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**ESTIMATING VARIANCES  
FOR STATISTICS CANADA HEALTH SURVEYS:  
A COMPARISON OF THE OPTIONS AVAILABLE TO USERS**

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Ivelina DeLeva and François Brisebois

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Statistics Canada

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# **ESTIMATING VARIANCES FOR STATISTICS CANADA HEALTH SURVEYS: A COMPARISON OF THE OPTIONS AVAILABLE TO USERS**

Ivelina DeLeva and François Brisebois <sup>1</sup>

## **ABSTRACT**

In the analysis of survey data, variance estimation is of critical importance. When dealing with data collected through complex survey designs, variance estimation is typically obtained using one of two methods: Taylor linearization or replication. This paper gives an overview of the variance estimation methods available to users and the software programs that support them. In particular, it compares the linearization method to one of the replication methods (the Bootstrap) in the context of their availability and flexibility in software packages. Three popular software packages were examined for these comparisons: SAS V8 (Taylor via SURVEYMEANS and Bootstrap via the BOOTVAR program), SUDAAN V9, and WesVar V4.2. The comparisons presented in this paper were done empirically using Statistics Canada health survey data from the Canadian Community Health Survey Cycle 1.2. The results show the differences and effects of using one method or one software program over another, as well as the ability of the software packages to incorporate the components of the survey design and weight adjustments into calculations.

**Key words:** Bootstrap; Taylor; Variance estimation; Weight adjustments; Software comparison.

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# ESTIMATION DE LA VARIANCE POUR LES ENQUÊTES SUR LA SANTÉ DE STATISTIQUE CANADA: COMPARISON DES OPTIONS DISPONIBLES AUX UTILISATEURS

Ivelina DeLeva et François Brisebois <sup>1</sup>

## RÉSUMÉ

Lors de l'analyse de données d'enquête, l'estimation de la variance est d'une importance cruciale. Dans le cas où les données sont recueillies via un plan de sondage complexe, l'estimation de la variance est habituellement accomplie en ayant recours à deux méthodes: la linéarisation de Taylor, ou l'approche par réplication. Ce document présente un survol des méthodes d'estimation de variances disponibles aux utilisateurs, de même que les progiciels supportant celles-ci. Plus particulièrement, la méthode de linéarisation de Taylor est comparée à une des méthodes par réplication (le Bootstrap) du point de vue de sa disponibilité et souplesse d'emploi dans les progiciels. Trois progiciels communément utilisés sont examinés: SAS V8 (Taylor via SURVEYMEANS, et Bootstrap via le programme BOOTVAR), SUDAAN V9, et WesVar V4.2. Les comparaisons empiriques présentées dans ce document sont effectuées à l'aide de données d'enquête sur la santé de Statistique Canada, plus précisément du Cycle 1.2 de l'Enquête sur la santé dans les collectivités canadiennes. Les résultats présentent les différences numériques et l'impact d'utiliser une méthode ou un progiciel plutôt qu'un autre, de même que la capacité des progiciels à incorporer dans les calculs les composantes du plan de sondage et des ajustements faits au poids.

Mots clés: Bootstrap; Taylor; Estimation de variance; Ajustement des poids; Comparaison de progiciels.

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# TABLE OF CONTENTS

1. INTRODUCTION	6
2. THE CANADIAN COMMUNITY HEALTH SURVEY (CCHS)	7
3. VARIANCE ESTIMATION METHODS	8
3.1 TAYLOR LINEARIZATION	8
3.2 BOOTSTRAP	8
3.3 REVIEW OF THE COMPARISONS IN THE LITERATURE	9
3.4 ADVANTAGES AND DISADVANTAGES OF THE BOOTSTRAP	10
3.5 VARIANCE ESTIMATION IN STC HEALTH SURVEYS	11
4. TOOLS / SOFTWARE FOR VARIANCE ESTIMATION	12
4.1 THE SOFTWARE: SAS V8	12
4.1.1 <i>Taylor variances</i>	12
4.1.2 <i>Bootstrap variances through the BOOTVAR macro program</i>	13
4.2 THE SOFTWARE: SUDAAN V9	14
4.2.1 <i>Taylor variances</i>	14
4.2.2 <i>Bootstrap variances</i>	16
4.3 THE SOFTWARE: WESVAR 4.2	16
4.3.1 <i>Bootstrap variances</i>	17
4.4 ALTERNATIVE WAYS TO USING THE SOFTWARE FOR VARIANCE ESTIMATION	17
4.4.1 <i>Use of average design effects</i>	17
4.4.2 <i>CV lookup tables</i>	18
5. RESULTS OF COMPUTATIONAL COMPARISONS	19
6. CONCLUSION	22
7. FUTURE WORK	23
ACKNOWLEDGEMENTS	23
REFERENCES	24
APPENDIX	26
SAMPLE CODE FOR BOOTVAR ESTIMATES	26
SAMPLE CODE FOR ESTIMATES IN FIGURE 1	26
SAMPLE CODE FOR ESTIMATES IN FIGURE 2	27



## 1. INTRODUCTION

Variance estimation is crucial when analyzing survey data. First, it indicates how precise computed estimates are, which guides analysts on how to interpret results before publishing. Next, variance estimation is required for the statistical testing of hypotheses about population parameters. When analyzing data from survey samples, computation of variance estimates must account for the specifics of the survey design used to collect the data. Moreover, variance estimation should also incorporate the effects of the various stages of weight adjustment. In most household surveys conducted by Statistics Canada, complex designs using stratification and clustering are used, and sampling weights are corrected to account for factors such as nonresponse and calibration. When dealing with such data, it is not always possible to obtain a closed form algebraic expression to estimate variances; therefore, one needs to rely on approximation methods. The two most commonly used approximation methods consist of Taylor series linearization (Taylor) and replication techniques. The Bootstrap method is one of several replication techniques, which has become the recommended method for a large number of Statistics Canada household surveys. Both Taylor and the Bootstrap are discussed more fully in further sections of this paper.

The main challenge faced by analysts in doing variance estimation using these approximation methods is finding a statistical software package that will support these methods, as well as offer the statistics/models of their interest. Most standard statistical software packages generally cannot support the correct use of survey data from a complex design, since they typically assume simple random sampling of elements. A number of packages include the Taylor variance estimation method under the condition that one can provide the variables containing survey design information such as the stratification and clustering (often referred to as PSU) variables. The challenge with software packages is even more evident when specifically using the Bootstrap method, since at the present time none of the most popular commercial statistical software packages directly support the method. In order to fill this gap, a macro program (the BOOTVAR) was created by Statistics Canada methodologists and distributed to analysts when the Bootstrap method was first adopted. In the end, both the Taylor and Bootstrap show some advantages and disadvantages from technical and practical points of view. Thus, analysts must often make a decision on which method and software package to use, without even knowing the impact that choice would have on their variance estimates.

