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# Comparison of ratio-synthetic, sample-size dependent and EBLUP estimators as estimators of food–animal productivity parameters

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#### Abstract

A comparison was made of three small-area sampling methods [two traditional design-based methods (ratio-synthetic, sample-size dependent) and one model-based method (EBLUP)] in estimation of some cow and sow population productivity parameters. Performance was evaluated in estimating both farm-specific mean responses and mean animal response over all farms using sample sizes of 100 and 25. Differences in results obtained with the cow and sow data are discussed in terms of the impact of sample size and population size on sampling method. There was a tendency for the model-based method to be the best performer in situations most likely to be operational when the sampling is done as part of a food–animal monitoring scheme. The situations are identified where the sample-size-dependent method performed best.  $\odot$  2002 Elsevier Science B.V. All rights reserved.

Keywords: Small-area estimation; Ratio-synthetic; Sample-size dependent; EBLUP

## 1. Introduction

Efficient sampling methodology will play an important role in achieving a level of monitoring of food–animal populations that comes close to the level achieved for some human populations. This is because the resources available for monitoring food–animal populations are only a very small fraction of those available for monitoring human populations. Our assessment of using composite estimation with two-stage repeated sample designs (Holt and Farver, 1992; Farver et al., 1997) revealed only moderate gains in efficiency relative to simple estimation in estimating the total response at each occasion

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and the total response over a sequence of successive measurement occasions. This was because intraclass correlations were too low in most cases to counteract the low correlation over time of corresponding animal responses. However, sizeable gains in relative efficiency were observed for estimating the difference between means or totals on successive measurement occasions because for several parameters, the responses at the farm level had high correlations over time.

One of the challenges associated with large-scale monitoring is to provide very accurate estimates of parameters for the population as a whole—but also for subpopulations (called ''domains''). These domains could be farms, counties or regions in a national monitoring scheme for health and productivity of food–animal populations. Often the sample sizes for the domains are so small that the standard errors at the domain level are too large to be useful; there might be no samples at all for some domains of interest. Ghosh and Rao (1994) gave a review of the so-called ''small-area-estimation methods'' which have evolved relatively recently for providing estimates for domains with small sample sizes. They appraised five alternative methods: synthetic, sample-size dependent, empirical best linear unbiased prediction (EBLUP), empirical Bayes and hierarchical Bayes estimation. Each of these methods makes use, in different ways, of information obtained from a census of the population at some starting or base time to estimate response parameters at a subsequent time. In the context of monitoring a population, the desired response parameters would be estimated multiple times using repeated measurement of the population after the base time. It is conventional to designate the base response as  $x$  and a subsequent response as y. Thus, an element sampled from the population would have an x-value and a vector of y-values (one y for each time the response was recorded after the base time). Ghosh and Rao (1994) included a comparison of small-area-estimation methods using an example based on **a single sample** of 38 response pairs  $(x, y)$  drawn from a synthetic population of size  $M = 114$  subjects divided across 16 small areas. The results seemed to favor model-based methods (EBLUP, empirical Bayes and hierarchical Bayes estimation) over the traditional design-based methods (synthetic and sample-size-dependent estimation). I undertook a more stringent evaluation of three of the small-area techniques compared by Ghosh and Rao; I used repeated sampling of the small domains at multiple times after the base period. The evaluation was made using a larger and a smaller sample size. My intention was also to provide direction for their use with some responses that commonly would be encountered in a large-scale evaluation of the productivity of food– animal populations.

## 2. Recent literature in small-area estimation

Four papers focus on various aspects of Baysian small-area estimation. Datta and Lahiri (1995) developed a robust hierarchical Bayes method to smooth small-area means when information is available on covariates; the procedure reduced the impact of outliers.

The paper by Farrell et al. (1997) relates to the prediction of small-area rates and proportions from auxiliary variables using nonlinear model-based approaches. These authors put forth an empirical Bayes method that uses only small-area summary statistics for both continuous and categorical predictor variables (rather than, more restrictively,

microdata from all individuals in a small area). Ghosh et al. (1998) extended the case of Baysian methods in solving small-area estimation problems when the survey data includes discrete and/or categorical variables. Yasui et al. (2000) compared various prior distributions that could be placed on area-specific risks in Baysian estimation of small area disease risks.

Three papers deal with the error of small-area estimators. Lahiri and Rao (1995) demonstrated the robustness of the Prasad–Roa estimator of the MSE (1990) (Prasad and Rao, 1990) of the EBLUP estimator under the Fay–Herriot model (1979) (Fay and Herriot, 1979) with respect to nonnormality of the small-area means. Singh et al. (1998) reviewed and compared (both analytically and empirically) Baysian and frequentist approaches to modification of the MSE to account for the extra variability induced by the usual need to estimate the variance components of small-area estimates. Datta and Lahiri (2000) provided an approximation to the MSE of the EBLUP estimator; their approximation is valid for a number of variance component methods including maximum likelihood and residual maximum likelihood (Cressie, 1992; Dick, 1995). Longford (1999) applied shrinkage estimators (both univariate and multivariate, the latter proposed by the author) to UK census data.

## 3. Materials and methods

Three small-area sampling estimators were evaluated: the ratio-synthetic (RS) estimator, the sample-size dependent (SD) estimator and the EBLUP estimator. These three smallarea estimators were evaluated on repeated samples taken from two data sets: one with repeated monthly measurements on cows and the second with repeated parity measurements on sows. The cow responses were collected at eight times during the milkproduction cycle from a population of 290 cows from 16 farms. The cow responses used were milk (pounds of milk produced by a cow in a 24 h period), fat-corrected milk (FCM, milk adjusted to a standard 3.5%-fat basis), butterfat (%fat), somatic-cell count (SCC) and linear score of SCC (L2). The sow responses used were gestation length, number live-born, birth weight, and weaning weight which were collected at five birthing from a population of 497 sows from 18 piggeries. More details about the cow and sow populations sampled are given in Table 1.

One set of 100 simple random samples (without replacement) of 100 cows (representative of a larger sample size) and a second set of 25 simple random samples of 100 cows (representative of a smaller sample size) were obtained from the population of cows using the random generator of BMDP.<sup>1</sup> Parallel sets of 100 simple random samples were similarly obtained from the population of sows. Each set of 100 simple random samples was processed separately but in the same manner as follows: a program was written using the SAS System<sup>2</sup> to obtain (based on each sample generated) the RS, SD and EBLUP estimates of the population farm-specific mean response values (milk, FCM, butterfat, SCC and L2 for cows and gestation length, number live-born, birth weight, and weaning weight

<sup>&</sup>lt;sup>1</sup> BMDP Statistical Software Inc., Los Angeles, CA.

<sup>&</sup>lt;sup>2</sup> SAS Institute Inc., Cary, NC.

