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Elusive Population Size**

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## Two-Step Centre Sampling for Estimating Elusive Population Size

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**Abstract.** The estimation of the size of an elusive population is a problem frequently addressed in many fields of applications. In the paper, under the assumption that each unit of the population is present at least in one centre of aggregation, a two step sampling strategy for the estimation of the population size is proposed. At the first step a sample of centres is selected, at the second step, from the selected centres, a sample of ultimate units is observed. The design extends the traditional network sampling introducing an additional step of selection. The properties of the Horvitz-Thompson type estimator are evaluated in a design-based approach: the estimator is admissible and consistent; the design is measurable. The approach is also used to estimate other descriptive parameters (the total and the mean of a study variable) for the same population. The expressions of the variance of all the proposed estimators and of their unbiased sample estimators are also proposed. The strategy is applied to a simulated population.

**Key words:** Two-step centre sampling, Network sampling, Centre of aggregation, Multiplicity, Horvitz and Thompson estimator

## 1 Introduction

The single step centre sampling was introduced by Blangiardo (1996) in order to obtain reliable information about elusive populations. Two different approaches for single step centre sampling have been developed in literature. Both are based on the following assumptions: each member of the population attends at least one centre of aggregation; the centres are known (or have been identified in previous surveys) and their number is finite. In the first approach (Mecatti and Migliorati 2001) an overall sample of individuals is selected drawing a simple random sample of fixed size independently from each centre and the distribution of population members among the aggregation centres is estimated and used in order to obtain an estimator for the mean of a characteristic of interest. Blangiardo, Migliorati and Terzera (2004) use this approach also to obtain an estimator of the population size.

In the other approach developed by Pratesi and Rocco (2002) a simple random sample of centres is selected and all the individuals of the sampled centres are considered. The individuals in the selected centres are assumed identifiable and they are stratified by their multiplicity (number of frequented centres). The network sampling theory is then adapted to the estimation of the population size (Birbaum and Sirken 1965). Diana et al (2003) use this approach also to obtain an estimator of the total and the mean of a study variable selecting the centres with unequal selection probability design.

Following this second approach, when the number of individuals in the selected centres is relevant, it is reasonable to propose a second step of selection. The individuals in the selected centres are listed and only a random sample of them is observed. For each selected ultimate unit we assume to know its multiplicity (the number of frequented

centers in the population). The design extends the traditional network sampling introducing an additional step of selection.

The methodology is useful also when the population is not elusive and several lists of the population members exist, but they are supposed to be incomplete or not well maintained. Many contributions explain how to use the lists jointly to estimate the population size (Haines, Pollock, Pantula, 2000; Pratesi, 2001) but they limit the analysis to situation where all the lists are considered. When the lists (capture occasions /centres) are many, it is reasonable to select a sample of them and, if the size of each list is relevant, it is natural to select a random sample of their units.

In section 2 the two-step selection procedure is described and the probabilities of inclusions are derived. Section 3 is devoted to the estimators of the population size and of the total and the mean of a study variable and to the properties of the two-step strategy. Concluding remarks, on the basis of a simulation study, described in section 4, are outlined in section 5.

## **2 The two-step centre sampling procedure**

Assume that the population is composed by units that are present at least in one centre. The objective is the estimation of  $N_c$ , the size of the population. The two steps sampling procedure first randomly selects  $m$  centres from the list of  $M$  centres of aggregation. Then, the list of the units in each selected centre is built and a simple random sample of units is independently selected from each centre. Since we assumed that each unit may be in more than one center, the final size of the sample  $n$  is generally less or equal to the direct summation of the centre sample sizes ( $\sum_{i=1}^m n_i \geq n$ ).

Each unit in the population has the possibility to be selected in the sample  $s$ , but the more are the centres at which a given unit is linked, the higher is the probability that the unit will be included in the sample.

### 2.1 The probability of inclusion of the first order

At the first-step the first order inclusion probability of unit  $i$ ,  $\pi_{i1}$ , depends on the number  $g$  of centres where the unit is present (its multiplicity) besides depending on the total number  $M$  of centres in the population and the number of selected centres  $m$ . The higher is its multiplicity, the higher is the probability that the unit is enclosed in the sample. The probability is constant for all the units with the same multiplicity.

$$\pi_{i1} = 1 - \frac{\binom{M-g}{m}}{\binom{M}{m}} \quad \text{or equivalently} \quad \pi_{i1} = \sum_h \frac{\binom{m}{h} \binom{M-m}{g-h}}{\binom{M}{g}} = \pi_g$$

with  $h = [\max(1, m+g-M), \dots, \min(g, m)]$  and  $\pi_g = 1, \forall g > M-m$ .

In order to define the second-step first order inclusion, let  $s_k$  be the event "the sample selected from the centre  $k$  includes the unit  $i$  given that  $i$  is in  $k$ ", then:

$$\pi_{i2|1} = \Pr\left(\bigcup_k s_k\right)$$

where the logic summation is extended on the number of events. This number depends on the number of selected centres  $m$  and on the multiplicity of the unit  $i$  in the selected centres. The probability depends also on the sampling fraction in the selected centers,

$\frac{n_k}{N_k}$ . The details for the derivation of the previous expression and an example are

reported in the Appendix A.

