Proportion estimation based on a partially rank ordered set sample with multiple concomitants in a breast cancer study

ARMIN HATEFI and MOHAMMAD JAFARI JOZANI
Department of Statistics, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2.

Abstract:

In this paper, we use partially rank-ordered set (PROS) sampling design with multiple concomitants in a breast cancer study and propose a method to estimate the proportion of patients with malignant (cancerous) breast tumours in a given population. Through extensive numerical studies, the performance of the estimator is evaluated under various concomitants with different ranking potentials (i.e., good, intermediate and bad) and tie-structures. We show that the PROS estimator with multiple concomitants based on the ranking information provided through some easy to obtain cytological characteristics that are associated with the malignancy of breast tumours performs better than its counterparts under simple random sampling (SRS) and ranked set sampling (RSS) designs with logistic regression models. As opposed to available RSS based methods in the literature, our proposed methodology allows to declare ties among the ranks and does not rely on the existence of any specific regression model assumptions.

Keywords: Breast cancer; Cytological characteristics; Malignant tumours; Multiple concomitants; Population proportion; Partial ranking; Ranked set sampling.

1 Introduction

In many medical studies, measuring the variable of interest (e.g., disease status) is difficult and involves complicated procedures that are usually time consuming and/or expensive. However, one may have access to several concomitant variables (e.g., laboratory and demographic characteristics) from the sampling units that can be quantified easily at little cost. In most applications, the auxiliary information is often used in the estimation process to make better inference about the parameter of interest. For example, in a diabetes study, Chen et al. (2005) used the body mass index, weight and buttocks circumference to provide efficient estimate of the diabetes status of patients. Or, in a cardiovascular disease study, due to the association between the smoking status, the body mass index, the dietary beta carotene intake and beta plasma concentration in blood (as the quantitative trait of interest), Schlattmann (2009) used these concomitants to better predict the incidents of cardiovascular diseases. In such examples, the sampling units can be

\[\text{Corresponding author}
\]

Email: Hatefi.ar@gmail.com & armin.hatefi@umanitoba.ca
ranked easily (at little cost) using the available concomitants prior to taking the final measurements on the variable of interest. In these settings one can use the information of these concomitants in the data collection process of the study to obtain more representative samples from the underlying population. Rank-based sampling designs such as ranked set sampling (RSS) and partially rank ordered set (PROS) sampling provide a collection of techniques to obtain and analyze these expensive measurements with the help of inexpensive information.

In this paper, we use the PROS sampling design with multiple concomitants in a breast cancer study and propose a methodology that can be used to better estimate the proportion of patients with cancerous tumours compared with the commonly used methodologies in the literature based on simple random sampling (SRS) and RSS designs. In breast cancer studies, the discrimination between malignant (cancerous) and benign (not cancerous) tumours is very important and requires a comprehensive biopsy procedure. Benign tumours are those that cannot spread to other parts of body and only grow locally. In contrast, malignant tumours are those that invade and destroy nearby tissues and spread to other parts of the body. To determine whether tumours are malignant or benign, samples of suspected masses are either surgically biopsied or verified by clinical re-examinations after 3 to 12 months following the aspiration of breast clumps. This is an invasive procedure that involves the physical extraction of tissue. The test is expensive, and the results tend to take some times to process. To accurately diagnose breast cancer based purely on a Fine Needle Aspiration (FNA), Wolberg and Mangasarian (1990) identified nine visually assessed cytological characteristics of an FNA sample in the Wisconsin Breast Cancer Data (WBCD) that are considered to be relevant to breast cancer determination and its diagnosis. As we explain in Section 2, these cytological characteristics (concomitants) are easy to obtain and can play an important role in the early discrimination between malignant and benign breast masses. More references pertaining to WBCD can be found in Wolberg and Mangasarian (1990) and Terpstra and Liudahl (2004) as well as the website of the data set (Bache and Lichman, 2013) and references therein.

Several studies have been done on the WBCD to show the benefits of using rank-based sampling techniques for breast cancer research. For example, Terpstra and Liudahl (2004) proposed an RSS-based methodology to estimate the probability of having malignant breast tumours and the proportion of patients with breast cancer in the WBCD when only a single concomitant is used in the data collection process. Although they proposed a more efficient estimator based on RSS data for the population proportion, their statistical methodology is only applicable in bivariate settings. In other words, one can take advantage of one and only one concomitant in the estimation of the population proportion. In the WBCD, however, there are multiple concomitants that are highly correlated with the malignancy of breast tumours and one might want to incorporate them simultaneously in to the estimation as well as the data collection process to improve the inference about the proportion of patients with malignant breast tumours. To this end,
Chen et al. (2005) proposed an RSS-based methodology using multiple concomitants to estimate the population proportion. However, their method is based on the logistic regression modeling assumption and, as we show in Section 4, even by using concomitants that are highly correlated with the response variable, the logistic regression model might not be statistically significant. This could be because in these applications the sample sizes are not necessary high. In the absence of such strong modeling assumption, it is not clear how the extra information should be incorporated in the estimation process in a more efficient way. In addition, the regression-based methodology requires training samples with measurements on both concomitants and the response variable to estimate the parameters of the model. In many applications, however, training samples are not available. Moreover, none of the one-concomitant RSS (Terpstra and Liudahl, 2004) and RSS-based logistic regression methods (Chen et al., 2005) allows to declare ties among the ranks in the ranking process of the RSS scheme. This is not realistic, especially for the WBCD where all the cytological concomitants are (categorical) ordinal variables taking on values between 1 to 10. In such a case, forcing rankers to assign unique ranks to the sampling units results in random assignment of the ranks and can lead to substantial amount of ranking error and consequently to poor/invalid statistical inference.

To overcome these problems, in this paper, we propose to use the partially rank ordered set (PROS) sampling technique (Ozturk, 2011) with multiple concomitants and construct more efficient estimate of the population proportion and apply it to the WBCD. In the PROS sampling technique, one can assign sampling units into partially rank-ordered subsets, instead of precisely ranking all sampling units in a set. Let $G = \{g_1, \ldots, g_l\}$ denote a partition of the integers $\{1, \ldots, H\}$ into $l$ mutually exclusive subsets $g_r = \{(r-1)m+1, \ldots, rm\}$, each of size $m$, where $g_r = \{(r-1)m+1, \ldots, rm\}$ and $m = H/l$. To construct a PROS sample from the population of interest, a set of $H$ units are first selected. Instead of ranking all units in the set, a ranker is asked to assign the sampling units into subsets that are partially rank-ordered so that units in subset $g_r$ have smaller ranks than units in subset $g_s$, when $s > r$; $r, s = 1, \ldots, l$. This can be done using concomitant variables or any other means that does not require measuring the variable of interest. From the subset $g_1$, a unit is selected at random for full measurement, say $Y[g_1]_1$. Selecting another $H$ units and again assigning them into subsets, we select a unit at random from the subset $g_2$ for full measurement, namely $Y[g_2]_1$. The process is continued until we obtain $Y[g_l]_1$ as the final measurement from the subset $g_l$. This results in a PROS sample of size $l$ as $Y[g_1]_1, \ldots, Y[g_l]_1$ and the whole process constitutes one cycle of the sampling procedure. The cycle can be repeated $n$ times to generate a PROS sample of size $nl$, denoted by $\{Y[g_]_r; r = 1, \ldots, l; i = 1, \ldots, n\}$. In the above description, the number of observations in each subset is assumed to be the same. However, one can easily relax this assumption with slight modifications in the notations. In this paper, as we illustrate in Subsection 2.1, we consider a general setting where we do not assume that the number of subsets and subset sizes are fixed through the sampling procedure. This is because, in practice, the number of subsets are actually determined by concomitants or
Table 1: An example of PROS sample

| Cycle | Set | Subsets | Observation |
|-------|-----|---------|-------------|
| 1     | \(U_1\) | \(G_1 = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\) | \(Y_{g_11}\) |
|       | \(U_2\) | \(G_2 = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\) | \(Y_{g_21}\) |
|       | \(U_3\) | \(G_3 = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\) | \(Y_{g_31}\) |
| 2     | \(U_1\) | \(G_1 = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\) | \(Y_{g_12}\) |
|       | \(U_2\) | \(G_2 = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\) | \(Y_{g_22}\) |
|       | \(U_3\) | \(G_2 = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\) | \(Y_{g_32}\) |

the ranking ability of rankers.