Dairy			Swine	
Farm	No. of cows	Days in milk, median, range	Farm	No. of sows
1	19	$32, 18 - 24$	1	29
$\overline{2}$	22	34, 19-49	$\mathfrak{2}$	29
$\overline{4}$	12	38, 26-66	8	31
5	17	21, 15–43	24	27
7	12	33, 15 - 49	26	12
8	18	33, 17-49	30	28
9	20	$32, 16 - 50$	40	15
10	21	$31, 18 - 50$	43	40
11	16	$30, 16 - 38$	44	40
12	19	35, 15-46	51	19
13	18	33, 22 - 48	58	19
16	18	25, 16-65	59	34
18	21	$27, 15 - 36$	61	20
19	20	25, 16 - 48	63	38
20	9	26, 18-49	66	22
21	28	29, 16-43	68	38
			70	28
			107	28
Overall	290	$31, 17 - 47^{\circ}$		497

Number of cows and sows from participating farms; distribution by farm of days in milk for cows at first monthly measurement

<sup>a</sup> Central 90% of the distribution.

for sows) at each time period subsequent to the first time period. Sample responses recorded at and/or population values (census information) of the first time period were used as base information for all estimates obtained at subsequent time periods as shown in Eqs.  $(1)$ – $(4)$  below.

The RS estimator (Purcell and Linacre, 1976; Ghangurde and Singh, 1977), in the context of the present repeated measurement scheme, has the form

$$
\hat{\mu}_{y_{ji}}^{\text{RS}} = \left(\frac{\overline{y}_j}{\overline{x}}\right) \mu_{x_i} \tag{1}
$$

where  $\hat{\mu}_{y_{ji}}^{RS}$  is the RS estimate of the mean response at time j for the *i*th farm; m the total number of animals in the sample (henceforth, referred to as the "sample size");  $\overline{y}_i$  the sample mean response at time j of the m animals selected;  $\bar{x}$  the sample mean response at the base time of the *m* animals selected and  $\mu_{x_i}$  the mean response at the base time for the *i*th farm.

This states that the farm-specific mean estimate at time  $j$ —whether or not the farm has been sampled at time j—is obtained by multiplying the population mean observed for the farm at the base time by the ratio of the sample mean response at time  $j$  of the  $m$  animals selected (from all farms sampled at  $j$ ) to the sample mean response at the base time of the  $m$ animals selected. This is the classic ratio estimator (Cochran, 1977; Lohr, 1999; Scheaffer et al., 1996) deriving efficiency from the auxiliary information provided at the base time. Typical of ratio estimators, the gain in precision might be offset by bias (particularly in cases of small sample sizes).

The SD estimator (Drew et al., 1982) has the form if  $f_i \geq F_i$  then

$$
\hat{\mu}_{y_{ji}}^{\text{SD}} = \hat{\mu}_{y_{ji}}^{\text{REG}} = \overline{y}_{ji} + \left(\frac{\overline{y}_j}{\overline{x}}\right) (\mu_{x_i} - \overline{x}_i)
$$
\n(2)

if  $f_i < F_i$  then

$$
\hat{\mu}_{y_{ji}}^{\text{SD}} = \frac{f_i}{F_i} (\hat{\mu}_{y_{ji}}^{\text{REG}}) + \left(1 - \frac{f_i}{F_i}\right) \hat{\mu}_{y_{ji}}^{\text{RS}}
$$
\n(3)

where  $f_i=(m_i/m)$ ,  $m_i$  is the total number of animals sampled from the *i*th farm,  $0 \le m_i \le M_i$ ;  $m = \sum_{i=1}^{N} m_i$ , the total number of animals in the sample, the sample size; N the total number of farms in the population;  $F_i = (M_i/M), M_i$  the total number of animals on the *i*th farm;  $M = \sum_{i=1}^{N} M_i$ , the total number of animals in the population;  $\hat{\mu}_{y_i}^{SD}$  the SD estimate of the mean response at time j for the *i*th farm;  $\hat{\mu}_{y_{ji}}^{REG}$  a "survey-regression" estimate of the mean response at time j for the *i*th farm;  $\overline{y}_{ii}$  the sample mean response at the jth time for the *i*th farm;  $\bar{y}$ , the sample mean response at time j of the m animals selected;  $\bar{x}$ the sample mean response at the base time of the m animals selected;  $\mu<sub>x</sub>$  the mean response at the base time for the *i*th farm;  $\bar{x}_i$  the sample response at the base time for the *i*th farm (using the  $m_i$  animals selected from the *i*th herd);  $\hat{\mu}_{y_{ji}}^{RS}$  the RS estimate of the mean response at time  $j$  for the *i*th farm.

This states that if the proportion of animals from a farm in a sample is equal to or greater than the proportion of animals from that farm in the total population of animals, the SD estimator is the classic regression estimator (Cochran, 1977; Lohr, 1999; Scheaffer et al., 1996). If the proportion of animals from a farm in a sample is less than the proportion of animals from that farm in the total population of animals, the SD estimator is the weighted composite of the regression estimator and the RS estimator with the weights being  $f_i/F_i$  and  $1 - f_i/F_i$ , respectively. Note that if none of the animals of a farm is selected in the sample (i.e.  $f_i = 0$ ), the SD estimator for that farm is the RS estimator.

The EBLUP estimator (Robinson, 1991; Harville, 1991) has the following form

$$
\hat{\mu}_{y_{ji}}^{\text{EBLUP}} = \hat{f}_i \overline{y}_{ji}^{\text{first component}} + (1 - f_i) [\hat{\beta}_{1j} + \hat{\beta}_{2j} \mu_{x_i}^*] + (1 - f_i) [\overline{y}_{jiw} - \hat{\beta}_{1j} - \hat{\beta}_{2j} \overline{x}_{iw}] \hat{\gamma}_{ji} \tag{4}
$$

where  $\hat{\mu}_{y_i}^{\text{EBLUP}}$  is the EBLUP estimate of the mean response at time j for the *i*th farm;  $f_i$  =  $(m_i/m)$ ,  $m_i$  the sample size of ith sampled farm, m the total number of animals in the sample, the sample size;  $\bar{y}_{ii}$  the sample mean response at the *j*th time for the *i*th farm;  $\hat{\beta}_{1i}$  and  $\hat{\beta}_{2i}$  are the estimated slope parameters from regression 3 given in Appendix A;  $\mu_{x_i}^*$  the mean base response for unsampled units of the *i*th farm;  $\overline{y}_{jiw} = \sum_{k=1}^{m_i} (y_{jik}/x_{ik}) / \sum_{k=1}^{m_i} (1/x_{ik});$  $\overline{x}_{iw} = m_i / \sum_{k=1}^{m_i} (1/x_{ik}); \hat{r}_{ji} = \hat{\sigma}_{v_j}^2 / (\hat{\sigma}_{v_j}^2 + \hat{\sigma}_{e_j}^2 / w_{ji}), \hat{\sigma}_{v_j}^2, \hat{\sigma}_{e_j}^2$  and  $w_{ji}$  are defined in Appendix A.

Although much more complex than the RS and SD estimators, the EBLUP estimator is also a weighted composite estimator. As will be shown below, the first and second components carry the most weight. The first component makes use of the farm-specific

means observed at the given recording  $j$  and the second component makes use of the mean base response of the animals that are not sampled at recording j.

