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# **Estimation After a Group Sequential Trial**

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#### Abstract

Group sequential trials are one important instance of studies for which the sample size is not fixed a priori but rather takes one of a finite set of pre-specified values, dependent on the observed data. Much work has been devoted to the inferential consequences of this design feature. Molenberghs et al (2012) and Milanzi et al (2012) reviewed and extended the existing literature, focusing on a collection of seemingly disparate, but related, settings, namely completely random sample sizes, group sequential studies with deterministic and random stopping rules, incomplete data, and random cluster sizes. They showed that the ordinary sample average is a viable option for estimation following a group sequential trial, for a wide class of stopping rules and for random outcomes with a distribution in the exponential family. Their results are somewhat surprising in the sense that the sample average is not optimal, and further, there does not exist an optimal, or even, unbiased linear estimator. However, the sample average is asymptotically unbiased, both conditionally upon the observed sample size as well as marginalized over it. By exploiting ignorability they showed that the sample average is the conventional maximum likelihood estimator. They also showed that a conditional maximum likelihood estimator is finite sample unbiased, but is less efficient than the sample average and has the larger mean squared error. Asymptotically, the sample average and the conditional maximum likelihood estimator are equivalent.

This previous work is restricted, however, to the situation in which the the random sample size can take only two values, N = n or N = 2n. In this paper, we consider the more practically useful setting of sample sizes in a the finite set  $\{n_1, n_2, \ldots, n_L\}$ . It is shown that the sample average is then a justifiable estimator, in the sense that it follows from joint likelihood estimation, and it is consistent and asymptotically unbiased. We also show why simulations can give the false impression of bias in the sample average when considered conditional upon the sample size. The consequence is that no corrections need to be made to estimators following sequential trials. When small-sample bias is of concern, the conditional likelihood estimator provides a relatively straightforward modification to the sample average. Finally, it is shown that classical likelihood-based standard errors and confidence intervals can be applied, obviating the need for technical

corrections.

**Some Keywords:** Exponential Family; Frequentist Inference; Generalized Sample Average; Joint Modeling; Likelihood Inference; Missing at Random; Sample Average.

## 1 Introduction

Principally for ethical and economic reasons, group sequential clinical trials are in common use (Wald, 1945; Armitage, 1975; Whitehead, 1997; Jennison and Turnbull, 2000). Tools for constructing such designs, and for testing hypotheses from the resulting data, are well established both in terms of theory and implementation. By contrast, issues still surround the problem of estimation (Siegmund, 1978; Hughes and Pocock, 1988; Todd, Whitehead, and Facey, 1996; Whitehead, 1999) following such trials. In particular, various authors have reported that standard estimators such as the sample average are biased. In response to this, various proposals have been made to remove or at least alleviate this bias and its consequences (Tsiatis, Rosner, and Mehta, 1984; Rosner and Tsiatis, 1988; Emerson and Fleming, 1990). An early suggestion was to use a conditional estimator for this Blackwell (1947).

To successfully address the bias issue, it is helpful to understand its origins. Lehman (1950) showed that it stems from the so-called *incompleteness* of the sufficient statistics involved, which in turn implies that there can be no minimum variance unbiased linear estimator. Liu and Hall (1999) and Liu et al (2006) explored this incompleteness in group sequential trials, for outcomes with both normal and one-parameter exponential family distributions. For these distributions, Molenberghs et al (2012) and Milanzi et al (2012) embedded the problem in the broader class with random sample size, which includes, in addition to sequential trials, incomplete data, completely random sample sizes, censored time-to-event data, and random cluster sizes. In so doing, they were able to link incompleteness to the related concepts of ancillarity and ignorability in the missing-data sense. By considering the conventional sequential trial with a deterministic stopping rule as a limiting case of a stochastic stopping rule, these authors were able to derive properties of families of linear estimators as well as likelihood-based estimators. The key results are as follows:(1) there exists a maximum likelihood estimator that conditions on the realized sample size (CL), which is finite sample unbiased, but has slightly larger variance and mean square error (MSE) than the SA ;(2) the sample average (SA) exhibits finite sample bias, although it is asymptotically unbiased; (3) apart from the exponential distribution setting, there is no optimal linear estimator, although the sample average is asymptotically optimal; (4) the validity of the sample average as an estimator also follows from standard ignorable likelihood theory.

Evidently, the CL is unbiased both conditionally and marginally with respect to the sample size. In contrast, the CL is marginally unbiased, but there exist classes of stopping rules where, conditionally on the sample size, there is asymptotic bias for some values of the sample sizes. Surprisingly, this is not of concern. Milanzi *et al* (2012) showed this for the case of two possible sample sizes, N = n and N = 2n. With such a stopping rule, it is possible that, for example when N = n, the bias grows unboundedly with n; when this happens though, the probability that N = n shrinks to 0 at the same rate. If strict finite sample unbiasedness is regarded as essential, the conditional MLE can be used, which, like the MLE, also admits the standard likelihood-based precision measures, although it is computationally intensive. This is a very important result and should be contrasted with the various precision estimators that have been developed in the past.

On the other hand, developments in Molenberghs *et al* (2012) and Milanzi *et al* (2012) show that despite finite sample bias, a correction may not be strictly necessary for SA. Further, its likelihood basis, implies it can be used in conjunction with standard likelihood-based measures of precision, such as standard errors and associated confidence intervals to provide valid inferences.

A major limitation of Molenberghs *et al* (2012) and Milanzi *et al* (2012) is the restriction to two looks of equal size. It is the main aim of this paper to extend this work to the practically more useful setting of multiple looks of potentially different sample sizes.

In Section 2, we introduce notation, describe the setting, the models, and the associated generic problem. In Section 3, we study the problems of incompleteness when using a stochastic stopping rule. The class of generalized sample averages in introduced in Section 6, and conditional and joint maximum likelihood estimators are derived. Their asymptotic properties are studied in Section 7. A simulation study is described in the Supplementary Materials, Section A.

# 2 Problem and Model Formulation

Consider a sequential trial with L pre-specified looks, with sample sizes  $n_1 < n_2 < \ldots, < n_L$ . Assume that there are  $n_j$  i.i.d. observations  $Y_1, \ldots, Y_{n_j}$ , from the *j*th look that follow an exponential family distribution with density

$$f_{\theta}(y) = h(y) \exp\left\{\theta y - a(\theta)\right\},\tag{1}$$

for  $\theta$  the natural parameter,  $a(\theta)$  the mean generating function, and h(y) the normalizing constant. Subsequent developments are based on a generic data-dependent stochastic stopping rule, which we write

$$\pi(N = n_j | k_{n_j}) = F\left(k_{n_j} | \psi\right) = F\left(k_{n_j}\right),\tag{2}$$

where  $K_{n_j} = \sum_{i=1}^{n_j} Y_i$  also has an exponential family density:

$$f_{n_j}(k) = h_{n_j}(k) \exp\left\{\theta k_{n_j} - n_j a(\theta)\right\}.$$
(3)

Our inferential target is the parameter  $\theta$ , or a function of this.

