Estimation for network snowball sampling: Preventing pandemics

Steve Thompson
Department of Statistics and Actuarial Science
Simon Fraser University, Burnaby, BC, Canada
thompson@sfu.ca

July 27, 2021

Abstract

Snowball designs are the most natural of the network sampling designs. They have many desirable properties for sampling hidden and hard-to-reach populations. They have been under-used in recent years because simple design-based estimators and confidence intervals have not been available for them. The needed estimation methods are supplied in this paper. Snowball sampling methods and accurate estimators with them are needed for sampling of the people exposed to the animals from which new coronavirus outbreaks originate, and to sample the animal populations to which they are exposed. Accurate estimates are needed to evaluate the effectiveness of interventions to reduce the risk to the people exposed to the animals. In this way the frequencies of major outbreaks and pandemics can be reduced. Snowball designs are needed in studies of sexual and opioid networks through which HIV can spread explosively, so that prevention intervention methods can be developed, accurately assessed, and effectively distributed.

Keywords: Snowball sampling, Network sampling, Adaptive sampling, Coronavirus pandemics, animal surveys, HIV, Design-based inference

1 Introduction

In network sampling, social links are followed from one person to another in selecting the sample of people from a subpopulation that might otherwise be hard to reach. The most natural of the network designs is snowball sampling, in which any number of the links out from each person may be followed. So if a person in the sample has two partners or contacts, either zero, one, or two of those contacts are added to the sample, depending the selection probabilities of the links. For another person in the sample with ten links to contacts, any number from zero to ten links may be followed. In turn, links out from the
Figure 1: A sample from a regular snowball design. Repeat selections of the same person are not allowed. This results in a network sample with tree structure.
Figure 2: A sample from a snowball design allowing repeat selections of the same person, but only by a different recruiter. This results in a sample with network structure more general than a tree.
new people in the sample are followed at the next wave. In this way the
sample may grow fast or slowly, depending on the link-tracing probabilities
and also depending on the numbers and configuration of the links in the social
network of the target population.

In some snowball surveys, a respondent is not allowed to recruit a person
who has already been recruited into the sample. This results in a network
sample with tree structure (Figure 1). In other cases it may be natural to
allow re-recruitments. Usually the survey protocol will not allow re-cruitment
of a person by the same person that recruited them earlier, but will allow
re-recruitment of a sample member by a different recruiter. This results in
samples with network structure more general than a treee (Figure 2). Note
that most people in the sample have roles as both recruitees and recruiters.

The nature of snowball sampling brings different people into the sample
with different probabilities. To estimate the characteristics of the target
population, such as mean number of partners or proportion of people with a
characteristic such as a risk-related behavior, the different inclusion
probabilities for different sample members should be taken into account. A
sample mean or sample proportion gives each person equal weight and so
results in an estimate that is biased in comparison to the actual population
mean or proportion. Unbiased estimators in this design-based sense have been
available for only simple forms of snowball sampling, such as a complete
one-wave snowball sample where the inclusion probabilities for the initial
sample are known. The problem with more general snowball samples, with
many waves and link-tracing probabilities less than one, is that the inclusion
probabilities are not known. In fact they can not be exactly calculated from
the sample data because they depend on the population network outside the
sample as well as within it, as well as depending on the sampling design.

This inference problem has kept snowball sampling designs from being
more widely used than they should be. In this paper we present new
estimators for key population characteristics from snowball samples. The
method is based on estimating the unit inclusion probabilities from the sample
data in interaction with the network sampling design. The method is
design-based and data-based. It does not assume a statistical form of model
for the population network.

Snowball designs are currently being used to collect data on people with
exposure to animals, in order to understand and prevent the emergence of
novel species of the coronavirus family that jump from animals to humans and
lead to emergence of epidemics or pandemics every few years. Snowball
designs are used in some studies of key populations at high risk for HIV, such
as sex workers, clients of sex workers, and networks of people who mis-use
opioids and other drugs that are in some cases injected. Contact-tracing
designs of people exposed to sexually transmitted diseases or exposed to
someone with the new disease covid-19, where the purpose is primarily to find
cases and make interventions, rather than inference, also are of snowball form.

Because the of the importance of the snowball studies of in relation to
emergence of outbreaks of new coronavirus species in humans, and the fact
that those studies are recent and not so well known, that example will be
described at some length next. Subsequent sections will describe the method
proposed here and evaluate it in relation to alternatives.

Snowball sampling designs have many important uses in the real world. In
this paper we will focus on three. One concerns the prevention of future
pandemics caused by emergence of new species in the coronavirus family. The
second, related to the first, involves spatial adaptive designs for animal species
with uneven distributions. The third involves studies of sexual and opioid
networks with high risk of HIV, the human immunodeficiency virus.

1.1 Outbreaks of new species of coronavirus in humans

Virus species of the coronavirus family are adept at transferring from one
mammal host species to another, adapting to the new host environment
through genetic mutations and recombinations ([Latinne et al., 2020]). These
can include transfers from bats, civets, raccoon dogs, pangolins and other
species to humans ([Graham and Baric, 2010], [Tang et al., 2020],
[Andersen et al., 2020], [Montgomery and Macdonald, 2020]). Bat species
are considered likely to be the main reservoir for viruses in the the coronavirus
family. These transfers to humans are moderately common. Most of these die
out as the person infected recovered or dies, or they infect just a few people
close to that person before dying out ([Zhou et al., 2020]). But a small
proportion of these transfer viruses catch on and become major outbreaks.

Since the start of the 21st Century there have been three major outbreaks
of coronavirus species in humans. These are SARS (the species SARS-CoV-1)
in 2002, the Middle East Respiratory Syndrome (MERS), in 2012, and
covid-19 (caused by the coronavirus species SARS-CoV-2), in 2019, and at the
time of this writing a worldwide pandemic. More such outbreaks and
pandemics are widely expected by virologists and epidemiologists unless some
interventions can make conditions less favorable to them.

[Li et al., 2019] used snowball sampling to obtain a sample across three
provinces in the south of China of 1596 people at-risk through their exposure
to animals. Eight study regions were selected in areas known to have diverse
coronaviruses in bat populations roosting close to human dwellings. The study
targeted “human populations that are highly exposed to bats and other
wildlife, including people who visit or work around bat caves, work in local live
animal markets, raise animals, or are involved in wildlife trade (e.g., wild
animal harvest, trade, transportation, and preparation), as identified by
previous exploratory ethnographic interviews.”

