Simple estimators for network sampling

Steve Thompson

1 Department of Statistics and Actuarial Science, Simon Fraser University, Burnaby, British Columbia, Canada

* thompson@sfu.ca

Abstract

A new estimation method is presented for network sampling designs, including Respondent Driven Sampling (RDS) and Snowball (SB) sampling. These types of link-tracing designs are essential for studies of hidden populations, such as people at risk for HIV. The simple idea behind the new method is to run a fast-sampling process on the sample network data to estimate the inclusion probabilities of the actual survey, and incorporate those in unequal probability estimators of population means and proportions.

Improved versions of the usual RDS and SB designs are also proposed, termed RDS+ and SB+, to obtain information on more of the within-sample links. In simulations using the network from the Colorado Springs study on the heterosexual spread of HIV, the new estimators produce in most cases lower bias and lower mean square than current methods. For the variables having the largest mean square errors with current estimators, the improvement with the new estimator is dramatic. The estimates are improved even more with the enhanced design versions. For estimating the population mean degree, the efficiency gains using he new method are 29 for RDS, 54 for RDS+, 26 for SB and 80 for SB+. This means for example, with the ordinary RDS design, the mean square error with the new estimator, same data, is 1/29 that of currently used estimators.

The new method is computationally intricate but is fast and scales up well. The new estimation method can be used to re-analyze existing network survey data. For new network sampling studies, it is recommended to use the improved designs as well as the new estimators.

Author summary

This paper presents new estimators of characteristics of hidden and hard-to-reach populations using data from network sampling designs. Network sampling designs such as Respondent-Driven Sampling and snowball sampling are important for studying hidden populations including key populations with high exposure to the HIV epidemic through drug injecting or sexual links. These surveys are essential for the understanding needed to bring relief to those affected and to reduce or end the epidemic.

Evaluations of the new estimators are carried out using data from a large-scale network study of a high-risk population. The new method produces more accurate estimates of population values in most cases compared to currently used methods. The increase in accuracy is achieved by eliminating most of the bias. The reason for the better performance of the new estimators is that they do not rely on unrealistic assumptions used by other estimators about how the sample is selected in the real world.
Instead, the new estimator uses a fast sampling process, similar to the real-world design, on the sample network data to estimate the relative probability of each person being included in the sample. These inclusion probability estimates are used in estimates of population characteristics.

Introduction

Network sampling consists of designs which at least in part follow network links from units already in the sample to add connected units to the sample. The fundamental problems in network sampling are to find the best designs for a given situation and then, given the sample data, to find effective inference methods for estimating characteristics of the population. Network sampling methods have long been used to investigate hidden and hard-to-reach populations, and in many cases provide the only feasible means to sample such a population. In this paper I introduce new simple estimators for inference from network samples that work for a variety of network sampling designs including the types most widely used.

The HIV/AIDS pandemic has provided motivation for the development and use of network sampling methods. The most recent UNAIDS report estimates that 36.9 million people worldwide are living with HIV, with 1.8 million new infections and 940,000 AIDS-related deaths annually. Academic work and public funding of research into network sampling methods for key populations at risk have increased dramatically since the late 1990s. A recent systematic review found over 460 peer-reviewed papers on Respondent Driven Sampling surveys, not including methodology studies, in 69 countries worldwide. Another recent paper reported finding 642 academic articles on Respondent-Driven Sampling. A search of the NIH funded grant database in 2012 found that over $100 million had been provided for grants with “Respondent-Driven Sampling” in the title or key words, while by 2015 the figure exceeded $180 million in NIH funding. Many of the actual RDS studies have been funded by the U.S. President’s Emergency Plan for AIDS Relief (PEPFAR) and the Centers for Disease Control and Prevention.

The potential benefit of these network sampling surveys in these key populations is huge. These link tracing methods provide the means to get into these hard to reach populations, to understand the biological and behavioral factors that enhance or inhibit the virus. Most of these surveys include a bioassay component, with saliva or blood samples taken, tested for HIV and other infections such as HSV2, and sometimes sequenced for HIV strain. In addition, the link-tracing samples find there way into the parts of the population where the spread of the virus is most explosive and hard to eradicate. These surveys bring with them interventions, such as HIV testing, referral for antiretroviral prescriptions, counseling, and condoms, to the people most in need of them. The understanding from these surveys is central to efforts to contain and bring down the epidemic globally. Estimates from these surveys provide essential input for simulations of the HIV epidemic and evaluations of intervention programs.

The simple idea behind the new estimates is to run a fast-sampling process, similar to the actual sampling design, on the sample network data, and use the fast-sample inclusion frequencies to estimate the unknown survey-inclusion probabilities and thereby estimate the population values. In effect the new method explores computationally the sample network topology to full full depth and weights each observation using all the network paths leading to that node, path-lengths affecting weights and redundant pathways lending increased weight. In contrast, the most widely used current methods either do not use the sample network data at all, using self reported degree instead, or using only the first-step depth of the sample network data by comparing numbers of connections within and between sets of nodes.
For computation there are two approaches to implementing the simple idea. One is to sample the network data repeatedly with a link-tracing design similar to the original design, from seed selection to target sample size. Because the design is without replacement, a smaller sample size needs to be used than was used in the original design. In this approach a sequence independent samples are selected, each one proceeding from seeds to target sample size. The second approach is to construct a sampling process that selects a sequence of samples that are not independent but have selection properties similar to the original design. These approaches are described in detail in the Methods section.

The inference method described in this paper uses data from network sampling designs such as Respondent Driven Sampling (RDS) and Snowball (SB) designs and produces estimates and confidence intervals for population means and proportions of the survey response variables. No assumptions are made about the population network. Instead, information about the network is extracted from the sample network data, that is, the data on links between sample nodes. From the sample network data the relative inclusion probabilities of the sample nodes are estimated, and design-based estimates of population values are made from those. Improved versions of the RDS and SB designs, termed RDS+ and SB+, are also proposed in this paper. The improved designs increase the number of sample links in the data, resulting in better estimates for little additional effort in data collection.

The basic difficulty for inference from link-tracing sampling designs is that the sampling procedure selects different units with different probabilities, depending on the unit’s place among the links of the population network. A widely used and much-studied estimator for use with unequal probability designs is the generalized unequal probability estimator (GUPE) \[5\], which divides each sample unit’s value by the unit’s inclusion probability and normalizes by the sample sum of the reciprocals of the inclusion probability. With most of the network sampling designs that are actually used for hidden populations, the inclusion probabilities are unknown and depend on network links beyond the sample data.

In practice modern network sampling designs for hidden populations work by handing out coupons to each person recruited into the sample, with which they can recruit people to whom they are linked. When any person comes in with a coupon, they are paid a small honorarium, as is the person who gave them the coupon. After being interviewed and in some cases undergoing medical tests, the new recruit is in turn given coupons with which to recruit new sample members. This process continues until target sample size is met. With RDS designs the number of coupons is usually limited to a small number such as 2 or three. With snowball designs the number of coupons given equals the number of partners reported, or else a high coupon limit is set, such as 15 or 25. The survey is started out with an initial sample, or “seeds” selected by survey personnel.

For a one-wave snowball design \[6\] offered a number of design-based and model-based approaches to estimating the size of a hidden population. For RDS surveys, Salganik and Heckathorn (SH) \[7\] introduced an estimator for mean degree which uses the form of the GUPE but with degree \(d_i\) of node \(i\) replacing the inclusion probability \(p_i\). This was based on the assumption that the recruitment process by which the sample was selected was similar to a with-replacement random walk, producing a Markov chain in which the current state of the chain is the currently selected node and on the assumption that the population network consisted of only a single connected component. Using a separate assumption that the sequence of selections having the attribute and not having the attribute was also a Markov chain they arrived at an estimator of the proportion of the population having the attribute. That estimator, in addition to using the self-reported degrees, uses the proportion of recruitment links
leading out from a group that go to the other group. In this way, their estimator uses information from the sample network link data, in addition to the sample node data such as attribute value and degree of a node. Heckathorn [8] extends that method to estimate the several proportions of a categorical variable and to estimate the group mean of a continuous variable.

The Volz-Heckathorn estimator (VH) [9], using the random walk approximation for the sampling design and assuming a single component in the population, uses the form of the GUPE with degree in place of inclusion probability for estimates of means of all types of node variables, whether attribute or more general numeric. This estimator does not use any of the recruitment link or other sample network data, only the node variable of interest and the node reported degree. The VH estimator is currently the most commonly used estimation method used with RDS surveys.

The Successive Sampling estimator of Gile [10] improves on the VH estimator for samples in which sample size $n$ is a substantial fraction of population size $N$. The improvement is based on the fact that the real sampling is done without replacement. The effect of the sampling fraction $n/N$ is adjusted for using a stochastic sampling algorithm to estimate the inclusion probabilities with a successive sampling without-replacement design in which at the $i$-th selection a node is selected with probability proportional to degree from among all units not already selected in the first $i-1$ steps. This procedure involves estimating iteratively the unit degrees in the whole population of size $N$, and therefore it requires knowledge or an estimate of population size $N$. The estimated inclusion probabilities $\hat{\pi}_i$ are then used in the GUPE form to estimate population means and proportions, for any type of node variable. When sample fraction $n/N$ is small, this estimator defaults to the VH estimator. A simple network model called the configuration graph model, which takes any arbitrary fixed degree distribution and randomly connects the link ends, is used to motivate the SS model.