## 2.1 Stochastic Rule As A Group Sequential Stopping Rule

. While the stopping rule seems different from the ones frequently used, it will later on be clear as to how it can be specified to conform to the commonly used stopping rules in the sequential trials. For instance, when the conditional probability of stopping of an exponential family form is chosen, e.g.,

$$F(k_n) = F(k) = \int_{z=-\infty}^{z=A(k)} \widetilde{f}_1(z)dz,$$
(4)

then an appealing form for the marginal stopping probability can be derived. Here  $\tilde{f}_1(z)$  can be seen as an exponential family member, underlying the stopping process. When the outcomes Yand hence K do not range over the entire real line, the lower integration limit in (4) should be adjusted accordingly, and the function A(k) should be chosen so as to obey the range restrictions. It is convenient to assume that  $\tilde{f}_1(z)$  has no free parameters; should there be the need for such, then they can be absorbed into A(k). Hence, we can write

$$\widetilde{f}_1(z) = \widetilde{h}_1(z) \exp\left\{-\widetilde{a}(0)\right\}.$$
(5)

Using (3) and (5), the marginal stopping probability becomes:

$$P(N = n) = \int_{k=-\infty}^{k=+\infty} \int_{z=-\infty}^{z=A(k)} f_{n,\theta}(k) \widetilde{f}_1(z) dz dk$$
  
=  $\exp\{-na(\theta) - \widetilde{a}(0)\} \int_{k=-\infty}^{k=+\infty} h_n(k) \left[\int_{z=-\infty}^{z=A(k)} \widetilde{h}_1(z) dz\right] e^{\theta k} dk$   
=  $\exp\{-na(\theta) - \widetilde{a}(0)\} \mathcal{L}\{H_1(A(k)) \cdot h_n(k)\},$  (6)

where

$$H_1(t) = \int_{z=-\infty}^{z=t} \tilde{h}_1(z) dz.$$

Milanzi et al (2012) studied in detail the behavior of stopping rules where

$$A(k) = \alpha_j + \beta k_{n_j} / n_j^m,$$

with  $\alpha_j$ ,  $\beta$  and m are constants specific to a design.

Choosing  $\beta \to \infty$  and  $\beta \to -\infty$  results into deterministic stopping or continuing thus corresponding to the stopping rules commonly used in sequential trials. The trial is stopped when (6) is greater than a randomly generated number from a Uniform(0,1). Note that the higher the evidence against (for) the null hypothesis, the higher the probability to stop. In the specific example of normally distributed responses, (1) can be chosen as standard normal. The value of  $\alpha$  is paramount to deciding the behavior of stopping boundaries. Consider, for example, O'Brien and Fleming stopping boundaries where it is difficult to stop in early stages; one can then specify  $\alpha_j$  such that the probability of stopping increases with the stages. In addition to the computational advantages and the associated practicality, we use the stochastic rule to maintain the focus of this paper, which is estimation.

### **3** Incomplete Sufficient Statistics

Several concepts play a crucial role in determining the properties of estimators following sequential trials: incompleteness, a missing at random (MAR) mechanism, ignorability, and ancillarity (Molenberghs *et al*, 2012). We consider the role of incompleteness first: a statistic s(Y) of a random variable Y, with Y belonging to a family  $P_{\theta}$ , is complete if, for every measurable function  $g(\cdot)$ ,  $E[g\{s(Y)\}] = 0$  for all  $\theta$ , implies that  $P_{\theta}[g\{s(Y)\} = 0] = 1$  for all  $\theta$  (Casella and Berger, 2001, pp. 285–286). Incompleteness is central to the various developments (Liu and Hall, 1999; Liu *et al*, 2006; Molenberghs *et al*, 2012) because of the the Lehman-Scheffé theorem which states that "if a statistic is unbiased, complete, and sufficient for some parameter  $\theta$ , then it is the best mean-unbiased estimator for  $\theta$ ," (Casella and Berger, 2001). In the present setting, the relevant sufficient statistic is not complete, and so the theorem *cannot* be applied here.

In line with extending the work of Molenberghs *et al* (2012) and Milanzi *et al* (2012) to a general number of looks, we explore incompleteness and its consequences in studies with more than two looks, using the stochastic rule.

In a sequential setting, a convenient sufficient statistic is (K, N). Following the developments in the

above papers, the joint distribution for (K, N) is:

$$p(K,N) = f_0(K,N) F(K_N),$$
 (7)

$$f_0(k_{n_1}, n_1) = f_{n_1}(k_{n_1}), (8)$$

$$f_0(k_{n_j}, n_j) = \int f_0(k_{n_{j-1}}, n_{j-1}) f_{n_j - n_{j-1}}(k_{n_j} - k_{n_{j-1}}) \left[ 1 - F(k_{n_{j-1}}) \right] dk_{n_{j-1}}.$$
 (9)

If (K, N) were complete, then there would exist a function g(K, N) such that E[g(K, N)] = 0 if and only if g(K, N) = 0, implying that

$$0 = \int g(k_{n_1}, n_1) f_{n_1}(k_{n_1}) F(k_{n_1}) dk_{n_1} + \sum_{j=2}^{L-2} \int g(k_{n_j}, n_j) H(k_{n_j}) F(k_{n_j}) dk_{n_j} + \int g(k_{n_L}, n_L) H(k_{n_L}) F(k_{n_L}) dk_{n_L},$$
(10)

with

$$H(k_{n_j}) = \left[ \int \underbrace{\cdots}_{j-1} \int f_0(k_{n_{j-1}}, n_{j-1}) f_{n_j - n_{j-1}}(k_{n_j} - k_{n_{j-1}}) \left[ 1 - F(k_{n_{j-1}}) \right] dk_{n_1} \dots dk_{n_{j-1}} \right].$$

Tedious but straightforward algebra results into:

$$g(k_{n_L}, n_L)\widetilde{H}(k_{n_L}) = -\sum_{j=1}^{L-1} \int g(z_j, n_j)\widetilde{H}(z_j)F(z_j)dz_j,$$
  
$$g(k_{n_L}, n_L) = \frac{\sum_{j=1}^{L-1} \int g(z_j, n_j)\widetilde{H}(z_j)F(z_j)dz_j}{\widetilde{H}(k_{n_L})}.$$

Assigning, for example, arbitrary constants to  $g(n_1, k_{n_1}), \ldots, g(n_{L-1}, k_{n_{L-1}})$ , a value can be found for  $g(n_L, k_{n_L}) \neq 0$ , contradicting the requirement for (K, N) to be complete, hence establishing incompleteness. From applying the Lehmann-Scheffé theorem, it follows that no best mean-unbiased estimator is guaranteed to exist. The practical consequence of this is that even estimators as simple as a sample average need careful consideration and comparison with alternatives. Nevertheless, the situation is different for non-linear mean estimators as illustrated for the conditional likelihood estimator.

# 4 Unbiased Estimation: Conditional Likelihood

An important drawback of linear mean estimators in the context of sequential trials is their finitesample bias. In connecting missing data and sequential trials theory, Molenberghs *et al* (2012) provided a factorization for the joint distribution of observed data and sample size that leads to an unbiased conditional likelihood mean estimator. For an arbitrary number of looks, the conditional distribution for  $N = n_1$  is:

$$f_{n_1}(n_1, k_{n_1}) = f_{n_1}(k_{n_1})F(k_{n_1}),$$
  

$$f_{n_1}(n_1) = \int f_{n_1}(k_{n_1})F(k_{n_1})dk_{n_1} = A_{n_1}(\mu),$$
  

$$f(k_{n_1}|n_1) = \frac{f_{n_1}(k_{n_1})F(k_{n_1})}{A_{n_1}(\mu)},$$

from which the log-likelihood, score, Hessian, and information follow as:

$$\ell_{n_1}(\mu) = \ln \left[ h_{n_1}(k_{n_1}) \right] + \theta k_{n_1} - n_1 \mu - \ln \left[ A_{n_1}(\mu) \right], \tag{11}$$

$$S_{n_1}(\mu) = k_{n_1} - \frac{B_{n_1}(\mu)}{A_{n_1}(\mu)} = k_{n_1} - E\left[K|N = n_1\right],$$
(12)

$$H_{n_1}(\mu) = -\left\{\frac{C_{n_1}(\mu)}{A_{n_1}(\mu)} - \left(\frac{B_{n_1}(\mu)}{A_{n_1}(\mu)}\right)^2\right\} = -\left\{E\left[K^2|N=n_1\right] - \left(E\left[K|N=n_1\right]\right)^2\right\}, (13)$$
  
$$I_{n_1}(\mu) = E\left[K^2|N=n_1\right] - \left\{E\left[K|N=n_1\right]\right\}^2,$$

where

$$B_{n_1}(\mu) = \int k_{n_1} f_{n_1}(k_{n_1}) dk_{n_1}$$
 and  $C_{n_1}(\mu) = \int k_{n_1}^2 f_{n_1}(k_{n_1}) dk_{n_1}$ .

