Population Size Estimation for Respondent-Driven Sampling and Capture-Recapture: A Unifying Framework

Mamadou Yauck
Department of Mathematics, Université du Québec à Montréal, Montréal, QC, Canada H3C 3P8
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Abstract

This paper deals with the estimation of population sizes for respondent-driven sampling (RDS), a variant of link-tracing sampling that leverages social networks over a number of waves to recruit individuals from hidden populations. The RDS process is mostly controlled by individual participants who might report on recruitment proposals, or nominations, that they have received or given. By considering all nominations given or received over a time period, one can create a capture-recapture dataset in which units are individuals who have received at least one nomination and capture occasions are either time intervals or recruitment waves, with the goal of estimating the size $N$ of the hidden population. In this paper, we argue that the underlying process that generated the RDS nomination data is that of a capture-recapture experiment. We then proposed a methodology for the estimation of the population size and investigated its performance against departures from classical capture-recapture assumptions.

Keywords: hidden population sampling; social networks; capture-recapture; population size.
1 Introduction

*Respondent-driven sampling* (RDS) is a variant of link-tracing sampling that aims to use social relationships to reach individuals from hard-to-reach populations, for which there is no sampling frame and membership may involve stigmatized behavior ([Heckathorn](#1997)). The RDS recruitment is conducted over a number of recruitment waves, with each recruited individual receiving a fixed number of *coupons* and being asked to recruit additional individuals, starting from initial *seed* participants. RDS provides three main advantages over traditional sampling methods. First, the recruitment occurs through many waves, allowing the process to sample farther from the initial seeds. Second, relying on individuals to recruit their peers into the study reduces privacy concerns associated with identifying participants’ personal networks and often boosts participation rates. Finally, participants usually report on the size of their personal network of contacts, allowing analyses to adjust for potential over- (or under-) sampling of those individuals who are more (less) likely to be recruited into the study.

A crucial information, which is generally not sought after in classical RDS studies, is the number of recruitment proposals that each recruited individual received throughout the process. In fact, recruiters are usually not aware of other individuals’ recruitment status. In this case, they might offer to recruit individuals who are already given coupons by other recruiters. Conversely, unrecruited individuals might initially refuse a coupon proposal by a neighbor, but later accept that of another recruiting neighbor. This action is called *nomination*. When recruiters reveal information about the nominations given and received, the underlying process, which will be denoted *RDSn*, might entails crucial information about the size of the target population.

The size $N$ of a hard-to-reach population, one of its main features, is generally unknown
in RDS studies. While there is an important and growing literature on the estimation of means and proportions, statistical methods for the estimation of the size of a hidden population is still an area of great research interest (Spiller et al., 2018). Approaches that rely on the successive sampling approximation to the RDS process have been developed (Handcock et al., 2015). Others methods rely on recruitment timing either in a frequentist framework (Berchenko et al., 2017) or a Bayesian framework (Crawford et al., 2018).

The use of capture-recapture methods for estimating the size of a hidden population is a well-known and proven approach (Otis et al., 1978). A capture-recapture experiment typically consists in repeatedly capturing, marking and releasing units back into the population. The goal of the statistical analysis is to estimate the number of missed units using information on the captured units. Capture-recapture methods have been largely overlooked in RDS studies for the estimation of $N$. The few existing methods that use the principle of capture-recapture consider the RDS sample as an initial capture and rely on other sources of information for subsequent capture events (Johnston et al., 2013; Paz-Bailey et al., 2011).