### 2.2 The probability of inclusion of the second order

The second order inclusion probabilities are defined on the two steps of selection as

$$\text{well: } \pi_{ij} = \pi_{ij1} \cdot \pi_{ij2|i}.$$

The probability  $\pi_{ij1}$  depends on the multiplicities of individual  $i$  and  $j$  (respectively  $g$  and  $g'$ ) and on the number of centres to which both the individuals belong (common centres,  $c$ ). Consider from now on, only  $g \leq g'$ , for the symmetry of the matrix of the probabilities of inclusion. The expression of the second order inclusion probability at the first step is:

$$\pi_{ij1} = \pi_g + \pi_{g'} - 1 + \frac{\binom{M-g-g'+c}{m}}{\binom{M}{m}} = \begin{cases} \pi_g & \text{if } c = g \\ \frac{\binom{c}{l} \binom{g-c}{h} \binom{g'-c}{k} \binom{M-g-g'+c}{m-l-h-k}}{\binom{M}{m}} & \text{otherwise} \end{cases}$$

where  $l$ ,  $h$  and  $k$  can assume the following values:

$$l = (0, \dots, \min(c, m));$$

$$\text{if } c=0 \text{ or } l=0, h = (1, \dots, \min(g-c, m-1)) \text{ and } k = (1, \dots, \min(g-c, m-h));$$

$$\text{if } l \neq 0, h = (0, \dots, \min(g-c, m-l)) \text{ and } k = (0, \dots, \min(g-c, m-l-h)).$$

The second order inclusion probabilities at the second step  $\pi_{ij2|i}$  are:

$$\pi_{ij2|i} = \Pr\left(\bigcup_{k,h} (s_k \cap (s_h | i))\right)$$

where  $s_k$  is the event “the sample selected from the centre  $k$  includes the unit  $i$  given that the unit  $i$  is in the centre  $k$ ” and  $s_h | i$  is the event “the sample selected from the center  $h$  includes the unit  $j$ , given that the unit  $i$  was selected and that the unit  $j$  is in the centre  $h$ ”. The logic summation is extended on the number of events  $s_k \cap (s_h | i)$ .

This number depends on number of selected centres  $m$ , on the multiplicity of the units  $i$

and  $j$  in the selected centres, and on the number of common centres in the selected centres. The details for the derivation of the previous expression and an example are reported in the Appendix A.

Note that under the condition that at least two centres are selected and that at least two units are selected from each of them, both the components of second order inclusion probability  $\pi_{ij1}$  and  $\pi_{ij2|1}$  are strictly positive and so  $\pi_{ij} = \pi_{ij1} \cdot \pi_{ij2|1} > 0 \quad \forall i, j$ .

### 3 The estimation of the population size and of the total and the mean of the study variable

#### 3.1 The unbiased estimation of the population size

The process of selection, described in the previous section produces two final complementary outcomes: the unit  $i$  is or is not in the sample  $s$ . The two events are described by an indicator variable  $I_i$  (1 if  $i \in s$ , 0 otherwise) and its expected value, the probability of inclusion in the sample, is calculated conditionally to the first step of selection:

$$E(I_i) = E_1(E(I_i | 1)) = E_1(E(I_{i1} \cdot I_{i2|1})) = E_1(I_{i1}) \cdot E(I_{i2|1}) = \pi_{i1} \cdot \pi_{i2|1} = \pi_i$$

where  $I_{i1}$  is the belonging indicator of  $i$  to one of the selected centres (at the first step the event “ $i$  is in  $s$ ” is equivalent to the event “one or more of the centres which  $i$  is linked to, is selected”), and  $I_{i2|1}$  is the indicator of the selection of unit  $i$  among the units of the selected centre.

An Horvitz-Thompson type estimator of  $N_c$  is:

$$\hat{N}_c = \sum_{i=1}^{N_c} \frac{I_i}{\pi_i} \text{ or equivalently } n_c = \sum_{i=1}^n \frac{1}{\pi_i}$$

with variance:

$$V(\hat{N}_c) = \sum_{i=1}^{N_c} \frac{V(I_i)}{\pi_i^2} + 2 \sum_{i < j}^{N_c} \frac{\text{cov}(I_i, I_j)}{\pi_i \pi_j}.$$

The proposed centre sampling design, under the condition that at least two centres are selected, is measurable (Särndal et al., 1992). In other words,  $\pi_{ij} > 0 \forall i, j$ . So the design allows the calculation of valid variance estimates. An unbiased estimator of the variance, which however may seldom assume non positive values, is:

$$v(\hat{N}_c) = \sum_{i=1}^n \frac{(1 - \pi_i)}{\pi_i} + 2 \sum_{i < j}^n \left( \frac{\pi_{ij}}{\pi_i \pi_j} - 1 \right) \cdot \frac{1}{\pi_{ij}}.$$

Under the two-step centre sampling design,  $\hat{N}_c$  is unbiased for  $N_c$  and, being an Horvitz-Thompson estimator, is admissible in the class of all the unbiased estimator of  $N_c$  (Cassel et al., 1977).

### 3.2 The unbiased estimator of the total of a study variable

The Horvitz-Thompson type estimator of  $Y$  is easily derived by the above expressions for the estimator of the population size:

$$\hat{Y} = \sum_{i=1}^{N_c} \frac{I_i \cdot y_i}{\pi_i} \text{ or equivalently } y = \sum_{i=1}^n \frac{y_i}{\pi_i}$$

with variance:

$$V(\hat{Y}) = \sum_{i=1}^{N_c} \frac{V(I_i) \cdot y_i^2}{\pi_i^2} + 2 \sum_{i < j}^{N_c} \frac{\text{cov}(I_i, I_j) \cdot y_i y_j}{\pi_i \pi_j}.$$



An unbiased estimator of the variance  $V(\hat{Y})$  is:

$$v(\hat{Y}) = \sum_{i=1}^n \frac{(1 - \pi_i) \cdot y_i^2}{\pi_i} + 2 \sum_{i < j}^n \left( \frac{\pi_{ij}}{\pi_i \pi_j} - 1 \right) \cdot \frac{y_i y_j}{\pi_{ij}}$$

Under the two-step centre sampling design,  $\hat{Y}$  is unbiased for  $Y$  and admissible in the class of all the unbiased estimator of  $Y$  (Cassel et al., 1977).