Similarly for  $N = n_j$  where j > 1, we have the conditional distribution:

$$f_{n_j}(n_j, k_{n_j}) = \widetilde{H}(k_{n_j}) F(k_{n_j}) \exp\left[\theta k_{n_j} - n_j a(\theta)\right], \qquad (14)$$

$$f_{n_j}(n_j) = \int \widetilde{H}(k_{n_j}) F(k_{n_j}) \exp\left[\theta k_{n_j} - n_j a(\theta)\right] = A_{n_j}(\mu), \tag{15}$$

$$f(k_{n_j}|n_j) = \frac{\widetilde{H}(k_{n_j})F(k_{n_j})\exp\left[\theta k_{n_j} - n_j a(\theta)\right]}{A_{n_j}(\mu)}.$$
(16)

The following expressions for the likelihood, score, Hessian, and information are:

$$\ell_{n_j}(\mu) = \ln[\tilde{H}(k_{n_j})F(k_{n_j})] + \theta k_{n_j} - n_j\mu - \ln A_{n_j}(\mu),$$
(17)

$$S_{n_j}(\mu) = k_{n_j} - \frac{B_{n_j}(\mu)}{A_{n_j}(\mu)} = k_{n_j} - E\left[K|N = n_j\right],$$
(18)

$$H_{n_j}(\mu) = -\left\{\frac{C_{n_j}(\mu)}{A_{n_j}(\mu)} - \left[\frac{B_{n_j}(\mu)}{A_{n_j}(\mu)}\right]^2\right\} = -\left\{E\left[K^2|N=n_j\right] - \left(E\left[K|N=n_j\right]\right)^2\right\}, (19)$$

$$I_{n_j}(\mu) = E\left[K^2 | N = n_j\right] - \left\{E\left[K | N = n_j\right]\right\}^2,$$
(20)

where

$$B_{n_j}(\mu) = \int k_{n_j} \widetilde{H}(k_{n_j}) F(k_{n_j}) \exp(\theta k_{n_j} - n_j a(\theta)) dk_{n_j},$$
  

$$C_{n_j}(\mu) = \int k_{n_j}^2 \widetilde{H}(k_{n_j}) F(k_{n_j}) \exp(\theta k_{n_j} - n_j a(\theta)) dk_{n_j} \quad (j > 1)$$

The overall information for the conditional likelihood estimator is given by

$$I_{c}(\mu) = \sum_{j=1}^{L} A_{n_{j}}(\mu) \left\{ \frac{C_{n_{j}}(\mu)}{A_{n_{j}}(\mu)} - \left[ \frac{B_{n_{j}}(\mu)}{A_{n_{j}}(\mu)} \right]^{2} \right\},$$
  
$$= \sum_{j=1}^{L} n_{j} a''(\theta) A_{n_{j}}(\mu) - \sum_{j=1}^{L} \frac{[B_{n_{j}}(\mu) - n_{j} a'(\theta) A_{n_{j}}(\mu)]^{2}}{A_{n_{j}}(\mu)}.$$
 (21)

From scores (12) and (18), it can be seen that conditional likelihood estimator is unbiased. Clearly, the bias correction in the CLE mirrors the bias expression of the SA, as can be seen from (33). Upon writing (12) and (18), as

$$S_{n_j}(\mu) = k_{n_j} - n_j \mu + \left[ n_j \mu - \frac{B_{n_j}(\mu)}{A_{n_j}(\mu)} \right],$$

the bias-correction factor in the CLE becomes even more apparent.

In contrast to the case of a fixed sample size, conditioning on the sample size in this case leads to loss of information, as can be seen by the subtraction of a positive factor in (21). This is a consequence of conditioning on a non-ancillary statistic, as discussed in Casella and Berger (2001).

Additionally, despite having the appealing property of finite sample unbiasedness, its non-linear nature comes with computational problems. Note that maximization of (11) and (14) requires simultaneous optimization and solution of multiple integrals. Unless small-sample unbiasedness is of paramount importance, consideration has to be given to the time and complexity of implementing the conditional likelihood.

## 5 Joint Likelihood Estimation

Likelihood methods, while allowing for a unified treatment across a variety of settings (e.g., data types, stopping rules), they do rely heavily on correct parametric specification. This should be taken into account when opting for a particular approach.

Selection model factorization for the joint distribution of observed data and sample size also leads to joint likelihood estimation (JLE). Employing the separability and ignorability concepts from the

missing data theory, it is known that under a missing at random (MAR) assumption, maximizing the joint likelihood is equivalent to maximizing the likelihood of the observed data only. This is crucial when considered against the background of Kenward and Molenberghs (1998), where it was shown that for frequentist inference and under the missing at random (MAR) assumption, the observed information matrix gives valid inferences. Other properties of joint likelihood estimation are explored below.

The joint distribution of the sufficient statistics (K, N) is given by:

$$f(K,N) = h_N(K) \exp\left[K\theta - Na(\theta)\right] \cdot \prod_{i=1}^{L-1} \left[1 - F(k_{n_j})\right] F(k_{n_L})^{I(i (22)$$

Because our stopping rule is independent of the parameter of interest, the log-likelihood, the score, the Hessian, and the expected information simplify as follows:

$$\ell(\mu) = \ln[h_N(K)] + K\theta - Na(\theta) + \ln\left\{\prod_{i=1}^{L-1} \left[1 - F(k_{n_j})\right]F(k_{n_L})^{I(i
(23)$$

$$S(\mu) = K - Na'(\theta), \tag{24}$$

$$H(\mu) = -Na''(\theta), \tag{25}$$

$$I(\mu) = \sum_{j=1}^{L} n_j a''(\theta) A_{n_j}(\mu).$$
(26)

In deriving the score (24) from (23) the rightmost term drops out, i.e., conventional ignorability applies. As a consequence, the maximum likelihood estimator (MLE) reduces to  $\hat{\mu} = a'(\theta) = K/N$ , the SA.

Because of the bias, a finite sample comparison among estimators needs to be based on the MSE. For  $\hat{\mu}$ , this is

$$\mathsf{MSE}(\widehat{\mu}) = \frac{1}{\sum_{j=1}^{L} n_j a''(\theta) A_{n_j}(\mu)} + \left[ \sum_{j=1}^{L} \frac{\left[ B_{n_j}(\mu) - A_{n_j} n_j \mu \right]}{n_j} \right]^2.$$
(27)

0

For the conditional likelihood estimate (CLE) the MSE is:

$$\mathsf{MSE}(\hat{\mu}_{c}) = \frac{1}{I_{c}(\mu)} = \frac{1}{\sum_{j=1}^{L} n_{j} a''(\theta) A_{n_{j}}(\mu)} + \frac{y}{\left[\sum_{j=1}^{L} n_{j} a''(\theta) A_{n_{j}}(\mu)\right]^{2} - y \sum_{j=1}^{L} n_{j} a''(\theta) A_{n_{j}}(\mu)},$$
(28)

where

$$y = \sum_{j=1}^{L} \frac{\left[B_{n_j}(\mu) - A_{n_j}n_j(\mu)\right]^2}{A_{n_j}(\mu)}.$$

The condition that  $MSE(\hat{\mu}) \ge MSE(\hat{\mu}_c)$  is equivalent to the requirement that

$$\left[\sum_{j=1}^{L} \frac{\left[B_{n_j}(\mu) - A_{n_j} n_j \mu\right]}{n_j}\right]^2 \ge \frac{1}{\sum_{j=1}^{L} n_j a''(\theta) A_{n_j}(\mu)}$$

holds. For the special case of equal sample sizes this can never be true, hence the SA has the smaller MSE. More generally, neither is uniformly superior in terms of MSE.