Sample members were given a questionnaire about risk-related and
protective behaviors and their experiences with flu-like and SARS-like
symptoms, and were given antibody tests for evidence of past infection with
bat coronavirus. The blood tests identified 9 individuals (0.6%) who were
positive for bat coronaviruses. 73 (5%) reported symptoms fever with cough
and shortness of breath or difficulty breathing within the last 12 months, and
227 (14%) reported fever with muscle aches, cough, or sore throat symptoms
within the last 12 months.

When asked about protective measures, among the 502 participants who purchased animals from wet markets in the past 12 months 194, (39%) had taken measures such as washing hands, purchasing live animals less often, or purchasing meat at supermarkets instead of live animal markets. Only 7 (1%) had considered wearing a mask while visiting the markets, with the same number having considered wearing gloves.

Each reported percentage is the unweighted sample mean (divided by 100). Much more accurate estimates for each of those quantities can be calculated using the method proposed in this paper.

The need for accurate estimates becomes acute when we consider evaluating the effectiveness of an intervention. Suppose an intervention program is introduced to a community to increase the wearing of gloves when working in the markets. We need to compare wearing gloves in the community before and after the intervention, or with the rate in a community without the intervention program. If the estimates are highly biased or erratic in their statistical properties, then the comparisons may be in error and lead to choosing the less effective intervention for roll-out on a larger scale.

A number of studies have sampled bats from their natural habitats, tested them for coronavirus species, and through phylogenetic analyses established their relationship to species that have infected or can infect humans ([Ge et al., 2013], [Li et al., 2005], [Wang et al., 2006], [Wang and Anderson, 2019], [Olival et al., 2017b], [Olival et al., 2017a], [Hu et al., 2017], [Corman et al., 2015]).

[Huong et al., 2020] sampled the animals, rather than the humans, along a supply chain in the wildlife trade in Vietnam. The animals on their way to market and restaurants were tested for infection with bat coronavirus species. They found that the infection rate increased along the supply chain. For example, field rats for food, in the possession of the trappers who catch them wild in the field, had a 21% infection rate. For rats in the markets, the infection rate was 32%. At the restaurants that served wild animal dishes, the infection rate in the rats was 56%. The presumed reason for the amplification of infection rate along the supply chain was overcrowding in the cages the animals were transported and held in, so that infection rapidly spread between the animals.

If the infection rate of the animals is higher at a point in the supply chain, then the risk to the people who work with them will be higher there.

The way to prevent future outbreaks and pandemics of emerging species of coronavirus in humans is to decrease the frequency of occurrences of transfers of coronaviruses from animals to people. Most of those transfer strains die out before producing any significant outbreak, but some small proportion of them will catch on to produce serious outbreaks as well as new pandemics. If there are less frequent transfers, there should be correspondingly less frequent outbreaks and pandemics.

So far in the 21st Century the serious outbreaks have come 7 and 10 years apart, so the next one could be anticipated to arrive not far in the future. If
through interventions the frequency of transfers could be reduced to one-third its current value, then the next outbreak instead of 7 or 10 years, might be 21 or 30 years in the future. The anticipated outbreaks before then would have been prevented.

Potential interventions suggested by the currently available studies would include programs to increase the use of protective measures like washing hands and use of gloves and masks in working with animals. To reduce the amplification of infection rates along the supply chain, safer and more humane transfer cages would need to be designed and required.

Sampling both of the people exposed to animals and of the animals they are potentially exposed to will be required to accurately assess the effectiveness of different intervention strategies and select thereby the best interventions to make. The key missing tool up to this point has been an accurate, robust estimation method for snowball sampling designs. The purpose of this paper is to present such a method.

1.2 Adaptive spatial designs for animal species

In addition to snowball sampling of the people exposed to animals, we need to sample the animals they are exposed to, in order to estimate the prevalence of coronavirus infection in those animals, and to obtain the genetic sequences of those virus. In some cases the sampling of the animals will be straightforward, using conventional sampling design features such as random sampling without replacement and stratification. This may be the case in markets and wildlife farms. If we need to sample wild animals living nearby the people, such as bats with natural roosting sites in trees, adaptive spatial designs could be useful.

The adaptive designs work by starting with an initial conventional sample, such as a random sample of spatial units. Whenever a significant number of animals is found in a sample unit, its neighboring units are added to the sample. If any of those has significance abundance, its neighbors in turn are added, and so on ([Thompson, 1990]). In ([Thompson, 2006], which was first about network designs for estimating prevalence of risk behaviors for HIV, it is shown that any of the spatially adaptive design can be re-framed as a network sampling problem (see also [Thompson, 2011]. In ([Thompson, 2006] this was done for a spatially uneven population of wintering waterfowl, and proved very effective there. In the same way the network sampling estimators proposed in the present paper can be used for adaptive spatial sampling designs and have some advantages in terms over previous estimators for adaptive sampling designs in terms of simplicity and flexibility.

The re-framing of an adaptive spatial design as network sampling works as follows. In the spatial setting suppose for simplicity the sampling units are square plots covering the study region. Convert each square plot to a circle representing a node in a network. If plot $i$ has animals in it, then if we observe $i$ it will lead us to any of its neighbors. So for a neighbor $j$ draw an arrow from $i$ to $j$. If unit $j$ has animals in it, then if it was observed first it would lead us
to $i$, so draw an arrow from $j$ to $i$. With arrows in both directions, the link between $i$ and $j$ is symmetric, so it can also be drawn as a simple line. Now suppose unit $j$ has no animal in it. Then it will not lead us to its neighbor $i$. So there is an arrow from $i$ to $j$ but not from $j$ to $i$. So the link is directional here, and we get a network that is partially directional. The estimation method work fine with the directional links in the network. This re-framing is illustrated in the figures of [Thompson, 2006] and [Thompson, 2011].

1.3 HIV-at-risk sexual networks, opioid networks

With the HIV epidemic the key populations at risk include people who inject drugs non-medically, people who sell or buy sex, or trade it for drugs or tangible goods, and men who have sex with men. To study these people and try to alleviate the epidemic, ethnographers and health outreach workers used link-tracing methods. In the 1980s and 1990s these were usually in the form of snowball designs.