### 3.3 The approximately unbiased estimator of the mean of a study variable

An approximately unbiased estimator for the population mean  $\bar{Y}$  is given by the weighted sample mean

$$\hat{\bar{Y}} = \frac{\hat{Y}}{\hat{N}_c}$$

Its approximate variance is:

$$V(\hat{\bar{Y}}) = \frac{1}{N_c^2} \sum_{i=1}^{N_c} \sum_{j=1}^{N_c} (\pi_{ij} - \pi_i \pi_j) \frac{(y_i - \bar{Y})(y_j - \bar{Y})}{\pi_i \pi_j}$$

and its sample estimator is:

$$v(\hat{\bar{Y}}) = \frac{1}{\hat{N}_c^2} \sum_{i=1}^n \sum_{j=1}^n \left( \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \right) \frac{(y_i - \hat{\bar{Y}})(y_j - \hat{\bar{Y}})}{\pi_i \pi_j}$$

## 4 Some empirical results

A Monte Carlo experiment was carried out on the simulated population given in Pratesi and Rocco (2002): in the following this population is indicated as *population 1*. The population size is  $N_c = 3100$  individuals, each individual frequents at least one of the

$M = 4$  centres ( $A, B, C, D$ ). The structure of *population 1* is described in Table 1 and Table 2: Table 1 contains the multiplicity profile of the population and the distribution of the study variable  $Y$  by profile. The partial totals  $Y_i$  associated to each profile are derived by the numerical example given in Diana et al. (2003). Table 2 summarizes the joint distribution of the population by centre and multiplicity profile.

**Table1.** Multiplicity profile of *population 1*

Multiplicity profiles	Centres				Frequency of the profile	Partial totals of the profile
	<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>		
Only 1 centre	1	0	0	0	200	3240
	0	1	0	0	300	4550
	0	0	1	0	400	6119
	0	0	0	1	300	4957
Only 2 centres	0	1	1	0	200	4960
	0	0	1	1	300	4476
	1	0	1	0	300	4954
	0	1	0	1	400	6607
	1	1	0	0	100	3111
	1	0	0	1	100	2938
Only 3 centres	1	1	1	0	200	4487
	1	0	1	1	50	2525
	1	1	0	1	100	2310
	0	1	1	1	100	2742
All 4 centres	1	1	1	1	50	2340
					3100	60316

Each row of Table 1 represents a possible multiplicity profile. In the example there are 4 multiplicity profiles: the profile “only one centre” occurs when the individual frequents only 1 centre; the profile “only two centres” occurs when the individual frequents only two of the four centres, and so on. The number of different occurrences of each profile is equal to the combination without replacement of the number of frequented centres on the total number of centres  $M = 4$ . For example, the profile “only two centres” can occur in 6 different manners.

**Table 2.** *Population 1: joint distribution by centre and multiplicity profile*

Multiplicity profile	Centre A		Centre B	
	Number of individuals	%	Number of individuals	%
Only 1 centre	200	18,18	300	20,69
2 centres	500	45,45	700	48,28
3 centres	350	31,82	400	27,59
4 centres	50	4,55	50	3,45
	1100	100	1450	100
Multiplicity profile	Centre C		Centre D	
	Number of individuals	%	Number of individuals	%
Only 1 centre	400	25,00	300	21,43
2 centres	800	50,00	800	57,14
3 centres	350	21,88	250	17,86
4 centres	50	3,13	50	3,57
	1600	100	1400	100

Given the partial totals  $Y_i$  associated to each profile, individual values of the study variable  $Y$  in *population 1* have been simulated in the following cases:

1. *uniform distribution in the profile*: the study variable for the individual  $i$  in the centre  $h$ , indicated by  $y_{ih}$ , is the result of the equal distribution of the profile partial total  $Y_i$  among the individuals with the same profile.
2. *normal distribution in the profile*: the study variable for the individual  $i$  in the centre  $h$  is normally distributed with mean equal to the profile mean,  $\bar{Y}_i = Y_i / N_i$ , and variance equal to  $(c.v(Y) \cdot \bar{Y}_i)^2$ , for different values of the coefficient of variation of the study variable:  $c.v(Y) = 0.5, 1, 2$ .
3. *lognormal distribution in the profile*: the study variable for the individual  $i$  in the centre  $h$  follows a lognormal distribution with mean equal to the profile mean,  $\bar{Y}_i = Y_i / N_i$ , and variance equal to  $(c.v(Y) \cdot \bar{Y}_i)^2$ , for different values of the coefficient of variation of the study variable:  $c.v(Y) = 0.5, 1, 2$ .

The synthesis of the distribution of the study variable by multiplicity profile for each of the simulated populations are reported in Appendix B: mean, total, standard deviation and coefficient of variation of the study variable  $Y$  in the population are shown for each occurrence of the multiplicity profile.

The experiment consisted in 1000 two-step centre random selections according to the following rules: a simple random sample of  $m = 2$  centres was drawn, then only a simple random sample of their units was observed. For each sample the estimates  $\hat{N}_c$  and  $v(\hat{N}_c)$ ,  $\hat{Y}$  and  $v(\hat{Y})$ ,  $\hat{\bar{Y}}$  and  $v(\hat{\bar{Y}})$ , were calculated. The sampling distribution of each of the above estimators, indicated by  $\hat{\theta}$ , is then summarized by its expected value,  $\hat{E}(\hat{\theta})$ , empirical bias  $d_{\hat{\theta}} = (\hat{E}(\hat{\theta}) - \theta) / \theta$ , sampling variance,  $v_1 = \hat{E}(\hat{\theta} - \hat{E}(\hat{\theta}))^2$ , and by the expected value of the variance estimator,  $v_2 = \hat{E}(v(\hat{\theta}))$ .