Table 1 illustrates a simple example of the construction of the PROS sampling design when \(H = 6, l = 3, m = 2\), the cycle size is \(n = 2\) and \(G = \{g_1, g_2, g_3\} = \{\{1, 2\}, \{3, 4\}, \{5, 6\}\}\). Each set contains six units that are assigned to three partially rank-ordered subsets using a ranking mechanism. The partial ranking indicates that ties have been declared among the ranks for the units within subsets; however, the subsets themselves are partially ordered. More specifically, subsets \(g_1\) include the units with the two smallest judgment ranks among the six units. Units in subsets \(g_2\) have judgment ranks greater than units in subsets \(g_1\) and smaller judgment ranks than units in subset \(g_3\). Units in subsets \(g_3\) have received the two highest judgment ranks among the units in each set. In each set, one of the units is finally selected for full measurement from the bold faced subsets in Table 1. The resulted PROS sample of size \(nl = 6\) is then denoted \(\{Y_{gri}; r = 1, 2, 3; i = 1, 2\}\).

Recently, the PROS sampling design has received considerable attention in the literature. For example, Hatefi and Jafari Jozani (2014) studied the information and uncertainty structures of PROS data. Ozturk and Jafari Jozani (2014) used PROS samples for estimation problems in finite population settings. Nazari et al. (2014) developed nonparametric kernel density estimators using PROS data. Hatefi et al. (2013) applied PROS sampling in mixture modeling to estimate the age structures of short-lived fish species. Ozturk (2013a) and Frey (2012) relaxed the assumption concerning the pre-specification of the number of subsets in each set. Due to different ranking potentials of the concomitants, the results of Ozturk (2013a) and Frey (2012) allow to declare as many subsets as desired for the accommodation of tied ranks among the units in the sets. Ozturk (2013a) also studied the statistical inference based on multi-observer RSS in the estimation of the population mean. Recently, Ozturk (2013b) used the properties of PROS samples under multiple auxiliary information in the estimation of the population mean and total in finite population settings.
In this study, using multiple concomitants, we first explore the benefits of employing PROS sampling technique for estimating the population proportion. Then, the estimation procedure will be applied to the WBCD to provide more accurate estimate of the proportion of patients with malignant breast tumours. To this end, Section 2 describes PROS sampling design using multiple concomitants for analysis of the WBCD. We propose an estimation procedure using multi-concomitant PROS samples for the population proportion in Section 3. In Section 4, through two numerical analyses, we study the performance of the multi-concomitant PROS procedure in the estimation of the proportion of patients with malignant breast tumours compared with those based on one-concomitant RSS and multi-concomitant RSS-based logistic regression methods. Summary and concluding remarks are finally presented in Section 5.

2 Multi-concomitant based sampling from the WBCD

Breast cancer accounts for one of the most important types of cancers in women and causes a significant rate of death worldwide. Most of breast cancer cases are discovered when a noticeable lump feels differently from the rest of breast tissues. The early detection of cancerous tumours is very important in the treatment of breast cancer. The earlier breast cancer is detected, the better it may be for the patients long-term health. Many breast cancer organizations, such as the American Breast Cancer Foundation, the Cancer Research UK and the Canadian Breast Cancer Foundation, are concerned about the incidence rate and prevalence of breast cancers in target populations at given times. To this end, regular studies are conducted to estimate the prevalence of malignant breast cancer tumours among the patients in the target population. This is usually done by estimating the proportion of patients with a new or previous malignant breast tumours. In this paper, we consider the WBCD data set as our population and show that PROS sampling design using multiple concomitants can be used as an efficient tool for estimating the proportion of patients in the population with malignant breast tumours. This data set was collected by Dr. William H. Wolberg (Department of Surgery, University of Wisconsin, Madison) and is available online at the UCI machine learning repository (Bache and Lichman, 2013).

Suppose the dichotomous variable $Y$ (hereafter called the Malignant Tumours) denotes the status of breast masses as malignant (success) or benign (failure) tumour. The malignancy of the breast tumours is determined through a comprehensive biopsy procedure. To accurately diagnose the breast tumour samples based purely on FNA, Dr. Wolberg identified nine visually assessed characteristics of an FNA sample and exploited them to determine the status of the tumour samples and start diagnosing them with proper procedures. To be more specific, assessing the epithelial cell clumps obtained through an standard method of breast FNAs, Wolberg and Mangasarian (1990) first identified eleven cytological characteristics of FNAs to distinguish between benign and malignant tumours. These eleven cytological characteristics of breast
FNAs were valued on a scale of 1 (normal) to 10 (most abnormal) by a doctor assessing the tissue cells through a microscope, such that 1 indicates the closest status to the benign while 10 represents the most anaplastic.\cite{3,4} Statistical analysis found that nine of these cytological characteristics play significant roles in the discrimination between malignant and benign breast masses. These nine cytological characteristics are as follows: the amount of thickness (Clump Thickness), the surrounding cells cohesion (Marginal Adhesion) of the epithelial cell aggregates, the size of an epithelial cell aggregate (Single Epithelial Cell Size) calculated as the diameter of the population of the largest epithelial cells relative to erythrocytes, the proportion of a single epithelial nuclei being bare of the peripheral cytoplasm (Bare Nuclei), the blandness of the nuclear chromatin (Bland Chromatin), the normality of nucleolus (Normal Nucleoli), the unusual mitoses (Mitoses), the uniformity in size (Uniformity of Cell Size) and the shape (Uniformity of Cell Shape) of the epithelial cell.

Table 2: Cytological concomitants and their correlations with Malignant Tumours in the WBCD.

| Concomitants         | ρ     | Concomitants              | ρ     |
|----------------------|-------|---------------------------|-------|
| Bare Nuclei          | 0.8226| Marginal Adhesion         | 0.7062|
| Uniformity of Cell Shape | 0.8218| Single Epithelial Cell Size | 0.6909|
| Uniformity of Cell Size | 0.8208| Mitoses                   | 0.4234|
| Bland Chromatin      | 0.7582| Subject ID                | -0.0847|
| Normal Nucleoli      | 0.7186| Independent Covariate     | -0.0317|
| Clump Thickness      | 0.7147|                           |       |

We use these nine easy to obtain cytological characteristics as concomitants associated with malignancy of the corresponding FNA sample to conduct the PROS sampling designs with multiple concomitants from the WBCD. Table 2 shows these concomitants and their correlations with the Malignant Tumours. In addition to these nine cytological concomitants, to explore the effect of unreliable concomitants (i.e., those with very low correlations with the Malignant Tumours), we treat the Subject ID (the unique code for each subject) as another concomitant in our numerical studies. Due to the nature of this concomitant, it is seen from Table 2 that its correlation with the Malignant Tumours is −0.0847. Also, to investigate the effect of an independent concomitant on the performance of our proposed methodology, we generated an independent ordinal variable, namely “Independent Covariate”, taking values on 1 to 10. This guarantees almost zero correlation between the Independent Covariate and the Malignant Tumours.