Fellows [11] introduces the Homophily Configuration Graph model, which for an arbitrary degree distribution allows the linkage probabilities to depend on attribute memberships. This model motivates the Homophily Configuration Graph Estimator (HCG), which uses the attribute variable group membership in a manner similar to SH and adjusts for large sampling fraction with the SS method. The method uses recruitment link data as in the SH and requires an estimate $\hat{N}$ as in SS. Fellows shows that the SH method works well under the configuration graph model and that HCG estimator works well under the homophily configuration graph model. Simulations show the method works well under homophily configuration graph model realizations as expect. It also works well for the attribute variables of the empirical Project 90 network, which is also used in the present paper, though he uses for the simulation only the largest connected component from that network. The method is described for estimating the mean of an attribute variable, which is the population proportion of that variable, as uses the estimate from the recruit links of transitions between the groups with the attribute and without.

Confidence interval methods commonly used with RDS designs include the Salganik bootstrap [12] for SH and VH, the Gile SS bootstrap [10] for SS. A recent evaluation of these methods, for means of binary variables and using simulations based on a statistical network model fitted to RDS data is [13]. A different bootstrap approach for RDS data called a Tree Bootstrap is described in [14].

Estimation methods based on the VH estimator are based on node degrees. The SH estimator goes one step further into the sample network by using the proportion of links within a group to the number going out from that group. In contrast the methods in [15], [16], and [17] use the full sample network. Minimally, the sample network includes only those links within the sample that were used in recruitment, plus the counterpart edge in the other direction to symmetrize the link. The more full version of
the sample network uses the set of all links that connect sample nodes. [15] requires the full sample subgraph in order to apply the Rao-Blackwell method to improve an initial unbiased estimator. [16] gives a method for estimating the sample subgraph from the recruitment graph, and [17] uses that estimated subgraph, together with an assumed model, to estimate the size of a hidden population. The method proposed here uses whatever sample network information is available. If that is only the recruitment graph, that alone is used in estimation. No attempt is made to estimate the sample subgraph. Estimation efficiency is improved if more within-sample links are known. These are the enhanced versions of the estimators. The best estimators result from designs which reveal all the within-sample links.

The methods such as VH, SH, SS, and HCG that use underlying Markov chain assumptions about the sampling design address estimation only with RDS type of designs using small numbers of coupons per participant, such as 2 or 3, limiting the number of recruits each recruiter can bring in. More general snowball types of designs, which issue as many coupons as the reported number of partners or sets a high maximum coupon limit such as 15 or 25, have not been addressed or evaluated for those methods. Each of the methods above, SH, VH, SS, and HCG uses in part the reciprocal of reported degree based on an approximating random walk assumption, so that each is related to the VH estimator. For estimating mean degree, SH defaults to VH. With large population size in relation to sample size, SS defaults to VH. And for estimating mean degree with large population relative to sample size, HCG defaults to VH.

The new method of inference proposed here works for any of the commonly used network sampling designs. This includes the snowball-like designs as well as the small-coupon-number designs. The new method estimates the population means or proportions of all types of variables in the same way, whether they are continuous, integer, or binary valued. It does not assume a network model producing networks with particular properties, nor does it assume the population network contains only one connected component. It does not assume the sampling design is similar to a with-replacement random walk design, nor that population values of variables of interest (node y-values) have any particular pattern or that the selected sequence of those values has Markov-chain properties.

Instead, the new method uses the sample network data and examines computationally its network topology. That is, it examines the patterns of connectedness in the links part of the sample $E_s$, and with a fast sampling process calculates the inclusion frequencies of those units in a network sampling design. The inclusion probability of a node $i$ is high if a lot of paths lead to it from other nodes. Multiple or redundant paths to it increase it’s probability of being included. The probabilities are influenced by the lengths of the different paths and by the inclusion probabilities of the other nodes on those paths. Further, the exact inclusion probabilities for units in the sample depend on sample paths that come in from wider network outside of the sample. So a fast sampling process restricted to the sample network, using link-tracing similar to the original design, is used. The long-term relative inclusion frequencies with the fast-sampling process are used as estimates of the relative inclusion probabilities. And these estimated inclusion probabilities are used to estimate the population characteristics.

The method is computationally efficient and scales up extremely well to larger sample sizes. In the simulations the new method gives better estimates of population values in most cases, compared to the compared to other estimators, and in some important cases the estimates are many times better with the new method. The estimates are in most cases better still with the improved improved (“plus”) versions of the network sampling designs.

In the empirical simulations of this paper the new estimators perform in most cases
better than the VH estimator, in terms of bias and mean square error. In some important cases, such as for estimating population mean degree, the new estimators perform very much better. The substantial bias of the VH estimator arises largely from the discrepancy between node degree and the actual inclusion probability of a node. This discrepancy in turn arises from the difference between an assumed with-replacement random walk in a strongly connected graph and the actual recruitment process used in surveys of hidden populations. The actual survey design is without-replacement, and with more than one coupon the selection process branches. The population network tends to have more than one component rather than being strongly connected. \[18\] and \[19\] call attention to the biases arising from these unrealistic assumptions. The methods of \[10\] and \[11\] serve to reduce the part of the without-replacement bias for the case of large sampling fractions. Even with a relatively small sample fraction as in the simulations of this paper, the without-replacement sampling and branching pattern produce marked differences from the random walk assumptions. While the bias of the VH estimator is higher with the snowball designs than with the small-coupon-number designs, it is large with both.

The new estimators do not rely on assumptions about Markov chain properties of the recruitments or transitions between respondent values, nor do they depend on the network having only one connected component. Instead, the new estimators explore the sample network data empirically. The exploration is done by selecting a sequence of samples from the network data using a fast sampling process having features similar to the real sample selection design. These features include branching, without-replacement selections, and a small rate or reseeding to be sure the sample does not get stuck in any single connected component.

By using the fast process that is similar to the real design and exploring with it the paths of all lengths reaching to and from each unit, the new estimators get more accurate estimates of the inclusion probabilities, which greatly reduces the bias of the estimates of population characteristics. Existing network survey data can be reanalyzed to obtain better estimates using the new estimators. For future surveys, the proposed data collection enhancements which provide information on additional within-sample links produce further estimation improvements. Considering the costs and benefits of these surveys worldwide, these improvements are well worth pursuing.

**Network sampling designs**

A network sample has the form

$$s = (U_s, E_s)$$

where \(U_s\) denotes the units, or nodes, in the sample and \(E_s\) denotes the edges, or links, in the sample. (“Nodes” and “Units” are used interchangeable, as are “edges” and “links” in this paper.) Edges may be directional or symmetric.

A network sampling design is a procedure for getting such a sample from a population. Usually edges are discovered through observing or interviewing sample nodes, and edges may be traced to add more nodes to the sample. The traced edges become part of the edge part of the sample. Additional within-sample edges, beyond those used for recruitment, can also be added to the sample by various means.

Two types of network sampling designs in current use for hard-to-access human populations include Respondent Driven Sampling (RDS) and Snowball Sampling (SB). In RDS, 1. a sample of initial units called “seeds” are selected by some means; 2. each member of the sample is given a small number of coupons, like two or three, with which to recruit new people who are connected to the sample member by the type of edge relationship of interest; 3. Those recruits who come in are themselves given coupons
with which to recruit additional people, and sampling continues until a target sample size is reached.

In Snowball Sampling designs, 1. a sample of seeds is selected; 2. each sample member is given as many coupons as their number of partners, or up to some high limit such as 15 or 25; 3. sampling continues until target sample size is reached.

The sample of nodes in these network designs applied to human populations includes the seeds and the people recruited in the subsequent waves of sampling. The data collected on these sample members includes interview responses on demographics and behavior and biological assay results such as results of blood or saliva tests for infections.

The sample of links includes all the relationships known between sample members. In ordinary RDS and Snowball sampling protocols, the only links known sample members are those links used in recruitment. So $E_s$ consists only of recruitment links. In this paper we consider also two enhancements of these designs, termed RDS Plus. In RDS plus, an RDS sample of nodes is selected and extra effort is made to obtain information on as many of the other links between sample members. Similarly, with the SB Plus design, additional effort is made to find the additional within-sample links. The Plus version of each design type obtains the same sample $U_s$ of nodes, but a larger sample $E_s$ of links.