The mean of each sampling distribution of 100 farm-specific mean estimates was computed along with its standard error. Also, for each sample generated, the mean animal response over all farms was computed as the weighted (by the population farm size,  $M_i$ ) mean of the farm-specific estimates. Average relative errors (AREs) and average squared errors (ASEs) (Ghosh and Rao, 1994) were computed as follows:

$$
ARE = \frac{1}{N} \frac{\sum_{i=1}^{N} |\hat{\mu}_{y_{ji}}^{\text{est.}} - \mu_{y_{ji}}|}{\mu_{y_{ji}}}, \qquad \text{ASE} = \sum_{i=1}^{N} (\hat{\mu}_{y_{ji}}^{\text{est.}} - \mu_{y_{ji}})^2
$$

where N is the number of herds;  $\hat{\mu}_{y_i}^{\text{est.}}$  the estimated mean response at time j for the *i*th farm; "est." designates the RS, SD or EBLUP estimate;  $\mu_{v_{ij}}$  the mean response at time j for the *i*th farm.

The mean of each distribution of 100 overall farm mean estimates, of 100 ARE (i.e. mean ARE) and 100 ASE (i.e. mean ASE) were obtained.

The effect of sample size on the results was evaluated as follows: an ''estimation event'' was defined as the estimation of one farm-specific mean response at one recording (for cow data) or one birthing (for sow data). In the case of the cow data, for each response variable, there were 16 farms for which farm-specific estimates of the mean response were made at seven recordings (recordings 2–8) for a total of 112 estimation events. In the case of the sow data, for each response variable, there were 18 farms for which estimates were made at four birthing (2–5) for a total of 72 estimation events. It is important to remember that a farm-specific mean is the mean of 100 means obtained by re-sampling the population 100 times. For each response variable, a frequency distribution was obtained by classifying each estimation event jointly by the estimator (RS, SD or EBLUP) providing the mean closest to the parameter being estimated using a sample size of 100 and using a sample size of 25. The Stuart–Maxwell test for independence of frequency distributions with matched pairs (Stuart, 1955; Maxwell, 1970; Fleiss and Everitt, 1971; Fleiss, 1981) was used to determine whether there was any significant change in estimator performance with a reduction in sample size from 100 to 25.

Two quantities were computed to assess the impact, over the 100 samples, of the regression estimator on the SD estimation for each farm. One quantity computed is what I call the ''impact percentage'' of the regression estimator on the SD farm-specific estimates. As noted above, the SD farm-specific estimate from a sampling trial had no component derived from the regression component when none of the animals of the given farm were included in the sample  $(m_i = 0)$ . This was regarded as a failure and a score of 0 was given to that trial. In a sampling trial when  $f_i \geq F_i$ , the SD farm-specific estimate was based solely on the regression estimator. This was regarded as a success and a score of 1 was given to that trial. In a trial when  $m_i > 0$  and  $f_i < F_i$ , the SD farm-specific estimate had a component based on the regression estimator and a component based on the RS estimator weighted by  $f_i/F_i$  and  $1 - f_i/F_i$ , respectively. This was regarded as a partial success and a score of  $f_i/F_i$  was given to the trial. The mean of these trial-specific scores over the 100 trials (multiplied by 100) is the impact percentage of the regression estimator on the SD farm-specific estimates.

Another quantity computed was the percentage of the 100 SD estimates having a regression-estimator component. This is the percentage of successes or partial successes in the 100 trials.

## 4. Results and discussion

## 4.1. Estimation of farm-specific mean animal response

Table 2 gives detailed results observed for milk with a sample size of 100. For space conservation, I have presented the estimates predicted at the 2–5 recordings only. These results are typical of those observed for the other cow responses. Note that the estimation procedures use sample or census information from the first recording to estimate the parameters at subsequent recordings. The results presented in Table 3 are the complete set of results observed for number of live-born piglets with a sample size of 100 and are typical of those observed for the other sow responses. The complete set of results obtained for all of the cow and sow responses using samples sizes of 100 and 25 are available from the author upon request.

Table 4 summarizes, from the complete set of such tables, the performance of the three estimators in estimating the farm-specific mean cow and sow responses. Table 4 gives, for each response variable, the frequency distribution obtained by classifying each estimation event (see definition given in Section 3) jointly by estimator (RS, SD or EBLUP) providing the mean closest to the parameter being estimated using a sample size of 100 and using a sample size of 25. For example, Table 4 shows that in estimating total milk, there were 63 estimation events in which the SD estimate was closest to the parameter being estimated using samples sizes of both 100 and 25, six estimation events in which the SD estimate was closest to the parameter being estimated using a sample size of 100 and the RS estimate was closest to the parameter being estimated using a sample of size 25, and nine estimation events in which the SD estimate was closest to the parameter being estimated using a sample size of 100 and the EBLUP estimate was closest to the parameter being estimated using a sample size of 25.

## 4.1.1. Large sample results

One finding exhibited in Table 4 is that when using a sample size of 100, the SD estimator provided estimates closest to the parameter being estimated in most of the estimation events using the cow data—but the EBLUP estimator provided estimates closest to the parameter being estimated in most of the estimation events using the sow data. Specifically, the SD estimator produced a farm-specific mean estimate that was closest to the farm-specific population mean in 73% of the estimation events involving all five of the cow responses using a sample size of 100 (Table 4), while the EBLUP estimator produced an estimate that was closest to the farm-specific population mean in 66% of the estimation events involving all four of the sow responses using a sample size of 100 (Table 4). I believe this difference in estimator performance with the cow and sow data when using a sample of size 100 relates to the difference in population sizes. With a sample size of 100, there remain 190 unsampled cows—but 397 (twice as many) unsampled sows. This is an

Comparison of RS, SD and EBLUP estimates of cow total milk (pounds/day) at four times during lactation  $(m^a = 100)$ 