The goal of this working paper is to provide analysts with a reference document that profiles both Taylor and Bootstrap variance estimation methods, in terms of both their theory and their accessibility in software programs. The paper also examines empirically the quantitative differences in the results obtained from the two methods via available software packages, using data from the Canadian Community Health Survey (CCHS), a survey conducted by Statistics Canada since September 2000. This should give analysts a better idea of the difference resulting from the choice of one method over another when certain software is used.

Many comparisons have been done both in the area of the different methods and in the area of the different software packages available. However, most of these studies make their comparisons on a fairly general level. This paper offers additional valuable information as it examines the methods in greater detail in conjunction with the capabilities of the software packages. One important factor for this paper is that the data used for its analyses is taken from a household health survey, so the conclusions and results are particularly applicable to the behaviour of this kind of data. Secondly, in



evaluating the performance of the variance estimation methods, this study looks at the impact of incorporating a post-stratification and a nonresponse adjustment. In addition to that, the paper discusses the use of the Bootstrap method in software programs that do not directly support it.

Section 2 introduces the CCHS, from which data was used for the empirical comparisons. A general overview of the survey is presented, as well as the survey design and weighting procedure specifics, since these aspects affect variance estimation. Section 3 presents the two variance estimation methods of interest for this paper: the Taylor series linearization method and the Bootstrap method. Some statistical software packages supporting these methods are examined and compared (in terms of variance estimation) in section 4. Section 5 provides the empirical results obtained from the two variance estimation methods, and outlines the differences observed from one software program to the other. Finally, sections 6 and 7 present a general conclusion and the future work left from the findings, respectively.

## **2. THE CANADIAN COMMUNITY HEALTH SURVEY (CCHS)**

The CCHS is one of Statistics Canada's largest household surveys. Its main objective is to provide reliable cross-sectional information on health status and health determinants at the national, provincial and regional levels. The strategy adopted to meet this objective was to implement a biennial cycle of data collection, which for the first year consists of a health region-level survey, and for the second year focuses on a specific health topic and provides data at the provincial level. More information on the biennial cycle strategy can be found in Béland, Bailie, Catlin and Singh (2000). The data used in this paper was collected from the second year of the first biennial cycle, more commonly referred to as Cycle 1.2.

The area frame used and maintained by the Canadian Labour Force Survey (LFS) was used to select the CCHS Cycle 1.2 sample of dwellings, using a stratified multi-stage design. A complete description of the LFS area frame is given in the *Methodology of the Canadian Labour Force Survey* (Statistics Canada, 1998), while Morano, Lessard and Béland (2000) address the changes made to the standard LFS sample selection process in order to meet the specific sample size requirements of the CCHS.

The weighting procedure for Cycle 1.2 included the traditional steps of nonresponse adjustment and calibration. Brisebois and Thivierge (2001) present the details of the weighting strategy used in the context of Cycle 1.1 of the CCHS, which similarly to Cycle 1.2, used the LFS area frame to select part of its sample. As mentioned earlier, ideally, the effect of all these weighting adjustments should be incorporated into variance estimation calculations. This issue will be discussed later in the comparisons of the variance estimation methods.

### 3. VARIANCE ESTIMATION METHODS

As explained above, variance estimation can be done using one of two types of estimation approaches: Taylor series linearization, or replication methods. Of the replication techniques, Balanced Repeated Replication (BRR), Jackknife (JK), and Bootstrap are some of the more commonly used methods. For National Population Health Survey (NPHS) data, the predecessor to the CCHS, the Bootstrap was recommended as the preferred method for variance estimation. Specifics on the methodology and reasons for this recommendation can be found in Yeo, Mantel, and Liu (1999). The following sections present the Taylor and Bootstrap methods in greater detail.

#### 3.1 Taylor Linearization

This method relies on the simplicity associated with estimating the variance of a linear statistic (Flores-Cervantes, 1997). The linearization of the statistic is done by taking the first order term of the Taylor series expansion around the mean to obtain a linear approximation of the statistic. Its variance is then estimated by the variance of this linear approximation using the usual variance formulas for linear statistics.

Studies done by Dipbo and Wolter (1984) investigate the more accurate second order Taylor approximations in the case of proportions. They observed that in these approximations, the first order term accounted for 100.8% of the variance when the stratum sample size was 6. These results indicate that first order Taylor approximations can in fact overestimate the variance for proportions. In addition to that, Dipbo and Wolter show that while the bias is reduced, the variance of the variance is increased and calculations are considerably more complex for the second order variances. For this reason, all of the software packages examined in this paper use the first order approximation, since the results produced are considered to be of decent quality and are obtained with relatively simple computations. Wolter (1985), however, cautions users that these first order approximations may be unreliable in the context of highly skewed populations.

#### 3.2 Bootstrap

The Bootstrap (Efron, 1979) can also be applied to estimating variances. In a review of re-sampling methods and their properties, Shao (1996) outlines the different variants of the Bootstrap, of which the rescaling Bootstrap proposed by Rao and Wu (1988) is the basis for variance estimation in complex survey designs. An extended version of this proposed Bootstrap (Rao, Wu, Yue, 1992) was implemented for the NPHS and CCHS surveys.

Similarly to other re-sampling methods, the Bootstrap method uses the existing sample as a population which is re-sampled to imitate the original sampling approach. In order to achieve high accuracy in computing a variance estimate, ideally, a number of completely new samples, each representative of the population, could be drawn individually to compute the same statistic. Since each of these separate samples would independently represent the population, the variance between the set of estimated statistics would be an accurate estimate of the variance of the statistic of interest. However, this approach would be extremely costly and highly impractical. So instead, since the existing sample is originally selected to be representative of the population, it is treated as if it were the population and is then re-sampled. In other words, a sub-sample is taken from the existing sample  $B$  times and the statistic is calculated for each of these  $B$  sub-

samples, called replicates. The variance is then estimated by the variance of this set of replicates.

### 3.3 Review of the comparisons in the literature

These methods, together with other re-sampling methods, have been compared both theoretically and empirically in numerous studies. Results vary from study to study as variance estimation in complex surveys depends on, and is influenced by, each element of the survey design. Consequently, two general schools of thought have emerged, usually based on empirical evidence supported by some theoretical justification: linearization is a more stable estimator and thus more reliable; versus, replication is an estimator that better reflects the survey design of a complex survey.