# 6 Generalized Sample Averages

To get a broad picture of the properties of the SA, which follows from JLE, we embed it into a broader class of linear estimator. Extending the definition in Molenberghs *et al* (2012), the generalized sample average (GSA) can be be defined as:

$$\bar{\mu}_g = \sum_{j=1}^L \frac{a_j}{n_j} k_{n_j},\tag{29}$$

for a set of constants  $a_1, \ldots, a_L$ . The SA follows as the special case where each  $a_j = 1$ . To explore the properties of the GSA, we make use of the fact that:

$$\int f_{n_1}(k_{n_1})dk_{n_1} + \sum_{j=2}^L \int \widetilde{H}(k_{n_j})F(k_{n_j})\exp(\theta k_{n_j} - n_j a(\theta))dk_{n_j} = 1,$$

and derive three useful identities:

$$\int f_{n_1}(k_{n_1})dk_{n_1} = 1 - \sum_{j=2}^{L} A_{n_j}(\mu), \qquad (30)$$

$$\sum_{j=1}^{L} B_{n_j}(\mu) = \sum_{j=1}^{L} n_j a'(\theta) A_{n_j}(\mu), \qquad (31)$$
$$\sum_{j=1}^{L} C_{n_j} = \sum_{j=1}^{L} 2n_j a'(\theta) B_{n_j}(\mu) - [n_j a'(\theta)]^2 A_{n_j}(\mu) + n_j a''(\theta) A_{n_j}(\mu).$$

Using identities (30) and (31), the expectation of (29) can then be formulated as

$$E\left[\bar{\mu}_{g}\right] = \frac{a_{1}}{n_{1}}B_{n_{1}}(\mu) + \sum_{j=2}^{L}\frac{a_{j}}{n_{j}}B_{n_{j}}(\mu)$$
  
$$= a_{1}\mu + \sum_{j=2}^{L}a_{1}A_{n_{j}}(\mu)\frac{n_{1}-n_{j}}{n_{1}}\left[\frac{n_{1}a_{j}-n_{j}a_{1}}{a_{1}(n_{1}-n_{j})}E\left\{\frac{K}{N}\middle|N=n_{j}\right\} - \mu\right], \qquad (32)$$

establishing the bias as a function of the difference between the marginal and conditional means. When (32) is unbiased, at least one value among  $a_1, \ldots, a_L$  will depend on  $\mu$ . This means that none of the GSA can be uniformly unbiased. Focusing on the SA, the expectation reduces to

$$E\left[\bar{\mu}\right] = \mu + \sum_{j=2}^{L} A_{n_j}(\mu) \frac{n_1 - n_j}{n_1} \left[ \frac{B_{n_j}(\mu)}{n_j A n_j(\mu)} - \mu \right]$$
  
=  $\mu + \sum_{j=2}^{L} A_{n_j}(\mu) \frac{n_1 - n_j}{n_1} \left[ E\left\{ \frac{K}{N} \middle| N = n_j \right\} - \mu \right],$  (33)

from which we get the bias as

$$\sum_{j=2}^{L} A_{n_j}(\mu) \frac{n_1 - n_j}{n_1} \left[ \frac{B_{n_j}(\mu)}{n_j A n_j(\mu)} - \mu \right] = \sum_{j=2}^{L} \frac{n_1 - n_j}{n_1 n_j} \left[ B_{n_j}(\mu) - A_{n_j} n_j \mu \right]$$
$$= \sum_{j=1}^{L} \frac{\left[ B_{n_j}(\mu) - A_{n_j} n_j \mu \right]}{n_j}.$$
(34)

Thus, the SA is unbiased when the conditional and marginal means are equal.

# 7 Asymptotic Properties

We now turn to the large-sample properties of the estimators discussed in the previous sections. When  $N \to \infty$ , approximately  $K \sim N(N\mu, N\sigma^2)$ , so normal-theory arguments can be used. Considering a first-order Taylor series expansion of  $F(k_{n_j})$  around  $n_j\mu$  results in  $F(k_{n_j}) \approx F(n_j\mu) + F'(n_j\mu)(k_{n_j} - n_j\mu)$ . Without loss of generality, consider a class of stopping rules for which  $F'(n_j) \xrightarrow{n \to \infty} 0$ . In this setting, the expressions derived above can be approximated by

$$A_{n_1}(\mu) \approx F(n_1\mu),$$
  

$$B_{n_1}(\mu) \approx F(n_1\mu)n_1\mu,$$
  

$$A_{n_j}(\mu) \approx \prod_{i=1}^{j-1} [1 - F(n_i\mu)]F(n_j\mu), \quad (j > 1)$$
  

$$B_{n_j}(\mu) \approx \prod_{i=1}^{j-1} [1 - F(n_i\mu)]F(n_j\mu)n_j\mu, \quad (j > 1).$$

These approximations will be useful in what follows.

#### 7.1 Asymptotic Bias

### **Conditional Likelihood Estimation**

We turn now to the asymptotic *conditional* behavior of the bias of the sample average *given the sample size*. Two cases are considered:

- **Case I.**  $F(n\mu) \xrightarrow{n \to \infty} a \in ]0,1[$  and  $F'(n\mu) \xrightarrow{n \to \infty} 0$ . For this case  $E[\bar{\mu}|N = n_j] \xrightarrow{n \to \infty} \mu$ , for  $j = 1, \ldots, L$ .
- **Case II.** Here, both the function  $F(\cdot)$  and its first derivative  $F(\cdot)$  converge to zero. When this happens, it does so for all but one of the sample sizes that can possibly be realized. The one exception is the sample size that will be realized, asymptotically, with probability one. Without loss of generality, we illustrate this case for stopping at the first look, assuming that the sample size realized at the first look corresponds to a set of values for  $\mu$  that do not contain the true one. Thus,  $F(n\mu) \xrightarrow{n\to\infty} 0$  and  $F'(n\mu) \xrightarrow{n\to\infty} 0$ . This case can correspond for particular forms of  $F(k_{n_j})$ . Given that K is asymptotically normally distributed, letting  $F(K) = \Phi(k)$  is a mathematically convenient choice from which it follows that  $F(n_j\mu) = \Phi(n_j\mu)$ . Consider first  $N = n_1$ . Then,

$$\lim_{n_1 \to \infty} E[\bar{\mu}|N=n_1] = \mu - \lim_{n_1 \to \infty} \frac{\phi(n_1\mu)\sigma^2}{\Phi(n_1\mu)},$$

of which the right hand term approaches 0/0. We therefore apply l'Hopital's rule and obtain:

$$\lim_{n_1 \to \infty} E[\bar{\mu}|N=n_1] = \mu - \lim_{n_1 \to \infty} \frac{-n_1 \mu \phi(n_1 \mu)}{\phi(n_1 \mu)} \to \infty,$$

with the sign opposite to that of  $\mu$ . Hence, conditional on the fact that stopping occurs after the first look, the estimate may grow in an unbounded way. However, recalling that  $F(n\mu)$ , the probability of stopping when  $N = n_1$ , also approaches zero, these extreme estimates are a the same time also extremely rare. In the same case, for  $N = n_j$  (j > 1),  $\lim_{n\to\infty} E[\bar{\mu}|N = n_j] \to \mu$ . So for these sample sizes no asymptotic bias occurs.