Farm		Second recording				Third recording				Fourth recording				Fifth recording		
	$\mu_2$	RS <sub>2</sub>	SD <sub>2</sub>	EBLUP <sub>2</sub>	$\mu_3$	RS <sub>3</sub>	SD <sub>3</sub>	EBLUP <sub>3</sub>	$\mu_4$	RS <sub>4</sub>	SD <sub>4</sub>	EBLUP <sub>4</sub>	$\mu_{5}$	$RS_5$	SD <sub>5</sub>	EBLUP <sub>5</sub>
$\mathbf{1}$	$89.1^{b}$	$86.1^\circ$ $0.13^{\circ}$	$89.2^{\rm d}$ 0.43	86.8 0.24	87.9	83.1 0.14	87.5 0.44	84.3 0.26	74.4	76.6 0.15	74.3 0.57	74.3 0.30	70.8	71.4 0.14	71.1 0.35	69.9 0.18
$\overline{c}$	72.9	74.5 0.11	72.5 0.38	74.6 0.21	73.4	71.9 0.12	72.4 0.40	73.4 0.23	71.9	66.3 0.13	70.4 0.30	69.6 0.18	64.8	61.8 0.12	63.5 0.47	64.3 0.25
3	88.5	83.1 0.13	87.8 0.79	85.4 0.41	78.7	80.3 0.14	79.0 0.51	79.2 0.20	76.1	74.0 0.14	75.4 0.67	74.0 0.29	66.6	68.9 0.14	67.3 0.68	67.5 0.25
$\overline{4}$	70.1	68.6 0.10	70.2 0.28	71.7 0.18	69.2	66.3 0.11	69.5 0.49	70.1 0.33	65.2	61.1 0.12	65.1 0.37	65.6 0.21	63.1	56.9 0.11	62.6 0.41	62.6 0.23
5	86.1	90.4 0.14	87.2 0.59	86.9 0.29	84.1	87.3 0.15	84.2 0.38	83.7 0.19	82.1	80.5 0.15	82.0 0.46	78.9 0.21	80.1	75.0 0.15	79.6 0.36	74.6 0.23
6	91.7	90.0 0.14	91.3 0.45	89.1 0.23	88.1	86.9 0.15	87.9 0.51	85.7 0.27	72.4	80.1 0.15	73.6 0.55	75.1 0.24	66.3	74.6 0.15	67.7 0.60	69.0 0.29
$\overline{7}$	89.4	92.6 0.14	89.8 0.56	89.0 0.30	91.1	89.4 0.15	90.3 0.50	87.7 0.25	83.6	82.4 0.16	82.7 0.67	80.2 0.31	73.8	76.8 0.15	73.5 0.71	72.6 0.34
8	80.3	78.9 0.12	79.9 0.32	79.9 0.18	73.0	76.2 0.13	73.2 0.39	75.0 0.22	69.2	70.2 0.14	68.7 0.46	70.0 0.23	65.7	65.4 0.13	65.2 0.43	65.8 0.22
9	85.1	90.5 0.14	85.6 0.33	86.2 0.17	80.2	87.4 0.15	81.1 0.43	82.2 0.26	77.0	80.6 0.15	77.0 0.32	76.8 0.18	74.1	75.0 0.15	73.8 0.34	72.1 0.18
10	73.3	71.9 0.11	73.1 0.28	74.2 0.16	72.4	69.4 0.12	72.3 0.28	72.7 0.18	67.0	64.0 0.12	66.8 0.32	67.3 0.17	61.7	59.6 0.12	61.7 0.33	62.9 0.15
11	73.1	69.8 0.11	72.0 0.33	73.2 0.17	72.4	67.4 0.12	71.7 0.36	71.9 0.22	65.3	62.2 0.12	64.3 0.44	65.6 0.23	61.7	57.9 0.11	60.0 0.48	62.0 0.23
12	76.8	76.7 0.12	76.8 0.46	77.7 0.25	71.4	74.1 0.13	71.5 0.37	73.7 0.18	64.7	68.3 0.13	64.2 0.42	67.5 0.19	66.8	63.6 0.13	66.1 0.33	65.9 0.17
13	82.5	83.9 0.13	82.7 0.32	82.6 0.18	77.7	81.1 0.14	78.1 0.35	78.8 0.20	73.5	74.7 0.14	73.8 0.31	73.5 0.17	71.6	69.6 0.14	71.5 0.44	69.9 0.24
14	72.8	73.0 0.11	71.8 0.35	73.5 0.26	76.0	70.5 0.12	74.2 0.50	73.8 0.44	69.0	65.0 0.13	68.0 0.34	68.0 0.23	62.0	60.5 0.12	61.4 0.34	62.7 0.24
15	89.2	91.2 0.14	89.6 0.48	88.3 0.17	84.3	88.0 0.15	85.3 0.44	84.4 0.18	80.8	81.2 0.16	80.8 0.47	78.5 0.27	69.8	75.6 0.15	70.7 0.43	70.7 0.16
16	81.6	79.9 0.12	81.1 0.43	80.9 0.29	76.6	77.2 0.13	75.9 0.42	76.9 0.22	71.5	71.1 0.14	71.1 0.47	71.3 0.24	63.1	66.3 0.13	63.1 0.42	64.9 0.23
Mean <sup>f</sup> Mare <sup>g</sup> Maseh	80.8	80.6 3.02 9.46	80.6 4.23 19.87	80.7 2.65 7.65	78.1	77.9 4.22 14.99	77.9 4.46 18.64	77.9 3.01 9.23	72.2	71.8 4.22 13.47	71.8 4.97 21.47	71.8 3.21 8.70	67.1	66.9 4.97 16.61	66.9 5.34 21.46	66.9 3.30 8.59

 $^{\rm a}$  Total number of responding animals over all herds.

<sup>b</sup> Farm-specific population mean, the parameter being estimated.

<sup>d</sup> Italic values indicate mean (within recording) closest (to nearest hundredth pound) to estimated parameter.

<sup>e</sup> Standard error (smallest for RS estimate within recording).

f Over all herds.

 $^{\mathbf{g}}$  Mare  $=$  mean ARE(%).

 $^{\rm h}$  Mase  $=$  mean ASE.

 $^{\rm c}$  Mean.

Comparison of RS, SD and EBLUP estimates of number of live-born piglets at four birthing  $(m^a = 100)$ 