2.1 Multi-concomitant PROS sampling

Let $(X, Y)\top$ denote a multivariate random variable when $Y$ represents the response variable following a Bernoulli distribution with parameter $p$ (i.e., probability of success) and $X = (X_1, X_2, \ldots, X_l); l \geq 1$
denotes the \( l \)-variate concomitants. In order to construct a PROS sample with multiple concomitants (hereafter called multi-concomitant PROS), we first specify two positive integers \( H \) as the set size and \( n \) as the cycle size. Throughout the paper, we assume that \( N = nH \), where \( N \) represents the total sample size and the number of observations from each judgment order class is \( n \). We now describe how to obtain a multi-concomitant PROS sample of size \( N \), while a numerical illustration is provided in Section 2.2. To measure the \( r \)-th judgment order statistic, say \( Y_{[r]}^i \) \((r = 1, \ldots, H; i = 1, \ldots, n)\) through this design, we randomly choose a set of \( H \) experimental units, \( U_i^{[r]} = \{u_{i1}, \ldots, u_{iH}\} \) from the population. Let \( K \) concomitants be available for the ranking purpose and suppose \( X_{k,i}^{[r]} = (X_{1,k,i}, \ldots, X_{H,k,i}) \) represents the values of the \( k \)-th concomitant, say \( X_k \), \( k = 1, \ldots, K \), for the sampling units in \( U_i^{[r]} \). After ranking the sampling units using \( X_{k,i}^{[r]} \), we construct the rank vectors as follows

\[
O_{k,i}^{[r]} = O(X_{1,k,i}, \ldots, X_{H,k,i}) = \{O_{1,k,i}, \ldots, O_{H,k,i}\}, \quad k = 1, \ldots, K,
\]

where \( O_{h,k,i} \) is the rank assigned to the unit \( u_{hi} \in U_i^{[r]} \). If ranking is done based on an ordinal variable (e.g., the cytological characteristics), the tied ranks may be produced. In this situation, all tied units in the set receive the same rank. If there is a negative correlation between the concomitant variable and the response variable \( Y \), the ranking operator is selected as \( O_{r,k,i} = H + 1 - O_{H+1-r,k,i} \), \( r = 1, \ldots, H \), to produce the necessary judgment order statistics. Note that \( O_{k,i}^{[r]} \) is the rank vector associated with units in the set \( U_i^{[r]} \) from which we derive the \( r \)-th judgement order statistic, \( Y_{[r]}^i \). For each \( O_{k,i}^{[r]} \), \( k = 1, \ldots, K; i = 1, \ldots, n \), we build an \( H \times H \) weight matrix, \( D_{k,i}^{[r]} \), whose rows and columns stand for the units of the set \( U_i^{[r]} \) and assigned judgment ranks, respectively. The entities of the \( D_{k,i}^{[r]} \) stand for the strength-of-weights of the ranking procedure. If there is no tie in the ranking vector \( O_{k,i}^{[r]} \), the \( h \)-th \((h = 1, \ldots, H)\) row and the \( O_{r,k,i} \)th column of the matrix \( D_{k,i}^{[r]} \) is one, and other entries of the \( h \)-th row are zero. If there are \( m \) tied ranks for the \( h \)-th unit \((u_{hi})\), then all the entries corresponding to the tied ranks in the \( h \)-th row will be \( 1/m \) and other entries of the row will be zero. In a similar fashion, we build \( D_{k,i}^{[r]} \) for all \( k = 1, \ldots, K \). To incorporate the ranking information obtained from all available concomitants in the selection of \( Y_{[r]}^i \), we focus on the weighted mean of the strength-of-weight matrices

\[
\bar{D}_i^{[r]} = \sum_{k=1}^{K} \alpha_k D_{k,i}^{[r]},
\]

where \( \sum_{k=1}^{K} \alpha_k = 1 \). The coefficients \( \alpha_k \) is chosen to reflect the importance of the concomitant variable \( X_k \) in the ranking process. Due to Stokes (1977), it is known that larger values for the correlation coefficient between a concomitant and the response variable results in a better precision for the corresponding concomitant-based RSS estimator. As proposed by Ozturk (2013b), we calculate

\[
\alpha_k = \frac{|\rho_k|}{\sum_{k=1}^{K} |\rho_k|},
\]
where $\rho_k$ denotes the correlation coefficient between $Y$ and $X_k, k = 1, \ldots, K$. Finally $Y_{[r]i}$ will be obtained from the unit having the maximum entry in the $r$-th column of $\bar{D}_{[r]}^{[i]}$. If the maximum is unique, say $s$, we observe $(Y_{[r]i}, \bar{\omega}_{[r]}^{[i]})$ as the multi-concomitant PROS sample, where $Y_{[r]i}$ is the response variable of the unit $u_{si}$ in the set $U_{[r]}^{[i]}$ and $\bar{\omega}_{[r]}^{[i]}$ will be the $s$-th row of the $\bar{D}_{[r]}^{[i]}$. However, if the maximum entry in the $r$-th column of $\bar{D}_{[r]}^{[i]}$ is not unique, we consider all the rows with the maximum weight. For all these rows, we calculate the concentration around $r$-th judgment order statistic. Then the $Y$-measurement of the unit with the highest concentration is identified as $Y_{[r]i}$. If the highest concentration is still not unique, one of the units is randomly selected for full measurement and we calculate its corresponding weight vector $\bar{\omega}_{[r]}^{[i]}$.

For a given weight vector $\bar{\omega}_{[r]}^{[i]} = (\bar{\omega}_{[r,1]}^{[i]}, \ldots, \bar{\omega}_{[r,H]}^{[i]}) \in \bar{D}_{[r]}^{[i]}$, we calculate the concentration around the $r$-th judgment order statistic as

$$\gamma_{r,i} = \sum_{t=1}^{H} (t - r)^2 \omega_{i}^{[r,t]}.$$ 

Small values of $\gamma_{r,i}$ imply a high concentration around the $r$-judgement rank. Finally the observed multi-concomitant PROS data are given by

$$\{ (Y_{[r]i}, \bar{\omega}_{[r]}^{[i]}), \ r = 1, \ldots, H; i = 1, \ldots, n \}.$$ 

Note that through multi-concomitant PROS sampling, we not only measure $Y_{[r]i}$ but also we calculate the weight vectors $\bar{\omega}_{[r]}^{[i]}$ related to the judgment ranks using combined ranking information from all the available concomitants. Moreover, $Y_{[r]i}$ and $\bar{\omega}_{[r]}^{[i]}$ are dependent random variables for fixed $i$ and $r$. In a similar vein, the PROS sampling based on $K$ concomitants can be extended to the PROS sampling under $K$ different rankers for only one concomitant. See Ozturk (2013a) for more details.

### 2.2 An illustrative example

To illustrate the construction of multi-concomitants PROS samples, we present a simple example based on the WBCD using $K = 4$ cytological characteristics as concomitants including the Subject ID ($k = 1$), Uniformity of Cell Size ($k = 2$), Uniformity of Cell Shape ($k = 3$) and Bare Nuclei ($k = 4$). Suppose we are interested in measuring the second judgment order statistic $Y_{[2]1}$ when the set size $H = 5$ and the cycle size $n = 1$.