Since linearization is a much older method, its stability has been illustrated by several empirical studies. Comparing three variance estimation methods using three sample designs, Kish and Frankel (1974) found that the variability was consistently lowest for Taylor estimates and highest for BRR, a method very similar to the Bootstrap. These results suggest that the Taylor estimator is more stable than the BRR estimator since the variability referred to in Kish and Frankel's conclusions is the variability of the variance. Wolter (1985) summarizes similar results from five Monte Carlo studies done during the previous 20 years focused on evaluating the accuracy of different variance estimators in finite samples. From these results collectively, Wolter makes two main conclusions. First, he points out that, in terms of the MSE and bias criteria, the Taylor method shows greater stability. Next, he explains that, from the point of view of confidence interval coverage (which is considered to be the most relevant criterion of accuracy), the replication methods are preferable.

In another study, using a sample with a stratified systematic design, Zhang (2001) shows that in some cases the Taylor method as implemented in SUDAAN may result in greater variance estimates than the Bootstrap. He obtained Bootstrap standard error estimates for proportions that were consistently smaller than those from the without replacement (WOR) and with replacement (WR) Taylor methods. The observed differences are attributed to the limitations in the design options available in SUDAAN, which are often not entirely appropriate for the underlying complex survey design.

Since replication methods can incorporate the effects of weight adjustments in variance estimation, it would be expected that they produce larger variances than methods only incorporating the design information in the calculations. In a more recent study, Valliant (2004) recognizes that replicate estimators are superior to linearization estimators precisely because they account for the various stages of weight adjustment, but found that this was the case only in a limited sense. The replicate estimator examined in his study (the Grouped Jackknife) tended to be a substantial overestimate especially with smaller sample sizes. On the other hand, linearization methods, as well as other variance estimators based on squared residuals, were found to yield underestimates.

Along the same lines, Flores-Cervantes (1997) explains how software programs using the Taylor method often do not offer the option to account for nonresponse or all levels of post-stratification adjustments. He points out that the variance estimate can in some cases be improved with post-stratification options, but the improvement would only reflect the reduction



in variance due to adjusting to control totals in one dimension. In replication, this is not a problem as the replicate weights can fully account for this effect when they are created, even if the post-stratification is of more than one dimension. Consistent with Flores-Cervantes, Kaufman (2000) states that the Bootstrap is expected to more correctly measure the variance (than Balanced Half Replicates or Jackknife) because it has more flexibility in adjusting for the dependent sampling (assuming an appropriate adjustment can be derived), as in the case of a finite population sample.

As discussed by Flores-Cervantes, the limitations of the Taylor variance estimates for currently available statistical packages come from the lack of flexibility in the existing options of the software programs. Taylor variances can, however, be computed to account for necessary adjustments using the method of estimating equations (EE). Much theory exists on this methodology, but there is still no software with built-in procedures that implement it. The EE approach to variance estimation relies on the fact that (finite) population parameters can be expressed as solutions to suitable "census" estimating equations. Consequently, parameter estimates may be obtained by solving sample EE, which incorporate design weights as well as adjustment factors based on post-stratification information. This approach is discussed in greater detail by Hidirolou, Rao, and Yung (1999), where results for Taylor variances reflecting design and post-stratification adjustments are derived for stratified multi-stage complex surveys. Yung, Hidirolou, and Rao (2001) extend these results to the case where weight adjustments are also made to account for nonresponse.

This approach in using estimating equations can be very appealing as it provides a unified method for estimating both simple and complex statistics (linear or not). However, while it is flexible in its ability to be used for any type of parameter, it has two important limitations: it requires that a suitable function  $u(\theta)$  is known for  $\theta$ , the parameter of interest, which can be difficult to find; and implementation in a computer system is entirely up to the user. Rao, Yung, and Hidirolou (2002) provide some directives and propose a general methodology for a computer implementation.

### **3.4 Advantages and disadvantages of the Bootstrap**

For surveys with a large number of PSUs, the Bootstrap can be perceived as preferable over the Jackknife because the number of replicates needed is not dictated by the number of PSUs. While the Jackknife requires a replicate for each sample PSU, the number of replicates for the Bootstrap is not dependent on such design specifics. Furthermore, in a study by Yeo, Mantel, and Liu (1999) using NPHS data, results indicated that Bootstrap CVs become more stable than the Jackknife, as  $B$  (the number of Bootstrap samples) increases. In addition to that, it is well established that Bootstrap has better properties for non-smooth statistics, such as percentiles. More generally, replication methods have an advantage over the Taylor linearization of statistics because they do not necessitate the derivation of linearization functions and derivatives which can sometimes be difficult or tedious, if not impossible (Shao, 1996).

As well as better representing the specifics of the sampling design and the weighting procedures, the Bootstrap method has further benefits for the purposes of data dissemination. Public-use micro-data files (PUMF) are released containing general demographic and health information of all sampled respondents. As explained in Yeo, Mantel, and Liu (1999), in order to use the Taylor method to estimate variances, access to design information is required. In

addition, to account for the first and second stage sampling fractions (also known as the finite population correction or fpc adjustment), more information (e.g. population counts) is required. However, for the protection of respondent confidentiality, such information does not appear in the PUMF, as it can potentially be used to identify a particular respondent. The creation of Bootstrap replicates does not solve this problem completely, but it makes it much more difficult for users to reveal geographical information about respondents.

Replicate methods such as the Bootstrap were originally considered to have a serious drawback of being strongly computer intensive. With the advent of faster and more powerful personal computers, this perspective became less of an issue. A more current challenge with using the Bootstrap method is the fact that it is not readily available in any commercial software programs as a direct procedure. However, because of its close resemblance with BRR, it is possible to use software that supports BRR variance estimation to get Bootstrap estimates. In general, use of the Bootstrap requires a bit more handling, so software using Taylor and Bootstrap is discussed in more detail in Section 4.

### **3.5 Variance Estimation in STC Health Surveys**

Statistics Canada's population health surveys (CCHS and NPHS) use complex survey designs to select multi-stage samples with a large number of PSUs. Since the Bootstrap estimator is able to incorporate both design elements and weight adjustments for a better, more accurate representation of the variance, it was selected as the method for variance estimation. Refer to Yeo, Mantel, and Liu (1999) for details on the reasons behind the adoption of the method.

To address the lack of software programs supporting the Bootstrap method, STC Population Health Survey Methodologists have developed BOOTVAR, a series of SAS (or SPSS) macros that allow users to carry out the calculations using the Bootstrap method. The BOOTVAR is primarily made available to all Statistics Canada health survey users through the dissemination of the data.