Farm	Second birthing				Third birthing			Fourth birthing				Fifth birthing				
	$\mu_2$	RS <sub>2</sub>	SD <sub>2</sub>	EBLUP <sub>2</sub>	$\mu_3$	RS <sub>3</sub>	SD <sub>3</sub>	EBLUP <sub>3</sub>	$\mu_4$	RS <sub>4</sub>	SD <sub>4</sub>	EBLUP <sub>4</sub>	$\mu_{5}$	$RS_{5}$	SD <sub>5</sub>	EBLUP,
$\mathbf{1}$	11.7 <sup>b</sup>	$10.2^{\circ}$ $0.03^{\rm d}$	8.5 0.10	$10.3^\circ$ 0.04	11.5	10.3 0.03	9.8 0.12	10.8 0.05	11.9	10.7 0.03	10.0 0.09	11.1 0.04	12.2	10.4 0.03	10.4 0.11	11.2 0.07
$\overline{2}$	10.3	11.0 0.03	11.0 0.11	10.6 0.04	11.5	11.1 0.03	11.6 0.12	11.1 0.06	11.2	11.5 0.03	11.4 0.15	11.1 0.05	11.5	11.2 0.04	11.8 0.13	11.3 0.07
3	9.7	11.2 0.03	11.9 0.12	10.8 0.05	10.2	11.3 0.03	11.3 0.09	10.6 0.05	10.9	11.6 0.03	12.0 0.12	11.1 0.07	10.5	11.4 0.04	11.6 0.12	10.8 0.06
$\overline{4}$	10.2	10.7 0.03	10.7 0.12	10.5 0.03	10.1	10.8 0.03	10.5 0.12	10.5 0.05	10.8	11.1 0.03	11.1 0.13	10.9 0.05	10.9	10.8 0.04	11.1 0.12	10.8 0.04
5	10.3	9.6 0.03	8.6 0.11	10.2 0.04	10.7	9.7 0.03	9.7 0.10	10.4 0.05	11.3	10.0 0.03	10.1 0.12	10.8 0.05	10.2	9.8 0.03	9.3 0.17	10.4 0.07
6	11.3	10.4 0.03	9.1 0.11	10.3 0.05	10.9	10.5 0.03	9.9 0.12	10.7 0.05	11.9	10.8 0.03	10.8 0.09	11.2 0.05	11.7	10.6 0.04	10.5 0.09	10.9 0.07
$\overline{7}$	10.1	11.2 0.03	11.4 0.12	10.6 0.05	9.9	11.2 0.03	10.7 0.14	10.5 0.06	10.7	11.6 0.03	11.3 0.10	10.9 0.04	11.6	11.3 0.04	12.2 0.14	11.2 0.05
8	10.2	10.9 0.03	10.7 0.09	10.5 0.04	10.6	10.9 0.03	10.8 0.10	10.7 0.04	9.8	11.3 0.03	10.3 0.09	10.7 0.05	10.6	11.0 0.04	10.8 0.09	10.7 0.04
9	10.0	11.0 0.03	11.3 0.08	10.5 0.04	9.9	11.1 0.03	10.9 0.07	10.4 0.05	10.8	11.4 0.03	11.5 0.08	11.0 0.04	10.3	11.2 0.04	11.0 0.08	10.5 0.05
10	9.4	10.7 0.03	11.2 0.11	10.5 0.03	10.2	10.8 0.03	10.9 0.10	10.5 0.04	9.9	11.1 0.03	11.0 0.11	10.8 0.04	9.4	11.0 0.04	10.5 0.12	10.3 0.05
11	10.4	8.4 0.03	6.1 0.19	9.6 0.09	10.2	8.4 0.02	7.3 0.13	10.0 0.06	10.1	8.7 0.02	8.0 0.14	10.4 0.05	9.5	8.5 0.03	7.4 0.13	10.0 0.05
12	9.4	10.8 0.03	11.6 0.09	10.5 0.04	9.7	10.9 0.03	10.7 0.10	10.2 0.06	10.2	11.2 0.03	11.4 0.10	10.8 0.04	10.3	11.0 0.04	11.5 0.12	10.7 0.06
13	10.5	11.9 0.04	12.5 0.17	10.9 0.06	12.0	12.0 0.03	13.0 0.15	11.5 0.06	12.6	12.4 0.03	13.5 0.17	11.7 0.07	12.1	12.1 0.04	13.0 0.13	11.3 0.07
14	11.9	12.5 0.04	12.3 0.07	11.1 0.05	12.2	12.6 0.03	12.4 0.08	11.6 0.05	11.6	13.0 0.03	12.0 0.08	11.4 0.04	10.8	12.7 0.04	11.3 0.09	10.8 0.04
15	8.4	10.5 0.03	11.7 0.14	10.4 0.05	9.8	10.6 0.03	11.3 0.11	10.4 0.05	10.3	10.9 0.03	11.8 0.13	10.8 0.05	8.8	10.7 0.04	10.2 0.18	9.9 0.09
16	10.0	11.5 0.03	12.2 0.10	10.8 0.04	11.1	11.5 0.03	12.3 0.10	11.2 0.05	11.5	11.9 0.03	12.5 0.13	11.3 0.06	11.4	11.6 0.04	12.4 0.10	11.2 0.06
17	10.5	9.8 0.03	8.6 0.12	10.1 0.05	10.5	9.9 0.03	9.4 0.10	10.3 0.04	11.5	10.2 0.03	10.4 0.10	11.0 0.03	11.0	10.0 0.03	9.9 0.10	10.7 0.05
18	8.9	11.7 0.04	13.5 0.10	10.9 0.04	9.6	11.8 0.03	12.2 0.11	10.6 0.06	10.6	12.2 0.03	13.1 0.10	11.1 0.04	9.8	11.9 0.04	12.2 0.12	10.4 0.08
Mean <sup>t</sup> Mare <sup>g</sup> Maseh	10.2	10.9 12.66 2.03	10.9 21.50 6.90	10.5 9.15 1.24	10.6	11.0 8.56 1.10	11.0 12.67 2.73	10.7 5.55 0.51	11.0	11.3 8.86 1.17	11.3 12.59 2.87	11.0 5.35 0.51	10.7	11.1 9.38 1.43	11.1 13.03 2.94	10.8 6.13 0.66

<sup>a</sup> Total number (over all herds) of responding animals.

<sup>b</sup> Farm-specific population mean, the parameter being estimated.

 $\rm ^c$  Mean.

<sup>d</sup> Italic values indicate mean (within recording) closest (to nearest hundredth number) to estimated parameter.

<sup>e</sup> Standard error (smallest for RS estimate within recording).

f Over all herds.

 $g$  Mare = mean ARE $(\%).$ 

 $h$  Mase  $=$  mean ASE.

For each response variable, the frequency distribution obtained by classifying each estimation event<sup>a</sup> jointly by estimator (RS, SD or EBLUP) providing the mean closest to the parameter being estimated with a sample sizes of 100 and  $25<sup>b</sup>$ 



<sup>a</sup> An estimation event is the estimation of one farm-specific mean response at one recording (for cow data) or one birthing (for sow data). In the case of the cow data, for each response variable, there were 16 farms for which estimates were made at seven recordings for <sup>a</sup> total of 112 estimation events. In the case of the sow data, for each response variable, there were 18 farms for which estimates were made at four birthing for <sup>a</sup> total of 72 estimation events.

<sup>b</sup> Cow data: total milk, FCM, butterfat, L2, SCC; sow data: number live-born, birthing weight, weaning weight, gestation length.

<sup>c</sup> Fat-corrected milk.

<sup>d</sup> Linear score of somatic-cell count.

e Somatic-cell count.

f p-Value for Stuart–Maxwell test for independence of frequency distributions with matched pairs.

important difference in that the second component of the EBLUP estimator (Eq. (4)) makes use of the mean base or reference response (the first recording in the case of the cow data or the first birthing in the case of the sow data) for unsampled animals of each farm. Table 5 gives the mean component values over the estimation events for the cow and sow responses. This table shows that with a sample size of 100, the second component for the cow responses is approximately two times the first component whereas the second component for the sow responses is approximately four times the first component. Use of the base information from so many unsampled sows provided the EBLUP estimator with a competitive advantage when estimating the sow parameters. The SD estimator does not make use of information from unsampled animals.