Table 3 shows a set of five units $U_{[2]}^{[1]} = \{u_{11}, u_{21}, u_{31}, u_{41}, u_{51}\}$ and their concomitants selected for ranking process in this example. To illustrate the effect of tie-structure in the example, we assume that tied-ranks may be declared in the ranking process using three cytological characteristics (i.e., $k \in \{2, 3, 4\}$). Unique ranks are also assigned to the units using the Subject ID. The tie-structures in this example are constructed as follow. The values of concomitants are assigned to the units in subsets $s_1 = \{1, 2\}, s_2 = \{3, 4\}, s_3 = \{5, 6\}, s_4 = \{7, 8\}$ and $s_5 = \{9, 10\}$ and these subsets are partially ranked so that units within
Table 3: Units of the set $U_1^{[2]}$ and their concomitants in the illustrative example.

| Concomitants | Uniformity of Cell Size | Uniformity of Cell Shape | Bare Nuclei |
|--------------|-------------------------|--------------------------|-------------|
| $k = 1$      | $k = 2$                 | $k = 3$                  | $k = 4$    |
| $u_{11}$     | 1033078                 | 1                        | 1           |
| $u_{21}$     | 1035283                 | 1                        | 1           |
| $u_{31}$     | 1016277                 | 8                        | 4           |
| $u_{41}$     | 1017122                 | 10                       | 10          |
| $u_{51}$     | 1044572                 | 7                        | 9           |

Each group receive the same rank and units in $s_h$ receive lower ranks than units in $s_{h'}$ when $h < h'$. For example, using the Bare Nuclei values reported in Table 3 for the judgment ranking process, units $u_{11}, u_{21}$ are declared tied at ranks $\{1, 2\}$, unit $u_{31}$ is uniquely ranked 3 and units $u_{41}, u_{51}$ receive tied ranks at $\{4, 5\}$.

Table 4: The tie-structures of the set $U_1^{[2]}$ and the ranks declared in the curly brackets.

| Concomitants | Units |
|--------------|-------|
| $k$          | $u_{11}$ | $u_{21}$ | $u_{31}$ | $u_{41}$ | $u_{51}$ |
| 1            | 1, $\{3\}$ | 1, $\{4\}$ | 1, $\{1\}$ | 1, $\{2\}$ | 1, $\{5\}$ |
| 2            | 1/2, $\{1,2\}$ | 1/2, $\{1,2\}$ | 1/2, $\{3,4\}$ | 1, $\{5\}$ | 1/2, $\{3,4\}$ |
| 3            | 1/2, $\{1,2\}$ | 1/2, $\{1,2\}$ | 1, $\{4\}$ | 1, $\{5\}$ | 1, $\{3\}$ |
| 4            | 1/2, $\{1,2\}$ | 1/2, $\{1,2\}$ | 1, $\{3\}$ | 1/2, $\{4,5\}$ | 1/2, $\{4,5\}$ |

Table 4 provides the tie-structures and ranks declared for the units of the set $U_1^{[2]}$. Under the Bare Nuclei, for instance, the weights are 1/2 for the $u_{11}, u_{21}$ tie-ranked at $\{1, 2\}$, 1 for $u_{31}$ ranked 3 and 1/2 for units $u_{41}, u_{51}$ tie-ranked at $\{4, 5\}$. Using the Subject ID, as noted earlier, we observe unique ranks (i.e., no tied-rank) for all the units in the first row of Table 4. From Table 4 we construct the weight matrix.
$D_{k,1}^2$, $k = 1, \ldots, 4$, based on these concomitants as follow

\[
D_{1,1}^{[2]} = \begin{bmatrix}
0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 1
\end{bmatrix}, \quad D_{2,1}^{[2]} = \begin{bmatrix}
\frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\
\frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\
0 & 0 & \frac{1}{2} & \frac{1}{2} & 0 \\
0 & 0 & 0 & 0 & 1
\end{bmatrix},
\]

\[
D_{3,1}^{[2]} = \begin{bmatrix}
\frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\
\frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1 \\
0 & 0 & 1 & 0 & 0
\end{bmatrix}, \quad D_{4,1}^{[2]} = \begin{bmatrix}
\frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\
\frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\
0 & 0 & \frac{1}{2} & \frac{1}{2} & 0 \\
0 & 0 & 0 & \frac{1}{2} & \frac{1}{2}
\end{bmatrix}.
\]

Using $\alpha = (0.0468, 0.0453, 0.4537, 0.4542)$ obtained based on the correlations between the concomitants $(k = 1, \ldots, 4)$ and the Malignant Tumours, we compute the average weight matrix as

\[
\bar{D}_{1}^{[2]} = \begin{bmatrix}
0.4766 & 0.4766 & 0.04680 & 0.00000 & 0.0000 \\
0.4766 & 0.4766 & 0.00000 & 0.04680 & 0.0000 \\
0.0468 & 0.0000 & 0.47685 & 0.47635 & 0.0000 \\
0.0000 & 0.0468 & 0.00000 & 0.22710 & 0.7261 \\
0.0000 & 0.0000 & 0.47635 & 0.24975 & 0.2739
\end{bmatrix},
\]

which will be used to identify the unit in the set $U_{1}^{[2]}$ for full quantification. Since our goal here is to measure the second judgment order statistic $Y_{1}^{[2]}$, we focus on the second column of $\bar{D}_{1}^{[2]}$. We observe that units $\{u_{11}, u_{21}\}$ both have the maximum chance to be the second order statistic in this set. Finally, having the higher concentration, the first unit $u_{11}$ is selected as the second judgment order statistic $Y_{1}^{[2]}$ from $U_{1}^{[2]}$ for full measurements. The observed data in this example is given by

\[
(Y_{[2]}, \bar{\omega}_{1}^{[2]}) = (Y_{[2]}, \{0.4766, 0.4766, 0.04680, 0, 0\}) ,
\]

where $\bar{\omega}_{1}^{[2]}$ is the first row of the matrix $\bar{D}_{1}^{[2]}$ (the row corresponding to $u_{11}$). Note that we also observe the concomitant values associated with the selected unit that can be used in the estimation of the probability of having malignant breast tumours using some regression models such as logistic regression.
3 Statistical procedures

3.1 Multi-concomitant PROS estimator

Let \( Y_{mp} = \{(Y_{r[i]}, \omega_{i}^{[r]}); r = 1, \ldots, H; i = 1, \ldots, n\} \) denote the multi-concomitant PROS sample of size \( nH \) with set size \( H \) and cycle size \( n \). Suppose \( Y_{r[i]} \) is the quantified \( r \)-th judgment order statistic and \( \omega_{i}^{[r]} = (\omega_{i}^{[r,1]}, \ldots, \omega_{i}^{[r,H]}) \) is its corresponding weight vector such that \( 0 \leq \omega_{i}^{[r,h]} \leq 1 \) and \( \sum_{h=1}^{H} \omega_{i}^{[r,h]} = 1 \). To exploit the tie-structure in the estimation of the population proportion \( p \), the quantified statistics are prorated to the judgment ranks, using the strength-of-weight probability vector. Due to Ozturk (2013b), the population proportion estimation under the multi-concomitant PROS data is calculated by

\[
\hat{p}_{mp} = \frac{1}{H} \sum_{h=1}^{H} \sum_{r=1}^{H} \sum_{i=1}^{n} \omega_{i}^{[r,h]} Y_{r[i]} = \sum_{r=1}^{H} \sum_{i=1}^{n} \omega_{i}^{[r]} Y_{r[i]},
\]

where \( \omega_{i}^{[r,h]} \) can be interpreted as the allocation of \( Y_{r[i]} \) to the \( h \)-th judgment rank, proportional to the strength of the agreement probability that \( h \) is the true rank of \( Y_{r[i]} \) \((h = 1, \ldots, H)\). Note that population proportion estimator using one-concomitant RSS (Terpstra and Liudahl, 2004) can be obtained as an special case of (1) using a single concomitant with no tie-structure.