Statistical methodologies for capture-recapture data can be used for RDSn data. For any recruitment wave, surveyers collect data corresponding to a list of individuals who have received or given a nomination. Each nomination in this context represents a capture. In Section 3 we argue that the underlying process that generated the RDSn data is that of a capture-recapture experiment. We then developed, in Section 4 a methodology for the estimation of $N$ in the presence of RDSn data, under a capture-recapture framework. The performance of our new methodology is investigated in Section 5 under departures from classical capture-recapture assumptions.
2 Population and sample structures

2.1 The graphical structure of the population

We consider a population of individuals connected by social ties. This underlying network structure can be represented by a graph \( G = (V, E) \), where \( V \) represents the set of vertices or nodes, with \( |V| = N \), and \( E \) denotes the set of edges or links shared by nodes. The ordered pair \((u, v) \in E\) denotes an edge, where \( u, v \in V \). For undirected graphs, \((u, v) \in E\) implies \((v, u) \in E\) whereas for directed graphs, \((u, v) \in E\) does not imply \((v, u) \in E\). Two vertices are said to be adjacent if they are linked by an edge. A path between two vertices is a sequence of distinct vertices that are adjacent. Two adjacent vertices are called neighbors. A graph is said to be connected if there is a path from any node to any other node (West, 2017).

Assumption 1. (Population graph). The population graph is an undirected, connected graph \( G = (V, E) \), where \( V \) and \( E \) are finite sets, with \( |V| = N \).

Under this assumption, one can reach any vertex from any other vertex in the graph. This is illustrated in Figure 1.

![Graph Image](image.png)

Figure 1: Representation of a graph of 9 vertices.

Let \( s_{jk} = 1 \) if \((j, k) \in E\) and \( s_{jk} = 0 \) otherwise, with \( s_{jj} = 0 \). We define \( d_j = \sum_{k=1}^{N} s_{jk} \)
as the number of vertices tied with the $j$th vertex of $G$; this represents the degree of the $j$th vertex.

2.2 The classical RDS process

We first describe the classical RDS process for sampling $n$ individuals from the finite population described in Section 2.1. The recruitment, in practice, works as follows. Seeds are first chosen by convenience, generally as volunteers from the target population. The newly recruited individuals report information for the survey, including their degrees $\{d_j\}$. These new recruits become recruiters, and the iterative process continues until a specified sample size is reached.

We assume that the RDS recruitment process takes place within the population graph $G$ and progresses across vertices’ ties, with seeds being chosen at random. Thus, recruitment only occurs between neighboring units. Further, we assume that no individual can be recruited more than once into the study, as it is the case in most RDS studies. Formally, the sampling procedure can be described as follows:

Step 1. In wave zero of recruitment, $s$ individuals are selected as seeds from the population, with probability proportional to degree.

Step 2. The selected seeds recruit individuals from among their unrecruited neighbors; the number of recruits is however bounded above by the number of coupons given to the seeds.

Step 3. The newly recruits are given coupons to recruit from among their unrecruited neighbors. The process continues iteratively until the sample size $n$ is reached.

The process is illustrated in Figure 2. At the end of the recruitment process, we observe all
connections between recruited individuals. Also, all recruited individuals report on their population degrees \( \{d_j\} \). In this paper, we assume that recruited individuals report on nominations that they have received or given at each wave. This underlying RDSn process is illustrated in Figure 3. At the end of the sampling process, the available information for the \( j \)th recruited individual is \( \{d_j, m^1_j, \ldots, m^\ell_j\} \), where \( m^k_j \) represents the number of nominations received by the \( j \)th individual at the \( k \)th recruitment wave, \( k = 1, \ldots, \ell \).

Figure 2: Illustration of the RDS sampling process. The seed is represented in dashed circles. Vertical arrows represent recruiter-recruit relationships.

Figure 3: Illustration of the RDSn process underlying the RDS process of Figure 2. The seed is represented in a dashed circle. Black arrows represent successful nominations, i.e. recruiter-recruit relationships; red arrows represent unsuccessful recruitment nominations. The time event of such nominations is not illustrated in this figure.
3 RDSn as a capture-recapture experiment

Consider a hidden population of $N$ individuals for which an RDS recruitment is being conducted over a finite time period. A member of the population is said to be captured if (i) the person receives a coupon proposal whether or not she/he takes up or refuses the nomination, and (ii) that nomination is recorded by the surveyer. If both conditions for capture are met, and that the probability of both events occurring is constant over time and across individuals, then the total number of captures, which counts the first capture and all nominations, could be thought to have been generated from a binomial distribution with a constant capture probability: this represents capture-recapture model $M_0$. This model implicitly assumes that the capture status of an individual does not affect that of a (non) neighboring individual. The independence assumption may not hold in practice as a recruiter who received a nomination rejection would probably look to recruit another neighboring individual instead of the one who gave the rejection. This will be discussed in Section 4.