#### 4.1 Estimation of the population size: empirical sampling distribution of $\hat{N}_c$

The variability of the estimator of the population size is a function of the first and second order probabilities of inclusion. They are determined, as shown in section 2, by the second step sampling fraction and by both the multiplicity of the single individuals and of the couples of individuals.

The results for different sampling fractions in the centres are reported in Table 4, which shows the effect of a constant sampling fraction for  $f = 20\%$ ,  $33\%$ , and of a variable sampling fraction obtained selecting the same number of individual  $n_i = 279$  from each centre in such a way that the average final sample size is the same than for  $f = 20\%$  ( $\bar{n} = 537$ ).

The effect of the multiplicity of the single individuals and of the couples of individuals is shown in Table 5. The same size of the population,  $N_c$ , can be reached moving the joint distribution of the individuals by centre and multiplicity profile. Then, the simulation study has been repeated in order to single out the effect on the variability of the estimator of the distribution by multiplicity profile. We moved the distribution by profile of Table 2 (*population 1*), given the marginal distribution of the individuals by centre. The target population has been modified as shown in Table 3 (*population 2*): in italics the percentage distribution by centre, given the multiplicity profile.

**Table 3.** Population 2: joint distribution by centre and multiplicity profile

Multiplicity profile	Centre A		Centre B	
	Number of individuals	%	Number of individuals	%
Only 1 centre	300	27,03 <i>24,39</i>	315	21,72 <i>25,61</i>
2 centres	500	45,05 <i>19,23</i>	685	47,24 <i>26,35</i>
3 centres	290	26,13 <i>17,58</i>	430	29,66 <i>26,06</i>
4 centres	20	1,80 <i>25,00</i>	20	1,38 <i>25,00</i>
	1110	100	1450	100
Multiplicity profile	Centre C		Centre D	
	Number of individuals	%	Number of individuals	%
Only 1 centre	280	17,50 <i>22,76</i>	335	23,93 <i>27,24</i>
2 centres	780	48,75 <i>30,00</i>	635	45,36 <i>24,42</i>
3 centres	520	32,50 <i>31,52</i>	410	29,29 <i>24,85</i>
4 centres	20	1,25 <i>25,00</i>	20	1,43 <i>25,00</i>
	1600	100	1400	100

The rationale of the modification is to mimic a situation that is likely in real life applications: centres which attract more people, in our simulation centre B and C, are

likely to attract individuals with higher multiplicity profile. In other words, under the assumption that each individual frequents at least one centre, crowded centres are more likely frequented by individuals who frequent also other centres. In the economy of our simulation this means that, given the centres, the percentage of individuals with multiplicity profile “only 3 centres” is higher in Table 3 than in Table 2 (centre B: 30% vs 28%, centre C: 33% vs 22%, centre D: 29% vs 18%). Given the multiplicity profile, centre B and C are more attractive for people with multiplicity 2 and 3: centre B attracts the 26% of those individuals and centre C, respectively, the 30% and 31% (see figures in italics in Table 3). Obviously this is not true for the individuals who frequent all the centres: the percentage is 25% for all the 4 centres.

**Table 4.** Sampling distribution of  $\hat{N}_c$  by sampling fraction

	$f$	$\bar{n}$	$\hat{E}(\hat{N}_c)$	$d_{\hat{N}_c}$	$v_1$	$v_2$	$d_v$
Constant fraction	20%	537	3110	0.0033	70377	72128	0.024
	33%	872	3110	0.0033	68840	70010	0.017
Variable fraction	$n_i = 279$	537	3111	0.0035	70908	71648	0.010

The empirical bias  $d_{\hat{N}_c} = (\hat{E}(\hat{N}_c) - N_c) / N_c$  is negligible for both the constant sampling fractions and also in case of variable sampling fraction. Also the empirical bias of the estimator of the variance,  $d_v = (v_1 - v_2) / v_1$ , is acceptable both in case of constant and variable sampling fractions. The effect of the increase in the sampling fraction on the variability of the population size estimator is in line with our expectations: when the sampling fraction increase both the sampling variance,  $v_1$ , and the expected value of the variance estimator,  $v_2$  decrease. Given the target population of Table 1 and 2, the exact

variance of the estimator  $\hat{N}_c$  under the one step centre design is 68266.67 (average sample size  $\bar{n} = 1441$ , see Pratesi and Rocco, 2002): the evidence seems to be that the second step of selection does not add a relevant quota to the variance. The increase of  $v_1$  is under about the 5% of the reference value for both the second step constant sampling fractions (3.1% for  $f = 20\%$ , 0.8% for  $f = 33\%$ ). Fixing the average sample size the results seem equivalent both for constant sampling fraction  $f = 20\%$  and variable sampling fraction  $n_i = 279$ .

The effect of the distribution of the individuals by centre and multiplicity profile can be seen from the results of Table 5. The simulation has been repeated for constant and variable sampling fraction for the two different target populations (*population 1* and *population 2*) described above. The variability of our estimator is highly influenced by the distribution of the individuals among the centres. It seems that an higher concentration of individuals with high multiplicity in crowded centres dramatically reduces the variability of our estimator: in case of *population 2* both  $v_1$  and  $v_2$  are more than the 80% lower than in *population 1*. The reduction in variability is obtained for constant and variable sampling fraction.