## 4. TOOLS / SOFTWARE FOR VARIANCE ESTIMATION

SAS, SUDAAN, and WesVar are three commonly used software programs for statistical analysis that support either or both Taylor and replication methods. More recently, STATA has become increasingly popular, but is not discussed in this paper. As indicated above, the Bootstrap and Taylor variance estimators were compared across the three software packages. Since each program has different capabilities, it requires its own set of steps to obtain the proper variance estimates. For the Taylor estimates, the specification of the design variables is required; and for the Bootstrap estimates, the specification of the Bootstrap replicates is required. The steps and considerations are outlined below and the results are presented in the next section with an evaluation of the performance of each method using CCHS Cycle 1.2 data.

### 4.1 The software: SAS V8

Until recently, the SAS software was only able to do SRS variance estimates, which are inappropriate and highly inaccurate for a complex survey design. In Version 8 of SAS, two built-in procedures (SURVEYMEANS and SURVEYREG) were added to the software package to deal with proper calculation of variance estimates for complex surveys using the Taylor linearization method. Two more procedures will be added in Version 9 (SURVEYFREQ and SURVEYLOGISTIC), which will allow for more options in this matter. In addition to that, even though Bootstrap is not directly available in SAS, the BOOTVAR macro-based program mentioned above (also available in SPSS) enables users to calculate Bootstrap variances.

#### 4.1.1 Taylor variances

- Taylor variances can be obtained using the SURVEYMEANS and SURVEYREG procedures in SAS V8 and SURVEYFREQ/SURVEYLOGISTIC in SAS V9.
- Specifying the sampling fraction for an fpc adjustment is an option for cases where the sampling fraction is large enough to have a significant impact on the variance. However, the formula behind the calculation at the moment is incomplete as it only accounts for the first stage sampling fraction adjustment (i.e. the variance between clusters) and omits the second stage sampling fraction (the within-clusters variance component).
- If the fpc is used for a two-stage design, the correction would be only partial and therefore an understatement of the variance. However, the formula is perfectly good for a single stage design as it accounts for any necessary fpc corrections at that level. This discrepancy should be corrected in a future version of the software.
- Formula used in SAS V8 for Taylor variances (with an fpc adjustment, but not accounting for the post-stratification adjustment) in terms of the SAS Online Documentation notation (SAS Institute, 1999):

$$\hat{V}(\hat{Y}) = \sum_{h=1}^H \frac{n_h(1-f_h)}{n_h-1} \sum_{i=1}^{n_h} (y_{hi} - \bar{y}_{h..})^2$$



where:

$h = 1, 2, \dots, H$  is the stratum number, with a total of  $H$  strata

$i = 1, 2, \dots, n_h$  is the cluster number within stratum  $h$ , with a total of  $n_h$  sampled clusters

$j = 1, 2, \dots, m_{hi}$  is the unit number within cluster  $i$  of stratum  $h$ , with a total of  $m_{hi}$  units

$n_h$  is the number of clusters in the sample

$N_h$  is the number of clusters in the frame

$$\hat{Y} = \sum_{h=1}^H \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} w_{hij} y_{hij}$$

$$y_{hi.} = \sum_{j=1}^{m_{hi}} w_{hij} y_{hij}$$

$$\bar{y}_{h..} = \left( \sum_{i=1}^{n_h} y_{hi.} \right) / n_h$$

$f_h = n_h / N_h$  is the first stage sampling fraction for stratum  $h$

- Since the design dealt with in this analysis is a two-stage design and for which sampling fractions at each level are considered small enough to be negligible, the focus was on Taylor variance estimates without an fpc adjustment. The formula for Taylor (no fpc) estimates is the same as the one shown above where the first stage sampling fraction is equal to zero (i.e.  $f_h = 0$ ).

#### 4.1.2 Bootstrap variances through the BOOTVAR macro program

- Bootstrap variances for totals, ratios, differences between ratios, and linear and logistic regression estimators can be obtained using the BOOTVAR macros (calculations are done as described by Yeo, Mantel, and Liu (1999)).
- Formula used in BOOTVAR for Bootstrap variances:

$$\hat{V}(\hat{B}) = \sum_{i=1}^b (\hat{B}_i - \bar{\hat{B}}) / b$$

where:

$\hat{B}_i$  are the point estimates obtained from the  $i^{th}$  Bootstrap replicate

$\bar{\hat{B}}$  is the average of the Bootstrap replicates,  $\hat{B}_i$

$\hat{B}$  is the estimate of the statistic (computed using the sampling weight)

$b$  is the number of Bootstrap replicate weights used (CCHS provides 500 Bootstrap weights)



## 4.2 The software: SUDAAN V9

The current version of the SUDAAN software (Version 9 was used) supports both the Taylor method and some replication methods for variance estimation, but not Bootstrap. However, it is possible to obtain Bootstrap variances by taking advantage of the similarity between Bootstrap and the BRR method, available in SUDAAN. Since the form of the Bootstrap variance estimator is the same as that of the BRR estimator, SUDAAN is in fact able to produce Bootstrap estimates given that you provide the Bootstrap replicate weights. More on this is presented in Section 4.2.2. Unlike SAS where the different methods of estimation require the use of different procedures, the approach in SUDAAN is to use the same procedure in each case, but to specify different options. Different estimation methods can be obtained using the DESIGN option, together with the corresponding components required for the selected method (e.g. indicating the replicate weights when using the BRR method).

### 4.2.1 Taylor variances

- A SAS-callable version of SUDAAN is available, which behaves as an addition to the standard SAS package (i.e. SUDAAN procedures and code can be used in the SAS environment).
- Taylor variance estimates for totals and ratios are obtained using the DESCRIPT, the CROSSTAB, and the RATIO (ratios only) procedures. For more details on how to use these procedures, refer to the SUDAAN User's Manual (Research Triangle Institute, 2001).
- As with SAS, it is possible to compute estimates with an fpc adjustment and estimates without such an adjustment; but unlike SAS, the formula here is complete and accounts for both sampling fractions in a two-stage design.
- Specifying a without replacement (WOR) design indicates that a finite population is used and requires the specification of sampling fractions (for the fpc adjustment) for each stage of sampling.
- Formula used in SUDAAN V9 for Taylor variances (WOR, not accounting for the post-stratification adjustment) in terms of the SUDAAN user guide notation (Research Triangle Institute, 2001):

$$\hat{V}_{WOR}(\hat{Y}) = \sum_{h=1}^H (1 - f_h) n_h s_h^2 + \sum_{h=1}^H f_h \sum_{i=1}^{n_h} (1 - f_{hi}) m_{hi} s_{hi}^2$$

where:

- $h = 1, 2, \dots, H$  is the stratum number, with a total of  $H$  strata
- $i = 1, 2, \dots, n_h$  is the cluster number within stratum  $h$ , with a total of  $n_h$  sampled clusters
- $j = 1, 2, \dots, m_{hi}$  is the unit number within cluster  $i$  of stratum  $h$ , with a total of  $m_{hi}$  sampled units
- $n_h$  is the number of clusters in the sample for stratum  $h$
- $N_h$  is the number of clusters in the frame for stratum  $h$
- $m_{hi}$  is the number of units that are sampled in cluster  $i$  of stratum  $h$
- $M_{hi}$  is the number of units in the frame for cluster  $i$  of stratum  $h$

$$\begin{aligned} \hat{Y} &= \sum_{h=1}^H \sum_{i=1}^{n_h} y_{hi.} & \text{and} & & y_{hi.} &= \sum_{j=1}^{m_{hi}} w_{hij} y_{hij} \\ s_h^2 &= \sum_{i=1}^{n_h} \frac{(y_{hi.} - \bar{y}_{h..})^2}{(n_h - 1)} & \text{and} & & \bar{y}_{h..} &= \left( \sum_{i=1}^{n_h} y_{hi.} \right) / n_h \\ s_{hi}^2 &= \sum_{j=1}^{m_{hi}} \frac{(w_{hij} y_{hij} - \bar{y}_{hi.})^2}{(m_{hi} - 1)} & \text{and} & & \bar{y}_{hi.} &= \left( \sum_{j=1}^{m_{hi}} y_{hij} \right) / m_{hi} \end{aligned}$$

and the first and second stage sampling fractions are (respectively):

$$f_h = n_h / N_h \quad \text{and} \quad f_{hi} = m_{hi} / M_{hi}$$

- The above formula is equivalent to the fpc formula in SAS V8 except that the SAS formula consists of only the first term and omits the second term of the above equation.
- Specifying a with replacement (WR) design will generate estimates with no fpc adjustment. SUDAAN treats this to be equivalent to a WOR design without the finite population correction.
- Formula used in SUDAAN V9 for Taylor variances (WR, not accounting for the post-stratification adjustment) in terms of the SUDAAN user guide notation (Research Triangle Institute, 2001):

$$\hat{V}_{WR}(\hat{Y}) = \sum_{h=1}^H n_h s_h^2$$

where all components in the equation are defined the same way as for the WOR variance formula

- As total stratum and cluster counts are often unavailable to data users, only Taylor variances without an fpc adjustment (WR design) were examined here.

### 4.2.2 Bootstrap variances

- Though there is no option for a Bootstrap design, Bootstrap variances can be obtained by specifying a BRR design and providing the externally generated Bootstrap weights as the replicate weights.
- Phillips (2004) discusses the differences and similarities between the Bootstrap and the BRR and demonstrates by way of example how to use the Bootstrap weights in SUDAAN (and WesVar) to compute Bootstrap variance estimates.
- Formula used in SUDAAN V9 for BRR variances in terms of the SUDAAN user guide notation (Research Triangle Institute, 2001):

$$\hat{V}_{BRR}(\hat{B}) = \frac{1}{b} \sum_{i=1}^b (\hat{B}_i - \tilde{B})^2$$

where:

$$\tilde{B} = \begin{cases} \hat{B} & \text{is used when the final sampling weight is specified and represents the estimate based on the full sample using the sampling weight} \\ \bar{\hat{B}} & \text{is used when the final sampling weight is not specified and represents the average of the replicate weights} \end{cases}$$

$\hat{B}_i$  is the point estimate obtained using the  $i^{th}$  replicate  
 $b$  is the total number of replicate weights used

- Note that the results produced in SUDAAN will differ from the ones obtained through BOOTVAR. When the final sampling weight is not specified, SUDAAN will produce the same variance estimates as BOOTVAR; however, the point estimate will correspond to the mean as computed from the bootstrap replicates. Conversely, including the final sampling weight in the procedure will produce the same point estimate as that of BOOTVAR, but the variance estimate would be computed around the final sampling weight. Although such small differences can be observed, both results are considered acceptable since the point estimate from the final sampling weight and the mean of the bootstrap replicates are asymptotically equivalent.

### 4.3 The software: WesVar 4.2

The WesVar Version 4.2 software supports replication methods only, but no Bootstrap explicitly. This software is more user-friendly than SAS and SUDAAN as it requires no programming. It consists of a graphical user interface containing a series of menus and options that the user can specify on a point-and-click basis.

### 4.3.1 Bootstrap variances

- Similarly to SUDAAN, Bootstrap variance estimates can be obtained using a BRR design and the externally generated Bootstrap replicate weights. For more details on the methods used by WesVar, refer to the WesVar User's Guide (Westat, 2002).
- Phillips (2004) provides a visual illustration using screenshots of the steps to be followed in obtaining Bootstrap variance estimates in WesVar.
- Formula used in WesVar 4.2 for BRR variances in terms of the WesVar User's Guide notation (Westat, 2002):

$$\hat{V}_{BRR}(\hat{B}) = c \sum_{i=1}^b (\hat{B}_i - \hat{B})^2$$

where:

$\hat{B}_i$  is the estimate of  $B$  based on the observations included in the  $i^{th}$  replicate

$\hat{B}$  is the full-sample estimate using the final sampling weight

$b$  is the total number of replicate weights used

$c$  is a constant that depends on the replication method (in this case  $c = \frac{1}{b}$ )

### 4.4 Alternative ways to using the software for variance estimation

As can be seen already, design information is a vital part in computing accurate variances. This information is usually included in survey datafiles, but is missing from public release datasets because it puts data confidentiality at risk. For the CCHS, since design identifiers represent finer geographical information than what is permitted on public-use microdata files (PUMF), they are not available to users of these files. The possibility of using and releasing collapsed versions of these identifiers have been studied but without success (Mayda et al., 1996). Therefore, for PUMF users, it is not possible to compute accurate variances using either Taylor or the bootstrap method. One could argue that performing the bootstrap method through the use of the externally generated replicate weights does not require knowledge of the design information. However, by the nature of the method, it would be possible to recreate stratum and PSU membership from patterns in the bootstrap weights, which makes the design information indirectly available when bootstrap weights are provided.

Faced with the impossibility of using appropriate variance estimation calculations, users of public release datasets still have recourse to some alternatives. One option consists of integrating average design effects into calculations of SRS variances, while another alternative rests on the use of CV look-up tables. Both of these (alternate methods) rely on approximate results which translate inevitably into a great loss of precision for variance estimates.