A number of procedures have been used in surveys for discovering the additional within-sample links. For instance, 1. multiple recruitments of a person by different recruiters can be allowed in the protocol, revealing additional within-sample links without having to do repeat interviews. 2. Unique identifiers of partners can be obtained and made anonymous but revealing more links than revealed through recruitments. An example of such a procedure is asking each sample member for names or phone numbers of partners, as well as their own name or phone numbers. The names or phone numbers can be changed to code values and the code values matched up to provide sample links. An effective anonymizing system for such unique identifiers is described by Fellows (2012) [20]. 3. Intensive in-community ethnographic or epidemiological field work can trace out and identify the individuals at both ends of partnership links, as has been done in studies of hard to access populations such as the Project 90 study providing the data for the evaluation simulations in this paper. The field ethnographic methods identify names of partners, with the actual names later being removed from the data, replaced by arbitrary ID numbers informative only within the data set.

**Fast sampling process**

Given the network sample $s = \{U_s, E_s\}$ obtained from the real world network sampling design, we obtain a sequence of fast samples

$$\{S_1, S_2, S_3, \ldots, S_T\}$$

from the network data using a fast-sampling process similar to the original design. $T$ is the number of iterations.

For unit $i \in U_s$, there is a sequence of indicator random variables:

$$\{Z_{i1}, Z_{i2}, Z_{i3}, \ldots, Z_{iT}\}$$

where $Z_{it} = 1$ if $i \in S_t$ and $Z_{it} = 0$ if $i \not\in S_t$, for $t = 1, 2, \ldots, T$, the number of iterations of the sampling process.

The average

$$f_i = \frac{1}{T} \sum_{t=1}^{T} Z_{it}$$
is used as an estimate of the relative inclusion probability of unit $i$ in the similar design used to obtain the data from the real world. If the real-world network design is done without replacement, then the fast-sampling process is also carried out without replacement.

In the first approach, each sample in the sequence proceeds from selection of seeds to target sample size. With this approach the samples in the sequence $\{S_1, S_2, S_3, ..., S_T\}$ are independent of each other.

In the second approach, some seeds are selected in the beginning and then each subsequent sample $S_t$ is selected dependent on the one before it, $S_{t-1}$. To get from $S_t$ to $S_{t-1}$ we probabilistically trace links out from $S_t$, randomly drop some nodes from $S_t$, and may with low probability select one or more new seeds. Theoretical advantages of the second approach are first, that the computation can be made very fast. Second, the sampling process is fast-mixing and once it reaches it’s stationary distribution every subsequent sample $S_t$ is in that distribution. The stationary distribution of the sequence of samples represents a balance between the re-seeding distribution, which can be kept small with a low rate of re-seeding, and the design tendencies arising from the link-tracing and the without-replacement nature of the selections.

In the independent sample approach, on the other hand, at each iteration new seeds are selected. Usually the seed selection is from a distribution that is different from the stationary distribution, so some number of waves of link tracing is needed to get closer to the probabilities of the original design. Even when target sample size is reached it may still be in a different distribution from the original sample selection procedure because, with the necessarily smaller sample size, the independent sample from the sample network data is not able to go as many waves.

Neither of the two computational implementation approaches can be expected to be precisely unbiased, in the design-based sense, because of the target sample size smaller than the actual sample size with the without-replacement sampling, and because the generalized unequal probability estimator, as a generalized ratio estimator, not being precisely unbiased even when the true inclusion probabilities are known. The implementation of the independent, repeated sample selection approach is straightforward based on the recruitment protocol of the original design. Because the fast sampling process approach is less familiar, it is described in more detail here.

For the fast sample process $S_t$, instead of selecting an entire sample from seeds to target sample size, the approach is to set up a sampling process. For the sampling process we start with seeds at iteration $t = 0$ and at each subsequent iteration a few links may be traced from the links out from $S_t$ and a few nodes removed from $S_t$ to obtain $S_{t+1}$. Tracings and removals are done with constant small probability and are independent, given current sample size. However, removals are only done if the sample size of $S_t$ is above target, and then with probability calculated to give an expected number of removals to go back to target.

Specifically, in the examples we trace the links out from the current sample $S_t$ independently, each with probability $p$. Nodes are removed from the sample independently with probability $q$. The removal probability $q$ is set adaptively to be $q_t = (n_t - n_{target})/n_t$ if $n_t > n_{target}$ and $q_t = 0$ otherwise, so that sample size fluctuates around its target during iterations. Sampling is without replacement in that a node in $S_t$ is not reselected while it remains in fast sample, but it may be reselected at any time after it is removed from the fast sample.

With this procedure, the sequence of fast samples $S_1, S_2, ...$ forms a Markov chain of sets, with the probability of set $S_t$ depending only on the previous set $S_{t-1}$. The sampling process is fast mixing, with the sample size fluctuating stochastically around the target.

The inclusion-indicator average $f_i$ converges in probability to the inclusion
probability for unit \( i \) in the fast-sample design process by the weak law of large numbers for Markov chains. These in turn approximate the inclusion probabilities of the real design to the extent that the sampling process design is similar to the real design. The effectiveness of this approximation must be evaluated with simulations, as is done in the next section.

Alternatively, one can use a fast design that is with replacement. An advantage of this is that a target sample size for the fast design can be used that equals the actual sample size used in obtaining the data. A disadvantage of using a with-replacement fast design is that in many situations the real design by with the data are collected is without-replacement.

If the fast-sample design is with replacement, let \( M_t(i) \) be the number of times node \( i \) is selected at iteration \( t \). The quantity \( g_i = (1/t) \sum_{t=1}^{t} M_t(i) \), the average number of selections up to iteration \( t \), estimates the expected number of selections for node \( i \) under the with-replacement design at any given iteration \( t \).

Fast sampling processes of these types are discussed in [21] and [22] for their potential uses as measures of network exposure of a node, or a measure of network centrality, or a predictive indicator of regions of a network where an epidemic might next explode. Calculation of the statistic \( f_i \) for each unit in the network sample can be used as an index of the network exposure of that unit. A high value of \( f_i \) indicates the unit has high likelihood of being reached by a network sample such as ours. It will also have a relatively high likelihood of being reached by a virus, such as HIV, that spreads on the same type of links by a link-tracing process that is broadly similar. A given risk behavior will be more risky for a person with high network exposure. For a person in a less well connected part of the network, the same behavior carries lower risk. Since a purpose of the surveys is to identify risk characteristics, an index of network exposure measures another dimension of that risk, beyond the individual behavior and health measures. Here, however, are interested in their usefulness for estimating population characteristics based on link-tracing network sampling designs.

### Estimators

The network sampling designs considered here select units with unequal probabilities. With unequal probability sampling designs, sample means and sample proportions do not provide unbiased estimates of their corresponding population means and proportions.

To estimate the mean of variable \( y \) with an unequal-probability sampling design, the generalized unequal probability estimator has the form

\[
\hat{\mu}_{\text{GUPE}} = \frac{\sum_y (y_i / \pi_i)}{\sum_y (1/ \pi_i)}
\]

where \( \pi_i \) is inclusion probability of unit \( i \).

With the network sampling designs of interest here, the inclusion probabilities \( \pi_i \) are not known and can not be calculated from the sample data. To circumvent this problem the Volz-Heckathorn Estimator uses degree, or self-reported number of partners, to approximate inclusion probability.

\[
\hat{\mu}_{\text{VH}} = \frac{\sum_y (y_i / d_i)}{\sum_y (1/ d_i)}
\]

in which \( d_i \) is the degree, the number of self-reported partners, of person \( i \).

The rationale for this approximation is that if the sampling design is a random walk with replacement, or several independent random walks with replacement and the
population network is connected, then the selection probabilities of the random walk design will converge over time to be proportional to the \( d_i \). Here connected means that each node in the population can be reached from any other node by some path, or chain of links, so that the population network consists of only one connected component. Biases in this estimator result from the use of without-replacement sampling in the real-world designs, the use of coupon numbers \( k \) greater than 1 making the design different from a random walk, population networks being not connected into a single component, or slow mixing due to specifics of the population network structure.

The simple idea of the new estimators proposed here is to run a fast sampling process similar to the real design on the sample network data. Then use the fast-sample inclusion frequencies to estimate the relative inclusion probabilities of the sample units. The sample network data is the link part of the network sample.

The simple estimator, with a non-replacement sampling design, is

\[
\hat{\mu} = \frac{\sum_{i \in s} (y_i / f_i)}{\sum (1 / f_i)} \tag{4}
\]

where there is no ambiguity we write \( i \in s \) for the summation over the nodes in the sample, rather than the more explicit \( i \in U_s \), and where \( f_i \) is inclusion frequency of the fast-sampling process run on the sample network data.

A simple variance estimator to go with the simple estimator is

\[
\hat{\text{var}}(\hat{\mu}) = \frac{1}{(\sum_{i \in s} 1 / f_i)^2} \sum_{i \in s} \frac{(y_i - \hat{\mu})^2}{f_i^2} \tag{5}
\]

An approximate \( 1 - \alpha \) confidence interval is then calculated as

\[
\hat{\mu} \pm z \sqrt{\hat{\text{var}}(\hat{\mu})} \tag{6}
\]

with \( z \) the \( 1 - \alpha/2 \) quantile from the standard Normal distribution.