Milanzi *et al* (2012) showed that a large class of stopping rules corresponds to either Case I or Case II. For example, for stopping rule  $\Phi(\alpha + \beta k/n)$ , they found that Case I applies. Switching to  $\Phi(\alpha + \beta k)$ ,  $F'(n\mu) = \beta \phi(\alpha + \beta n\mu)$  which again tends to zero. However,  $\Phi(\alpha + \beta n\mu)$  may tend to either zero or one. For a general rule  $F(k) = \Phi(\alpha + \beta kn^m)$ , with m any real number,  $F'(n\mu)$ converges to zero whatever m is. Further,  $F(n\mu)$  converges to  $\Phi(\alpha + \beta\mu)$  for m = -1,  $\Phi(\alpha)$  for m < -1, and  $\Phi(\pm \infty)$  (i.e., 0 or 1) for m > -1.

### Joint Likelihood Estimation

Recall that the bias for the SA was given by (34), which asymptotically tends to the limit

$$\lim_{n \to \infty} \sum_{j=1}^{L} \frac{\prod_{i=1}^{j-1} [1 - F(n_i \mu)] F(n_j \mu) n_j \mu - \prod_{i=1}^{j-1} [1 - F(n_i \mu)] F(n_j \mu) n_j \mu}{n_j} \longrightarrow 0.$$

Although the sample average is generally finite-sample biased for data-dependent stopping rules, it is asymptotically unbiased and hence can be considered an appropriate candidate for practical use following a sequential trial. Emerson (1988) established the same result for two possible looks and further noted that this property is not relevant in group sequential trials, because large sample sizes are unethical, hence making the study of small sample properties crucial. On the other hand, results from a comprehensive analysis, comparing randomized controlled trials (RCTs) stopped for early benefit (truncated) and RCTs not stopped for early benefit (non-truncated), indicated that treatment effect was over-estimated in most of truncated RCTs regardless of the pre-specified stopping rule used (Bassler et al, 2010). They further advocate stopping rules that demand large number of events. In their exploration of properties of estimators, Milanzi et al (2012) showed that in the general class of linear mean estimators, only the sample average has the asymptotic unbiasedness property, thus giving it an advantage in cases where asymptotic unbiasedness would play a role. The sample average is asymptotically unbiased in all cases, and additionally conditionally asymptotically unbiased, even in the case of an arbitrary number of looks. Further, under the usual likelihood regularity conditions, the SA is then consistent and asymptotically normally distributed, and the likelihood-based precision estimator and its corresponding confidence intervals are valid. Care has to be exercised when working under the MAR assumption, as is the case here, because the observed information matrix rather than the expected information matrix should be used to obtain precision estimators to ensure their validity. Kenward and Molenberghs (1998) noted that, provided that use is made of the likelihood ratio, Wald, or score statistics based on the observed information, then reference to a null asymptotic  $\chi^2$  distribution will be appropriate.

This conventional asymptotic behavior contrasts with the idiosyncratic small-sample properties of the SA derived in Section 6.

## 7.2 Asymptotic Mean Square Error

Given that the bias for the sample average tends to zero as the sample size increases and that  $\sum_{j=1}^{L} B_{n_j}(\mu) - A_{n_j}(\mu) n_j \mu \xrightarrow{n \to \infty} 0$ , it follows that

$$\lim_{n \to \infty} \mathsf{MSE}(\widehat{\mu}) = \lim_{n \to \infty} \mathsf{MSE}(\widehat{\mu}_c) \to \frac{1}{\sum_{j=1}^L n_j a''(\theta) A_{n_j}(\mu)}$$

# 8 Simulation Study

#### 8.1 Design

The simulation study has been designed to corroborate the theoretical findings on the behavior of the likelihood estimators, in comparison to commonly used biased adjusted estimators. Assume a clinical trial comparing a new therapy to a control, designed to follow O'Brien and Fleming's group sequential plan with four interim analyses.

The objective of the trial is to show that the mean response from the new therapy is higher than that of the control group. Let  $Y_{it} \sim N(\mu_t, 1)$  and  $Y_{ic} \sim N(\mu_c, 1)$  be the responses from subject *i* in the therapy and control groups, respectively. The null hypothesis is formulated as  $H_0: \theta = \mu_t - \mu_c = 0$ vs.  $H_1: \theta = \theta_1 > 0$ . Further, allow a type I error of 2.5% and 90% power to detect the clinically meaningful difference.

Given that we are interested in asymptotic behavior, different values of the clinically meaningful difference,  $\theta_1 = 0.5, 0.25$ , and 0.15 are considered to achieve different sample sizes, with smaller  $\theta_1$  corresponding to larger sample size.

With the settings described above, datasets are generated as follows; at each stage,  $Y_{it} \sim N(2, 1)$ ,  $i = 1 \dots n_j$ ,  $j = 1 \dots 4$  and  $Y_{ic} \sim N(\mu_c, 1)$ , where  $\mu_c = 1.5$ , 1.75, and 1.85 for the first, second, and third setting, respectively. These also serve as the true mean values under which the bias is being considered.

Estimation proceeds by obtaining the maximum likelihood estimator (sample average:  $\hat{\mu}_t - \hat{\mu}_c$ ) at each stage and applying the stopping rule:

$$F(k_{n_j}) = \Phi\left(\alpha_j + \beta \frac{k_j}{n_j}\right), \qquad (j = 1...4),$$

where  $\beta = 100$  to represent the rules applied to the group sequential trials case (Milanzi *et al*, 2012). To follow the behavior of O'Brien and Fleming boundaries (where early stopping is difficult), a value of  $\alpha$  is chosen to make sure that the probability of stopping increases with the increase in number of looks, i.e.,  $\alpha_j = [2(h - j + 1)]/h\alpha_1$ , where  $\alpha_1 = -50$ , -25, and -15, for  $\theta_1 = 0.5$ , 0.25, and 0.15, respectively, and h is the number of planned looks. Obviously, the choice of  $\alpha_j$  depends on the design and goals of the trial. In this setting,  $\alpha_1$  was chosen such that  $P(N = n_3 | \theta = \theta_1) \ge 0.5$  and to make early stopping difficult. The decision to stop is made when  $F(k_{n_j}) > U$ , where  $U \sim \text{Uniform}(0, 1)$ ; otherwise, we continue. For example if  $F(k_{n_j}) = 0.70$ , then the probability of continuing is 30% and

for large values of  $\beta$ ,  $F(k_{n_j}) \in \{0, 1\}$ .

The objective of the simulation is to show that the performance of the CLE as the mean estimator after a group sequential trial and compare MLE to other bias adjusted estimators. We further show that MLE confidence intervals obtained by using the observed information matrix, lead to valid conclusions.

Other estimators obtained include: the mean unbiased estimator (MUE), the bias adjusted estimator (BAM; Todd, Whitehead, and Facey 1996), and Rao's bias-adjusted estimator (RBADJ; Emerson and Fleming 1990).

Additional simulations with two possible looks and a smaller value of  $\beta$  for both joint and conditional likelihood are presented in the Appendix.

#### 8.2 Results

Table 1 gives the mean estimates for different estimators of  $\theta$ . On average, the MLE exhibits large relative bias compared to the bias adjusted estimates, for example, for  $\theta_1 = 0.15$ , which corresponds to a maximum sample size of 1949, relative bias for MLE is 6% compared to 0.7% for CLE. The conditional likelihood estimator performs as expected with consistently small bias under all the three scenarios. On the other hand, the MLE shows asymptotically unbiased behavior, seen by the reduction (though small) in relative bias as sample size increases. This is not the same for BAM and RBADJ.