**Table 5.** Sampling distribution of  $\hat{N}_c$  by target population

Sampling fraction	target	$\bar{n}$	$\hat{E}(\hat{N}_c)$	$d_{\hat{N}_c}$	$v_1$	$v_2$	$d_v$
$f = 20\%$	<i>population 1</i>	537	3110	0.0033	70377	72128	0.0249
$f = 20\%$	<i>population 2</i>	534	3095	-0.0015	13068	12496	-0.0348
$n_i = 279$	<i>population 1</i>	537	3111	0.0035	70908	71648	0.0104
$n_i = 278$	<i>population 2</i>	536	3095	-0.0015	13141	12657	-0.0368

4.2 Estimation of the population total and mean: empirical sampling distribution of  $\hat{Y}$  and of  $\hat{\bar{Y}}$

The two step centre sampling allows for the unbiased estimation of the total of the study variable and the approximately unbiased estimation of the population mean. The empirical sampling distribution of the estimators  $\hat{Y}$  and of  $\hat{\bar{Y}}$  has been summarized in Tables 6 and 7 for different distribution of the study variable  $Y$  in the population. The simulation has been carried out selecting 1000 two step centre samples from *population 1* with constant sampling fraction ( $f = 20\%$ ) at the second step.

Table 6. Sampling distribution of  $\hat{Y}$  ( $Y=60316, f = 20\%, \bar{n} = 537$ )

Population 1	$\hat{E}(\hat{Y})$	$d_{\hat{Y}}$	$v_1 \times 10^{+7}$	$v_2 \times 10^{+7}$	$d_v$
uniform distribution in the profile	60475	0.0062	1.2717	1.2855	0.0108
normal distribution in the profile – cv=0.5	60496	0.0030	1.4850	1.4301	-0.0370
normal distribution in the profile – cv=1	60527	0.0035	2.0641	1.9209	-0.0694
normal distribution in the profile – cv=2	60677	0.0060	4.8560	4.4885	-0.0757
lognormal distribution in the profile – cv=0.5	60483	0.0028	1.4369	1.4313	-0.0039
lognormal distribution in the profile – cv=1	60482	0.0027	1.8791	1.8340	-0.0240
lognormal distribution in the profile – cv=2	60474	0.0026	3.1946	3.0606	-0.0420

The results in Tables 6 and 7 confirm that the variability of the total and mean estimators is linked to the variability of the study variable in the population: the empirical sampling variance  $v_1$  increases when the coefficient of variation in the



population increases. This happens for normal, lognormal and uniform distribution of the study variable in the profile. The expected value of the variance estimator  $v_2$  follows the same pattern.

Table 7. Sampling distribution of  $\hat{Y}$  ( $\bar{Y} = 19.4568$ ,  $f = 20\%$ ,  $\bar{n} = 537$ )

Population 1	$\hat{E}(\hat{Y})$	$d_{\hat{Y}}$	$v_1$	$v_2$	$d_v$
uniform distribution in the profile	19.4891	0.0017	0.3469	0.4194	0.0724 <sup>(*)</sup>
normal distribution in the profile – cv=0.5	19.4949	0.0020	0.5312	0.5921	0.0609 <sup>(*)</sup>
normal distribution in the profile – cv=1	19.5039	0.0024	1.0960	1.1311	0.0320
normal distribution in the profile – cv=2	19.5491	0.0047	3.9189	3.8951	-0.0061
lognormal distribution in the profile – cv=0.5	19.4907	0.0017	0.4764	0.5719	0.0956 <sup>(*)</sup>
lognormal distribution in the profile – cv=1	19.4890	0.0017	0.8931	0.9922	0.0991 <sup>(*)</sup>
lognormal distribution in the profile – cv=2	19.4847	0.0014	2.1937	2.2629	0.0315

<sup>(\*)</sup> when  $v_1$  is less than 1 we have considered  $d_v = (v_1 - v_2)$  rather than  $d_v = (v_1 - v_2)/v_1$

Given the target population of Table 1 and 2, the exact variance of  $\hat{Y}$  and  $\hat{Y}$  under the one step centre design are, respectively, 11749234.7 and 0.314 (average sample size  $\bar{n} = 1441$ , see Diana et al. 2003). The second step of selection add to this variance a variable quota depending on the distribution of the study variable in the profiles.

Note that in a single step selection we observe completely the multiplicity profiles of the individuals which are present in one of the selected centres. In other words, the selection of the centres induces the “selection” of the multiplicity profiles. When there is a second step of selection we observe only part of the multiplicity profiles selected at

the first step: the part that corresponds to the individuals which are in the centres and are selected at the second step. When the distribution of the study variable in the profile is uniform, this does not cause an appreciable increase in the variability of the estimators. For the uniform distribution we have only a relative increase of the 8% for the total estimator  $\hat{Y}$  and of the 10% for the mean estimator  $\hat{\bar{Y}}$ . In the other situations (normal and lognormal distributions with different cvs) the variance increases dramatically. For the simulated populations where the two estimators reach the highest variability (see Tables 6 and 7: normal distribution in the profile with  $cv=2$ ) the variability of the estimators is more than doubled: we have 48560000 vs 11749235 for the total estimator  $\hat{Y}$  and 3.9189 vs 0.314 for the mean estimator  $\hat{\bar{Y}}$ .

The enlargement of the sampling fraction produces on the variability of the two estimators  $\hat{Y}$  and  $\hat{\bar{Y}}$  the same effect seen for the population size estimator: when the sampling fraction increases both the sampling variance,  $v_1$ , and the expected value of the variance estimator,  $v_2$  decrease (see Table 8 that reports the results for the uniform distribution of the study variable in the profile).