Table 5

Effect of sample size on the mean component values of the EBLUP estimator (Eq. (4)) over all estimation events<sup>a</sup> for the cow and sow responses

Response variable	Sample size $(m)^b$	Component of Eq. (4)						
		First component	Second component	Third component				
Cow data								
Total milk	100	23.5	44.4	2.3	70.2			
	25	5.9	61.9	2.3	70.1			
FCM <sup>c</sup>	100	24.1	45.7	0.0	69.8			
	25	6.1	63.8	$-0.0$	69.9			
Butterfat	100	1.3	2.4	0.0	3.7			
	25	0.3	3.4	$-0.0$	3.7			
L2 <sup>d</sup>	100	1.0	1.9	$-0.0$	2.9			
	25	0.2	2.6	$-0.0$	2.8			
SCC <sup>e</sup>	100	68.9	130.6	0.1	199.6			
	25	17.4	193.2	0.4	211.0			
Sow data								
Number live-born	100	2.2	8.6	$-0.0$	10.8			
	25	0.5	10.2	0.0	10.7			
Birthing weight	100	7.2	28.1	$-0.0$	35.3			
	25	1.8	33.6	$-0.0$	35.4			
Weaning weight	100	24.8	96.9	0.0	121.7			
	25	6.2	115.9	$-0.0$	122.1			
Gestation length	100	23.3	91.9	$-0.0$	115.2			
	25	5.8	109.4	0.0	115.2			

<sup>a</sup> An estimation event is the estimation of one farm-specific mean response at one recording (for cow data) or one birthing (for sow data). In the case of the cow data, for each response variable, there were 16 farms for which estimates were made at seven recordings for a total of 112 estimation events. In the case of the sow data, for each response variable, there were 18 farms for which estimates were made at four birthing for a total of 72 estimation events.<br><sup>b</sup> Total number of responding animals over all herds.

<sup>c</sup> Fat-corrected milk.

<sup>d</sup> Linear score of somatic-cell count.

<sup>e</sup> Somatic-cell count.

Table 6 shows that over all farms with  $m = 100$ , the regression-impact percentage for cows (87.2%) was significantly higher  $(p = 0.014)$  than that for sows (84.8%). Thus, the cow SD farm-specific estimates would be relatively less biased than the corresponding SD farm-specific estimates for sows because they are less contaminated by the RS component. This most likely contributed to the difference noted in the performance of the SD estimator when estimating the farm-specific mean responses using the cow and sow data with a sample size of 100.

## 4.1.2. Effect of lowering the sample size from 100 to 25

The SD estimator provided the estimate closest to the cow parameter being estimated using sample sizes of 100 and 25 in 49.8% of the total number of estimation events (over all response variables). With the sow data, the EBLUP estimator provided the estimate closest to the parameter being estimated using sample sizes of 100 and 25 in 57.6% of the total number of estimation events. However, Table 4 shows that a reduction in sample size from 100 to 25 resulted in some movement away from the SD estimator in the case of the cow data and away from the EBLUP estimator in the case of the sow data. Subjecting the frequency tables for the cow responses to the Stuart–Maxwell test for independence of frequency distributions with matched pairs (Stuart, 1955; Maxwell, 1970; Fleiss and Everitt, 1971; Fleiss, 1981) revealed that a reduction in sample size from 100 to 25 resulted in significant change in estimator performance in terms of producing a farm-specific mean estimate that was closest to the parameter being estimated in the case of SCC ( $p < 0.0001$ ), L2 ( $p = 0.0001$ ), and butterfat ( $p = 0.007$ ) and a marginally nonsignificant change in the case of FCM  $(p = 0.06)$ . The same test applied to the frequency tables for the sow responses revealed no significant change in estimator performance when the sample size was reduced from 100 to 25, although the result for gestation length was only marginally nonsignificant ( $p = 0.055$ ). Subsequent analyses recommended by Fleiss (1981) demonstrated that for SCC, L2 and butterfat, the number of estimation events when the SD-produced estimate was the closest to the parameter being estimated using a sample size of 100 and either the EBLUP- or RS-produced estimate was closest to the parameter being estimated using a sample size of 25 was highly significantly greater than the number of estimation events when either the EBLUP- or RS-produced estimate was closest to the parameter being estimated using a sample size of 100 and the SD-produced estimate was the closest to the parameter being estimated using a sample size of 25. For each response, the computed  $\chi^2$ -value was nearly equal in magnitude to the corresponding Stuart–Maxwell  $\chi^2$ -value.

In searching for an explanation of the changes in estimator performance on the cow responses observed with changes in sample size, I first focused on the impact of sample size on the three components of the EBLUP estimator (Eq. (4)). Table 5 shows that for all cow and sow responses, the first two components exhibited major changes when the sample size was reduced from 100 to 25. For all responses, when the sample size was reduced from 100 to 25, the major decrease in the first component was compensated by a nearly equivalent increase in the second component. Thus, the EBLUP estimates remained remarkably stable when the sample size was reduced from 100 to 25.

The apparent stability of the EBLUP estimator over change in sample size helped to direct attention to the SD estimator to explain the changes in estimator performance on the

Table 6

Summary by cow and sow farm of the effect of sample size  $(m)^{a}$  on the percentage of the 100 sampling trials for which the SD estimator had a regression-estimator component and on the impact percentage of the regressionestimator on the SD farm-specific estimates



<sup>a</sup> Total number of responding animals over all herds.

<sup>b</sup> See text for method used to derive the impact percentage.

cow responses observed with changes in sample size. In evaluating the performance of the SD estimator, it is important to assess the influence of the regression estimator on the SD estimator because a stronger regression-estimator influence means a weaker ratio-estimator influence and hence a smaller chance for bias in the SD estimates. SD estimates based on larger sample sizes most likely will have a component derived from the regression estimator. Our results demonstrated this to be the case with a sample size of  $m = 100$ . Table 6 shows that for all cow and sow farms, with  $m = 100$ , at least 96% and often 100% of the 100 farm-specific SD estimates generated by repeated sampling of the farm contained a component derived from the regression estimator. The mean percentage over all cow farms (99.8%) did not differ significantly ( $p = 0.27$ ) from that for sow farms (99.4%). These percentages each dropped significantly ( $p < 0.0001$ ) when the sample size was reduced to 25; 79.6% for cow farms and 75.2% for sow farms (Table 6).

The drop in sample size from 100 to 25 was accompanied by a highly significant  $(p < 0.0001)$  drop in the mean impact percentage of the regression estimator on the SD farm-specific estimates from 87.2 to 69.3% for cow data and from 84.8 to 67.0% for sow data. This represents a major increase in the impact of the RS component of the SD estimator. Thus, the SD estimator is most likely to be more biased and hence ''off-target'' with the smaller sample size. This provided more opportunity for the EBLUP estimator (whose second component increased sufficiently to compensate for a reduction in its first component with the sample-size reduction) to be closer to the parameter being estimated. This seems to be the most plausible explanation for the moderate decline in the performance of the SD estimator with the cow data using a sample size of 25. It is not an improvement in the EBLUP estimator but a decline in the performance of the SD estimator (due to a greater impact of the RS estimator component) coupled with the EBLUP estimator exhibiting little overall change.

I was unable to observe an easily interpretable relationship of the correlation between the first recording and subsequent recordings for milk and the performance of the SD estimator. The regression-estimator component of SD would be expected to perform best at high correlations. Table 7 gives the correlations between the first recording and subsequent recordings for all cow and sow variables. The table shows that the correlations observed for milk were among the highest observed for the response variables considered. This might have enabled milk to be more resistant to the movement from SD to EBLUP with a reduction in sample size from 100 to 25. However, butterfat was as resistant as milk to the movement from SD to EBLUP with sample-size change—but its correlations were considerably lower. The correlations noted for SCC were very low and it was SCC that exhibited the largest number of changes from SD to EBLUP. Yet, the second highest number of changes from SD to EBLUP was noted for L2 which had moderate correlations like butterfat. Change is clearly not solely a function of correlation because an inspection of the 24 individual changes from SD to EBLUP observed for L2, e.g., revealed that only 14 of such changes were associated with relatively low correlations.