One could imagine the number of coupons increasing over time as the number of recruiters grows, even for a short period of time, giving potential recruits an increased chance of being captured. This could be thought of as a time effect with large (small) capture probabilities in periods when the number of coupons is more (less) important, defining capture-recapture model $M_t$.

Capture probabilities may vary across individuals as one might expect people with more popularity, particular traits characterized by homophily, or the tendency for individuals to recruit others with similar traits, or interest in the study to have higher chances of being enrolled or nominated. This type of heterogeneity can be modeled with a binomial distribution with random capture probabilities, leading to model $M_h$. Note that the heterogeneity model $M_h$ implicitly relaxes the independence assumption of models $M_0$ and $M_t$. Further,
a time effect in catchability is indirectly accounted for with model $M_h$ \cite{Link2003, Rivest and Baillargeon2013}.

Two important challenges need to be tackled in the process of arguing for RDSn as a capture-recapture experiment. First, one needs to properly define a capture occasion in the context of an RDS study. In a capture-recapture setting, capture occasions (usually time intervals) are defined and completely controlled by surveyors. In RDS studies, the recruitment process is mostly controlled by participants, including the timeframe for nominations. Second, classical closed population capture-recapture models, which include $M_0$, $M_t$ and $M_h$, assume that population units are available for capture at the beginning of each occasion. This is not the case in RDS since, for any given time interval, only individuals who share ties with recruiters at that time will be available for nomination. Further, a capture-recapture experiment requires a value for the number of capture occasions while RDS studies set out a desired sample size or, in some cases, a number of recruitment waves.

**Assumption 2. (An RDSn nomination occasion).** An RDS recruitment wave represents an RDSn nomination occasion.

In the context of modeling RDSn data as generated from a capture-recapture experiment, this assumption implies that a recruitment wave in an RDS study corresponds to a capture occasion in a traditional capture-recapture study.

4 Modeling of RDSn data

Consider a hidden, networked population of size $N$ described in Section 3 on which an RDS experiment is conducted for $\ell > 1$ waves. This section presents some notations and assumptions, and discusses the likelihood function given the observed data.
4.1 Notations and assumptions

A capture history for an individual in the population is a sequence of 0 (miss) and (1) capture summarized in a vector of size $\ell$, $\omega = (1, 0, \ldots, 0)$. Let $\omega^d$ denote a direct capture history, i.e. occurring in the selection of seed participants, with elements $\omega^d_i = 1$ if the $i$th individual is selected as a seed, and $\omega^d_i = 0$ otherwise. For the $i$th individual, the number of neighbors who received a nomination at the start of the $j$th wave is denoted $A_{ij}$. Let $n_{ind}$ be the number of uniquely captured individuals from the first to the last wave; let $n$ represent the number of uniquely captured individuals throughout the experiment. Finally, we define $p_{ij}$ as the probability of receiving a nomination for the $i$th individual at the $j$th wave. A model for the observed data will be denoted $M_\alpha$, where $\alpha$ represents the source of variation in catchability.

We now present some assumptions regarding the mechanism of the underlying nomination process. These assumptions focus on the network component of the target population and the ways in which neighbors conduct their relationships.

Assumption 3. (No interaction interference). Interactions between two neighbors cannot be affected by other population units’ actions.

This assumption implies that the relationship between two neighbors in terms of nominations is independent of outside events. In particular, the probability of receiving a nomination depends only on individual characteristics of the involved pair.