While point estimates are useful in giving the picture of the magnitude of the difference, confidence intervals (CI) are highly important in decision making. A comparison of adjusted confidence intervals provided with the RCTdesign package in R (Emerson *et al*, 2012), to the likelihood based confidence intervals, obtained by using observed variance as precision estimates, indicates that their coverage probabilities are comparable. The coverage probabilities were (94.6%, 94.6%, 97.6%) for the adjusted CI and (93.8%, 92.8%, 96.8%) for MLE based CI, for the three settings in the order of increasing sample size. Using the same design parameters, we also investigated the type I error rate for MLE and adjusted estimators, by setting  $\theta_1 = 0$  and obtaining the percentage times the confidence interval does not contain zero. Type I error rates for likelihood based CI were (5.6%, 6.4%, 2.8%), which are similar to those based on adjusted CIs, (5.4%, 4.8%, 2.8%) for the three settings in the order of increasing sample size. Certainly, using either of the CIs will lead to similar conclusions, which makes the simpler and well known sample average a good estimator candidate for analysis after group

sequential trials.

At first sight, it looks like there may be less practical interest, given this similarity. However, the implications should not be underestimated. There is a general feeling that adjustments need to be made. As is clear from earlier work in the literature and from this manuscript, corrections are computationally challenging. In contrast, the standard joint likelihood estimator being the ordinary sample average, is extremely simple. Thus, our results may simplify calculations in important ways. We also explore the bias of each of the estimators at the sample level in contrast to the averaged bias as presented in Table 1. Recall that we had 500 samples for each setting, Table 2 gives the proportion of samples whose estimates' relative bias fell into a specified category. The CLE had a reverse trend of the other estimators where a only few estimated had large bias. Indeed, it is hard to pick a preferred estimator among the others estimators based on these results since each of the estimator has about 75% of the estimates having relative bias of > 10%. It is also clear from Figure 1, which plot the difference in relative bias, between each of the bias adjusted estimates and MLE, that none of the estimates discussed above is uniformly unbiased in comparison to MLE, i.e is some instances MLE may do better.

**Table 1:** Mean estimates (Est.) and relative bias (R.Bias) for the three different settings of O'Brien and Fleming's design. Parameters common to all the three settings include, power=90%, type I error=0.025,  $H_0: \theta = 0$  vs.  $H_1: \theta = \theta_1 > 0$ , where only the detectable difference ( $\theta_1$ ) was changed to initiate change in maximum sample size (Size). MLE is the maximum likelihood estimate, BAM is the bias-adjusted maximum likelihood estimator, RBADJ is the Rao bias-adjusted estimator, MUE is the median unbiased estimator, and CLE is the conditional likelihood estimator.

	Ν	ЛГЕ	В	AM	RE	BADJ	Ν	/IUE	C	LE
Size	Est.	R.Bias								
176	0.5448	(0.0895)	0.5142	(0.0285)	0.5019	(0.0037)	0.5251	(0.0502)	0.5026	(0.0052)
702	0.2665	(0.0661)	0.2508	(0.0031)	0.2473	(0.0108)	0.2557	(0.0228)	0.2476	(0.0094)
1949	0.1595	(0.0635)	0.1489	(0.0070)	0.1469	(0.0209)	0.1520	(0.0130)	0.1511	(0.0071)

**Table 2:** Results from three different settings of O'Brien and Fleming's design. Parameters common to all three settings include: power=90%, type I error=0.025,  $H_0: \theta = 0$  vs.  $H_1: \theta = \theta_1 > 0$ , where only the detectable difference ( $\theta_1$ ) was changed to initiate change in maximum sample size (Size). Out of 500 datasets generated for each setting, we compare the percentage of estimates (Prop. as a percentage) whose relative bias falls in the specified range (R.Bias as a percentage). MLE is the maximum likelihood estimate, BAM is the biased adjusted maximum likelihood estimator, RBADJ is Rao's bias-adjusted estimator, MUE is the median unbiased estimator, and CLE is the conditional likelihood estimator.

			Pro	op.(%)		
$ heta_1(Size)$	R.Bias(%)	BAM	RBADJ	MUE	MLE	CLE
0.5(176)	$\leq 0.99$	2.6	2.0	2.2	2.2	76.3
	1 - 4.99	8.4	11.4	11.0	10.6	13.2
	5 - 10	10.6	11.6	12.6	15.0	7.9
	> 10	78.4	75.0	74.2	72.2	2.6
0.25(702)	$\leq 0.99$	2.0	3.2	1.4	2.6	81.3
	1 - 4.99	7.2	9.0	8.8	9.0	12.5
	5 - 10	9.4	9.8	10.8	9.8	2.1
	> 10	81.4	78.0	79.0	78.6	4.2
0.15(1949)	$\leq 0.99$	2.6	1.8	1.4	2.2	55.6
	1 - 4.99	7.4	13.2	8.0	13.2	33.3
	5 - 10	9.2	9.0	11.8	11.0	8.9
	> 10	80.8	76.0	77.6	74.4	2.2

# 9 Concluding Remarks

As a result of the bias associated with joint maximum likelihood estimators following sequential trials, much work has been applied to providing alternative estimators. The origin of the problem lies with the incompleteness of the sufficient statistic for the mean parameter (Lehman, 1950), implying, among others, that there is no best unbiased linear mean estimator.

Using stochastic stopping rules, which encompass the deterministic stopping rules used in sequential trials as special cases, we have studied the properties of joint maximum likelihood estimators afresh,

in an attempt to enhance our understanding of the behavior of estimators (for both bias and precision) based on data from such studies. We have focused on one-parameter exponential family distributions, which encompasses several response types, including but not limited to binary, normal, Poisson, exponential, and time-to-event data.

First, the incompleteness of the sufficient statistic when using a stochastic stopping rule has been established. Using a generalized sample average, it is noted that in almost no case is there an unbiased estimator. Even when such an estimator does exist, with a completely random sample size, it cannot be uniformly best.

Second, there exist an unbiased estimator resulting from the likelihood of the observed data conditional on the sample size. While appealing, the conditional estimator is computationally more involved, because there is no closed-form solution. Although for a sequential trial with a deterministic stopping rule, the ordinary sample average is finite-sample biased, it can be been shown both directly and through likelihood arguments, that it is asymptotically unbiased and so remains a good candidate for practical use. Further, it is computationally trivial, has a correspondingly simple estimator of precision, derived from the observed information matrix and hence a well behaved asymptotic likelihood-based confidence interval. In addition, the mean square error of the sample average is smaller than that of the estimator based on the conditional likelihood. Asymptotically, the mean square errors of both estimators converge.

Third, there is the subtle issue that the sample average may be asymptotically biased for certain stopping rules, when its expectation is considered conditionally on certain values of the sample size. However, this is not a real practical problem because this occurs only for sample sizes that have asymptotic probability zero of being realized. We placed emphasis on joint and conditional likelihood estimators. While in the former the stopping rule is less present than sometimes thought, it is not in the latter. Also, when alternative frequentist estimators are considered, the stopping rule is likely to play a role in synchrony with the rule's influence on hypothesis testing due to the duality between hypothesis testing and confidence intervals.

While in some circumstances other sources of inaccuracy may overwhelm the issue studied here, we believe that it is useful to bring forward implications of our findings for likelihood-based estimation. Our findings, especially for the simulations in the Appendix, indicate that bias decreases relatively rapidly with sample size, but there are subtle differences depending on stopping rule considered. In

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this sense, fixed rules are different from Z-statistic based rules (Emerson 1988, p. 5; Jennison and Turnbull, 2000).

In conclusion, the sample average is a very sensible choice for point, precision, and interval estimation following a sequential trial.