The variance estimator is based on, and simplified from, the Taylor series linear approximation theory for generalized unequal probability estimator. Linearization leads to the estimator of the variance of the generalized estimator

\[
\hat{\text{var}}(\hat{\mu}_{\text{GUPE}}) = \frac{1}{(\sum_{i \in s} 1 / \pi_i)^2} \sum_{i \in s} \sum_{j \in s} \hat{\Delta}_{ij} \frac{(y_i - \hat{\mu}_{\text{GUPE}})(y_j - \hat{\mu}_{\text{GUPE}})}{\pi_i \pi_j} \tag{7}
\]

where

\[
\hat{\Delta}_{ij} = \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}}
\]

where \( \pi_{ij} \) is the joint inclusion probability for units \( i \) and \( j \). A good discussion of the approach is found in [23], with this variance estimator on p. 178 of that work.

Consider an estimator of the variance using the full variance expression with the fast-sample frequencies \( f_i \) in place of the \( \pi_i \) and, in place of the joint inclusion probability \( \pi_{ij} \), the frequency \( f_{ij} \) of inclusion of inclusion of both units \( i \) and \( j \) in the fast sampling process. This would give

\[
\hat{\text{var}}(\hat{\mu}) = \frac{1}{(\sum_{i \in s} 1 / f_i)^2} \sum_{i \in s} \sum_{j \in s} \hat{\Delta}_{ij} \frac{(y_i - \hat{\mu})(y_j - \hat{\mu})}{f_i f_j} \tag{8}
\]

where

\[
\hat{\Delta}_{ij} = \frac{f_{ij} - f_i f_j}{f_{ij}}
\]
The double sum in the variance estimate expression will have \( n(n-1)/2 \) terms in which \( i \neq j \). The most influential of these terms are the ones in which the joint frequency of inclusion \( f_{ij} \) is relatively large. Because of the link tracing in the fast sampling process, sample unit pairs with a direct link between them will tend occur together more frequently than those without a direct link. An estimator using only those pairs with known links between them in the sample data would be

\[
\hat{\sigma}^2(\hat{\mu}) = \frac{1}{(\sum_{i \in S} 1/f_i)^2} \left( \sum_{i \in U_s} \left( f_i - 1 \right) \frac{(y_i - \hat{\mu})^2}{f_i} - \sum_{(i,j) \in E_s} \Delta_{ij} \frac{(y_i - \hat{\mu})(y_j - \hat{\mu})}{f_i f_j} \right)
\]  

(9)

where \( E_s \) is the sample edge set. That is, \( E_s \) consists of the known edges \((i,j)\) between pairs of units in the sample data. In general the size of the sample edge set \( E_s \) will be much smaller than the \( n^2 \) possible sample node pairings \((i,j)\), or the \( n(n-1)/2 \) pairings with \( i \neq j \), where \( n \) is the sample size.

A further simplification and approximation for estimating the variance of the estimator is to use only the diagonal terms, that is,

\[
\hat{\sigma}^2(\hat{\mu}) = \frac{1}{(\sum_{i \in S} 1/f_i)^2} \sum_{i \in S} \frac{(1-f_i)(y_i - \hat{\mu})^2}{f_i}
\]  

(10)

Dropping the coefficients \((1-f_i)\), each of which is less than or equal to one, gives an estimate of variance that is larger, leading to wider, more conservative confidence intervals.

If the real-world network sampling design and correspondingly the fast sampling process are with replacement, the estimator of \( \mu \) is

\[
\hat{\mu} = \frac{\sum_{i \in S} m_i y_i / g_i}{\sum_{i \in S} m_i / g_i}
\]  

(11)

in which \( m_i \) is the number of times unit \( i \) is selected in the real design and \( g_i \) is the average number of selection counts of unit \( i \) in the fast sampling process.

With a with-replacement fast design the corresponding variance estimator is

\[
\hat{\sigma}^2(\hat{\mu}) = \frac{1}{(\sum_{i \in S} m_i / g_i)^2} \sum_{i \in S} \frac{m_i (y_i - \hat{\mu})^2}{g_i^2}
\]  

(12)

If \( x_i \) is another variable, an estimator of the ratio \( R = \mu_y/\mu_x \) of the mean of \( y \) to the mean of \( x \) is

\[
\hat{R} = \frac{\sum_{i \in S} y_i / f_i}{\sum_{i \in S} x_i / f_i}
\]  

(13)

with simple variance estimator

\[
\hat{\sigma}^2(\hat{R}) = \frac{1}{(\sum_{i \in S} x_i / f_i)^2} \sum_{i \in S} \frac{(y_i - x_i \hat{\mu})^2}{f_i^2}
\]  

(14)

The source C code of the algorithm for the fast sampling processes and calculation of the inclusion frequencies \( f_i \) on which the estimators are based can be found at stevenkthompson/simple on https://github.com.
Simulations

For an empirical population with which to evaluate the effectiveness of the proposed inference method we use the network data from the Colorado Springs Study on the heterosexual spread of HIV. Called the Project 90 study, it was carried out to delineate the behaviors and network characteristics of a high risk population including sex workers, clients of sex workers, drug users and associated people. The study was carried out by members of the El Paso County Health Department and was supported by the Centers for Disease Control and Prevention (CDC) [24]. In this study, every effort was made to trace the sexual, drug, and social relationships of the members of this at-risk population, identifying names and characteristics of each partner and later destroying the data on names or unique identifiers while retaining the anonymized network structure. Since this effort was far more thorough than is usual the case in network studies, this network data set is highly suitable as a simulation population from which to sample and evaluate network sampling and inference methods. For studies of hidden and hard-to-reach human populations, this is the most relevant of available network data sets for simulations evaluating methodologies.

We use here the complete data set placed by Matt Salganik in the archive maintained by the Princeton Office of Population Research (https://opr.princeton.edu/archive/p90/). The data set has N = 5492 people and L = 21,644 links between those people. The links represent social, sexual, and drug-related relationships and are symmetric. The data set includes 13 attribute variables on each person, including gender (male = 0, female = 1), sex work, client of sex worker, unemployed and other variables, some risk-related and some not, described in the data archive. The links are not identified by type, so the presence of a link between two people indicates there is at least one of the relationship types social, sexual, or drug related.

The data network of 5492 nodes and 21,644 has 108 separate components, the largest of which contains 4430 nodes, followed by components of sizes 50, 42, 26, and so on down to components of size 2.

For the simulation I used the entire Project 90 archive data set with its 108 components as more realistically representing other real populations of interest than would using using solely the largest component, as has sometimes been done in other methodology studies. All missing item responses have been arbitrarily changed to zero, so that the number of nodes and sample sizes for each of the variables are the same and so comparisons of estimation methods are not influenced by different sample sizes for different variables or by choices in how to handle missing values.

Option and rate values uses in the simulations were as follow. For the original without-replacement the coupon limit was 3 for RDS and RDS+ and 25 for SB and SB+. Less that 4 percent of people in the population have degree more than 25, so that with the snowball designs the number of coupons would equal their number of partners for more than 96 percent of the population. The target number of seeds was 240 and the target sample size was 1200. Seeds were selected by Bernoulli random selections with the desired expected sample size; coupons had an expiration date 28 days from date of issue; each day before sample size was reached; there was Bernoulli probability 0.00001 of selecting re-seeds, but this was hardly ever done; from the units outside the sample. The Bernoulli probability each day of tracing any link out of the sample where the coupon had not expired was 0.004. On average, 19 percent of the links within the sample were traced by coupon redemptions.

For the without-replacement fast sampling process the target sample size was 400; the Bernoulli link tracing probability on links out was 0.5 and the Bernoulli probability of node removals from the sample was also 0.5; re-seed Bernoulli probability for the nodes outside the sample was 0.1. The fast sampling process was the same, free to
follow links and unrestrained by coupons, for each of the four original designs.

In each simulation run the new estimator is calculated along with the VH estimator and the sample mean. Like the new estimator, the VH works the same for all types of variables, whether binary or more general numeric, and does not not require an estimate of population size. Because of the relatively small sampling fraction .22 in the simulations, the SS estimator here would be expected to be similar to the VH estimator, if the estimate of N for the SS estimator was accurate or biased upward. The SH estimator would be identical to the VH estimator for estimating mean degree. The HCG would be similar to the VH for estimating mean degree, because of the small sample fraction.

Separate simulations were done for each of the four sampling designs RDS, RDS+, SB, and SB+. Simulations for each of the four designs were carried out with the following steps.

1. From the population of N = 5492 people and L = 21,644 links, select a target sample of n = 1200 people, using RDS, RDS+, SB, or SB+. To start each sample, a target of 240 seeds are selected at random. A small number of additional seeds may be selected in the process of reaching the target sample size of 1200.

2. Calculate the $f_i$ with fast samples $S_1, S_2, ..., S_T$. The number of iterations $T$ used was 10,000. The target sample size for each $S_t$ in the sequence was 400, or one-third of the sample size $n = 1200$. Estimate means of degree and 13 other variables, using the new estimator $\hat{\mu}$, the Volz-Heckathorn estimator $\hat{\mu}_{VH}$ and the sample mean or proportion.