4.2 Likelihood function

The observed RDSn dataset is given by $\{\omega^d_i, m^j_i, A_{ij}; i = 1, \ldots, N, j = 1, \ldots, \ell\}$, where $\omega^d_i = 0$ and $m^j_i = 0$ for each of the $N - n$ missed individuals. Let $\mathcal{F}_j = \sum_{i=1}^N 1_{A_{ij} > 0}$ be the set of individuals sharing at least a tie with a nominated individual at the $j$th occasion,
with $|\mathcal{F}_j| \leq N$ for all $j = 1, \ldots, \ell$. We assume that individuals are ordered in such a way that $i = 1, \ldots, n$ indexes captured units, and $i = n + 1, \ldots, N$ indexes all missed units throughout the experiment. The likelihood function for $(N, \{p_{ij}\})$ given the observed data can be expressed as

$$L(N, \{p_{ij}\}) = L_1(N, \{p_{i0}\}) \times L_2(N, \{p_{ij; j \geq 1}\}),$$  \hspace{1cm} (1)$$

where

$$L_1(N, \{p_{i0}\}) = \frac{N!}{s!(N-s)!} \prod_{i=1}^{N} p_{i0}^{\omega_{i0}} (1 - p_{i0})^{1-\omega_{i0}},$$  \hspace{1cm} (2)$$

and

$$L_2(N, \{p_{ij; j > 1}\}) \propto \prod_{j=1}^{\ell} \prod_{i=1}^{n_{ind}} p_{ij}^{m_{ij}} (1 - p_{ij})^{\omega_{ij} - m_{ij}} \times \prod_{j=1}^{\ell} \prod_{i=n_{ind}+1}^{n} (1 - p_{ij})^{A_{ij}}.$$  \hspace{1cm} (3)$$

The first component of the likelihood, $L_1$, is based on the distribution probability of $\{\omega_{i0}\}$. The second component $L_2$ is based on the distribution of $\{\omega_{ij}^{ind}\}$ conditional on $\{A_{ij}, m_{ij}\}$; it deals with the network component of the sampling process. When $p_{ij} = p$, the likelihood function $L$ corresponds to that of homogeneous model $M_0$; $p_{ij} = p_j$ gives model $M_t$ while model $M_h$ assumes individual variations in indirect catchability ($p_{ij} = p_i$). When variations in indirect catchability are both individual and temporal, the likelihood is that of model $M_{th}$.

Two main challenges are associated with the likelihood functions given in (2) and (3). For models involving heterogeneity, the set of parameters $\{p_{i0}\}$ cannot be estimated given the observed data. This might be dealt with by positing a distributional assumption on the parameters and working under a generalized mixed effects model framework. Further, the network information $\{A_{ij}\}$ is not readily available to surveyors; its collection might require additional time and resources. To overcome the latter problem, one might work
with the information on whether or not a nomination occurred at least once during a given recruitment wave. The next section addresses both issues.

### 4.3 Capture-recapture model \(M_{th}\) for RDSn data

Let \(\omega_{ind}\) represents an indirect capture history, which entails information on nominations from neighbors, with elements \(\omega_{ij}^{ind} = 1_{m_i > 0} = 1\) if the \(i\)th individual is nominated once at the \(j\)th occasion \((j > 1)\), and \(\omega_{ij}^{ind} = 0\) otherwise. The overall capture history is given by \(\omega = (\omega^d, \omega^{ind})\). Let \(p_\omega\) be the predicted frequency for \(n_\omega\). Under model \(M_{th}\), capture probabilities \(\{p_{ij}\}\), for \(i = 1, \ldots, N\) and \(j = 0, \ldots, \ell\) can be expressed as

\[
\log\left( \frac{p_{ij}}{1 - p_{ij}} \right) = a_i + \beta_j, \tag{4}
\]

where \(\{a_i\}\) are independent random variables with common c.d.f \(H(x)\), \(\{\beta_j\}\) are fixed effects. Given \(\{a_i\}\) and following (4), the probability of observing capture history \(\omega\) is given by