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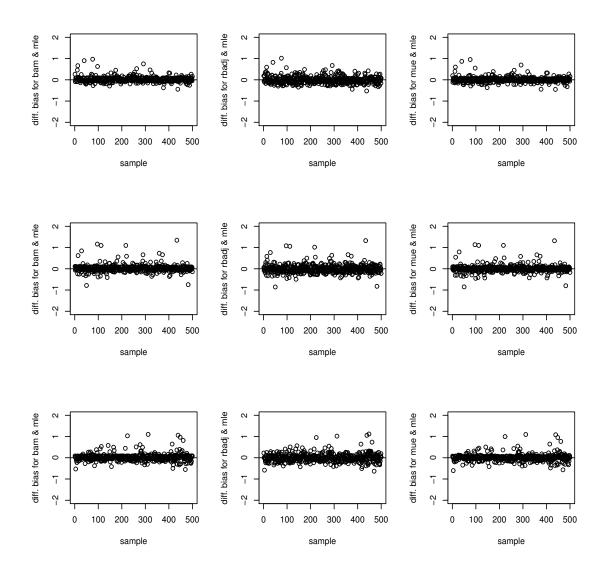
# References

Armitage, P. (1975) Sequential Medical Trials. Oxford: Blackwell.

- Bassler, D., Briel, M., Montori, V. M., Lane, M., Glasziou, P., Zhou, Q., Heels-Ansedell, D., Walter, S.D., Guyatt, G.H. and the STOPIT-2 Study Group. (2010). Stopping randomized trials early for benefit and estimation of treatment effects. Systematic review and meta-regression analysis. *Journal of the American Medical Association*,**303**, 1180–1187.
- Blackwell, D. (1947). Conditional expectation and unbiased sequential estimation. *Annals of Mathematical Statistics*, **18**,105-110.
- Casella, G. and Berger, R.L. (2001). Statistical Inference. Pacific Grove: Duxbury Press.
- Emerson, S.S. (1988). Parameter estimation following group sequential hypothesis testing. *PhD dissertation*. University of Washington.
- Emerson, S.S. and Fleming, T.R. (1990). Parameter estimation following group sequential hypothesis testing. *Biometrika*, **77**, 875–892.
- Emerson, S.S., Gillen, D.L., Kittelson, J.K., Emerson, S.C., and Levin, G.P (2012). RCTdesign: Group Sequential Trial Design. R package version 1.0.
- Hughes, M.D. and Pocock, S.J. (1988). Stopping rules and estimation problems in clinical trials. *Statistics in Medicine*, **7**, 1231–1242.

- Jennison, C. and Turnbull, B.W (2000). Group Sequential Methods With Applications to Clinical Trials. London: Chapman & Hall/CRC.
- Kenward, M.G. and Molenberghs, G. (1998) Likelihood based frequentist inference when data are missing at random. *Statistical Science*, **13**, 236–247.
- Lehmann, E.L. and Stein, C. (1950). Completeness in the sequential case. *Annals of Mathematical Statistics*, **21**, 376–385.
- Liu, A. and Hall, W.J. (1999). Unbiased estimation following a group sequential test. *Biometrika*, **86**, 71–78.
- Liu, A., Hall, W.J., Yu, K.F., and Wu, C. (2006). Estimation following a group sequential test for distributions in the one-parameter exponential family. *Statistica Sinica*, **16**, 165–81.
- Milanzi, E., Molenberghs, G., Alonso, A., Kenward, M.G., Aerts, M., Verbeke, G., Tsiatis, A.A., and Davidian, M. (2012). Properties of estimators in exponential family settings with observation-based stopping rules. *Submitted for publication*.
- Molenberghs, G., Kenward, M.G., Aerts, M., Verbeke, G., Tsiatis, A.A., Davidian, M., Rizopoulos, D. (2012). On random sample size, ignorability, ancillarity, completeness, separability, and degeneracy: sequential trials, random sample sizes, and missing data. *Statistical Methods in Medical Research*, 00, 000–000.
- Rosner, G.L. and Tsiatis, A.A. (1988). Exact confidence intervals following a group sequential trial: A comparison of methods. *Biometrika*, **75**, 723–729.
- Siegmund, D. (1978). Estimation following sequential tests. *Biometrika*, **64**, 191–199.
- Tsiatis, A.A., Rosner, G.L., and Mehta, C.R. (1984). Exact confidence intervals following a group sequential test. *Biometrics*, **40**, 797–803.
- Todd, S., Whitehead, J., and Facey, K.M. (1996). Point and interval estimation following a sequential clinical trial. *Biometrika*, **83**, 453–461.
- Wald, A. (1945). Sequential tests of statistical hypotheses. *The Annals of Mathematical Statistics*, 16, 117-186.

- Whitehead, J. (1997). The Design and Analysis of Sequential Clinical Trials (2nd ed.). New York: John Wiley & Sons.
- Whitehead, J. (1999). A unified theory for sequential clinical trials. *Statistics in Medicine*, **18**, 2271–2286.



**Figure 1:** Difference in relative bias between MLE and each the biased adjusted estimates (BAM, RBADJ and MUE). The first row is for  $\theta_1 = 0.5$ , second row,  $\theta_1 = 0.25$  and third row, |

# **Estimation After a Group Sequential Trial**

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# **Supplementary Materials**

These Supplementary Materials contain a full description of the additional simulation settings and results where we consider different forms of the stopping rule and study asymptotic unbiasedness and mean square error for both joint and conditional likelihood.

# A Simulation Study

## A.1 Design

This simulation study has been designed to corroborate the theoretical findings on the behavior of joint and conditional likelihood estimators. For this it is sufficient to take a sequential trial setting in which N can take two possible sample sizes: N = n or N = 2n. For the first set of simulations, we generate  $Y_i \sim N(\mu, 1)$ , (i = 1, ..., n), after which  $F = \Phi(\alpha + \beta k/n)$  is evaluated. The decision to stop or continue is reached by generating  $Q \sim U(0, 1)$ . If  $Q \leq F$ , then the trial is stopped, otherwise we generate another  $Y_i \sim N(\mu, 1)$  i = n + 1, ..., 2n. Finally, the estimate of  $\mu$  is obtained by maximizing the relevant likelihood (joint or conditional). The following values were chosen:  $\mu = 2$ ; 4; 10 and n = 25; 50; 250; 500; 5000. Values of  $\alpha$  and  $\beta$  were fixed at 0.1 and 0.01, respectively. A total of one million simulations were done for each setting, to ensure that even very small effects could be detected.

In the second set of simulations, the stopping rule is changed to  $F = \Phi(\alpha + \beta k)$ , for which the

conditional expectation of the SA may grow without bound.

#### A.2 Results

In Tables 3 and 4, we present the operational characteristics of the mean estimators from the joint and conditional likelihood respectively, for the stopping rule of the form  $F = \Phi (\alpha + \beta k/n)$ . The magnitude of both bias and MSE are comparable between the two tables, supporting the theoretical findings that the sample average is asymptotically unbiased and that the MSEs converge as sample size increases. A further set of simulation results is provided in Supplementary Materials A.

Tables 5 and 6 are the counterparts for stopping rule  $F = \Phi(\alpha + \beta k)$ . Note that there are fewer entries in Table 5, because, for larger sample sizes, the probability of stopping at N = n decreases, to the extent that not enough data remain to meaningfully complete the simulations. Though not very extreme, the magnitude of relative bias is noticeably higher for N = n than for N = 2n. The good news is that, overall, the marginal estimate will be driven by cases stopping at N = 2n, whose estimates have a very small bias and small MSE.

### **B** Simulation Study for Stopping Rule $\Phi(\alpha + \beta k)$

## **B.1 Simulation Settings**

The results presented in this section are from the simulation study run with the purpose of investigating the behavior of the joint and conditional likelihood estimators in non-fixed sample size trials. The sample size N can take the values n and 2n.