Steps 1 and 2 were repeated 1000 times for each of the four designs.

Using the 1000 values for each estimators, together with the known population values, the mean square error (MSE), Bias, and Confidence Interval Coverage were calculated.

Confidence intervals were calculated for the new estimator using the simple variance estimator described in the previous section. Confidence interval coverage for each estimate was calculated as the proportion of intervals, out of 1000, that covered the true mean of the variable.

Results

The results of the simulations are summarized in the figures. The numerical results on which the figures are based are in the tables of SI Tables. Figures 1 and 2 show the results for estimating mean degree. Fig 1 plots the MSE for estimating mean degree with the new estimator (vertical axis) against the MSE of the VH estimator for each of the four designs RDS, RDS+, SB, and SB+. For a point below the diagonal line the MSE is lower with the new estimator. Each point here is far below the line. The relative efficiencies (MSE(VH)/MSE(Simple)) corresponding to the four points and given in Tables 1-4 of SI Tables are 29 for RDS, 54 for RDS+, 26 for SB and 80 for SB+. This means for example that with a standard RDS study and using the same data, the new estimator has one-twenty-ninth the MSE as does the VH estimator. With each of the four designs, the MSE is large for the VH estimator and is low for the new estimator. The lower mean square errors of the new estimator are achieved by eliminating most of the bias.
Fig 1. For estimating mean degree, MSE of the new estimator (vertical axis) is plotted against MSE of the VH estimator. Each point represents a design. The new estimator has much lower MSE for each of the designs.

A measure of how much is gained by identifying the within-sample links beyond those used in recruitment is obtained by comparing the relative efficiency for estimating mean degree using the simple estimator for each of the “plus” designs with the corresponding standard designs in Fig 1. Using the simple estimator in each case, the efficiency gains are $\text{MSE}(\text{RDS})/\text{MSE}(\text{RDS}+) = 1.83$ and $\text{MSE}(\text{SB})/\text{MSE}(\text{SB}+) = 3.00$ (using the MSE values from Tables 1-4 of S1 Tables).

Figure 2 shows the same relationships but for the bias of the estimator of mean degree instead of MSE. Each point again represents a design and the absolute bias with the new estimator is on the vertical axis while the absolute bias for the VH estimator with the four designs. For instance, with RDS, the bias in estimating mean degree with the new estimator is .32 while the bias with VH is -2.46 (Table 1 of S1 Tables). For each of the four designs the bias of the VH estimator is large and the bias of the new estimator. Further, the bias of the VH estimator is worse with the SB and SB+ designs using 25 coupons than it is with the RDS and RDS+ designs using 3 coupons. That is to be expected since the VH estimator is based on the approximating assumption of a random walk design, and the more coupons handed out the more branching in recruitment, and the designs get even farther from the assumed random walk.

Fig 2. Bias in estimating mean degree. Bias of the new estimator (vertical axis) is plotted against bias of the VH estimator. Each point represents a different design. The new estimator has much less bias for each of the designs.

Also we see in Fig 2 that the new estimator is able to take advantage of the extra link information of the enhanced (+) designs to further reduce bias, while the VH estimator is not able to benefit from the extra sample network information of the enhanced designs.

For estimating the population proportion of each of the 13 attribute variables, the MSE comparisons are given in the four Figures 3-6. Here each plot is for just one of the designs RDS, RDS+, SB, and SB+. Each point represents a different binary variable, as identified in the legend. Once again, a point below the diagonal indicates the MSE is lower with the new estimator compared to the VH estimator. The pattern in each plot is that the MSE is lower with the new estimator than with the VH estimator, except for some of the points near the origin where the MSE is very small with both estimators.

Fig 3. MSE with design RDS for estimating population proportion for each of the 13 attribute variables.

Fig 4. MSE with design RDS+ for estimating population proportion for each of the 13 attribute variables.

Fig 5. MSE with design SB for estimating population proportion for each of the 13 attribute variables.

Fig 6. MSE with design SB+ for estimating population proportion for each of the 13 attribute variables.
A similar pattern for bias is shown in the four Figures 7-10. While neither estimator has uniformly lower bias for all variables, the new estimator has the lower bias except for cases where the bias is small with either estimator.

**Fig 7.** Bias with design RDS for estimating population proportion for each of the 13 attribute variables.

**Fig 8.** Bias with design RDS+ for estimating population proportion for each of the 13 attribute variables.

**Fig 9.** Bias with design SB for estimating population proportion for each of the 13 attribute variables.

**Fig 10.** Bias with design SB+ for estimating population proportion for each of the 13 attribute variables.

The exact MSE and Bias numeric results are shown in Tables 1-4 of SI Tables. The last two columns on the right in those tables show relative efficiency of the new estimator compared to VH or sample mean, and relative absolute bias. The column “eff” gives in the VH section of the table gives MSE(VH)/MSE(Simple) for each of the variables, and “rbias” gives |Bias(VH)|/|Bias(Simple)|. Values above 1.0 are favorable to the new estimator and values below 0.0 are favorable to VH, and show the details of the points clustered near the diagonal line and origin in the plots. The unweighted sample means, which have higher biases in most but not all cases, are included in the tables for reference.

Confidence interval widths and coverage probabilities were calculated only for the proposed estimator and are given in Tables 5-8 of SI Tables with each table for one of the four designs. The target coverage is .95. “AV $\tilde{SD}$” is the square root of the average value of $\tilde{\text{Var}}(\hat{\mu})$ over the 1000 runs. “AV width/2” is the average half-width of the confidence interval. “Coverage” in the tables is the coverage probability, the proportion of the 1000 simulation runs in which the confidence interval covers the true value.

Most of the coverage probabilities and in the 80s and 90s percents. Where coverage is lower than that, it is in most cases because the estimator has a bias similar in magnitude to it’s standard deviation, so that a symmetric confidence interval based on an estimate of that standard deviation will tend to be off-center. For this reason this same confidence interval method would not be recommended for the VH estimator with it’s tendency to have larger biases.

Although the simulations here compare the new estimator directly only to the VH estimator and the sample mean, the estimate of mean degree with the SS estimator is the same as with the VH estimator, so the SS estimate of mean degree will have the same bias and MSE as the VH estimate. With the sampling fraction $n/N = 0.22$ here, the SS and HCG estimates of mean degree should also be approximately like the VH estimator.

The SI Tables also document the historical advance of the estimators such as VH and SH over what went before them. Earlier link-tracing studies of hidden populations by field ethnographers, anthropologists, epidemiologists had no alternatives to reporting the results of their findings as sample means and proportions (25, 26 include reviews of earlier studies). From the tables we can see for example for estimating population mean degree, the efficiency gain of the VH, and for SH with is the same for mean...
Comparing the new estimators to the sample means and proportions the relative efficiencies can be read directly from the “eff” column of the SI Tables. The efficiency gain of the new estimator over the sample mean for estimating population mean degree is for RDS 198.54, for RDS+ 362.80, for SB 146.54, and for SB+ 439.49. The new estimators are made possible by better understanding of networks and of network sampling designs, faster computers, and computational data structures and algorithms which were not available two decades ago.

**Discussion and conclusions**

The simple estimators introduced here for network sampling use the sample network data and a fast sampling process similar to the actual sampling design used to collect the data. Inclusion frequencies of the fast sampling process estimate the relative inclusion probabilities of the actual design. These estimated inclusion probabilities are in turn used to form the sampling weights for estimates of population means and proportions.

The new estimators move beyond the approximating Markov chain assumptions about the recruitment of people into the sample or about the transitions in the recruitments different values of binary variables. The new estimators do not assume that the population network has only a single connected component. The discrepancy between such assumptions and reality has led to biases and high mean square errors in the estimators that depend on them.

The availability of these new estimators should free investigators to use different types of network sampling designs as they wish. For instance, the new estimators work as well with snowball designs that are virtually unlimited by imposed coupon limits as they do for designs that limit recruitment coupons to few. The practice of restricting recruitment coupons to small numbers such as two or three might make sense for some studies, in order to reach farther into a hidden population as opposed to exploring key areas of the population more thoroughly. The use of small coupon numbers was motivated originally by the hope that it would make the sampling closer to a random walk so that the estimation biases would not be too large. With the new estimators investigators can choose whatever coupon limits make sense for the study. Also for studies of at-risk key populations it may make sense to follow risk related links, such as drug injection related links or sexual links. With the new estimators, it is not necessary to follow more general links such as friendships in the hope that they connect the entire population into a single component.

The new estimators work as well for quantitative or continuous variables as for binary variables. The assumption about Markov transitions between states of a binary variable have led some estimation methods to be developed only for estimating the means of binary variables. In modern network surveys of hidden populations some of the most important variables are quantitative, such as number of sessions of sex in a period or frequency of drug injection activity, as well as number of partners. These quantitative variables are also the most likely to be related to the sampling inclusion probabilities and so benefit the most from better estimates of those inclusion probabilities.

Existing data from network sampling studies can be reanalyzed using the new methods. For new studies investigators could consider using the enhanced data collection methods that obtain more information about within-sample links, that produce better estimates with the same number of people in the sample.
Supporting information

S1 Tables. Tables for Simple estimators for network sampling.