\[
P(\omega|\{a_i\}) = \sum_{i=1}^{N} \prod_{j=0}^{\ell} p_{ij}^{\omega_{ij}} (1 - p_{ij})^{1 - \omega_{ij}}
= \sum_{i=1}^{N} \exp\left\{ \sum_{j=0}^{\ell} \omega_{ij} \beta_j + (\sum_{j=0}^{\ell} \omega_{ij}) a_i \right\} \prod_{j=0}^{\ell} \left\{ 1 + \exp(a_i + \beta_j) \right\}, \tag{5}
\]

The marginal probability of \(\omega\) satisfies

\[
P(\omega) \propto \int_{-\infty}^{+\infty} \prod_{j=0}^{\ell} \left\{ 1 + \exp(a_i + \beta_j) \right\} dH(a). \tag{6}
\]

If we assume that there is a distribution \(K(x)\) satisfying

\[
dK(x) \sim \frac{dH(x)}{\prod_{j=0}^{\ell} \left\{ 1 + \exp(a_i + \beta_j) \right\}}
\]
and that the corresponding distribution is gaussian $N(0, \tau)$, it follows that (Rivest and Baillargeon, 2007)

$$\mu_\omega = N \mathbb{P}(\omega) = \exp \left\{ \gamma + \sum_{j=0}^\ell \omega_j \beta_j + \left( \sum_{j=0}^\ell \frac{\omega_j}{\sqrt{2}} \right)^2 \tau \right\},$$

(7)

where $\gamma$ represents the logarithm of the expected frequency for the missed individuals. A more general formulation of (7) for a specific set of distributions is given by

$$\mu_\omega = \exp \left\{ \gamma + \sum_{j=0}^\ell \omega_j \beta_j + \tau \psi \left( \sum_{j=0}^\ell \omega_j \right) \right\},$$

(8)

where $\psi(y) = \log \{ \int \exp(yx) dK(x) \}$ is a convex function such that $\psi(0) = 0$. For Darroch’s model denoted $M_{Dh}$, which posits a normal distribution for heterogeneity, one has $\psi(\sum_j \omega_j) = (\sum_j \omega_j / \sqrt{2})^2$; a model with a mixture of Poisson distribution, denoted $M_{Ph,a}$, gives $\psi(\sum_j \omega_j) = \exp(a \sum_j \omega_j) - 1$, $a > 1$; a Gamma mixture model for heterogeneity, denoted $M_{Gh,\lambda}$, gives $\psi(\sum_j \omega_j) = - \log(\sum_j \omega_j + \lambda) + \log(\lambda)$, $\lambda > 1$; see Rivest and Baillargeon (2007) for a complete description of closed population heterogeneity models.

In this paper, we assume that the observed frequencies $n_\omega$ have independent Poisson distributions with expectation $\mu_\omega$ (Cormack, 1989):

$$n_\omega \sim \text{Poisson} \left( \mu_\omega \right).$$

(9)

Equations (9) and (8) yield a log-linear model for the RDSn capture-recapture data. This model can be fitted using a Poisson regression; an estimator for the size of the hidden population is then given by $\hat{N} = n + e^{\hat{\gamma}}$, with an estimated variance of $v(\hat{N}) = e^{\hat{\gamma}} (1 + e^{\hat{\gamma}}) v(\hat{\gamma})$, where $v(\hat{\gamma})$ is the variance of the intercept for the Poisson regression; it represents the element (1,1) of the Fisher information matrix for $(\gamma, \{\beta_j\}, \tau)$. Finally, the probability of observing at least one nomination is

$$p^* = \frac{\sum_{\omega \in \Omega} \mu_\omega}{\exp \gamma + \sum_{\omega \in \Omega} \mu_\omega},$$

(10)
where $\Omega$ is the set of all observable nomination histories, with $|\Omega| = 2^{t+1} - 1$. For the simplest model $M_0$, one has $\gamma = \log\{N(1-p)^{t+1}\}$, $\beta = \log\{p/(1-p)\}$, and $p^* = 1 - \{1 + \exp(\beta)\} = 1 - (1 - p)^{t+1}$. A time effect model $M_t$ gives $\gamma = \log\{N \prod_{j=0}^{t}(1 - p_j)\}$, $\beta_j = \log\{p_j/(1 - p_j)\}$, and $p^* = 1 - \prod_{j=0}^{t}(1 + \exp(\beta_j)^{-1} = 1 - \prod_{j=0}^{t}(1 - p_j)$.