Snowball sampling methods were used in [Potterat et al., 1999] to obtain data on the entire network and people of a population at risk for heterosexual and drug-related spread of HIV. In the study, investigators endeavoured to find the individuals at both ends of every relevant relationship. Because of the relative geographic isolation of the high-risk population, they were able to obtain essentially the entire population and its network structure. This population data set has been invaluable to studies of network sampling and estimation methodologies. It is used in this paper for the simulations to evaluate the effectiveness of the proposed estimators for snowball network designs in comparison with other estimation methods.

Snowball sampling designs, the most freely-branching of the network designs, are useful for studying the sexual and injection-related networks in which HIV spreads. [Peters et al., 2016] and [Campbell et al., 2017] report on a study in which contact tracing was used after an HIV outbreak associated with opioid misuse in Indiana had spread rapidly. The traced network together with phylogenetic data from sequencing of virus strains was used to determine where the outbreak started and how it spread.

Snowball designs are generally the preferred network sampling method for bringing interventions to benefit a population. Contact tracing for sexually transmitted diseases has long used snowball sampling. An individual who tests positive for the disease is asked to identify all their recent sexual partners. Investigators attempt to find each of those partners, inform them of their potential exposure, test then for the infection and, if the test is positive, to treat them to cure the infection and then in turn try to trace all their partners and do the same. In the current coronavirus pandemic, contact tracing of individuals who test positive involves finding all their recent contacts and at minimum to advise those individuals to self-isolate for a period. And in the more thorough versions, the contacts when found are also tested and, if a test is positive, that person’s contacts are traced as well.

For HIV there is currently no cure or vaccine available. There are effective
interventions such as increasing use of condoms and targeting condom use to the early period in any new relationship. In [Thompson, 2017] it is shown that distributing such an intervention program to some proportion of the population using a snowball network design is highly effective in comparison to the same intervention distributed to the same proportion of the population by other methods.

1.4 Snowball sampling

Early uses of network sampling for hard-to-reach populations typically used snowball sampling methods. Ethnographers studying drug users and other hidden populations wanted to know as many of the relationships in the community so tried to follow every referral to social partners. The data was summarized by unweighted sample means and proportions [Spreen, 1992, Heckathorn, 1997, and Thompson and Collins, 2002]. Design-based estimates of population values from relatively simple network sampling designs were obtained by Birnbaum and Sirken, 1965 and Frank, 1977, Frank and Snijders, 1994, and Birnbaum and Sirken, 1965.

Snijders, 1992 reviewed the literature on snowball sampling for inference about population values. The estimates at that time were limited to the more simple snowball designs, such as one-wave designs with symmetric. He concluded that snowball sampling is more suited for inference about the links than for inference about the nodes. [Heckathorn, 2011] [Handcock and Gile, 2011] look at different uses of the term “snowball sampling”.

Model-based methods can work well for snowball designs but, in addition to requiring a stochastic network model for the population, may be limited too specific forms of snowball designs, such as ones in which all links are traced out to a certain number of waves ([Chow and Thompson, 2003a], Chow and Thompson, 2003b, Thompson and Frank, 2000).

Pattison et al., 2013 assume an exponential random graph model and describe a conditional estimation strategy for estimating parameters of the model, with attention to computational efficiency so that large samples can be handled. The focus is on identifying structural characteristics of the population network, such as stars and triangles of various types.. Values of nodes, such as whether an animal is infected or the person handling it wears gloves, are not usually included in this type of model. The method appears to work well for its intended purposes. [Handcock and Gile, 2007] provide an informative discussion of design characteristics in relation to model-based inferences for network samples. [Handcock and Gile, 2010] describe a Bayesian model based approach for inference from snowball samples. The method works well but is limited to specific types of snowball designs, such as those where every like is followed out to some wave. The main limitation of the model-based estimation methods for snowball sampling may be to scale-up, because the Markov Chain Monte Carlo method required in the computations get slow as sample size increases. [Atkinson and Flint, 2001] review the
methodology for snowball sampling and conclude that snowball sampling is highly effective for finding members of a hidden population but that statistical inference from snowball samples was at the time of their writing problematical. 

[Thompson, 2006] gives a design-based strategy for snowball network designs with estimation based on one or another simple, if inefficient, initial estimator. That estimate is improved using the Rap-Blackwell method, which finds the conditional expectation of the initial estimator given the minimal sufficient statistics. In the network designs considered the minimal sufficient statistics is the set of distinct units in the sample, not counting repeat selections and not distinguishing order of selection. The estimates obtained are exactly unbiased and are very efficient, having low variance because of the Rao-Blackwell improvement. However, the method requires control over the initial design that may not be achieved in practice with hard-to-reach populations, and because of the Markov Chain Monte Carlo needed to do the Rao-Blackwell computations, may be limited in terms of scale up to large sample sizes.

In contrast to snowball sampling, the methodology of Respondent-Driven-Sampling ([Heckathorn, 1997]), limited the number of contacts a respondent could refer to a small number, typically 3. Estimators for these designs based on random walk theory and assumptions of Markov transitions in the sampling between values of attribute variables of respondents were given in [Salganik and Heckathorn, 2004], [Heckathorn, 2007], and [Volz and Heckathorn, 2008]. In a random walk design only one link is traced from the currently selected person, and the sampling is done with replacement. If a random walk is run in a network consisting of a single connected component, the long term frequency of inclusion of node $i$ is proportional to $d_i$. Variations on these early approaches, still relying on the assumption of a random walk design or Markov transitions include [Gile, 2011], [Baraff et al., 2016], and [Rohe et al., 2019].

Among network sampling designs, a snowball design is at the opposite end of the spectrum from a random walk design. A freely-branching snowball design allows unlimited branching, up to however many links are available, and is usually carried out without-replacement. For these reasons the estimators based on the random walk assumption have never been recommended for snowball designs, nor should they be.

The idea of the new estimation method is very simple. We run a sampling process similar to the actual survey design on the sample network data and use the inclusion frequencies in the sampling process to estimate the inclusion probability of each sample unit in the real-world sampling. With the estimated inclusion probabilities, well-established sampling inference methods can be used for population estimates and confidence intervals. Two approaches to the re-sampling are repeated re-samples and a Markov chain resampling process. For the simulations we use the resampling process because it is computationally much faster.