Tables 1-4 correspond to the four network sampling designs RDS, RDS+, SB, and SB+ respectively.

Tables 5-8 give confidence interval coverages and widths for the same four designs.

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S1. Tables for Simple estimators for network sampling.

Tables 1-4 correspond to the four network sampling designs RDS, RDS+, SB, and SB+ respectively.

Tables 5-8 give confidence interval coverages and widths for the same four designs.
|        | SIMPLE | actual | E.est | bias   | sd     | mse   | eff | rbias |
|--------|--------|--------|-------|--------|--------|-------|-----|-------|
| degree | 7.88   | 8.20   | 0.321723 | 0.324316 | 0.208686 | 1.00 | 1.00 |
| nonwhite | 0.24   | 0.25   | 0.010975 | 0.021323 | 0.000575 | 1.00 | 1.00 |
| female  | 0.43   | 0.43   | 0.001933 | 0.021844 | 0.000481 | 1.00 | 1.00 |
| worker  | 0.05   | 0.06   | 0.003294 | 0.009343 | 0.000998 | 1.00 | 1.00 |
| procurer | 0.02   | 0.02   | 0.001547 | 0.004637 | 0.000244 | 1.00 | 1.00 |
| client  | 0.09   | 0.09   | 0.000607 | 0.014468 | 0.000210 | 1.00 | 1.00 |
| dealer  | 0.06   | 0.07   | 0.006345 | 0.010341 | 0.000147 | 1.00 | 1.00 |
| cook    | 0.01   | 0.01   | 0.000187 | 0.002191 | 0.000045 | 1.00 | 1.00 |
| thief   | 0.02   | 0.02   | 0.001593 | 0.006493 | 0.000290 | 1.00 | 1.00 |
| retired | 0.03   | 0.03   | 0.000251 | 0.007735 | 0.000060 | 1.00 | 1.00 |
| homemakr | 0.06  | 0.06   | -0.000003 | 0.001096 | 0.000119 | 1.00 | 1.00 |
| disabled | 0.04  | 0.04   | 0.000857 | 0.008706 | 0.000077 | 1.00 | 1.00 |
| unemploy | 0.16  | 0.17   | 0.006356 | 0.015811 | 0.000290 | 1.00 | 1.00 |
| homeless | 0.01  | 0.01   | 0.000491 | 0.005062 | 0.000026 | 1.00 | 1.00 |
| VH      |        |        |        |        |        |       |     |       |
| degree  | 7.88   | 5.42   | -2.458292 | 0.221049 | 6.092061 | 29.19 | 7.64 |
| nonwhite | 0.24   | 0.26   | 0.020619 | 0.020615 | 0.000850 | 1.48 | 1.88 |
| female  | 0.43   | 0.41   | -0.024778 | 0.021961 | 0.001096 | 2.28 | 12.82 |
| worker  | 0.05   | 0.05   | -0.004860 | 0.010110 | 0.000126 | 1.28 | 1.48 |
| procurer | 0.02   | 0.01   | -0.003472 | 0.003454 | 0.000024 | 1.00 | 2.24 |
| client  | 0.09   | 0.13   | 0.038377 | 0.017908 | 0.001793 | 8.55 | 63.20 |
| dealer  | 0.06   | 0.07   | 0.001294 | 0.010499 | 0.000112 | 0.76 | 0.20 |
| cook    | 0.01   | 0.01   | -0.001309 | 0.002985 | 0.000011 | 0.63 | 7.00 |
| thief   | 0.02   | 0.02   | -0.000879 | 0.006085 | 0.000038 | 0.85 | 0.55 |
| retired | 0.03   | 0.03   | 0.002616 | 0.008131 | 0.000073 | 1.22 | 10.41 |
| homemakr | 0.06  | 0.05   | -0.008380 | 0.008862 | 0.000149 | 1.25 | 2627.83 |
| disabled | 0.04  | 0.04   | -0.005227 | 0.007436 | 0.000083 | 1.08 | 6.10 |
| unemploy | 0.16  | 0.13   | -0.027922 | 0.013437 | 0.000960 | 3.31 | 4.39 |
| homeless | 0.01  | 0.01   | -0.000674 | 0.004199 | 0.000026 | 0.70 | 1.37 |
| ŷ       |        |        |        |        |        |       |     |       |
| degree  | 7.88   | 14.31  | 6.432272 | 0.240921 | 41.432166 | 198.54 | 19.99 |
| nonwhite | 0.24   | 0.28   | 0.039685 | 0.016599 | 0.001850 | 3.22 | 3.62 |
| female  | 0.43   | 0.46   | 0.032543 | 0.011160 | 0.001184 | 2.46 | 16.83 |
| worker  | 0.05   | 0.09   | 0.040418 | 0.006369 | 0.001674 | 17.06 | 12.27 |
| procurer | 0.02   | 0.03   | 0.015857 | 0.003242 | 0.000262 | 10.96 | 10.25 |
| client  | 0.09   | 0.07   | -0.015363 | 0.006984 | 0.000285 | 1.36 | 25.30 |
| dealer  | 0.06   | 0.12   | 0.054326 | 0.007186 | 0.003003 | 20.40 | 8.56 |
| cook    | 0.01   | 0.01   | 0.001482 | 0.002368 | 0.000088 | 0.47 | 7.93 |
| thief   | 0.02   | 0.04   | 0.014693 | 0.004091 | 0.000233 | 5.20 | 9.22 |
| retired | 0.03   | 0.03   | -0.000726 | 0.004055 | 0.000017 | 0.28 | 2.89 |
| homemakr | 0.06  | 0.07   | 0.007519 | 0.006176 | 0.000995 | 0.80 | 2357.91 |
| disabled | 0.04  | 0.06   | 0.014319 | 0.005355 | 0.000234 | 3.05 | 16.70 |
| unemploy | 0.16  | 0.25   | 0.090330 | 0.010243 | 0.008264 | 28.46 | 14.21 |
| homeless | 0.01  | 0.02   | 0.003988 | 0.002808 | 0.000024 | 0.92 | 8.12 |
Table 2. RDS+ Design

| SIMPLE Design | Actual | E. est | Bias  | SD   | MSE   | Eff  | RBias |
|---------------|--------|--------|-------|------|-------|------|-------|
| degree        | 7.88   | 7.82   | -0.064183 | 0.33123 | 0.113762 | 1.00 | 1.00  |
| nonwhite      | 0.24   | 0.22   | -0.016216 | 0.023923 | 0.000835 | 1.00 | 1.00  |
| female        | 0.43   | 0.44   | 0.011235 | 0.027851 | 0.000902 | 1.00 | 1.00  |
| worker        | 0.05   | 0.05   | 0.002313 | 0.011178 | 0.000130 | 1.00 | 1.00  |
| procurer      | 0.02   | 0.01   | -0.000711 | 0.004308 | 0.000019 | 1.00 | 1.00  |
| client        | 0.09   | 0.07   | -0.017189 | 0.015128 | 0.000524 | 1.00 | 1.00  |
| dealer        | 0.06   | 0.06   | -0.006107 | 0.009508 | 0.000128 | 1.00 | 1.00  |
| cook          | 0.01   | 0.01   | -0.000597 | 0.004478 | 0.000020 | 1.00 | 1.00  |
| thief         | 0.02   | 0.02   | -0.002592 | 0.005953 | 0.000042 | 1.00 | 1.00  |
| retired       | 0.03   | 0.03   | -0.002589 | 0.008533 | 0.000080 | 1.00 | 1.00  |
| homemakr      | 0.06   | 0.06   | 0.000696 | 0.013245 | 0.000176 | 1.00 | 1.00  |
| disabled      | 0.04   | 0.04   | -0.001669 | 0.009565 | 0.000094 | 1.00 | 1.00  |
| unemploy      | 0.16   | 0.16   | -0.001582 | 0.018396 | 0.000341 | 1.00 | 1.00  |
| homeless      | 0.01   | 0.01   | -0.000682 | 0.005280 | 0.000028 | 1.00 | 1.00  |