#### 4.4.1 Use of average design effects

The design effect is a commonly used indicator that measures the impact of computing variance estimates according to a given survey design compared to what would be obtained



under a simple random sampling (SRS) scheme. Since most statistical packages treat sample data as if they were resulting from a SRS design, which is often not the case, it is possible to use the design effect to "correct" variance estimates produced under SRS assumptions to obtain a better picture of the variability contained in the estimates. Given that design effects will vary from one characteristic to another, average design effects are often reported to data users as a tool to apply an "average" correction to SRS variances. In its PUMF documentation, CCHS publishes average design effects for various subpopulations mostly consisting of geographical areas of interest such as provinces and health regions.

A more direct approach of using these average direct effects consists in the creation of what is commonly referred as a design-adjusted weight. This adjusted weight is obtained by dividing each individual sampling weight by the average design effect corresponding to the population of interest. Using this design-adjusted weight will result in variances that incorporate an average effect of the design on variance estimates, therefore accounting in part for the complex survey design effect.

#### **4.4.2 CV lookup tables**

Look-up tables of coefficients of variation, or simply CV look-up tables, are often provided with public release datasets as a tool to quickly obtain a general idea of the sampling variability associated with estimates of totals and proportions for categorical variables. Many Statistics Canada surveys publish such tables with their PUMFs, and CCHS is one of them. Sets of tables are usually produced for different subpopulations of interest that are covered by the survey; CCHS typically provides CV tables to be used for estimates computed either at the national, provincial, or health region levels.

The basis of each CV table is the average design effect computed for the population it covers. Design effects are calculated for a subset of key survey characteristics and an average value is chosen. Approximate CV tables are then obtained by calculating the variance under simple random sampling and incorporating the design effect into the calculation (Phillips and Kaushal, 1998).

## 5. RESULTS OF COMPUTATIONAL COMPARISONS

The computational analyses were primarily done to compare the Taylor method to the Bootstrap method from an empirical perspective, as implemented in the software packages discussed in Section 4. Estimates of totals and their respective variances were computed for variables of a post-strata domain, which is equivalent to estimating the variance for proportions. But before those results are presented, it is important to briefly look at how the BOOTVAR (the program distributed with Statistics Canada Health Survey data) compares to SUDAAN and WesVar in estimating Bootstrap variances. The formulae and details in sections 4.1 to 4.3 illustrate the differences between these packages. For the results in this study, point estimates of the total were identical for BOOTVAR and WesVar, but differed slightly for SUDAAN. The discrepancy observed comes from the fact that for an appropriate variance computation, no final sampling weight was given in the SUDAAN program, so the point estimate was computed as the average of the replicate Bootstrap weights.

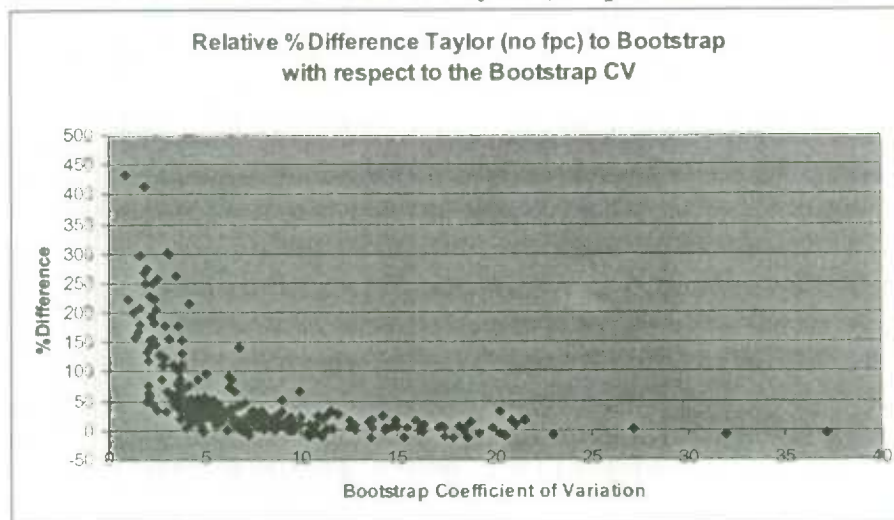
In terms of the variance estimates, the WesVar estimate was the one that differed from the other two. The observed difference was small and entirely due to the restrictions of the program; while BOOTVAR computes the variance around the mean of the replicate estimates, WesVar does it directly around the estimate itself. Unlike SUDAAN, WesVar does not allow the user to omit specifying this option, so that the calculation would be done using the full sample estimate.

Figure 1 presents a comparison of the results of higher interest: those of Bootstrap (using BOOTVAR) versus Taylor (no fpc). SAS and SUDAAN produce identical results for Taylor variances when using the same specifications. However, since SUDAAN offers more options, which are exploited later, all Taylor results presented here were obtained through SUDAAN. The data in Figure 1 expresses the difference between the Taylor and Bootstrap variance estimates in terms of the relative percent differences of these estimates graphed against the corresponding coefficients of variation (CVs). Clearly, the plot displays a strong trend for the SUDAAN Taylor variances to be greater than the BOOTVAR. The difference is considerable since on average the Taylor variances are relatively 54% larger than the Bootstrap. However, in this case, there are many weighting factors that the Bootstrap accounts for and the Taylor does not which are reflected in this difference.

Flores-Cervantes (1997) supports such an outcome by explaining how certain post-stratification adjustments reduce the variance but are not reflected in software program procedures using the Taylor method. Furthermore, providing empirical evidence for such results, Zhang (2001) found that in his study, Taylor variance estimates from stratified WOR and WR using SUDAAN are bigger than Bootstrap estimates for his proportion estimators.