The estimation method and why it works are described more exactly in the Methods section.
2 Methods

2.1 The new estimation method

In traditional survey sampling with unequal probabilities of inclusion for different people, typical estimators divide an observed value \( y_i \) for the \( i \)th person by the inclusion probability \( \pi_i \) that person. A variable of interest \( y_i \) can be binary, for example 1 if the person tests positive for a virus and 0 otherwise, or can be more generally quantitative, such as viral load. The inverse-weighting gives an unbiased or low-bias estimate of the population proportion or mean of that variable. In network surveys the inclusion probabilities are unknown so they need to be estimated.

The estimators described in this report first estimate the inclusion probability of each person in the sample by selecting many resamples from the network sample data using a design that adheres in key features to the actual survey design used to find the sample. In particular, the resampling design is a link-tracing design done without-replacement and with branching, as was the original design. The frequency \( f_i \) with which an individual is included in the resamples is used as an estimate of that person’s inclusion probability \( \pi_i \).

What we do is select \( T \) resamples \( S_1, S_2, \ldots, S_T \) from the sample network data. There are two approaches to selecting the sequence of resamples. In the repeated-samples approach each resample is selected independently from seeds and progresses step-by-step to target resample size independently of every other resample, so we get a collection of independent resamples. In the sampling-process approach each resample \( S_t \) is selected from the resample \( S_{t-1} \) just before it by randomly tracing a few links out and randomly removing a few nodes from the previous resample and using a small rate of re-seeding so we do not get locked out of any component by chance. It is this Markov resampling process approach that we use for the simulations in this paper because it is so computationally efficient.

For an individual \( i \) in the original sample, there is a sequence of zeros and ones \( Z_{i1}, Z_{i2}, \ldots, Z_{iT} \), where \( Z_{it} = 1 \) if that person is included in resample \( S_t \) and is 0 if the person is not included in that resample. The inclusion frequency for person \( i \) is

\[
f_i = \frac{1}{T} (Z_{i1} + Z_{i2} + \ldots + Z_{iT})
\]

Individuals centrally located in sample components tend to have high values of \( f_i \). That is because there are more paths, and paths of higher probability, leading the sample to those individuals. Also, individuals in larger components tend to have larger \( f_i \) than individuals in smaller components, so that the method is estimating inclusion probability of an individual relative to all other sample units, not just those in the same component or local area or the sample. This is because of the self-allocation of the branching design, even in the absence of re-seeding, to areas of the social network having more links and connected paths.
The estimator of the mean of a characteristic \( y \) in the hidden population is then

\[
\hat{\mu}_f = \frac{\sum (y_i/f_i)}{\sum (1/f_i)}
\]

(2)

where each sum is over all the people in the sample. If the actual inclusion probabilities \( \pi_i \) were known and replaced the \( f_i \) in Equation 2 we would have the generalized unequal probability estimator \( \hat{\mu}_\pi \) of [Brewer, 1963]. A simple variance estimator to go with \( \hat{\mu}_f \) is

\[
\hat{\text{var}}(\hat{\mu}) = \frac{1}{n(n-1)} \sum_s \left( \frac{ny_i/f_i}{\sum_s (1/f_i)} - \hat{\mu}_f \right)^2
\]

(3)

An approximate \( 1 - \alpha \) confidence interval is then calculated as \( \hat{\mu} \pm z \sqrt{\hat{\text{var}}(\hat{\mu})} \), with \( z \) the \( 1 - \alpha/2 \) quantile from the standard Normal distribution.

### 3 Results

The new estimators are evaluated and compared with the current estimates using the network data on the hidden population at risk for HIV enumerated in the Colorado Springs study on the heterosexual transmission of HIV [Potterat et al., 1999], also known as the Project 90 study. The study was so thorough in finding every linked person that it provides the most relevant network data set that can be considered as an entire at-risk population for the purpose of comparing sampling designs and estimators. In the simulations, the population size is 5,492, the number of people in the data set. From this population a sample of 1,200 people is selected, using a snowball design. For resampling the target resample size is 400. For each of 1,000 samples of size 1,200 each, 10,000 resamples were selected, each resample of size about 400. The population and the simulation methods are described in more detail in the Methods section.

The most commonly used estimator with network surveys in current practice is the VH estimator. The other variations in use such as SH are related to it and are based on the same assumptions plus the additional assumption of a first-order Markov process in transitions between node attribute values during the sampling. The SH estimator is used mainly for binary attribute variables. For categorical variables it has the property that the proportion estimates do not add to one without extra adjusting of one kind or another, and it is not well suited to continuous variables.

#### 3.1 Mean degree and concurrency

Among the most important quantities to estimate in relation to spread of HIV are the means and proportions of link-related variables. Two of widespread interest are mean degree and concurrency. Mean degree is the average number of partners per person in the population. The most common definition of concurrency is the proportion of people in the population who have two or
Figure 3: Mean squared error for three estimators of mean number of partners (mean degree), with a regular snowball design (left) and with a snowball design allowing re-recruitment of a person by different recruiters (right). The three estimators are the sample mean (Y-BAR, white), weighting by reciprocal of self-reported degree (VH, yellow), and the new estimator (NEW, black). Small MSE is good, so the new estimator is performing much the best.
Figure 4: Mean squared error for three estimators of concurrency, with a regular snowball design (left) and with a snowball design allowing re-recruitment of a person by different recruiters (right). The three estimators are the sample mean (Y-BAR, white), weighting by reciprocal of self-reported degree (VH, yellow), and the new estimator (NEW, black).
more partners. This and related definitions of concurrency and their role in spreading HIV are discussed in [Kretzschmar and Morris, 1996], [Morris and Kretzschmar, 1997], and [Admiraal et al., 2016]. A high number for either of these is an indication that an epidemic could spread rapidly in the population once it starts there. With the reference data set we are using for the simulations, a link indicates either a sexual relationship, a drug relationship, or a friendship relationship. Because friendship is included, the proportion of people with at least one relationship is very close to 1.00. Therefore we use a definition of concurrency here, which might be called “k-concurrency with k=10,” where a person is concurrent if they have more than 10 relationships. The true proportion of this is .82. The purpose here is to compare estimation methods for the mean of a characteristic of a node that is highly related to links. Because inclusion probabilities in network sampling depend on the pattern of links in the population in interaction with the design, these variables are the most sensitive to choice of estimator.