| VH Design     | Actual | E. est | Bias  | SD   | MSE   | Eff  | RBias |
|---------------|--------|--------|-------|------|-------|------|-------|
| degree        | 7.88   | 5.42   | -2.457134 | 0.227604 | 6.089313 | 53.53 | 38.28 |
| nonwhite      | 0.24   | 0.26   | 0.020821 | 0.021244 | 0.001049 | 1.16 | 2.18  |
| female        | 0.43   | 0.41   | -0.024457 | 0.021244 | 0.001049 | 1.16 | 2.18  |
| worker        | 0.05   | 0.05   | -0.004943 | 0.009720 | 0.000119 | 0.91 | 2.14  |
| procurer      | 0.02   | 0.01   | -0.003419 | 0.003376 | 0.000023 | 1.21 | 4.81  |
| client        | 0.09   | 0.13   | 0.037166 | 0.018657 | 0.000239 | 1.21 | 4.81  |
| dealer        | 0.06   | 0.06   | 0.000927 | 0.010374 | 0.000108 | 3.30 | 2.16  |
| cook          | 0.01   | 0.01   | -0.001510 | 0.002819 | 0.000010 | 0.50 | 2.53  |
| thief         | 0.02   | 0.02   | -0.000778 | 0.005826 | 0.000035 | 0.82 | 0.30  |
| retired       | 0.03   | 0.03   | 0.002589 | 0.008051 | 0.000072 | 0.90 | 1.00  |
| homemakr      | 0.06   | 0.05   | -0.008324 | 0.008794 | 0.000147 | 0.83 | 11.95 |
| disabled      | 0.04   | 0.04   | -0.005882 | 0.007681 | 0.000094 | 0.99 | 3.52  |
| unemploy      | 0.16   | 0.13   | -0.029356 | 0.013133 | 0.001034 | 3.03 | 18.56 |
| homeless      | 0.01   | 0.01   | -0.000674 | 0.004227 | 0.000018 | 0.65 | 0.99  |

| \( \bar{y} \) Design | Actual | E. est | Bias  | SD   | MSE   | Eff  | RBias |
|----------------------|--------|--------|-------|------|-------|------|-------|
| degree               | 7.88   | 14.30  | 6.419863 | 0.240330 | 41.27297 | 362.80 | 100.02 |
| nonwhite             | 0.24   | 0.28   | 0.039531 | 0.017219 | 0.001859 | 2.23 | 2.44  |
| female               | 0.43   | 0.47   | 0.032806 | 0.011357 | 0.001205 | 1.34 | 2.92  |
| worker               | 0.05   | 0.09   | 0.040330 | 0.005867 | 0.001661 | 12.75 | 17.44 |
| procurer             | 0.02   | 0.03   | 0.016056 | 0.003326 | 0.000269 | 14.10 | 22.57 |
| client               | 0.09   | 0.07   | -0.015742 | 0.007279 | 0.000301 | 5.57 | 0.92  |
| dealer               | 0.06   | 0.12   | 0.054282 | 0.006950 | 0.002995 | 23.45 | 8.89  |
| cook                 | 0.01   | 0.01   | 0.001442 | 0.002335 | 0.000008 | 0.37 | 2.42  |
| thief                | 0.02   | 0.04   | 0.014605 | 0.004005 | 0.000229 | 4.44 | 5.63  |
| retired              | 0.03   | 0.03   | -0.000696 | 0.003973 | 0.000016 | 0.20 | 0.27  |
| homemakr             | 0.06   | 0.07   | 0.007271 | 0.006181 | 0.000091 | 0.52 | 10.44 |
| disabled             | 0.04   | 0.06   | 0.014378 | 0.005299 | 0.000235 | 2.49 | 8.61  |
| unemploy             | 0.16   | 0.25   | 0.089440 | 0.010143 | 0.008102 | 23.77 | 56.54 |
| homeless             | 0.01   | 0.02   | 0.003962 | 0.002762 | 0.000023 | 0.82 | 5.81  |
| Table 3. SB Design | SIMPLE actual | E.est | bias | sd       | mse     | eff | rbias |
|-------------------|----------------|-------|------|----------|---------|-----|-------|
| degree            | 7.88           | 8.32  | 0.441944 | 0.283595 | 0.275741 | 1.00| 1.00  |
| nonwhite          | 0.24           | 0.26  | 0.016708 | 0.021857 | 0.000757 | 1.00| 1.00  |
| female            | 0.43           | 0.43  | 0.000794 | 0.022492 | 0.000507 | 1.00| 1.00  |
| worker            | 0.05           | 0.06  | 0.005829 | 0.009198 | 0.000119 | 1.00| 1.00  |
| procurer          | 0.02           | 0.02  | 0.003119 | 0.004730 | 0.000332 | 1.00| 1.00  |
| client            | 0.09           | 0.09  | 0.004746 | 0.013939 | 0.000217 | 1.00| 1.00  |
| dealer            | 0.06           | 0.07  | 0.010055 | 0.01421  | 0.000210 | 1.00| 1.00  |
| cook              | 0.01           | 0.01  | 0.000493 | 0.006341 | 0.000500 | 1.00| 1.00  |
| thief             | 0.02           | 0.03  | 0.003097 | 0.006341 | 0.000500 | 1.00| 1.00  |
| retired           | 0.03           | 0.03  | 0.005531 | 0.008084 | 0.00066  | 1.00| 1.00  |
| homemakr          | 0.06           | 0.06  | -0.001243| 0.008084 | 0.000066 | 1.00| 1.00  |
| disabled          | 0.04           | 0.04  | 0.001952 | 0.008947 | 0.000084 | 1.00| 1.00  |
| unemploy          | 0.16           | 0.17  | 0.010233 | 0.015945 | 0.000359 | 1.00| 1.00  |
| homeless          | 0.01           | 0.01  | 0.000955 | 0.005008 | 0.00026  | 1.00| 1.00  |
| VH actual E.est   | 7.88           | 5.19  | -2.689333| 0.200484 | 7.272708 | 26.38| 6.09  |
| nonwhite          | 0.24           | 0.27  | 0.031928 | 0.021830 | 0.001496 | 1.98| 1.91  |
| female            | 0.43           | 0.39  | -0.040046| 0.021358 | 0.002060 | 4.07| 50.42 |
| worker            | 0.05           | 0.05  | -0.002207| 0.008953 | 0.000855 | 0.72| 0.38  |
| procurer          | 0.02           | 0.01  | -0.001881| 0.003648 | 0.000017 | 0.52| 0.60  |
| client            | 0.09           | 0.15  | 0.064678 | 0.019204 | 0.004552 | 21.00| 13.63 |
| dealer            | 0.06           | 0.07  | 0.005755 | 0.010947 | 0.000193 | 0.92| 0.85  |
| cook              | 0.01           | 0.01  | -0.001647| 0.002800 | 0.000011 | 0.71| 8.54  |
| thief             | 0.02           | 0.02  | 0.002400 | 0.006449 | 0.000047 | 0.95| 0.77  |
| retired           | 0.03           | 0.03  | 0.005040 | 0.008598 | 0.000099 | 1.51| 9.48  |
| homemakr          | 0.06           | 0.05  | -0.012866| 0.008499 | 0.000238 | 1.99| 10.35 |
| disabled          | 0.04           | 0.04  | -0.006002| 0.007144 | 0.000087 | 1.04| 3.07  |
| unemploy          | 0.16           | 0.17  | -0.030449| 0.012518 | 0.001084 | 3.02| 2.98  |
| homeless          | 0.01           | 0.01  | -0.000407| 0.002695 | 0.000030 | 1.16| 5.03  |
| y actual E.est    | 14.24          | 6.353473| 0.199600| 0.404643| 46.54| 14.38 |
| nonwhite          | 0.24           | 0.30  | 0.057156 | 0.017098 | 0.003559 | 4.70| 3.42  |
| female            | 0.43           | 0.46  | 0.025163 | 0.011382 | 0.000763 | 1.51| 31.68 |
| worker            | 0.05           | 0.09  | 0.047583 | 0.005640 | 0.002296 | 19.36| 8.16  |
| procurer          | 0.02           | 0.02  | 0.019414 | 0.003096 | 0.000386 | 12.04| 6.22  |
| client            | 0.09           | 0.09  | -0.003272| 0.007314 | 0.000054 | 0.25| 0.07  |
| dealer            | 0.06           | 0.13  | 0.062425 | 0.006891 | 0.003944 | 18.81| 6.21  |
| cook              | 0.01           | 0.01  | 0.001548 | 0.002158 | 0.000007 | 0.48| 8.03  |
| thief             | 0.02           | 0.04  | 0.017620 | 0.004041 | 0.000327 | 6.55 | 5.67  |
| retired           | 0.03           | 0.03  | 0.000793 | 0.004157 | 0.000018 | 0.27| 1.49  |
| homemakr          | 0.06           | 0.06  | 0.003303 | 0.006172 | 0.000049 | 0.41| 2.66  |
| disabled          | 0.04           | 0.06  | 0.015175 | 0.005137 | 0.000257 | 3.06| 7.78  |
| unemploy          | 0.16           | 0.26  | 0.094812 | 0.009945 | 0.009088 | 25.32| 9.26  |
| homeless          | 0.01           | 0.02  | 0.004798 | 0.002695 | 0.000030 | 1.16| 5.03  |
### Table 4. SB+ Design