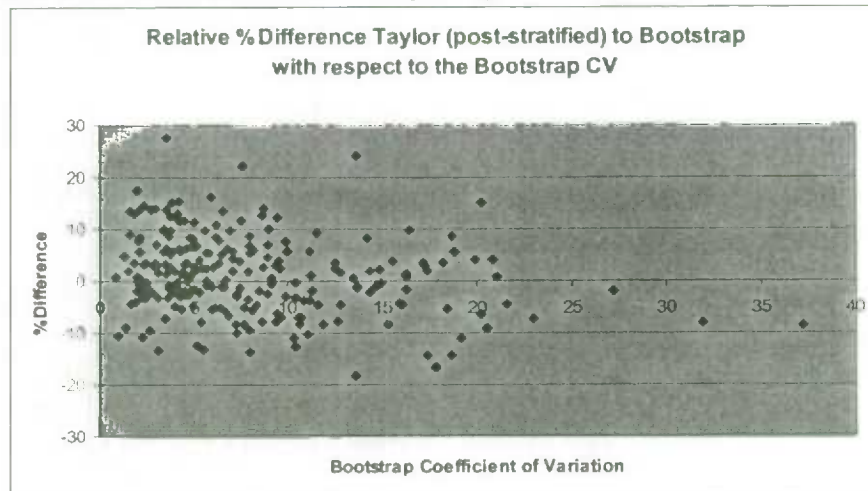
In addition to that, the data in Figure 1 displays an inverse relationship between the relative differences and the CVs of the estimates. In other words, for estimates of higher quality (having a small CV), the difference between the Taylor variance estimates and the Bootstrap variance estimates is quite large as computed by the software. Conversely, for estimates of lower quality (having a large CV), the difference is extremely small and almost negligible.

**Figure 1: Relative Percent Differences of Taylor (no fpc) and Bootstrap Variances**



As post-stratification adjustments appear to have such a large effect on the variance and are so important for obtaining better accuracy, post-stratified Taylor variance estimates were computed using SUDAAN, the only software package among the ones examined in this study with this capability for the Taylor method. Figure 2 displays how those results compare to the BOOTVAR estimates. The data is presented in the same fashion as in Figure 1 and shows a much closer relationship between the variances. Here, the plot is much more evenly dispersed around the zero, but still shows a bit of a tendency to be more positive than negative. Accounting for the post-stratification adjustment in the Taylor method brings the variances closer together, but the software computes the Taylor variance to be still higher than the Bootstrap by an average relative percent difference of 1.3% and a median of 1.0%. This slight positive difference can be interpreted as the combined effect of incorporating the nonresponse adjustment in variance calculations and of using different methods. However, since the two methods should produce similar results for large samples such as the one used here, it can be inferred that the positive difference in Figure 2 represents to a large degree the effect of the nonresponse adjustment reflected in the Bootstrap estimates but not in the Taylor. If the negligible fpc effect on variance estimates varies between methods, then it could be considered as an additional factor in explaining the difference observed.

**Figure 2: Relative Percent Differences of Taylor (post-stratified) and Bootstrap Variances**

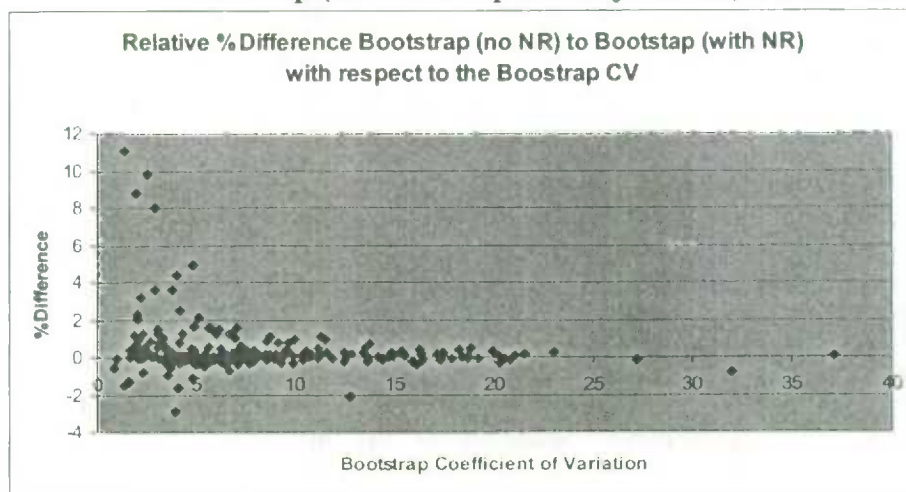




The above results would indicate that the nonresponse adjustment contributes to the variance by decreasing it. Such a hypothesis is confirmed by Mantel, Nadon, and Yeo (2000) in the context of the National Population Health Survey (NPHS), a close relative to the CCHS in terms of design and weighting procedures. Mantel, Nadon and Yeo found that the nonresponse adjustment to the weights had a decreasing effect on the variance that was small and virtually negligible, whereas the final calibration (post-stratification) effects were larger by an order of magnitude. Similar results regarding adjustments for nonresponse in the context of imputation are also confirmed by Beaumont (2004). Moreover, the results in Figure 2 show that there is no strong tendency for the relative differences to behave inversely to the CVs, since the points in the plot are more or less evenly dispersed at all levels of the CV. This would suggest that the two methods produce variance estimates that are relatively close regardless of the variability of the point estimate.

Since the Taylor variance from SUDAAN has, at this point, reached its limits in terms of feasible adjustments, it is not possible to obtain estimates that would encompass all of the elements that the Bootstrap estimates do in the BOOTVAR. Even the latest Version 9 of the SUDAAN software does not provide the option to account for the nonresponse in the Taylor variance estimates. Therefore, to get a sense of how big that nonresponse effect is (not clear from the results in Figure 2), using BOOTVAR, Bootstrap estimates were computed with replicate weights that didn't incorporate the nonresponse adjustment and ones that did. The results are shown in Figure 3, where the average relative percent difference is 0.4% with a median still larger than zero showing that Bootstrap variances without the nonresponse adjustment are slightly larger than the ones that include the adjustment.

**Figure 3: Relative Percent Differences of Bootstrap (without nonresponse adjustment) and Bootstrap (with nonresponse adjustment) Variances**



The above results illustrate the insignificant effects of the nonresponse adjustment for this data and show consistency with the conclusions of Mantel, Nadon, and Yeo (2000).

## 6. CONCLUSION

In summary, two acceptable and popular options used by health surveys analysts consist of using the Bootstrap weights with the BOOTVAR program, or using the Taylor linearization method with the SUDAAN software to do their variance estimation. The theory and empirical results presented in this study show that these two methods are not fully comparable and differ in many ways. Figure 4 illustrates the comparisons between methods and software presented in the preceding sections.