The bars in Figure 3 show the mean squared error of three estimators for estimating mean degree with the regular snowball design. We include the sample mean as an estimator because it is the one most commonly used to summarize the results in a snowball survey. We include the estimator $\hat{\mu}_d = \sum [(y_i/d_i)/\pi_i]$, which uses the self-reported degree $d_i$ as in place of the inclusion probability $\pi_i$ in Brewer’s estimator, because it is widely used, though not recommended for snowball sampling. It would be the correct estimator, equal to Brewer’s, if the design used had been a random walk instead of a snowball design, and if the self-reported degrees were accurate. It was used by [Salganik and Heckathorn, 2004] to estimate mean degree and by [Volz and Heckathorn, 2008] for estimating any kind of variable. We abbreviate it here VH.

Looking at the actual numbers represented in Figure 3 with the snowball design the MSEs of y-bar, VH, and the new estimator are respectively 40.453589, 7.249053, and 0.264755. Dividing the MSE of the sample mean by that of the new estimator gives the relative efficiency of the new estimator as 153. The relative efficiency of the new estimator for the VH estimator is 29. The high MSE of the sample mean and VH for snowball sampling is almost entirely due to bias. For any estimator MSE = Variance + (Bias)$^2$. For the sample mean, the bias squared is over 99% of the variance. For the VH the squared bias is 99% of the variance. So a bar plot of the bias of the estimators looks almost exactly the same as the bar plot for MSE in Figure 3.

The large biases result from using the wrong sampling weights in the estimators in relation to the actual inclusion probabilities $\pi_i$. The new estimator estimates those inclusion probabilities using the sample network of the data in interaction with the actual snowball design used or a close approximation to it. Because the estimated inclusion probabilities $f_i$ come out close to proportional to the actual inclusion probabilities $\pi_i$, the bias is virtually eliminated with the new estimation method.

For the snowball design allowing re-recruitments the relative efficiency of the new estimator to y-bar for estimating mean degree is 329, and to VH the
relative efficiency of the new estimator is 59. The high MSEs of $y$-bar and VH again are mostly due to bias.

For the estimate of $k$-concurrency, with $k = 10$, the MSE values with the regular snowball design for $y$-bar, VH, and the new estimator are 0.010717 0.043369 0.000447. The relative efficiency of the new estimator to the sample mean is 24. The relative efficiency of the new estimator to the VH estimator is 97. The squared bias accounts for 99% of the MSE of $y$-bar, and 98% of the MSE of the VH estimator.

For the snowball design allowing re-recruitments the relative efficiency of the new estimator to $y$-bar for estimating $k$-concurrency, with $k = 10$, is 17, and to VH the relative efficiency of the new estimator is 70. The high MSEs of $y$-bar and VH again are explained largely by the bias due to the incorrect weightings relative to the inclusion probabilities of the snowball design used in the survey.

Notice also that the magnitudes of MSE of $y$-bar and VH reverse in relation to each other, with VH performing better than $y$-bar for mean degree and worse than VH for $k$-concurrency. When the sampling weights of estimators differ significantly from the inclusion probabilities of the survey, the estimators not only perform poorly in most cases, but the performance is erratic, depending on the exact configuration of values of variables of interest and of the sampling weights in the population. In the present study, only the new estimator, with its inclusion probabilities estimated from the sample data and the actual design, performed consistently well for every variable and with each design.

### 3.2 Attribute variables

The Colorado Springs Study node data includes 13 individual attribute variables such as sex worker, client of sex worker, or unemployed. These are variables 1 through 13 in Table 1. For an individual, the value is 1 if the individual has the attribute and 0 otherwise. The object for inference for each attribute is to estimate the proportion of people in the population having that attribute. Most of these variables, such as sex or race or employment status, are not strongly or consistently related to inclusion probabilities. Still, for design-based estimators to work well it helps to have the estimated inclusion probabilities close to the actual inclusion probabilities. For the simulations, missing values were arbitrarily set to zero so that sample sizes would be the same for all variables.

With a conventional simple random sampling design for estimating a population proportion, the mean squared error of the estimate is a parabola-shaped function of the actual population proportion. The actual proportion has to be between zero and one. The MSE is highest when the actual proportion is one-half and the MSE is zero when the actual proportion is zero or one. With the network designs and their unequal inclusion probabilities the situation is more complex, but it is still the case that the actual proportion has to be between zero and one and that the MSE will be
Figure 5: With the regular snowball design, the mean squared error of three estimators of population proportion for each of 13 individual attributes. The three estimators are the sample mean (Y-BAR, white), weighting by reciprocal of self-reported degree (VH, yellow), and the new estimator (NEW, black). The new estimator (black) is compared to the current estimator (yellow). To help see the pattern, the MSE for estimating the compliment of each attribute is also shown. The compliment of sex work client, for example, is not-client. A parabolic curve is fitted by weighted least squares to the MSEs of the new estimator (solid line) and the current estimator (dashed line). The new estimator MSEs have the lowest fitted curve and the best fit.
Figure 6: With the snowball design allowing re-recruitments, the mean squared error of three estimators of population proportion for each of 13 individual attributes. The three estimators are the sample mean (Y-BAR, white), weighting by reciprocal of self-reported degree (VH, yellow), and the new estimator (NEW, black). The new estimator (black) is compared to the current estimator (yellow). To help see the pattern, the MSE for estimating the compliment of each attribute is also shown. The compliment of sex work client, for example, is not-client. A parabolic curve is fitted by weighted least squares to the MSEs of the new estimator (solid line) and the current estimator (dashed line). The new estimator MSEs have the lowest fitted curve and the best fit.
zero if the actual proportion is zero or one.

To help see the pattern in the mean squared errors for estimating the population proportions of the 13 attribute variables, the MSE for each variable is plotted in Figure 3 against the actual proportion of people having that attribute in the Colorado Springs study population. For each of the 13 variables, we can also estimate the proportion for its complement. The compliment of “client”, for example, is “not client”. The proportion for the compliment is 1 minus the proportion with the attribute, and the MSE for estimation of the compliment is the same as the the MSE for estimation of the original variable. This gives us 26 variables for each plot in Figure 3, with actual proportions ranging from near 0 to near 1. The original variables are on the left, since the actual proportions are all less than one-half. The compliment variables provide redundant information but clarify the pattern in the MSEs.