**Table 8.** Sampling distributions of  $\hat{Y}$  and  $\hat{\bar{Y}}$  for different sampling fractions

Sampling fraction	Estimator	$\hat{E}(\hat{\theta})$	$d_{\hat{\theta}}$	$v_1$	$v_2$	$d_v$
$f = 20\%$	$\hat{Y}$	60475	0.0062	1.2717	1.2855	0.0108
$f = 33\%$	$\hat{Y}$	60487	0.0028	1.2261	1.2290	0.0023
$f = 20\%$	$\hat{\bar{Y}}$	19.489	0.0017	0.3469	0.4194	0.0724 <sup>(*)</sup>
$f = 33\%$	$\hat{\bar{Y}}$	19.491	0.0018	0.3224	0.3917	0.0693 <sup>(*)</sup>

<sup>(\*)</sup> when  $v_1$  is less than 1 we have considered  $d_v = (v_1 - v_2)$  rather than  $d_v = (v_1 - v_2)/v_1$

## 5 Concluding remarks

The two-step centre sampling adapts and extends the network sampling introducing an additional selection step. This is appreciable when the centres aggregate many units: time and costs of the survey decrease and, at the same time, the proposed estimators of the population size ( $\hat{N}_c$ ), of the total ( $\hat{Y}$ ) and of the mean ( $\hat{\bar{Y}}$ ) have good properties.

The approach is completely design based, the design is measurable.

The estimator of the population size ( $\hat{N}_c$ ) is admissible, is unbiased and has good empirical properties when we consider efficiency in term of variance and compare it with the one associated to one-step centre sampling.

At the increasing of the final sample size the variance of the two steps estimator vanishes. In other words the sufficient condition for the consistency of the estimator is tenable. In fact, the behaviour of the estimator when the final sample size increases can be explored following the two steps of selection: at first, moving the size of the simple random sample in the selected centre to the population size of the centres themselves, and then increasing the number of selected centres. In the second step given the selected centres, the limit situation is reached when all the sampling fractions in the centres are equal to one. This case corresponds to the selection in one step of a sample of  $m$  centres with complete enumeration of the individuals in the selected centres. At the increasing of the number  $m$  till  $M$  (for elusive populations of increasing size  $M$  can remain constant or increase as well) the most of the terms in the variance of the estimator vanish (see Pratesi and Rocco, 2002).

The variability of the population size estimator  $\hat{N}_c$  is highly influenced by the distribution of the individuals among the centres. This is an advantage of the estimator in real life applications where it is likely that individuals with high multiplicity are

concentrated in crowded centres. In this situation, the variability of our estimator decreases. The reduction in variability is obtained for constant and variable sampling fraction.

The estimator of the total ( $\hat{Y}$ ) is admissible and unbiased. The estimator of the mean ( $\hat{\bar{Y}}$ ) is approximately unbiased. As we expected, the variability of both the estimators is linked to the variability of the study variable in the population: both the sampling variance,  $v_1$ , and the expected value of the variance estimator,  $v_2$ , increase when the coefficient of variation in the population increase. The contribution of the second step of selection to the sampling variance of  $\hat{Y}$  and  $\hat{\bar{Y}}$  is mainly due to the distribution of the study variable in the profiles. The variability of the two step estimators can become relevant in case of high variability of the distribution of the variable in the profiles.

#### Appendix A. Derivation of the second step inclusion probabilities

*The second step inclusion probability of the first order*

Let  $s_k$  be the event “the sample selected from the center  $k$  includes the unit  $i$ ”, equivalent to the event “the unit  $i$  belongs to the sample selected from the center  $k$ ”, then

$$\pi_{i2|1} = \Pr\left(\bigcup_k s_k\right) = \sum_k P(s_k) - \sum_{k<l} P(s_k \cap s_l) + \sum_{k<l<h} P(s_k \cap s_l \cap s_h) - \dots + (-1)^{q+1} P(s_k \cap s_l \cap \dots \cap s_q)$$

where the logic summation is extended on the number  $q$  of events  $s_k$ .

The probabilities of the events  $s_K$  depends on the second step sampling design and also on the multiplicity of the individual in the selected centres which is less or equal to  $g$  (the multiplicity of the individual in the population).

To fix the ideas, let assume to select a simple random sample of  $m = 2$  centres that aggregate, respectively,  $N_1$  and  $N_2$  ultimate units and select from them again a simple random sample of  $n_1$  and  $n_2$  individuals. In this case, the second-step inclusion probability, determined by the sampling fractions  $\frac{n_k}{N_k}$  in the selected centres, is:

$$\pi_{i2||} = \begin{cases} \frac{n_1}{N_1} & \text{if } i \text{ belongs only to the first selected centre} \\ \frac{n_2}{N_2} & \text{if } i \text{ belongs only to the second selected centre} \\ \frac{n_1}{N_1} + \frac{n_2}{N_2} - \frac{n_1}{N_1} \cdot \frac{n_2}{N_2} & \text{if } i \text{ belongs to both the selected centres} \end{cases}$$

#### *The second step inclusion probability of the second order*

Only the couples of units who are at least in one of the selected centres have a non zero probability to be sampled at the second step.