3.2 RSS-based Logistic regression estimator

Chen et al. (2005) used multiple concomitants to obtain an RSS-based estimator of the population proportion using a logistic regression model on concomitants \( X \) as follows

\[
p = \frac{\exp(\beta_0 + \beta^T X)}{1 + \exp(\beta_0 + \beta^T X)},
\]

where \( p \) is the corresponding probability of success, \( \beta_0 \) is the intercept parameter and \( \beta \) is the vector of slope parameters. It is assumed that there is a "training data set" consisting of the values of the concomitants as well as the response variable. Chen et al. (2005) requires the training data set to estimate the parameters of the logistic regression model in (2) (i.e., \( \beta_0 \) and \( \beta \)). Let \( X_r \) denote the vector of concomitants associated with the \( r \)-th individual in a set of size \( H \). Chen et al. (2005) estimates the probability of success \( \hat{p}_r \) \((r = 1, \ldots, H)\) based on the fitted logistic regression model and use them for ranking the sampling units with binary response variable \( Y \) to obtain an RSS sample of size \( nH \) given by \( \{Y_{r[i]}, r = 1, \ldots, H; i = 1, \ldots, n\} \). Finally, they propose an RSS-based estimator of the population proportion \( p \) as follow

\[
\hat{p}_l = \frac{1}{nH} \sum_{r=1}^{H} \sum_{i=1}^{n} Y_{r[i]}.
\]
We refer to this method as the multi-concomitant RSS-based logistic regression method for estimating \( p \).

### 3.3 Standard deviation reduction

To evaluate the performance of the multi-concomitant PROS estimator \( \hat{p}_{mp} \), we compare the average, standard deviation (SD) as well as the SD reduction of \( \hat{p}_{mp} \) with those of the counterpart estimators under simple random sampling (SRS), one-concomitant RSS (Terpstra and Liudahl, 2004) and multi-concomitant RSS-based logistic regression methods (Chen et al., 2005). Let \( \bar{\hat{p}}_{mp} = \frac{1}{J} \sum_{j=1}^{J} \hat{p}_{mp}^j \), where \( \hat{p}_{mp}^j \) is the multi-concomitant PROS estimate of \( p \) obtained from the \( j \)-th replicate, \( j = 1, \ldots, J \). The SD of \( \hat{p}_{mp} \) is then computed by

\[
SD(\hat{p}_{mp}) = \left\{ \frac{1}{J - 1} \sum_{j=1}^{J} (\hat{p}_{mp}^j - \bar{\hat{p}}_{mp})^2 \right\}^{1/2}. \tag{4}
\]

Similar to Chen et al. (2005), since \( p \) is known, using the finite population correction (population size is \( N' \)), we calculate the SD of the population proportion estimator based on a SRS sample of size \( m \) as follows

\[
SD(\hat{p}_{srs}) = \left\{ \frac{N' - m}{N' - 1} \times \frac{p(1-p)}{m} \right\}^{1/2}. \tag{5}
\]

From (4) and (5), the percentage of reduction in the sample SD (SD reduction) by using \( \hat{p}_{mp} \) instead of \( \hat{p}_{srs} \) is computed by

\[
SD\text{ reduction}(\hat{p}_{mp}, \hat{p}_{srs}) = \left( 1 - \frac{SD(\hat{p}_{srs})}{SD(\hat{p}_{mp})} \right) \times 100.
\]

The average and SD and SD reduction measures can similarly be obtained for other estimation procedures.

### 4 Breast cancer data analysis

In this section, we use the WBCD as the underlying population of interest, to evaluate the performance of \( \hat{p}_{mp} \) for estimating the proportion of patients with malignant breast cancer tumour and compare it with its counterparts under SRS, one-concomitant RSS and multi-concomitant RSS-based logistic regression methods. The WBCD consists of 699 subjects in where the tumour of 266 subjects have been identified as malignant. For this study, the response variable is the "Malignant Tumours" that follows a Bernoulli distribution with probability of success \( p = 0.3499 \). Through two numerical studies, we first evaluate the performance of \( \hat{p}_{mp} \) for estimating the proportion of patients with malignant breast tumours compared with its counterparts under SRS, one-concomitant RSS and multi-concomitant RSS-based logistic regression methods. Then, we investigate the effect of tie-structures on the performance of \( \hat{p}_{mp} \).
Study 1: One-concomitant and multi-concomitant RSS procedures

In this study, we evaluate the performance of the population proportion estimators under different sampling procedures. We focus on SRS estimator of \( p \), one-concomitant RSS-based estimator (Terpstra and Liudahl, 2004), multi-concomitant RSS-based logistic regression estimator (Chen et al., 2005), and our proposed multi-concomitant PROS estimator given in (1). The sample size (i.e., number of measured units) is fixed at 54 for each setting. To calculate the average, SD and SD reduction measures, each estimation procedure is replicated 50,000 times. Since the population proportion is \( p = 0.3499 \) (with population size \( N' = 699 \)), the SD of \( \hat{p}_{srs} \) based on a SRS without replacement of size 54 is given by

\[
SD(\hat{p}_{srs}) = \sqrt{\frac{699 - 54}{699 - 1} \times \frac{0.3499(1 - 0.3499)}{54}} = 0.0623. \tag{6}
\]

To evaluate the performance of one-concomitant RSS-based estimator, we select five single concomitants for the ranking process of the RSS technique. These include Bare Nuclei, Uniformity of Cell Shape and Uniformity of Cell Size which have the highest correlations with the Malignant Tumours, as well as the Normal Nucleoli, the Subject ID and Independent Covariate which, respectively, have intermediate, very low and almost zero correlations with Malignant Tumours to study the effect of different ranking abilities on the performance of one-concomitant RSS-based estimator of \( p \). The RSS design with set sizes \( H = 3, 6 \) and 9 are then applied to obtain the RSS estimates under these five single concomitants.

| Table 5: Averages and SDs (in bracket) of 50,000 estimates of the malignant proportion. |
|-----------------------------------------------|-----------------|-----------------|-----------------|-----------------|
| **Sampling Designs**                         | **SRS**         | **RSS with H=3** | **RSS with H=6** | **RSS with H=9** |
| Bare Nuclei                                  | 0.4466(0.0623)  | 0.3296(0.0557)  | 0.3130(0.0487)  | 0.3207(0.0442)  |
| Uniformity of Cell Shape                     | 0.4473(0.0623)  | 0.3281(0.0547)  | 0.3049(0.0456)  | 0.3069(0.0389)  |
| Uniformity of Cell Size                      | 0.4472(0.0623)  | 0.3262(0.0540)  | 0.3033(0.0449)  | 0.3076(0.0384)  |
| Normal Nucleoli                              | 0.4468(0.0623)  | 0.3369(0.0573)  | 0.3274(0.0516)  | 0.3279(0.0477)  |
| Subject ID                                   | 0.4466(0.0623)  | 0.3558(0.0596)  | 0.3549(0.0576)  | 0.3524(0.0555)  |
| Independent Covariate                        | 0.4472(0.0623)  | 0.3408(0.0588)  | 0.3111(0.0558)  | 0.3208(0.0547)  |

Tables 5 and 6 provide the average, SD and SD reduction values of these five one-concomitant RSS estimates obtained through 50,000 replicates. Our results show that RSS estimators based on single concomitant perform well in the estimation of \( p \) for all the set sizes compared with their SRS counterparts. Focusing on Uniformity of Cell Shape as the ranking concomitant, for instance, the sample SD of the RSS estimator compared with that of SRS estimator reduces from 13.34% for set size \( H = 3 \) to 38.39% for set size \( H = 9 \). Due to the fact that the Subject ID and Independent Covariate have the smallest correlations with the Malignant Tumours, as expected, the percent reduction in SD of one-concomitant RSS-based
estimator under these concomitants are low for all the set sizes. However, as the set size increases the SD reductions of the one-concomitant RSS-based estimators increases.