The MSE with the new estimator (black in plots) is lower than that of the current estimator in all cases except for some of the ones with actual proportion near to zero for which the MSE is very small with either estimator. While the MSEs of the new estimator fall rather close to the fitted parabola (solid line), the MSEs of the current estimator are more erratic and the fitted parabola (dashed line) is higher. The overall higher MSEs and erratic pattern with the current estimator result from the discrepancies between actual inclusion probabilities and those used in estimation.

| name             | actual | E.se  | width | coverage |
|------------------|--------|-------|-------|----------|
| 1 nonwhite       | 0.24   | 0.023 | 0.04  | 0.91     |
| 2 female         | 0.43   | 0.029 | 0.06  | 0.98     |
| 3 sex work       | 0.05   | 0.010 | 0.02  | 0.94     |
| 4 procures       | 0.02   | 0.005 | 0.01  | 0.96     |
| 5 sex-work client| 0.09   | 0.016 | 0.03  | 0.95     |
| 6 sells drugs    | 0.06   | 0.011 | 0.02  | 0.92     |
| 7 makes drugs    | 0.01   | 0.004 | 0.01  | 0.80     |
| 8 stealing       | 0.02   | 0.007 | 0.01  | 0.94     |
| 9 retired        | 0.03   | 0.009 | 0.02  | 0.92     |
| 10 homemaker     | 0.06   | 0.011 | 0.02  | 0.94     |
| 11 disabled      | 0.04   | 0.009 | 0.02  | 0.95     |
| 12 unemployed    | 0.16   | 0.017 | 0.03  | 0.96     |
| 13 homeless      | 0.01   | 0.005 | 0.01  | 0.86     |
| 14 no. partners  | 7.88   | 0.287 | 0.56  | 0.70     |
| 15 concurrency   | 0.82   | 0.035 | 0.07  | 1.00     |

The parabolas in the plots have form MSE = ap(1 − p) where p is the actual proportion, which is known for each of the 13 attribute variables in the simulation population. The coefficient a measures the height of the fitted parabola for a given estimator-design combination. Since the relationship is linear with increasing variance in the quantity p(1 − p), the weighted least
Table 2: SB re-recruit design: Confidence Interval Coverage, median is .92

| name              | actual | E.se  | width | coverage |
|-------------------|--------|-------|-------|----------|
| 1 nonwhite        | 0.24   | 0.024 | 0.05  | 0.97     |
| 2 female          | 0.43   | 0.031 | 0.06  | 0.98     |
| 3 sex work        | 0.05   | 0.010 | 0.02  | 0.93     |
| 4 procures        | 0.02   | 0.005 | 0.01  | 0.81     |
| 5 sex-work client | 0.09   | 0.016 | 0.03  | 0.95     |
| 6 sells drugs     | 0.06   | 0.011 | 0.02  | 0.95     |
| 7 makes drugs     | 0.01   | 0.004 | 0.01  | 0.75     |
| 8 stealing        | 0.02   | 0.007 | 0.01  | 0.90     |
| 9 retired         | 0.03   | 0.009 | 0.02  | 0.91     |
| 10 homemaker      | 0.06   | 0.012 | 0.02  | 0.92     |
| 11 disabled        | 0.04   | 0.010 | 0.02  | 0.92     |
| 12 unemployed     | 0.16   | 0.018 | 0.03  | 0.95     |
| 13 homeless        | 0.01   | 0.005 | 0.01  | 0.80     |
| 14 no. partners   | 7.88   | 0.267 | 0.52  | 0.85     |
| 15 concurrency    | 0.82   | 0.038 | 0.07  | 0.99     |

Squares regression estimator of the coefficient $a$ is a simple ratio estimator. Consider that the variable $y = \text{MSE}$ linearly increases with the variable $x = p(1 - p)$ and that the variance of $y$ about this line increases with $x$, approximately linearly. From weighted regression results this suggests, as an estimator for the slope $a$, the ratio estimator $\hat{a} = \sum y_i / \sum x_i$. So for an overall comparison of the estimator y-bar with the new estimator, let $a_{\text{ybar}}$ and $a_{\text{new}}$ represent the estimated parameters of the respective lines. The ratio $a_{\text{ybar}} / a_{\text{new}}$ is simply the sum of the MSEs with y-bar divided by the sum of the MSEs with the new estimator, because the $x$-values are the same with each design, so their sums divide out. Thus the ratio of the estimated parabola parameters $a$ is simply the ratio of the average MSE for the two designs. It’s also the ratio of heights of the two parabolas at any point. This ratio provides a measure of average relative efficiency of the two designs.

For the regular snowball design, the overall relative efficiency of the new estimator to the sample mean is $a_{\text{ybar}} / a_{\text{new}} = 0.02231997 / 0.002791733 = 8.0$. The relative efficiency of the new estimator to the VH estimator is $0.01079285 / 0.002791733 = 3.9$.

For the snowball design allowing re-recruitments, the overall relative efficiency of the new estimator to the sample mean is $a_{\text{ybar}} / a_{\text{new}} = 0.02244716 / 0.002445438 = 9.2$. The relative efficiency of the new estimator to the VH estimator is $0.01078216 / 0.002445438 = 4.4$. To see these relative parabola heights in Figures 5 and 6, note the position of zero on the vertical axis.

Confidence interval coverage probabilities for each variable for each of the 15 variables are given in Tables 1 and 2. The median coverage probability of the intervals for the 15 characteristics estimated with each of two designs is .94.
4 Discussion and conclusions

Snowball designs are the most natural of the network designs and have many desirable properties. They self-allocate so that most of the sample size goes into the most highly connected parts of the population. This leads investigators to those areas where risk of spread of a virus is highest. This makes snowball designs highly effective for distributing an intervention such as a vaccine to a population.

Snowball designs have been used less than they should be because a simple design-based estimator has not been available. The new method of this paper provide such estimators.

Snowball designs and accurate estimators to go with them are needed for preventing new pandemics from the coronaviruses family of viruses. They are needed for understanding sexual networks on which HIV spreads and opioid misuse networks which spread their own harms and occasionally provide explosive terrain for HIV. The new estimators can also be used for adaptive spatial designs for hard-to-sample animal species, by translating the spatial structure into network form.