#### 4.1.3. Standard errors

The smallest standard errors of the farm-specific means nearly always were observed with the RS estimates. Considering the 736 estimation events of this study over all cow responses except SCC (16 farms  $\times$  seven recordings  $\times$  four responses = 448 estimation events) and

Recording	Milk		FCM <sup>a</sup>		Butterfat		$L2^b$		SCC <sup>c</sup>		
	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted	
Cow data											
2	0.62	0.57	0.40	0.36	0.19	0.18	0.46	0.45	0.11	0.11	
3	0.58	0.53	0.39	0.36	0.23	0.23	0.33	0.32	0.07	0.08	
4	0.50	0.48	0.33	0.31	0.22	0.23	0.23 0.26		0.09	0.08	
5	0.40	0.36	0.22	0.19	0.18	0.18	0.24	0.22	0.05	0.04	
6	0.33	0.28	0.17	0.13	0.17	0.18	0.15	0.12	0.03	0.04	
7	0.33	0.27	0.19	0.14	0.21	0.23	0.24	0.22	0.21	0.20	
8	0.26	0.20	0.12	0.04	0.11	0.10	0.22	0.18	0.22	0.19	
Median	0.40	0.36	0.22	0.19	0.19	0.18	0.24	0.22	0.09	0.08	
<b>Birthing</b>	Number live-born		Birth weight		Weaning weight		Gestation length				
	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted			
Sow data											
2	0.08	0.07	0.17	0.16	0.11	0.13	0.39	0.30			
$\mathfrak{Z}$	0.19	0.17	0.19	0.15	0.12	0.10	0.40	0.32			
4	0.20	0.20	0.23	0.18	0.15	0.11	0.41	0.37			
5	0.20	0.20	0.25	0.22	0.07	0.04	0.39	0.37			
Median	0.195	0.185	0.21	0.17	0.115	0.105	0.395	0.345			

Table 7Correlations (unadjusted and adjusted for farm) of cow response at first recording and subsequent recordings and of sow response at first birthing and subsequent birthing

a Fat-corrected milk.

<sup>b</sup> Linear score of somatic-cell count.

<sup>c</sup> Somatic-cell count.

all sow responses (18 farms  $\times$  four recordings  $\times$  four responses = 288 estimation events), the standard errors obtained with the RS estimates were the smallest in 99.0% of the estimation events using a sample size of 100 animals. This percentage dropped only to 92.5% using a sample size of 25. The standard errors obtained with the EBLUP estimates were the next smallest in 98.1 and 92.4% of the estimation events using sample sizes of 100 and 25, respectively. The standard errors for the EBLUP and SD estimates would be expected to be larger than those of the RS estimates because the EBLUP and SD estimators have multiple components (with error associated with each component)—whereas the RS estimator is a single-component estimator. The finding that the EBLUP standard errors were consistently smaller than those of the SD estimator is support for the use of the EBLUP estimator in addition to that based on its strong performance in estimating the farm-specific means reported above.

The standard error results for the SCC response were not parallel to those described above for the other variables. Of the 112 estimation events involving SCC, the standard errors obtained with the RS estimates were the smallest for 53.6% of the events and those obtained with the EBLUP estimates were the smallest for 44.6% of the events using a sample size of 100 animals. These percentages were 67.0% (RS) and 31.2% (EBLUP) using a sample size of 25. I attribute these results to the extremely high variability in the SCC responses of a cow, even within the same location.

### 4.2. Estimation of mean animal response over all farms

#### 4.2.1. Mean over all farms

The complete results of the comparison of the RS, SD and EBLUP estimates of mean animal responses *over all farms* are available upon request from the author. The following summarizes these results:

*Milk*. With a sample size of 100, all three estimators gave the same overall farm mean estimate of milk (to the nearest 10th of a pound) at six of the seven recordings. When the sample size was reduced to 25, no single estimator demonstrated a clear advantage.

FCM. The EBLUP estimator generated the overall farm mean estimate closest to the parameter being estimated in five of the seven recordings with a sample size of 100. At the other two recordings, the EBLUP estimate was tied for being closest to the parameter being estimated with that produced by RS in one case and by both of the other estimators in the other case. The EBLUP estimator gave up some of this advantage to the SD estimator when the sample size was reduced to 25.

Butterfat. The results obtained with a sample size of both 100 and 25 were not supportive of any estimator.

L2. The EBLUP estimator generated the overall farm mean estimate closest to the parameter being estimated at all seven recordings with a sample size of 100. When the sample size was reduced to 25, the RS estimate was closest to the parameter being estimated at four recordings.

SCC. With a sample size of 100, the RS estimates were closest to the parameter being estimated at three recordings, the EBLUP at two recordings and the SD estimator at one recording. The EBLUP estimator produced estimates closest to the parameter being estimated at all seven recordings when the sample size was reduced to 25; all EBLUP estimates were considerably closer to the parameter being estimated than those produced by the RS and SD estimators.

Sow responses. The EBLUP estimator provided the mean estimate closest to the overall farm mean being estimated in 28 of 32 cases (four response variables  $\times$  four birthing  $\times$ two sample sizes). This performance is reflective of the excellent performance by the EBLUP estimator when estimating the farm-specific sow parameters.

It may seem surprising that the EBLUP estimator, which was definitively outperformed by the SD estimator in estimating farm-specific mean cow responses using a sample size of 100, could perform as well or better than the SD estimator in estimating the mean over all farms. Space does not permit detailing how this happened in the case of each cow response variable, but some insight into what happened over all cow responses is obtained by consideration of the L2 case with a sample size of 100, where, as noted above, the EBLUP estimator was closest to the overall farm parameters being estimated at all seven recordings. At the sixth recording, the EBLUP estimates were closest to the farm-specific parameter being estimated for 11 of the 16 farms. So at this recording, the excellent performance by the EBLUP estimator at the farm-specific level enabled it to produce an overall farm estimate closest to the corresponding parameter being estimated. This is how the EBLUP estimator was able to produce overall farm estimates closest to the corresponding parameters being estimated in nearly all cases with the sow responses using both large and small sample sizes.

A much different explanation has to be offered at the second recording where the SD estimator was closest to the farm-specific parameter being estimated for 15 farms and the RS estimator was closest for the remaining farm and yet the EBLUP estimator produced a mean estimate over all farms that was closest to the overall farm mean being estimated. For 14 of the 16 farms, the SD and EBLUP estimator produced means that were both below (eight farms) or both above (six farms) the parameter being estimated and the SD estimator was closer to the parameter. But for the remaining two farms, with 12 and 21 cows, respectively, the SD estimate was slightly below the parameter being estimated while the EBLUP estimate was considerably above the parameter—enough above to pull the EBLUP overall farm estimate closer to the parameter being estimated. This rather extreme result was also seen at the third recording.