The second step inclusion probability of the second order is the probability of the union of several events  $E_{kh}$ , each of them representing a way in which the couple  $i, j$  is enclosed in the final sample:

$$\pi_{ij2||} = \Pr \left( \bigcup_{k,h} (E_{kh}) \right)$$

where  $E_{kh} = (s_k \cap (s_h | i))$ ;  $s_k$  is the event "the sample selected from the center  $k$  includes the unit  $i$ ";  $s_h | i$  is the event "the sample selected from the center  $h$  includes

the unit  $j$  given that the unit  $i$  was selected". The logic summation is extended on the number of events  $E_{kh}$ . Let the size of this set be indicated by  $q$ :

$$\pi_{j|2j} = \Pr\left(\bigcup_{k,h} (E_{kh})\right) = \sum_k P(E_k) - \sum_{k<l} P(E_k \cap E_l) + \sum_{k<l<h} P(E_k \cap E_l \cap E_h) - \dots + (-1)^{q+1} P(E_k \cap E_l \cap \dots \cap E_q)$$

The probabilities of the events  $E_{ij}$  depends on the second step sampling design, on the multiplicity of each unit in the selected centres and on the number of selected centres to which both the units belong (common centres,  $c$ ). Again, this multiplicity is less or equal to  $g$ , the multiplicity of the individual in the population. Also the number of common selected centres is less or equal to  $c$ , the common centres in the population.

For the sake of simplicity, let assume again to select a simple random sample of units at both the steps ( $m=2$  centres,  $n_1$  and  $n_2$  individuals), the second order inclusion probabilities  $\pi_{j|2j}$  are such that:

$$\pi_{j|2j} = \begin{cases} \frac{n_1}{N_1} \cdot \frac{n_2}{N_2} & \text{if } i \in 1 \text{ and } j \in 2 \\ \frac{n_1}{N_1} \cdot \frac{n_1 - 1}{N_1 - 1} & \text{if } i, j \in 1 \\ \frac{n_2}{N_2} \cdot \frac{n_2 - 1}{N_2 - 1} & \text{if } i, j \in 2 \\ \frac{n_1}{N_1} \left( \frac{n_2}{N_2} + \frac{n_1 - 1}{N_1 - 1} - \frac{n_2}{N_2} \cdot \frac{n_1 - 1}{N_1 - 1} \right) & \text{if } i \in 1 \text{ and } j \in 1,2 \\ \frac{n_2}{N_2} \left( \frac{n_1}{N_1} + \frac{n_2 - 1}{N_2 - 1} - \frac{n_1}{N_1} \cdot \frac{n_2 - 1}{N_2 - 1} \right) & \text{if } i \in 2 \text{ and } j \in 1,2 \\ \frac{n_1}{N_1} \left( \frac{n_2}{N_2} + \frac{n_1 - 1}{N_1 - 1} - \frac{n_2}{N_2} \cdot \frac{n_1 - 1}{N_1 - 1} \right) + \frac{n_2}{N_2} \left( \frac{n_1}{N_1} + \frac{n_2 - 1}{N_2 - 1} - \frac{n_1}{N_1} \cdot \frac{n_2 - 1}{N_2 - 1} \right) - \frac{n_1}{N_1} \cdot \frac{n_2}{N_2} \cdot \left( \frac{n_1 - 1}{N_1 - 1} + \frac{n_2 - 1}{N_2 - 1} - \frac{n_1 - 1}{N_1 - 1} \cdot \frac{n_2 - 1}{N_2 - 1} \right) & \text{if } i, j \in 1 \text{ and } i, j \in 2 \end{cases}$$

Appendix B. Simulated distributions of the study variable  $Y$ 

Table B1. Normal population,  $\bar{Y} = 19.4568$ ,  
 $\sigma^2 = \sigma_w^2 + \sigma_b^2 = 164.6211 = 115.0986 + 49.5225$ ,  $c.v(Y) = 0.6594$

Centres				Frequency of the profile	$Y_i$	$\bar{Y}_i$	$\sigma_i(Y)$	$c.v_i(Y)$
Centre A	Centre B	Centre C	Centre D					
1	0	0	0	200	3240	16.20	8.70	0.54
0	1	0	0	300	4550	15.17	7.86	0.52
0	0	1	0	400	6119	15.30	7.54	0.49
0	0	0	1	300	4957	16.52	8.20	0.50
0	1	1	0	200	4960	24.80	10.81	0.44
0	0	1	1	300	4476	14.92	7.52	0.50
1	0	1	0	300	4954	16.51	8.33	0.50
0	1	0	1	400	6607	16.52	8.14	0.49
1	1	0	0	100	3111	31.11	17.47	0.56
1	0	0	1	100	2938	29.38	16.31	0.56
1	1	1	0	200	4487	22.44	12.02	0.54
1	0	1	1	50	2525	50.50	31.36	0.62
1	1	0	1	100	2310	23.10	10.95	0.47
0	1	1	1	100	2742	27.42	10.91	0.40
1	1	1	1	50	2340	46.80	25.84	0.55

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Table B2. Normal population,  $\bar{Y} = 19.4568$ ,  
 $\sigma^2 = \sigma_w^2 + \sigma_b^2 = 552.2312 = 502.7087 + 49.5225$ ,  $c.v(Y) = 1.2078$

Centres				Frequency of the profile	$Y_i$	$\bar{Y}_i$	$\sigma_i(Y)$	$c.v_i(Y)$
Centre A	Centre B	Centre C	Centre D					
1	0	0	0	200	3240	16.20	16.58	1.02
0	1	0	0	300	4550	15.17	15.87	1.05
0	0	1	0	400	6119	15.30	15.02	0.98
0	0	0	1	300	4957	16.52	15.98	0.97
0	1	1	0	200	4960	24.80	20.18	0.81
0	0	1	1	300	4476	14.92	15.09	1.01
1	0	1	0	300	4954	16.51	16.86	1.02
0	1	0	1	400	6607	16.52	16.16	0.98
1	1	0	0	100	3111	31.11	36.34	1.17
1	0	0	1	100	2938	29.38	34.18	1.16
1	1	1	0	200	4487	22.44	25.05	1.12
1	0	1	1	50	2525	50.50	74.09	1.47
1	1	0	1	100	2310	23.10	22.13	0.96
0	1	1	1	100	2742	27.42	20.12	0.73
1	1	1	1	50	2340	46.80	60.54	1.29