Accurate estimation with snowball designs requires estimating the inclusion probabilities $\pi_i$ from the data taking the actual survey sampling design into account. Sample means and proportions do not provide good estimates or data summaries for snowball samples. Estimators that weight observations by the reciprocal of the unit’s degree also do not work well with snowball sampling designs.

The new estimates are fast to compute, scale up well, and are based on the data and the design actually used rather than unrealistic assumptions. They are low-bias, accurate, and give reliable confidence intervals.

Acknowledgements

This research was supported by Natural Science and Engineering Research Council of Canada (NSERC) Discovery grant RGPIN327306. I would like to thank John Potterat and Steve Muth for making the Colorado Springs study data available and for their generous help explaining it. I would like to express appreciation for the participants in that study who shared their personal information with the researchers so that it could be made available in anonymized form to the research community and contribute to a solution to HIV and and addiction epidemics and to basic understanding of social networks.

References

[Admiraal et al., 2016] Admiraal, R., Handcock, M. S., et al. (2016). Modeling concurrency and selective mixing in heterosexual partnership networks with
applications to sexually transmitted diseases. *The Annals of Applied Statistics*, 10(4):2021–2046.

[Andersen et al., 2020] Andersen, K. G., Rambaut, A., Lipkin, W. I., Holmes, E. C., and Garry, R. F. (2020). The proximal origin of sars-cov-2. *Nature medicine*, 26(4):450–452.

[Atkinson and Flint, 2001] Atkinson, R. and Flint, J. (2001). Accessing hidden and hard-to-reach populations: Snowball research strategies. *Social research update*, 33(1):1–4.

[Baraff et al., 2016] Baraff, A. J., McCormick, T. H., and Raftery, A. E. (2016). Estimating uncertainty in respondent-driven sampling using a tree bootstrap method. *Proceedings of the National Academy of Sciences*, 113(51):14668–14673.

[Birnbaum and Sirken, 1965] Birnbaum, Z. and Sirken, M. G. (1965). Design of sample surveys to estimate the prevalence of rare diseases: three unbiased estimates, vital and health statistics, series 2. *Government Printing Office, Washington, DC*.

[Brewer, 1963] Brewer, K. (1963). Ratio estimation and finite populations: Some results deducible from the assumption of an underlying stochastic process. *Australian Journal of Statistics*, 5(3):93–105.

[Campbell et al., 2017] Campbell, E. M., Jia, H., Shankar, A., Hanson, D., Luo, W., Masciotra, S., Owen, S. M., Oster, A. M., Galang, R. R., Spiller, M. W., et al. (2017). Detailed transmission network analysis of a large opiate-driven outbreak of hiv infection in the united states. *The Journal of infectious diseases*, 216(9):1053–1062.

[Chow and Thompson, 2003a] Chow, M. and Thompson, S. K. (2003a). A bayesian approach to estimation with link-tracing sampling designs. *Survey Methodology*, 29:197–205.

[Chow and Thompson, 2003b] Chow, M. and Thompson, S. K. (2003b). Estimation with link-tracing sampling designs a bayesian approach. *Survey Methodology*, 29(2):197–206.

[Corman et al., 2015] Corman, V. M., Baldwin, H. J., Tateno, A. F., Zerbinati, R. M., Annan, A., Owusu, M., Nkrumah, E. E., Maganga, G. D., Oppong, S., Adu-Sarkodie, Y., et al. (2015). Evidence for an ancestral association of human coronavirus 229e with bats. *Journal of virology*, 89(23):11858–11870.

[Frank, 1977] Frank, O. (1977). Survey sampling in graphs. *Journal of Statistical Planning and Inference*, 1(3):235–264.

[Frank and Snijders, 1994] Frank, O. and Snijders, T. (1994). Estimating the size of hidden populations using snowball sampling. *Journal of Official Statistics*, 10:53–53.
[Ge et al., 2013] Ge, X.-Y., Li, J.-L., Yang, X.-L., Chmura, A. A., Zhu, G., Epstein, J. H., Mazet, J. K., Hu, B., Zhang, W., Peng, C., et al. (2013). Isolation and characterization of a bat sars-like coronavirus that uses the ace2 receptor. *Nature*, 503(7477):535–538.

[Gile, 2011] Gile, K. J. (2011). Improved inference for respondent-driven sampling data with application to hiv prevalence estimation. *Journal of the American Statistical Association*, 106(493):135–146.

[Graham and Baric, 2010] Graham, R. L. and Baric, R. S. (2010). Recombination, reservoirs, and the modular spike: mechanisms of coronavirus cross-species transmission. *Journal of virology*, 84(7):3134–3146.

[Handcock and Gile, 2010] Handcock, M. and Gile, K. (2010). Modeling social networks from sampled data. *The Annals of Applied Statistics*, 4(1):5–25.

[Handcock and Gile, 2007] Handcock, M. S. and Gile, K. (2007). Modeling social networks with sampled or missing data. *Center for statistics and the social sciences working paper no.75. University of Washington, Department of Statistics*.

[Handcock and Gile, 2011] Handcock, M. S. and Gile, K. J. (2011). Comment: On the concept of snowball sampling. *Sociological Methodology*, 41(1):367–371.

[Heckathorn, 1997] Heckathorn, D. D. (1997). Respondent-driven sampling: a new approach to the study of hidden populations. *Social problems*, 44(2):174–199.

[Heckathorn, 2007] Heckathorn, D. D. (2007). Extensions of respondent-driven sampling: Analyzing continuous variables and controlling for differential recruitment. *Sociological Methodology*, 37(1):151–208.

[Heckathorn, 2011] Heckathorn, D. D. (2011). Comment: Snowball versus respondent-driven sampling. *Sociological Methodology*, 41(1):355–366. PMID: 22228916.