Table 6: Percent SD reductions of RSS estimators relative to SRS estimator of the malignant proportion.

| Concomitants          | RSS with set size |
|-----------------------|-------------------|
|                       | H=3   | H=6   | H=9   |
| Bare Nuclei           | 10.5713| 21.9384| 29.1293|
| Uniformity of Cell Shape | 12.2834| 26.8765| 37.5440|
| Uniformity of Cell Size | 13.3495| 27.9003| 38.3916|
| Normal Nucleoli       | 8.1039 | 17.2002| 23.4274|
| Subject ID            | 4.3091 | 7.5649 | 11.0161|
| Independent Covariate | 5.6549 | 10.4947| 12.2978|

Now, we consider estimation of the population proportion using multi-concomitant PROS and RSS-based logistic regression estimators (Chen et al., 2005). We then compare them with the results obtained under one-concomitant RSS estimator (Terpstra and Lindahl, 2004). We consider nine ranking models corresponding to different choices of concomitants, as described in Table 7. Models 1, 2 and 9 focus on concomitants which have the highest (Bare Nuclei) and the lowest (Subject ID and Independent Covariate) correlation coefficients with the Malignant Tumours, respectively. These models will help us to simultaneously explain the effect of different ranking potentials on the performance of the malignant proportion estimators. We can also compare them with the results presented in Tables 5 and 6 for one-concomitant RSS method. Models 3 and 4 are two-concomitant based ranking models whose logistic regression models are significant. These models allow us to compare the performance of multi-concomitant PROS with that of the RSS-based logistic regression model in the estimation of malignant proportion.

Model 5 and 6 are two ranking models using three concomitants for ranking purposes. Model 5 includes three concomitants with the highest correlations with the Malignant Tumours, while Model 6 involves two best ranking variables along with the worst ranking variable. These models explain the effect of the worst ranking variable in the presence of the best ranking variables. Lastly, Model 7 consists of the best ranking variable along with the 3 ranking variables with intermediate correlations with the Malignant Tumours while Model 8 only consists of three concomitants with intermediate ranking abilities that are used in Model 7. This assists us to explain how much precision is lost by using intermediate ranking variables when we do not have access to the best ranking variable.

The PROS samples using multi-concomitants are constructed as described in Section 2. We use the tie-structure model introduced by Frey (2012). For instance, focusing on a concomitant, say $X_1$, we divide $X_1$ with a nonnegative $c$, $X_1/c$, and then round it to the nearest integer. Let $X_1^*$ denote the discretized
Table 7: Various ranking models using various concomitants.

| Ranking Models | Explanatory variables | Degree of association with Malignant Tumour | Significance of the Model at $\alpha = 0.05$ |
|----------------|-----------------------|---------------------------------------------|---------------------------------------------|
| Model 1        | Bare Nuclei           | Very Strong                                 | Yes                                         |
| Model 2        | Subject ID            | Very Low                                    | No                                          |
| Model 3        | Bare Nuclei, Normal Nucleoli | Very Strong, Intermediate                  | Yes                                         |
| Model 4        | Bare Nuclei, Single Epithelial Cell Size | Very Strong, Intermediate                  | Yes                                         |
| Model 5        | Bare Nuclei, Uniformity of Cell Size, Uniformity of Cell Shape | Very Strong, Very Strong, Very Strong | No                                          |
| Model 6        | Bare Nuclei, Uniformity of Cell Size, Subject ID | Very Strong, Very Strong, Very Low | No                                          |
| Model 7        | Bare Nuclei, Normal Nucleoli, Clump Thickness, Bland Chromatin | Very Strong, Intermediate, Intermediate, Intermediate | No                                          |
| Model 8        | Normal Nucleoli, Clump Thickness, Bland Chromatin | Intermediate, Intermediate, Intermediate | Yes                                         |
| Model 9        | Independent Covariate | No association                              | No                                          |

Table 8: Averages (AV), SDs (SD) and percent SD reductions (PSR) of 50,000 $\hat{p}_{mp}$ using various ranking models with set sizes $H = \{3, 6, 9\}$.

| Models        | H=3     | H=6     | H=9     |
|---------------|---------|---------|---------|
|               | AV      | SD      | PSR     | AV      | SD      | PSR     | AV      | SD      | PSR     |
| Model 1       | 0.3437  | 0.0507  | 18.5899 | 0.3303  | 0.0444  | 28.7434 | 0.3334  | 0.0422  | 32.2968 |
| Model 2       | 0.3562  | 0.0594  | 4.6454  | 0.3546  | 0.0578  | 7.3142  | 0.3506  | 0.0558  | 10.5121 |
| Model 3       | 0.3388  | 0.0495  | 20.6386 | 0.3233  | 0.0405  | 35.0739 | 0.3237  | 0.0361  | 42.0048 |
| Model 4       | 0.3336  | 0.0510  | 18.1295 | 0.3143  | 0.0399  | 35.9273 | 0.3130  | 0.0356  | 42.8559 |
| Model 5       | 0.3322  | 0.0480  | 23.0078 | 0.3219  | 0.0376  | 39.6046 | 0.3184  | 0.0322  | 48.4163 |
| Model 6       | 0.3358  | 0.0487  | 21.8970 | 0.3234  | 0.0367  | 41.1436 | 0.3224  | 0.0334  | 46.3639 |
| Model 7       | 0.3282  | 0.0491  | 21.1707 | 0.3181  | 0.0388  | 37.8145 | 0.3182  | 0.0338  | 45.8352 |
| Model 8       | 0.3281  | 0.0510  | 18.2574 | 0.3165  | 0.0411  | 34.0816 | 0.3048  | 0.0359  | 42.4212 |
| Model 9       | 0.3411  | 0.0591  | 5.2142  | 0.3199  | 0.0569  | 8.6820  | 0.3197  | 0.0547  | 12.2053 |

version of $X_1/c$. Then, units with the same discretized value are declared as the tied-ranks in the set. This discretization process is considered for all available concomitants. The multi-concomitant PROS data are finally generated through the combined ranking information from all available concomitants with the possibility of tie-structures. For more information, see Ozturk (2013a) and Frey (2012).

As mentioned earlier, there are two disadvantages associated with RSS-based logistic regression estimation procedure (Chen et al., 2005). The first disadvantage is that a ‘training sample’, which requires the
quantification of the Malignant Tumours, is needed to estimate the logistic regression model for the ranking process involved in RSS sampling; however, the multi-concomitant PROS estimation procedure does not need the training data set. To fit the RSS-based logistic regression model, a ‘training sample’ of size 100 was taken at random from the WDBC. This training data set is used for estimating the probabilities of success and performing the ranking process required for RSS estimation procedure of Chen et al. (2005).

Under only the Bare Nuclei ranking variable, \( \hat{p}_{mp} \) performs very well in the estimation of the malignant proportion. The sample SD reduction of \( \hat{p}_{mp} \) using Model 1 (Table 8) accounts for 18.58% for \( H = 3 \) and 32.29% for \( H = 9 \) while precision gained by the counterpart estimators for \( H = 3 \) are almost 10% and 29% for \( H = 9 \) in Table 6 and Table 9 respectively. This indicates the superiority of \( \hat{p}_{mp} \) over its counterparts even with one concomitant for ranking. The relative efficiency (RE) is another valuable measure to compare the performance of the estimation procedures (Terpstra and Luidahl, 2004). The relative efficiency can be considered as the ratio of variances of two estimators as
\[
RE(\hat{p}_{mp}, \hat{p}_l) = \frac{Var(\hat{p}_{mp})}{Var(\hat{p}_l)},
\]
and can be interpreted as the ratio of the required sample sizes to obtain the same precision for the two estimation procedures, say \( N_l = RE(\hat{p}_{mp}, \hat{p}_l)N_{mp} \), where \( N_l \) and \( N_{mp} \) are the total sample sizes of the estimation procedures. From Tables 8 and 9 focusing on the SDs of \( \hat{p}_{mp} \) and \( \hat{p}_l \) using Models 3 and 4 for \( H = 3 \), \( \hat{p}_l \) requires samples of sizes 61 and 58, respectively, to be as precise as \( \hat{p}_{mp} \) with sample size 54 in the estimation of the proportion of malignant tumours.