| SIMPLE | actual | E.est | bias  | sd    | mse   | eff  | rbias |
|--------|--------|-------|-------|-------|-------|------|-------|
| degree | 7.88   | 7.90  | 0.021062 | 0.302342 | 0.091854 | 1.00 | 1.00  |
| nonwhite | 0.24   | 0.23  | -0.014272 | 0.022637 | 0.000716 | 1.00 | 1.00  |
| female  | 0.43   | 0.44  | 0.009500  | 0.028160 | 0.000883 | 1.00 | 1.00  |
| worker  | 0.05   | 0.06  | 0.004619  | 0.010680 | 0.000135 | 1.00 | 1.00  |
| procurer | 0.02   | 0.02  | 0.000393  | 0.004503 | 0.00020  | 1.00 | 1.00  |
| client  | 0.09   | 0.08  | -0.012822 | 0.014368 | 0.000371 | 1.00 | 1.00  |
| dealer  | 0.06   | 0.06  | -0.002589 | 0.009764 | 0.000102 | 1.00 | 1.00  |
| cook    | 0.02   | 0.02  | -0.001522 | 0.005890 | 0.000037 | 1.00 | 1.00  |
| thief   | 0.03   | 0.03  | -0.001919 | 0.008887 | 0.00083  | 1.00 | 1.00  |
| homemakr | 0.06   | 0.06  | -0.000201 | 0.013147 | 0.000173 | 1.00 | 1.00  |
| disabled | 0.04   | 0.04  | -0.000747 | 0.009763 | 0.000096 | 1.00 | 1.00  |
| unemploy | 0.16   | 0.16  | 0.002081  | 0.018748 | 0.000356 | 1.00 | 1.00  |
| homeless | 0.01   | 0.01  | -0.000520 | 0.005489 | 0.000030 | 1.00 | 1.00  |

| VH | actual | E.est | bias  | sd    | mse   | eff  | rbias |
|----|--------|-------|-------|-------|-------|------|-------|
| degree | 7.88   | 5.19  | -2.696262 | 0.19265 | 7.306935 | 79.55 | 128.01 |
| nonwhite | 0.24   | 0.27  | 0.033787  | 0.022481 | 0.001647 | 2.30  | 2.37  |
| female  | 0.43   | 0.39  | -0.040785 | 0.021366 | 0.002136 | 2.42  | 4.29  |
| worker  | 0.05   | 0.05  | -0.002137 | 0.009592 | 0.00097  | 0.71  | 0.46  |
| procurer | 0.02   | 0.02  | -0.002142 | 0.003493 | 0.000017 | 0.82  | 5.46  |
| client  | 0.09   | 0.15  | 0.004674  | 0.019057 | 0.000173 | 1.00  | 1.00  |
| dealer  | 0.06   | 0.07  | 0.008032  | 0.010880 | 0.000183 | 12.26 | 5.04  |
| cook    | 0.01   | 0.01  | 0.001583  | 0.002833 | 0.000011 | 0.49  | 4.19  |
| thief   | 0.02   | 0.02  | 0.001872  | 0.006667 | 0.000048 | 1.30  | 1.23  |
| retired | 0.03   | 0.03  | 0.004935  | 0.008288 | 0.000093 | 1.13  | 2.57  |
| homemakr | 0.06   | 0.05  | -0.012813 | 0.008266 | 0.000232 | 1.34  | 63.75 |
| disabled | 0.04   | 0.04  | -0.006037 | 0.007086 | 0.000087 | 0.90  | 8.08  |
| unemploy | 0.16   | 0.13  | 0.029953  | 0.012773 | 0.000106 | 2.98  | 14.39 |
| homeless | 0.01   | 0.01  | -0.000834 | 0.003959 | 0.000016 | 0.54  | 1.60  |

| y | actual | E.est | bias  | sd    | mse   | eff  | rbias |
|--|--------|-------|-------|-------|-------|------|-------|
| degree | 7.88   | 14.23 | 6.350544 | 0.199966 | 40.369395 | 439.49 | 301.52 |
| nonwhite | 0.24   | 0.30  | 0.058552 | 0.017339 | 0.003729 | 5.21  | 4.10  |
| female  | 0.43   | 0.46  | 0.024115 | 0.011285 | 0.000709 | 0.80  | 2.54  |
| worker  | 0.05   | 0.10  | 0.047787  | 0.005815 | 0.002317 | 17.12 | 10.35 |
| procurer | 0.02   | 0.03  | 0.019401  | 0.003265 | 0.000387 | 18.95 | 49.43 |
| client  | 0.09   | 0.09  | -0.000469 | 0.007308 | 0.00054  | 0.14  | 0.04  |
| dealer  | 0.06   | 0.13  | 0.062280  | 0.006782 | 0.003925 | 38.46 | 24.05 |
| cook    | 0.01   | 0.01  | 0.001604  | 0.002308 | 0.000008 | 0.37  | 4.25  |
| thief   | 0.02   | 0.04  | 0.017384  | 0.004104 | 0.000319 | 8.62  | 11.42 |
| retired | 0.03   | 0.03  | 0.000792  | 0.004025 | 0.000017 | 0.20  | 0.41  |
| homemakr | 0.06   | 0.06  | 0.003582  | 0.005951 | 0.000048 | 0.28  | 17.82 |
| disabled | 0.04   | 0.06  | 0.015048  | 0.005170 | 0.000253 | 2.64  | 20.14 |
| unemploy | 0.16   | 0.26  | 0.095478  | 0.010154 | 0.009219 | 25.91 | 45.87 |
| homeless | 0.01   | 0.02  | 0.004603  | 0.002667 | 0.000287 | 0.93  | 8.85  |
| Table 5. RDS Design: Confidence Interval Coverage |
|-----------------------------------------------|
| name | actual | halfwidth | coverage |
|------|--------|-----------|----------|
| degree | 7.88   | 0.58      | 0.80     |
| nonwhite | 0.24   | 0.04      | 0.92     |
| female  | 0.43   | 0.05      | 0.97     |
| worker  | 0.05   | 0.02      | 0.95     |
| procurer | 0.02   | 0.01      | 0.92     |
| client  | 0.09   | 0.03      | 0.94     |
| dealer  | 0.06   | 0.02      | 0.95     |
| cook    | 0.01   | 0.01      | 0.79     |
| thief   | 0.02   | 0.01      | 0.92     |
| retired | 0.03   | 0.02      | 0.92     |
| homemakr | 0.06   | 0.02      | 0.94     |
| disabled | 0.04   | 0.02      | 0.94     |
| unemploy  | 0.16   | 0.03      | 0.95     |
| homeless | 0.01   | 0.01      | 0.84     |

| Table 6. RDS+ Design: Confidence Interval Coverage |
|-----------------------------------------------|
| name | actual | halfwidth | coverage |
|------|--------|-----------|----------|
| degree | 7.88   | 0.65      | 0.94     |
| nonwhite | 0.24   | 0.04      | 0.85     |
| female  | 0.43   | 0.06      | 0.93     |
| worker  | 0.05   | 0.02      | 0.92     |
| procurer | 0.02   | 0.01      | 0.76     |
| client  | 0.09   | 0.03      | 0.70     |
| dealer  | 0.06   | 0.02      | 0.79     |
| cook    | 0.01   | 0.01      | 0.64     |
| thief   | 0.02   | 0.01      | 0.67     |
| retired | 0.03   | 0.02      | 0.86     |
| homemakr | 0.06   | 0.03      | 0.92     |
| disabled | 0.04   | 0.02      | 0.89     |
| unemploy  | 0.16   | 0.04      | 0.94     |
| homeless | 0.01   | 0.01      | 0.68     |

| Table 7. SB Design: Confidence Interval Coverage |
|-----------------------------------------------|
| name | actual | halfwidth | coverage |
|------|--------|-----------|----------|
| degree | 7.88   | 0.59      | 0.72     |
| nonwhite | 0.24   | 0.04      | 0.87     |
| female  | 0.43   | 0.05      | 0.97     |
| worker  | 0.05   | 0.02      | 0.95     |
| procurer | 0.02   | 0.01      | 0.95     |
| client  | 0.09   | 0.03      | 0.96     |
| dealer  | 0.06   | 0.02      | 0.92     |
| cook    | 0.01   | 0.01      | 0.81     |
| thief   | 0.02   | 0.01      | 0.94     |
| retired | 0.03   | 0.02      | 0.92     |
| homemakr | 0.06   | 0.02      | 0.93     |
| disabled | 0.04   | 0.02      | 0.94     |
| unemploy  | 0.16   | 0.03      | 0.94     |
| homeless | 0.01   | 0.01      | 0.86     |
### Table 8. SB+ Design: Confidence Interval Coverage

| name      | actual | halfwidth | coverage |
|-----------|--------|-----------|----------|
| degree    | 7.88   | 0.66      | 0.96     |
| nonwhite  | 0.24   | 0.04      | 0.89     |
| female    | 0.43   | 0.06      | 0.94     |
| worker    | 0.05   | 0.02      | 0.95     |
| procurer  | 0.02   | 0.01      | 0.87     |
| client    | 0.09   | 0.03      | 0.76     |
| dealer    | 0.06   | 0.02      | 0.85     |
| cook      | 0.01   | 0.01      | 0.65     |
| thief     | 0.02   | 0.01      | 0.73     |
| retired   | 0.03   | 0.02      | 0.83     |
| homemakr  | 0.06   | 0.03      | 0.92     |
| disabled  | 0.04   | 0.02      | 0.90     |
| unemploy  | 0.16   | 0.04      | 0.95     |
| homeless  | 0.01   | 0.01      | 0.67     |
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