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**Table B3.** Normal population,  $\bar{Y} = 19.4568$ ,

$$\sigma^2 = \sigma_w^2 + \sigma_b^2 = 2.9331e + 003 = 2.8836e + 003 + 49.5225, \text{ c.v.}(Y) = 2.7835$$

Centres				Frequency of the profile	$Y_i$	$\bar{Y}_i$	$\sigma_i(Y)$	$c.v_i(Y)$
Centre A	Centre B	Centre C	Centre D					
1	0	0	0	200	3240	16.20	30.25	1.87
0	1	0	0	300	4550	15.17	32.33	2.13
0	0	1	0	400	6119	15.30	29.76	1.95
0	0	0	1	300	4957	16.52	30.36	1.84
0	1	1	0	200	4960	24.80	35.64	1.44
0	0	1	1	300	4476	14.92	30.38	2.04
1	0	1	0	300	4954	16.51	34.53	2.09
0	1	0	1	400	6607	16.52	31.89	1.93
1	1	0	0	100	3111	31.11	78.97	2.54
1	0	0	1	100	2938	29.38	75.60	2.57
1	1	1	0	200	4487	22.44	54.68	2.44
1	0	1	1	50	2525	50.50	232.50	4.60
1	1	0	1	100	2310	23.10	45.16	1.96
0	1	1	1	100	2742	27.42	34.80	1.27
1	1	1	1	50	2340	46.80	184.13	3.93

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**Table B4.** Lognormal population,  $\bar{Y} = 19.4568$ ,

$$\sigma^2 = \sigma_w^2 + \sigma_b^2 = 152.5066 = 102.9841 + 49.5225, \text{ c.v.}(Y) = 0.6347$$

Centres				Frequency of the profile	$Y_i$	$\bar{Y}_i$	$\sigma_i(Y)$	$c.v_i(Y)$
Centre A	Centre B	Centre C	Centre D					
1	0	0	0	200	3240	16.20	7.14	0.44
0	1	0	0	300	4550	15.17	7.25	0.48
0	0	1	0	400	6119	15.30	7.06	0.46
0	0	0	1	300	4957	16.52	8.65	0.52
0	1	1	0	200	4960	24.80	13.49	0.54
0	0	1	1	300	4476	14.92	7.14	0.48
1	0	1	0	300	4954	16.51	8.23	0.50
0	1	0	1	400	6607	16.52	9.15	0.55
1	1	0	0	100	3111	31.11	15.00	0.48
1	0	0	1	100	2938	29.38	14.84	0.51
1	1	1	0	200	4487	22.44	10.05	0.45
1	0	1	1	50	2525	50.50	24.97	0.49
1	1	0	1	100	2310	23.10	11.89	0.51
0	1	1	1	100	2742	27.42	12.00	0.44
1	1	1	1	50	2340	46.80	20.50	0.44

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**Table B5.** Lognormal population,  $\bar{Y} = 19.4568$ ,  
 $\sigma^2 = \sigma_w^2 + \sigma_b^2 = 430.9115 = 381.389 + 49.5225$ ,  $c.v.(Y) = 1.0698$

Centres				Frequency of the profile	$Y_i$	$\bar{Y}_i$	$\sigma_i(Y)$	$c.v_i(Y)$
Centre A	Centre B	Centre C	Centre D					
1	0	0	0	200	3240	16.20	13.13	0.81
0	1	0	0	300	4550	15.17	13.65	0.90
0	0	1	0	400	6119	15.30	13.91	0.91
0	0	0	1	300	4957	16.52	17.75	1.07
0	1	1	0	200	4960	24.80	26.54	1.07
0	0	1	1	300	4476	14.92	13.50	0.91
1	0	1	0	300	4954	16.51	16.13	0.98
0	1	0	1	400	6607	16.52	18.97	1.15
1	1	0	0	100	3111	31.11	29.26	0.94
1	0	0	1	100	2938	29.38	27.80	0.95
1	1	1	0	200	4487	22.44	17.67	0.79
1	0	1	1	50	2525	50.50	46.52	0.92
1	1	0	1	100	2310	23.10	23.63	1.02
0	1	1	1	100	2742	27.42	22.95	0.84
1	1	1	1	50	2340	46.80	34.78	0.74

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**Table B6.** Lognormal population,  $\bar{Y} = 19.4568$ ,  
 $\sigma^2 = \sigma_w^2 + \sigma_b^2 = 1.2390e+003 = 1.1894e+003 + 49.5225$ ,  $c.v.(Y) = 1.8091$

Centres				Frequency of the profile	$Y_i$	$\bar{Y}_i$	$\sigma_i(Y)$	$c.v_i(Y)$
Centre A	Centre B	Centre C	Centre D					
1	0	0	0	200	3240	16.20	21.43	1.32
0	1	0	0	300	4550	15.17	22.70	1.50
0	0	1	0	400	6119	15.30	26.03	1.70
0	0	0	1	300	4957	16.52	36.10	2.18
0	1	1	0	200	4960	24.80	46.07	1.86
0	0	1	1	300	4476	14.92	22.95	1.54
1	0	1	0	300	4954	16.51	29.39	1.78
0	1	0	1	400	6607	16.52	37.25	2.26
1	1	0	0	100	3111	31.11	49.79	1.60
1	0	0	1	100	2938	29.38	48.37	1.65
1	1	1	0	200	4487	22.44	27.48	1.23
1	0	1	1	50	2525	50.50	75.83	1.50
1	1	0	1	100	2310	23.10	43.06	1.86
0	1	1	1	100	2742	27.42	38.74	1.41
1	1	1	1	50	2340	46.80	50.24	1.07

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