[Huong et al., 2020] Huong, N. Q., Nga, N. T. T., Long, N. V., Luu, B. D., Latinne, A., Pruvot, M., Phuong, N. T., Quang, L. T. V., Hung, V. V., Lan, N. T., Hoa, N. T., Minh, P. Q., Diep, N. T., Tung, N., Ky, V. D., Roberton, S. I., Thuy, H. B., Long, N. V., Gilbert, M., Wicker, L., Mazet, J. A. K., Johnson, C. K., Goldstein, T., Tremeau-Bravard, A., Ontiveros, V., Joly, D. O., Walzer, C., Fine, A. E., and Olson, S. H. (2020). Coronavirus testing indicates transmission risk increases along wildlife supply chains for human consumption in viet nam, 2013-2014. *PLoS ONE*, 15(8):1–20.
[Kretzschmar and Morris, 1996] Kretzschmar, M. and Morris, M. (1996). Measures of concurrency in networks and the spread of infectious disease. *Mathematical biosciences*, 133(2):165–195.

[Latinne et al., 2020] Latinne, A., Hu, B., Olival, K. J., Zhu, G., Zhang, L., Li, H., Chmura, A. A., Field, H. E., Zambrana-Torrelio, C., Epstein, J. H., et al. (2020). Origin and cross-species transmission of bat coronaviruses in China. bioRxiv.

[Li et al., 2019] Li, H., Mendelsohn, E., Zong, C., Zhang, W., Hagan, E., Wang, N., Li, S., Yan, H., Huang, H., Zhu, G., et al. (2019). Human-animal interactions and bat coronavirus spillover potential among rural residents in southern China. *Biosafety and Health*, 1(2):84–90.

[Li et al., 2005] Li, W., Shi, Z., Yu, M., Ren, W., Smith, C., Epstein, J. H., Wang, H., Crameri, G., Hu, Z., Zhang, H., et al. (2005). Bats are natural reservoirs of sars-like coronaviruses. *Science*, 310(5748):676–679.

[Montgomery and Macdonald, 2020] Montgomery, R. A. and Macdonald, D. W. (2020). Covid-19, health, conservation, and shared wellbeing: Details matter. *Trends in Ecology & Evolution*.

[Morris and Kretzschmar, 1997] Morris, M. and Kretzschmar, M. (1997). Concurrent partnerships and the spread of HIV. *AIDS*, 11(5):641–648.

[Olival et al., 2017a] Olival, K. J., Hosseini, P. R., Zambrana-Torrelio, C., Ross, N., Bogich, T. L., and Daszak, P. (2017a). Erratum: Host and viral traits predict zoonotic spillover from mammals. *Nature*, 548(7669):612–612.

[Olival et al., 2017b] Olival, K. J., Hosseini, P. R., Zambrana-Torrelio, C., Ross, N., Bogich, T. L., and Daszak, P. (2017b). Host and viral traits predict zoonotic spillover from mammals. *Nature*, 546(7660):646–650.

[Pattison et al., 2013] Pattison, P. E., Robins, G. L., Snijders, T. A., and Wang, P. (2013). Conditional estimation of exponential random graph models from snowball sampling designs. *Journal of mathematical psychology*, 57(6):284–296.

[Peters et al., 2016] Peters, P. J., Pontones, P., Hoover, K. W., Patel, M. R., Galang, R. R., Shields, J., Blosser, S. J., Spiller, M. W., Combs, B., Switzer, W. M., et al. (2016). HIV infection linked to injection use of oxymorphone in Indiana, 2014–2015. *New England Journal of Medicine*, 375(3):229–239.

[Potterat et al., 1999] Potterat, J. J., Rothenberg, R. B., and Muth, S. Q. (1999). Network structural dynamics and infectious disease propagation. *International journal of STD & AIDS*, 10(3):182–185.

[Rohe et al., 2019] Rohe, K. et al. (2019). A critical threshold for design effects in network sampling. *The Annals of Statistics*, 47(1):556–582.
Salganik and Heckathorn, 2004] Salganik, M. J. and Heckathorn, D. D. (2004). Sampling and estimation in hidden populations using respondent-driven sampling. *Sociological methodology*, 34(1):193–240.

[Snijders, 1992] Snijders, T. A. (1992). Estimation on the basis of snowball samples: how to weight? *Bulletin of Sociological Methodology/Bulletin de Méthodologie Sociologique*, 36(1):59–70.

[Spreen, 1992] Spreen, M. (1992). Rare populations, hidden populations, and link-tracing designs: What and why? *Bulletin of Sociological Methodology/Bulletin de Methodologie Sociologique*, 36(1):34–58.

[Tang et al., 2020] Tang, X., Wu, C., Li, X., Song, Y., Yao, X., Wu, X., Duan, Y., Zhang, H., Wang, Y., Qian, Z., et al. (2020). On the origin and continuing evolution of sars-cov-2. *National Science Review*.

[Thompson, 2011] Thompson, S. (2011). Adaptive network and spatial sampling. *Survey Methodology*, 37(2):183–196.

[Thompson, 1990] Thompson, S. K. (1990). Adaptive cluster sampling. *Journal of the American Statistical Association*, 85(412):1050–1059.

[Thompson, 2006] Thompson, S. K. (2006). Adaptive web sampling. *Biometrics*, 62(4):1224–1234.

[Thompson, 2017] Thompson, S. K. (2017). Adaptive and network sampling for inference and interventions in changing populations. *Journal of Survey Statistics and Methodology*, 5(1):1–21.

[Thompson and Collins, 2002] Thompson, S. K. and Collins, L. M. (2002). Adaptive sampling in research on risk-related behaviors. *Drug and Alcohol Dependence*, 68:57–67.

[Thompson and Frank, 2000] Thompson, S. K. and Frank, O. (2000). Model-based estimation with link-tracing sampling designs. *Survey methodology*, 26(1):87–98.

[Volz and Heckathorn, 2008] Volz, E. and Heckathorn, D. D. (2008). Probability based estimation theory for respondent driven sampling. *Journal of official statistics*, 24(1):79.

[Wang and Anderson, 2019] Wang, L.-F. and Anderson, D. E. (2019). Viruses in bats and potential spillover to animals and humans. *Current opinion in virology*, 34:79–89.

[Wang et al., 2006] Wang, L.-F., Shi, Z., Zhang, S., Field, H., Daszak, P., and Eaton, B. T. (2006). Review of bats and sars. *Emerging infectious diseases*, 12(12):1834.
[Zhou et al., 2020] Zhou, P., Yang, X.-L., Wang, X.-G., Hu, B., Zhang, L., Zhang, W., Si, H.-R., Zhu, Y., Li, B., Huang, C.-L., et al. (2020). A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, 579(7798):270-273.