The second disadvantage associated with the RSS-based logistic regression model is the requirement of the logistic regression model assumption. To show the impact of such assumption, we used forward and backward selection methods for all concomitant-based ranking models introduced in Table 7 as well as other possible models based on available concomitants. In the case of one-concomitant ranking model, the regression models based on Uniformity of Cell Shape, Bland Chromatin, Clump Thickness and Marginal Adhesion were not significant. Models 2, 5, 6, 7 and 9 are considered as examples of ranking models were their corresponding logistic regression models are not significant.

From Table 8 focusing on Models 1 and 5, we take the advantage of multi-concomitant PROS sampling schemes and improve the precision of \( \hat{p}_{mp} \) from 18.58% for \( H = 3 \) and 32.29% for \( H = 9 \) under Model 1 (using only the Bare-Nuclei concomitant) to 23.00% for \( H = 3 \) and 48.41% for \( H = 9 \) under Model 5 in which we benefit from the full ranking information of the best three ranking variables in the estimation of the proportion of patients with malignant tumours. Considering Models 5 and 6, it is seen that the precision gain of \( \hat{p}_{mp} \) under Model 6 is slightly less than that under Model 5. This illustrates the effect of the bad ranker on the estimation; however, the discrepancy is not too large. This may reflect the benefit of multi-concomitant PROS procedure in which the good rankers downside the impact of a bad ranker. Focusing on Models 1, 7 and 8 under \( H = 3 \), it is apparent that the percentage of SD reduction increases from 18.58% under Model 1 to 21.17% under Model 7. This indicates that the excellence of \( \hat{p}_{mp} \) based...
on only the Bare Nuclei concomitant can be increased by using more intermediate ranking concomitants. Comparing Models 7 and 8, it is seen that using highly correlated concomitants for the ranking process plays an important role in the accuracy of \( \hat{p}_{mp} \) in the estimation of the proportion of patients with malignant tumours. Moreover, we see from Table 8 that precision gain of \( \hat{p}_{mp} \) is almost the same under Models 1 and 8. This is interesting as if there is no highly correlated concomitant associated with the Malignant Tumours for the ranking process, one can still estimate the proportion of malignant breast tumours reasonably well using multiple cytological characteristics having intermediate correlations with the Malignant Tumours.

**Study 2: Analysis of the tie-structures**

Here we study the properties of \( \hat{p}_{mp} \) for estimating the population proportion under different tie-structures. To this end, we compare the performance of \( \hat{p}_{mp} \) using different multi-concomitant PROS samples of fixed size \( nH = 54 \) with set sizes \( H \in \{2, 3, 6\} \) and various tie-structures associated with \( c \in \{1, 1.5, 3, 4\} \). The tie-structures in PROS samples are constructed as described in Study 1 using discretization formula (Frey, 2012).

The tie-structure is selected roughly proportional to \( c = \delta/H \) where \( H \) is set size and \( \delta \) is the range for the associated concomitant variable. This selection approximately assigns the same number of categories to the subsets and proposes roughly balanced PROS samples; however, it should be noted that the final samples may not be necessarily balanced, since the units are assigned to the subsets based on different ranking potentials of concomitants. Although the ordinal concomitants consist of 10 categories, since category 9 is rarely observed compared with other categories, we used \( \delta = 9 \) (instead of 10) in the selection of tie-structures for these concomitants. More specifically, when the set size \( H = 2 \), the tie-structure is \( c = \delta/H = 4.5 \sim 4 \). For set size \( H = 3 \), we use the tie-structure \( c = \delta/H = 3 \). Similarly \( c = \delta/H = 1.5 \)
Table 10: Results of 50,000 replicates of $\hat{p}_{mp}$ when no tie-structure (i.e., $c = 1$ for all set sizes $H = \{2, 3, 6\}$) is allowed in sampling.

| Ranking Models | $H$ | Average | SD   | SD Reduction | Lower Bound | Upper Bound | Length of CI |
|----------------|-----|---------|------|--------------|-------------|-------------|--------------|
| Model 1        | 2   | 0.3378  | 0.0576 | 7.6567       | 0.2440      | 0.4333      | 0.1893       |
|                | 3   | 0.3455  | 0.0513 | 17.6955      | 0.2616      | 0.4302      | 0.1686       |
|                | 6   | 0.3298  | 0.0451 | 27.5769      | 0.2560      | 0.4044      | 0.1484       |
| Model 2        | 2   | 0.3611  | 0.0601 | 3.6514       | 0.2590      | 0.4630      | 0.2040       |
|                | 3   | 0.3565  | 0.0601 | 3.6224       | 0.2592      | 0.4619      | 0.2028       |
|                | 6   | 0.3545  | 0.0576 | 7.5525       | 0.2593      | 0.4463      | 0.1870       |
| Model 5*       | 2   | 0.3295  | 0.0564 | 9.5027       | 0.2369      | 0.4236      | 0.1868       |
|                | 3   | 0.3327  | 0.0487 | 21.9011      | 0.2526      | 0.4120      | 0.1594       |
|                | 6   | 0.3124  | 0.0399 | 36.0475      | 0.2468      | 0.3781      | 0.1313       |
| Model 3        | 2   | 0.3333  | 0.0568 | 8.9168       | 0.2390      | 0.4276      | 0.1886       |
|                | 3   | 0.3377  | 0.0497 | 20.2667      | 0.2563      | 0.4196      | 0.1634       |
|                | 6   | 0.3227  | 0.0410 | 34.2832      | 0.2558      | 0.3902      | 0.1345       |
| Model 5        | 2   | 0.3294  | 0.0559 | 10.3764      | 0.2382      | 0.4226      | 0.1845       |
|                | 3   | 0.3344  | 0.0486 | 22.0833      | 0.2546      | 0.4141      | 0.1595       |
|                | 6   | 0.3154  | 0.0386 | 38.0544      | 0.2525      | 0.3793      | 0.1268       |
| Model 8        | 2   | 0.3314  | 0.0571 | 8.3292       | 0.2410      | 0.4262      | 0.1853       |
|                | 3   | 0.3338  | 0.0512 | 17.7815      | 0.2489      | 0.4188      | 0.1699       |
|                | 6   | 0.3050  | 0.0414 | 33.5407      | 0.2379      | 0.3739      | 0.1360       |
| Model 9        | 2   | 0.3499  | 0.0591 | 5.2576       | 0.2407      | 0.4444      | 0.2037       |
|                | 3   | 0.3406  | 0.0587 | 5.7845       | 0.2222      | 0.4444      | 0.2222       |
|                | 6   | 0.3109  | 0.0555 | 10.8859      | 0.2037      | 0.4074      | 0.2037       |