**Figure 4: Summary of comparisons done between methods and software**

	Bootstrap	Taylor
Post-stratification and Nonresponse adjustment	BOOTVAR (code in appendix 10.1)	N/A
Post-stratification No nonresponse adjustment	BOOTVAR	SUDAAN (DESCRIPT) (code in Appendix 10.3)
No post-stratification No nonresponse adjustment	N/A	SAS (SURVEYMEANS) (code in Appendix 10.2)

As can be seen from the above results, variances obtained using the Taylor method without any adjustments are much greater than those obtained using the Bootstrap replicates (Figure 1). In an effort to make the Taylor variance more comparable to the Bootstrap, applying post-stratification adjustments showed that the variance decreases substantially (Figure 2). This is not a surprising outcome since the post-stratification effect for the data used here is magnified by the fact that the estimates in the results are all of a post-strata domain. In addition to that, the nonresponse adjustment appeared to further decrease the variance, even if by a small amount (Figure 3). However, for analysts, even if the nonresponse adjustment is negligible, it is not actually possible to obtain post-stratified Taylor variance estimates using SUDAAN. The reason for this is because the final weights on the master file are already post-stratified, so post-stratification of already post-stratified weights would not reflect the true reduction in the variance. Thus, from a practical point of view, the only Taylor variance that is available to users is the no-fpc variance where only the design information is specified. Since this alternative to the Bootstrap generally overestimates the variance (at least for the data used in this analysis), users should use it with caution, or limit its use for explanatory work. Given that the Bootstrap captures all the variability by incorporating both design and weighting information into the calculation, it remains the recommended method.

## 7. FUTURE WORK

The results summarized in the previous sections were obtained on the basis that the sampling fractions in the sample were small and had a negligible effect on the variance. However, even if the fractions are small, they are not zero and consequently do have some impact. Fpc adjustments were not done in this study as the information required is generally not available to users. Moreover, at the moment, such a correction is possible both in SUDAAN and in SAS for a single-stage design, but is only accurate in SUDAAN for a two-stage sample, such as the one used for this analysis.

As a preliminary look at the degree of improvement of accounting for the fpc in the variance calculations, estimates were obtained using the CCHS 1.2 Department of National Defense datafile (a single stage sample used as a supplement to CCHS 1.2). Since this supplemental sample did not require calibration and had high sampling fractions, it represented a purer source for this investigation. Due to the high sampling fractions within all strata, Bootstrap weights were generated incorporating the fpc adjustment, as described in Rao and Wu (1988). Using this dataset and the same statistical packages as for the main analysis, Bootstrap and Taylor variances were obtained on a subset of the same variables as those used for the CCHS 1.2 results presented earlier. A relative difference that was much smaller was observed between the fpc adjusted Taylor and Bootstrap variances. In fact, 39 out of the 44 variance estimates were within 5% of each other. Furthermore, these preliminary results indicate no tendency for Taylor (with fpc) to be larger than the Bootstrap, as was the case for the no-fpc comparison. This suggests that further investigation of fpc adjustments may reveal a closer relationship between the linearized method and the Bootstrap.

Alternatively, considering the Bootstrap currently used for CCHS data, it may be of interest to investigate results obtained from a larger set of Bootstrap replicates. For variance estimation, the convergence of the estimate is extremely important in achieving accuracy. Some preliminary measures of the convergence of the variance estimates presented in the above analysis indicated that some of the estimates were of questionable convergence. As a validation to the above results, estimates of questionable quality were excluded and the remaining results were observed to reveal the same trends as those summarized in the previous section. Though replicate convergence criteria did not impact the conclusions in this study, it may be of some merit to investigate it more thoroughly.

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## APPENDIX

### Sample code for BOOTVAR estimates

```
libname in1 "C:\Cycle1.2\VarianceProject\MasterFile";
libname in2 "C:\Cycle1.2\Master\Bootstrp\Data";
libname out "C:\Cycle1.2\VarianceProject\MasterFile\Out";

*-----ESTIMATES USING BOOTVAR IN SAS-----;

*analysis file, bootstrap weights file;
%let Mfile = in1.c12;
%let bsamp = in2.b5;

*breakdown variables, number of b-weights, macro file needed;
%let classes = geob_prv;
%let B = 500;
%include "C:\Cycle1.2\Master\Bootstrp\SAS\Macro_v20.sas";

*estimates;
%total(asthma);
%total(diabetes);
%total(married);
%total(single);

%output;

*saving the results in a file;
data out.sas_bs;
    set &result;
run;

* end of program;
```

### Sample code for estimates in Figure 1

```
libname in1 "C:\Cycle1.2\VarianceProject\MasterFile";
libname out "C:\Cycle1.2\VarianceProject\MasterFile\Out";

*-----SAS TAYLOR ESTIMATES no fpc (TOTALS AND RATIOS)-----;
proc surveymeans data=in1.c12 alpha=0.05 clsum cv std sum varsum;
    domain geob_prv;
    cluster cluster;
    strata stratum;
    var    asthma diabetes married single;
    weight wtsb_m;
    ods output Domain=out.sas_tl;
run;

* end of program;
```

## Sample code for estimates in Figure 2

```
libname in1 "C:\Cycle1.2\VarianceProject\MasterFile";
libname out "C:\Cycle1.2\VarianceProject\MasterFile\Out";

*-----SUDAAN TAYLOR ESTIMATES no fpc - poststratified (TOTALS AND RATIOS)-----;
proc sort data=in1.c12_post;
    by stratum cluster;
run;

proc descript data=in1.c12_post filetype=SAS design=WR;
    nest          stratum cluster;
    weight        wgt17;
    subgroup      geob_prv agegrp dhhb_sex;
    levels        10 4 2;
    recode        geob_prv=(10 11 12 13 24 35 46 47 48 59);
    postvar       geob_prv agegrp dhhb_sex;
    postwgt       38030.11 37161.17 78885.32 81189.24 71480.64
                  71718.59 27046.93 33292.65 10140.23 9905.7 19739
                  20341.2 17218.06 17446.45 7459.36 9791.41 62495.56
                  61083.47 132125.86 140619.65 118582.88 122155.19 51152.78
                  68171.79 49987.54 48233.97 110474.9 112283.97 96574.61
                  97781.86 39636.97 53039.25 488950 467401.62 1129443.2
                  1096109.61 962440.81 984777.69 386561.31 525291.28 803372.33
                  771009.59 1891110.22 1895310.52 1403210.44 1454945.89 632692.44
                  804229.22 76240.3 73127.37 159515.86 155358.63 127691.39
                  129998.13 62000.52 80940.71 72540.86 68044.55 132210.14
                  132130.74 110124.6 109030.45 59360.28 75357.64 233894.38
                  221841.71 499199.59 480913.56 353996.82 343857.73 133701.5
                  161422.12 275531.56 267468.64 616177.33 624180.67 513082.41
                  520287.98 232031.86 283230.63;
    var           asthma diabetes married single;
    catlevel      4*1;
    table         geob_prv;
    output/filename="out.sd_post" filetype=SAS replace tablecell=all;
run;

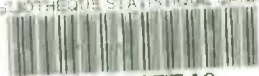
* end of program;
```







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