5 Empirical simulation study

A simulation study was conducted using a real-world dataset of individuals sharing social network relationships from the Colorado Springs Project 90 study [Klovdahl et al., 1994]. Data on thirteen (13) demographic variables and risk behaviors were collected on drug users and their sexual and needle-sharing associates, and sex workers and their partners, from 1988 through 1992. Around 600 participants reported on their network of contacts within the community, allowing the knowledge of the entire network of social ties. The corresponding social network of 5493 individuals and 21644 connections is distributed among 125 different connected clusters. The largest cluster, which is illustrated in Figure 4, had 81% of the population (4430 individuals) sharing 85% of the social relationships (18407 ties). The goal of the study was to investigate the relationship between the social network structure and the dynamics of HIV transmission in a community of high-risk heterosexuals.
The goal of this simulation study is to investigate the performance of our methodology when the classical RDS recruitment process discussed in Section 2.2, which includes nomination across recruitment waves, is considered. This is a clear departure from classical capture-recapture experiments for two main reasons. First, the number of captures in the first occasion is not fixed as it is the case for the number of seed participants in wave zero of recruitment. The second reason, which is very critical in assessing the validity of inference for \( N \), is that only a portion of the population is available for recruitment at the start of the second wave onwards wave: only individuals who share ties with potential recruiters are available for nominations.

From the largest cluster of the Project 90 network, we simulated RDS samples using the following procedure. First, we randomly selected \( s = 2550 \) seeds with probability
proportional to degree. Each seed recruited, without replacement, \( c = 5, 10 \) neighbors; we assume that each seed successfully recruits one individual on average. Unsuccessful recruitment attempts are considered nominations; the number of nominations for each seed equals the number of coupons minus the number of recruitments. Second, the newly recruited individuals are also given the same number of coupons to recruit among their unrecruited neighbors. The process goes on for \( \ell = 5, 10 \) waves.

The model that provides the best fit for the data, given the RDS recruitment process described in the previous paragraph, was selected in a pool of 8 models: \( M_0, M_t, M_{Ph2}, M_{Dh}, M_{Gh,3.5}, M_{Pth2}, M_{Dth}, M_{Gth,3.5} \). As can be seen in Table 2 (see Appendix), models \( M_t, M_{Pth2}, M_{Dth}, M_{Gth,3.5} \) offer a good fit. However, model \( M_t \) offers consistently the best fit across all simulation scenarios (see further comparisons with the Bayesian Information Criterion in Table 3 of the Appendix).

We finally investigated the performance of the population size estimator under model \( M_t \). We simulated 5000 RDS samples from the Project 90 data and computed the relative bias, the standard error for the relative bias, the coverage and the relative length of the 95% profile confidence interval for \( N \) as can be seen in Table 1. The relative bias is less or equal to 5% and the coverage for the 95% confidence interval is within 3% of its nominal value at most. The results show that departures from a classical capture-recapture sampling process induces negligible bias.
Table 1: Departure from the RDSn process: relative bias (RB), standard error for the relative bias (SE), coverage (Cov) and relative length (RLCI) of the 95% confidence interval for the estimation of \( N \) under capture-recapture model \( M_t \) for a specified number of seeds (s), coupons (c) and capture occasions (\( \ell \)).

