuals in these drug networks (both those enrolled and not enrolled in START) are likely at an increased risk for disease acquisition compared with those in lower prevalence drug using networks. As noted, network-based interventions could effectively reach members of high HIV prevalence drug use networks who were and were not enrolled in the study through diffusion.

Despite the limitations discussed, our findings highlight the interplay between network and neighborhood correlates of HIV and drug/sex risk behaviors and can be used to guide the development of more effective interventions to reduce health disparities. Interestingly, individuals in high HIV prevalence networks were more likely to have recently been enrolled in drug treatment, which suggests a venue for targeted interventions. Our data also suggest that the influence of HIV may extend beyond six degrees of separation. Thus, network-driven approaches, which also take features of the social/structural environment into account, may be appropriate to reduce HIV transmission and/or to support care seeking and HIV drug adherence for HIV-positive individuals, but further research is needed to better characterize neighborhood factors associated with HIV-clustering among drug-using populations in New York City.

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