for the case when $H = 6$. Also, note that $c = 1$ indicates that no-tie structure is created through PROS sampling; however, we may still observe tied-ranks in the estimation procedure because of the nature of the concomitants. For the Subject ID we have $\delta = 13390977$ and the tie-structures are selected roughly proportional to $\delta/H$ for different set sizes $H \in \{2, 3, 6\}$. In this study, we consider 6 sets of concomitants (as ranking models) for the ranking purpose. These include Models 1, 2, 3, 5, 8 and 9 of Table 7 as well as Model 5* using the Bare Nuclei and the Uniformity of Cell Shape as two good ranking variables. We obtain $\hat{p}_{mp}$ based on different multi-concomitant PROS samples and then the estimation procedures are replicated 50,000 times. We calculate the averages and SD of 50,000 malignant proportion estimates for each setting. To evaluate the effect of different tie-structures on the performance of $\hat{p}_{mp}$ in the estimation of malignant proportion, the reduction gained in sample SD of $\hat{p}_{mp}$ under each setting is compared with \textsuperscript{6} under its counterpart based on without replacement SRS sample of size 54. For each setting, we also study 90% non-parametric confidence intervals (CIs) for the population proportion, where the lower bound (Lower Bound) and upper bound (Upper Bound) of the intervals are computed as the empirical 5% and 95% quantiles of the proportion of malignant breast tumours estimates. We also calculate the length of
the confidence intervals for each setting as another measure of performance. Tables 10 and 11 show the results of the estimation procedures under PROS scheme using different tie-structures.

Table 11: Results of 50,000 replicates of \( \hat{p}_{mp} \) using different tie-structures (\( c = \{4, 3, 2\} \) when set size \( H = \{2, 3, 4\} \), respectively) in sampling.

| Ranking Models | \( H \) | Average | SD | SD Reduction | Lower Bound | Upper Bound | Length of CI |
|----------------|-------|--------|----|--------------|-------------|-------------|-------------|
| Model 1        | 2     | 0.3341 | 0.0567 | 9.1005 | 0.2413 | 0.4288 | 0.1875 |
|                | 3     | 0.3441 | 0.0505 | 18.9653 | 0.2609 | 0.4275 | 0.1665 |
|                | 6     | 0.3306 | 0.0446 | 28.4310 | 0.2579 | 0.4047 | 0.1468 |
| Model 2        | 2     | 0.3498 | 0.0608 | 2.4816 | 0.2411 | 0.4446 | 0.2035 |
|                | 3     | 0.3487 | 0.0601 | 3.6394 | 0.2414 | 0.4447 | 0.2034 |
|                | 6     | 0.3550 | 0.0593 | 4.7922 | 0.2599 | 0.4498 | 0.1898 |
| Model 5*       | 2     | 0.3334 | 0.0555 | 10.9221 | 0.2436 | 0.4259 | 0.1823 |
|                | 3     | 0.3310 | 0.0489 | 21.5385 | 0.2507 | 0.4113 | 0.1606 |
|                | 6     | 0.3220 | 0.0400 | 35.8855 | 0.2568 | 0.3885 | 0.1317 |
| Model 3        | 2     | 0.3345 | 0.0566 | 9.2023 | 0.2424 | 0.4284 | 0.1861 |
|                | 3     | 0.3384 | 0.0492 | 21.0232 | 0.2576 | 0.4194 | 0.1619 |
|                | 6     | 0.3234 | 0.0407 | 34.7509 | 0.2567 | 0.3901 | 0.1334 |
| Model 5        | 2     | 0.3319 | 0.0556 | 10.7361 | 0.2407 | 0.4246 | 0.1839 |
|                | 3     | 0.3318 | 0.0487 | 21.9182 | 0.2524 | 0.4124 | 0.1600 |
|                | 6     | 0.3216 | 0.0376 | 39.6662 | 0.2606 | 0.3842 | 0.1236 |
| Model 8        | 2     | 0.3337 | 0.0571 | 8.3607 | 0.2425 | 0.4282 | 0.1857 |
|                | 3     | 0.3278 | 0.0509 | 18.4197 | 0.2456 | 0.4114 | 0.1659 |
|                | 6     | 0.3166 | 0.0410 | 34.1925 | 0.2493 | 0.3841 | 0.1348 |
| Model 9        | 2     | 0.3468 | 0.0596 | 4.3587 | 0.2521 | 0.4451 | 0.1930 |
|                | 3     | 0.3411 | 0.0592 | 5.0599 | 0.2423 | 0.4416 | 0.1993 |
|                | 6     | 0.3196 | 0.0569 | 8.7842 | 0.2258 | 0.4133 | 0.1874 |

From Tables 10 and 11 we observe that when the set size increases from 2 to 6, \( \hat{p}_{mp} \) performs better in the estimation of the proportion of patients with malignant breast tumours, resulting in increase in the SD reductions and decrease in the length of the CIs. Comparing Tables 10 and 11 it is apparent that appropriate selection of tie-structures improves the precision of \( \hat{p}_{mp} \) in the estimation of malignant proportion. As noted earlier, using suitable tie-structures for one-concomitant RSS-based estimator, one can make better inference about the determination of malignancy of breast tumours than the one based on the estimation procedure proposed by [Terpstra and Liudahl (2004)](#).

5 Summary and concluding remarks

In many medical studies, measuring the variable of interest is costly, time consuming or difficult, but a small number of sampling units can be ranked easily using some easy to obtain concomitants and
this can be done at little cost. In these situations, rank-based sampling designs such as RSS and PROS sampling techniques can be efficiently employed to obtain more representative samples from the underlying population and make better inference about the parameter of interest. In this paper, we investigate the properties of PROS sampling design with multiple concomitants for estimating the proportion of patient with malignant tumours in a breast cancer study using the Wisconsin Breast Cancer Data (WBCD) as the population of interest. In this application, the discrimination between the malignant and benign breast tumours requires a comprehensive biopsy procedure which is often time consuming and costly. However, there are nine visually assessed cytological characteristics that are usually used to more accurately diagnose the breast cancer status. These concomitants can be used to obtain better samples from the underlying population using multi-concomitant PROS sampling technique and possibly better estimate the population proportion. To show this, we proposed an estimator of the population proportion using multi-concomitant PROS sample and, through extensive numerical studies, investigated the effect of different ranking potentials of the concomitants (i.e., good, intermediate and bad) on the performance of this estimator compared with its counterparts under SRS, one-concomitant RSS and multi-concomitant RSS-based logistic regression methods. Numerical analysis shows that multi-concomitant PROS estimator performs very well compared with its SRS counterpart and those proposed by Terpstra and Liudahl (2004) as well as Chen et al. (2005). Unlike the estimator of Terpstra and Liudahl (2004) which is restricted to only one concomitant for the ranking process, multi-concomitant PROS estimator takes the full benefit of multiple concomitants and provides significant improvement in the estimation of proportion. Although the RSS-based logistic regression method of Chen et al. (2005) uses multiple concomitants in the estimation of \( p \), their estimation method requires the logistic regression modeling assumptions. In the absence of such strong modeling assumptions, it is not clear how the extra information should be incorporated in an efficient way. In the WBCD, through different examples, we illustrated that such assumptions are not satisfied even if we use concomitants that are highly correlated with the Malignant Tumours. Our proposed method can efficiently incorporate as many concomitants as available into the estimation, regardless of such modeling assumptions. Another advantage of our method is the simple form of our estimator which is simply the weighted average of the PROS sample estimates. In addition, the methods proposed in Terpstra and Liudahl (2004) and Chen et al. (2005) do not allow to declare ties in ranks in the ranking process of RSS technique. This is not realistic, in particular for the analysis of the WBCD, where all the cytological concomitants are ordinal variables taking on values between 1 to 10. Multi-concomitant PROS sampling design, through partial ranking, not only eliminates this restriction but also results in more accurate estimators. It is worth mentioning that the proposed methodology in this paper can be applied to other medical studies as well.
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