| s   | c   | \( \ell \) | \( RB(\hat{N}) \) | \( SE[RB(\hat{N})] \) | 95% Cov. | RLCI |
|-----|-----|---------|-----------------|-----------------|---------|------|
| 5   | 5   | 0.07    | 0.01            | 0.96            | 0.79    |
| 10  | 0.05| 0.006   | 0.94            | 0.39            |
| 25  |     |         |                 |                 |
| 10  | 5   | 0.02    | 0.005           | 0.96            | 0.35    |
| 10  | 0.01| 0.003   | 0.95            | 0.18            |
| 50  |     |         |                 |                 |
| 5   | 5   | 0.04    | 0.006           | 0.96            | 0.37    |
| 10  | 0.04| 0.005   | 0.92            | 0.20            |
| 50  |     |         |                 |                 |
| 10  | 5   | 0.01    | 0.004           | 0.94            | 0.17    |
| 10  | <0.01| 0.002  | 0.93            | 0.09            |

6 Discussion

The estimation of the size of a hard-to-reach population under RDS raises challenging theoretical and methodological issues. This paper has argued that, by leveraging information on recruitment proposals, capture-recapture methods can be used to estimate the size of the target population. Although deviations from classical capture-recapture assumptions are shown to induce negligible bias, improved models are needed to provide a more realistic picture of RDS recruitment processes. This will be the object of future work.
Appendix

Departure from a classical capture-recapture sampling process: model selection

Table 2: Deviances (Dev) over degrees of freedom (df), Dev/df, for 10 closed population capture-recapture models fitted to 1000 simulated RDSn datasets for a specified number of seeds (s), coupons (c) and capture occasions (ℓ).

| s   | c  | ℓ   | M₀  | Mₜ  | Mₕ₂  | M₝ₜ  | Mₜ₢₅ | Mₚₙ₂  | Mₚₜ₂  | Mₚₜ₃  | Mₚₜ₅  |
|-----|----|-----|-----|-----|------|------|------|------|------|------|------|
| 5   | 5  | 0.84| 0.57| 0.84| 0.84 | 0.55 | 0.55 | 0.55 |
| 10  | 0.12| 0.08| 0.12| 0.12| 0.12 | 0.08 | 0.08 | 0.08 |
| 25  | 1.09| 0.82| 1.09| 1.09| 1.09 | 0.81 | 0.81 | 0.81 |
| 10  | 0.23| 0.17| 0.23| 0.23| 0.23 | 0.17 | 0.17 | 0.17 |
| 50  | 1.55| 0.81| 1.57| 1.57| 1.57 | 0.80 | 0.80 | 0.80 |
| 10  | 0.26| 0.15| 0.26| 0.26| 0.26 | 0.15 | 0.15 | 0.15 |
| 10  | 1.82| 0.97| 1.85| 1.85| 1.85 | 0.97 | 0.97 | 0.97 |
| 10  | 0.48| 0.32| 0.48| 0.48| 0.48 | 0.32 | 0.32 | 0.32 |
Table 3: Bayesian Information Criterion (BIC) for 10 closed population capture-recapture models fitted to 1000 simulated RDSn datasets for a specified number of seeds ($s$), coupons ($c$) and capture occasions ($\ell$).

| $s$ | $c$ | $\ell$ | $M_0$  | $M_\ell$ | $M_{Pth,2}$ | $M_{Dh}$ | $M_{Gh,3.5}$ | $M_{Pth,2}$ | $M_{Dh}$ | $M_{Gh,3.5}$ |
|-----|-----|-------|--------|----------|-------------|---------|---------------|-------------|---------|---------------|
| 5   | 5   | 25    | 98.24  | 113.30   | 103.65      | 103.57  | 103.55        | 118.71      | 118.62  | 118.61        |
|     |     | 50    |        |          |             |         |               |             |         |               |
| 10  | 5   | 25    | 311.32 | 333.53   | 317.42      | 317.19  | 317.18        | 339.63      | 339.40  | 339.39        |
|     |     | 50    |        |          |             |         |               |             |         |               |

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