The results at the other recordings were more complex. For example, at the fourth recording, the SD estimate was closer to the farm parameter being estimated in 11 farms and the EBLUP estimate was closer in the remaining five farms. In both sets of farms, the SD and EBLUP estimates were either both above or both below the farm parameter being estimated or one was above and the other below. The net impact was that the EBLUP overall farm estimate was closer to the population overall farm mean.

#### 4.2.2. ARE and ASE results

The mean (over 100 repeated sampling trials) AREs and ASEs obtained with the EBLUP estimator were the smallest in 96.1 and 88.2%, respectively, of the 51 cases of estimating the mean response over all farms over all cow responses (seven recordings  $\times$ five responses  $=$  35 cases) and all sow responses (four recordings  $\times$  four responses  $=$ 16 cases) using a sample size of 100. When the sample size was lowered to 25, these percentages fell to 76.5 and 58.8%, respectively. With only a single exception, when the

mean ARE and ASE obtained with the EBLUP was not the smallest, that obtained by the RS estimator was the smallest. So in estimating the mean over all farms, the enhanced $\hat{A}$  precision of the estimates obtained by the EBLUP estimator—coupled with the closeness of these estimates to the parameter—makes the EBLUP estimator an attractive option.

#### 4.3. General discussion

It is recognized that most production parameters are now recorded in computer systems and in some contexts there is less need to sample such data bases. However, if some agency desires to monitor a population to get the ''big picture'' of the health and productivity of the population over a large number of farms and to do it frequently and in a timely manner, certainly sampling will be involved to enhance the convenience and cost effectiveness of the process. In such an undertaking, the farm-specific estimates might not be as relevant to the individual farm—but having farm-specific mean estimates close to the parameter being estimated lends credibility to the sampling process used to produce the estimated mean responses over all farms.

The full utility of small-area-estimation methods would be realized when applied to infectious-disease monitoring where the expense of testing all individual animals may be high relative to the cost of visiting the farm and getting set up to collect samples. Smallarea-estimation methods also would be more directly applicable in monitoring the status of some nutrient in animals; probably there would not be complete information on the farm and it would be too costly to obtain such information without sampling. It should also be remembered that farms in some countries do not have the same data-collection and -storage capabilities as farms in extremely developed countries. Small-area estimation could be very useful in monitoring animal health and production in these countries providing both farm-specific and over-all-farm estimates.

The present study is not exhaustive; it was not intended to be exhaustive but rather to be a start. Among the many avenues for future work that could be proposed, I am particularly interested in the application of these methods to binary responses because of their obvious relevance in epidemiology and in a similar in-depth applied evaluation of the Baysian approaches that have been proposed.

## 5. Conclusion

The present results would seem to favor the EBLUP estimator in situations where a lower proportion of the total population of sampling units would be sampled. This is the situation that would be desired in the context of monitoring a large food–animal population constrained by limited resources. The EBLUP estimator appears to compensate adequately for changes in sample size; the SD estimator seems to be more affected by the diminished influence of its regression component as the sample size is reduced. Errors associated with mean estimates (both farm-specific and over all farms) produced using the EBLUP estimator frequently offer enhanced precision to EBLUP estimates—complementing their strong validity attributes.

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## Appendix A

Regressions required to obtain EBLUP estimate:

1.  $(y_{jik} - \overline{y}_{jiw})/x_{ik}^{1/2}$  on  $(x_{ik} - \overline{x}_{iw})/x_{ik}^{1/2}$  to obtain SSE $(1)_j$  to estimate  $\sigma_{e_j}^2$ ,  $\hat{\sigma}_{e_j}^2 = \frac{\text{SSE}(1)_j}{m - n - 1}$ 

where  $y_{jik}$  is the response at time j of the kth sampled animal from the ith farm;  $\overline{y}_{jik} = \sum_{k=1}^{m_i} (y_{jik}/x_{ik}) / \sum_{k=1}^{m_i} (1/x_{ik});$   $x_{ik}$  the base time response of the kth sampled animal from the *i*th farm;  $\overline{x}_{iw} = m_i / \sum_{k=1}^{m_i} (1/x_{ik}); m = \sum_{i=1}^{N} m_i$ , the total number of responding animals, the sample size;  $m_i$  the sample size of *i*th sampled farm,  $0 \leq m_i \leq M_i$ ; M<sub>i</sub> the total number of animals on the *i*th farm; *n* the total number of farms sampled.

- 2.  $y_{jik}/x_{ik}^{1/2}$  on  $[1/x_{ik}^{1/2}, x_{ik}^{1/2}]$  to obtain SSE(2)<sub>j</sub> to estimate  $\sigma_{v_j}^2$ , shown below.
- 3.  $(y_{jik} \hat{\alpha}_{ji}\overline{y}_{jiw})/x_{ik}^{1/2}$  on  $[(1 \hat{\alpha}_{ji})/x_{ik}^{1/2}, (x_{ik} \hat{\alpha}_{ji}\overline{x}_{iw})/x_{ik}^{1/2}]$  to estimate  $\beta_{1j}$  and  $\beta_{2j}$ , where  $\hat{\alpha}^{}_{ji} = 1 - (1 - \hat{\gamma}^{}_{ji})^{1/2}; \quad \hat{\gamma}^{}_{ji} = \hat{\sigma}^2_{v_j}/(\hat{\sigma}^2_{v_j} + (\hat{\sigma}^2_{e_j}/w_{ji.})); \quad w^{}_{ji.} = \sum_{k=1}^{m_i} w^{}_{jik}; \quad w^{}_{jik} = 1/k^2_{jik};$  $k_{jki} = x_{ik}^{1/2}.$

Note: all three regressions are through the origin. Computation of  $\hat{\sigma}_{\nu_j}^2$ 

$$
\hat{\sigma}^2_{v_j} = max(0, \tilde{\sigma}^2_{v_j})
$$

where  $\tilde{\sigma}_{v_j}^2 = \eta_{**j}^{-1} [SSE(2)_j - (n-p)\hat{\sigma}_{ej}^2]$ ;  $\eta_{**j} = \sum_{i=1}^n w_{ji} (1 - w_{ji} \underline{x}_{iv}' \underline{A}_j^{-1} \underline{x}_{iw})$ ;  $w_{ji} = \sum_{k=1}^{m_i} w_{jik}$ ;  $\mathbf{x}_{iw} = [1, \bar{x}_{iw}],$  a 1×2 vector;  $\bar{x}_{iw} = m_i / \sum_{k=1}^{m_i} (1/x_{ik}); \underline{A}_j =$  $\left[\sum_{i=1}^{n} \sum_{k=1}^{m_i} (1/x_{ik}) \right]_{n}^{n}$ <br> $\sum_{i=1}^{n} \sum_{k=1}^{m_i} x_{ik}\right],$ 

a 2  $\times$  2 matrix;  $x_{ij}$  is the base time response of the kth sampled animal from the *i*th farm; *n* the total number of farms sampled;  $m_i$  the sample size of the *i*th sampled farm.

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