Specifically, we generated  $Y_i \sim N(\mu, 1)$   $i = 1 \dots n$ , from which  $F = \Phi(\alpha + \beta k)$  is calculated, with  $K = \sum_{i=1}^{n} Y_i$ . The decision to stop or continue is reached by generating  $Q \sim U(0, 1)$  and that if  $Q \leq F$ , the trial stops, otherwise we generate another  $Y_i \sim N(\mu, 1)$   $i = n + 1 \dots 2n$ . Finally the estimate of  $\mu$  is obtained by maximizing the relevant likelihood (joint or conditional). The following values were considered:  $\mu = 2; 4; 10$  and n = 25; 50; 250; 500; 5000. To also allow for small effects to show up, a total of 1 million simulations were done for each setting.

#### **B.2 Simulation Results**

The results indicate small biases in all cases, the highest bias value being 0.1%, which comes from the conditional likelihood estimator for N = 25 and  $\mu = 2$ . In general, though, the conditional likelihood

**Table 3:** Estimates were obtained by maximizing the joint likelihood (sample average) and averaging was done over estimates from all the simulated samples; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9997	.00014	0.02904	1.67065	2.3288
50	2	2.0001	.00007	0.01452	1.76743	2.2329
250	2	1.9999	.00005	0.00291	1.89581	2.1040
500	2	2.0000	.00001	0.00145	1.92638	2.0736
5000	2	2.0000	.00001	0.00015	1.97675	2.0233
25	4	3.9998	.00006	0.02888	3.67160	4.3279
50	4	4.0001	.00002	0.01444	3.76801	4.2322
250	4	4.0001	.00002	0.00289	3.89630	4.1038
500	4	4.0000	.00001	0.00144	3.92663	4.0734
5000	4	4.0000	.00000	0.00014	3.97681	4.0232
25	10	9.9997	.00003	0.02841	9.67427	10.3252
50	10	10.0001	.00001	0.01421	9.76993	10.2303
250	10	10.0001	.00001	0.00284	9.89715	10.1030
500	10	10.0000	.00000	0.00142	9.92723	10.0728
5000	10	10.0000	.00000	0.00014	9.97700	10.0230

**Table 4:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits, respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9997	.00031	0.02904	1.67061	2.3288
50	2	2.0001	.00010	0.01454	1.76728	2.2329
250	2	2.0000	.00000	0.00290	1.89594	2.1041
500	2	2.0001	.00006	0.00713	1.85669	2.1434
5000	2	2.0000	.00001	0.00015	1.97675	2.0233
25	4	4.0000	.00004	0.02888	3.67186	4.3282
50	4	4.0001	.00013	0.01445	3.76798	4.2323
250	4	4.0000	.00000	0.00289	3.89622	4.1038
500	4	4.0001	.00005	0.00144	3.92666	4.0734
5000	4	4.0000	.00001	0.00014	3.97681	4.0232
25	10	10.0000	.00004	0.02841	9.67458	10.3255
50	10	10.0001	.00010	0.01422	9.76984	10.2304
250	10	10.0000	.00002	0.00284	9.89709	10.1029
500	10	10.0001	.00005	0.00142	9.92726	10.0728
5000	10	10.0000	.00001	0.00014	9.97700	10.0230

**Table 5:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples where we stopped at N = n; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits, respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.98573	0.00714	0.04009	1.59438	2.3771
50	2	1.95704	0.02148	0.02062	1.68982	2.2243
250	2	1.90287	0.04856	0.01343	1.77891	2.0268
25	4	3.97778	0.00555	0.04022	3.58737	4.3682
50	4	3.85891	0.03527	0.03438	3.62663	4.0912
25	10	9.97525	0.00248	0.04061	9.58325	10.3673

estimator shows little or no bias. For the sample average, comparing the overall results with the ones conditional on sample size, reveals that the bias is slightly higher in the conditional estimates than the marginal ones for the small sample size. The asymptotic behavior of bias is in line with theory, given that it decreases with increasing sample size. Loss of information in the conditional estimates is noticeable but very small in the settings studied, again in line with theory.

Details are provided in Tables 13-18.

# **C** Simulation Study for Stopping Rule $\Phi(\alpha + \beta k/n)$

#### C.1 Simulation Settings

The results presented here are from a simulation study run with the purpose of investigating the behavior of joint and conditional likelihood estimators in non-fixed sample size trials. In contrast to Section B.1 the stopping rule is now  $F = \Phi\left(\alpha + \beta \frac{k}{n}\right)$ . All other settings are as in Section B.1.

#### C.2 Simulation Results

The results show small biases in all cases, the highest bias value being 0.1%, which comes from the conditional likelihood estimate for N = 25 and  $\mu = 2$ , though in general the conditional likelihood

**Table 6:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples where we continued to N = 2n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $\frac{|(\mu - \hat{\mu})|}{\mu}$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits, respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	2.0033	.00166	0.02001	1.72613	2.2805
50	2	2.0067	.00332	0.01004	1.81065	2.2027
250	2	2.0001	.00003	0.00200	1.91241	2.0877
500	2	2.0000	.00002	0.00100	1.93805	2.0620
5000	2	2.0000	.00001	0.00010	1.98041	2.0196
25	4	4.0025	.00061	0.02001	3.72526	4.2796
50	4	4.0057	.00144	0.01003	3.80974	4.2017
250	4	4.0001	.00002	0.00200	3.91241	4.0877
500	4	4.0000	.00001	0.00100	3.93805	4.0620
5000	4	4.0000	.00000	0.00010	3.98041	4.0196
25	10	10.0003	.00002	0.02000	9.72306	10.2774
50	10	10.0001	.00000	0.01000	9.80405	10.1961
250	10	10.0001	.00001	0.00200	9.91241	10.0877
500	10	10.0000	.00000	0.00100	9.93805	10.0620
5000	10	10.0000	.00000	0.00010	9.98041	10.0196

**Table 7:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9985	.00077	0.02550	1.68972	2.3072
50	2	1.9990	.00052	0.01136	1.79192	2.2060
250	2	2.0001	.00003	0.00200	1.91241	2.0877
500	2	2.0000	.00002	0.00100	1.93805	2.0620
5000	2	2.0000	.00001	0.00010	1.98041	2.0196
25	4	3.9991	.00024	0.02272	3.70628	4.2918
50	4	3.9998	.00004	0.01018	3.80238	4.1973
250	4	4.0001	.00002	0.00200	3.91241	4.0877
500	4	4.0000	.00001	0.00100	3.93805	4.0620
5000	4	4.0000	.00000	0.00010	3.98041	4.0196
25	10	10.0001	.00001	0.02009	9.72242	10.2779
50	10	10.0001	.00000	0.01000	9.80405	10.1961
250	10	10.0001	.00001	0.00200	9.91241	10.0877
500	10	10.0000	.00000	0.00100	9.93805	10.0620
5000	10	10.0000	.00000	0.00010	9.98041	10.0196

**Table 8:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples where we stopped at N = n; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.98573	0.00714	0.04009	1.59438	2.3771
50	2	1.95704	0.02148	0.02062	1.68982	2.2243
250	2	1.90287	0.04856	0.01343	1.77891	2.0268
25	4	3.97778	0.00555	0.04022	3.58737	4.3682
50	4	3.85891	0.03527	0.03438	3.62663	4.0912
25	10	9.97525	0.00248	0.04061	9.58325	10.3673

estimator shows little or no bias. Comparing the marginal and conditional estimators for the sample average reveals that the bias is slightly higher in the conditional estimators than the marginal ones for the small sample size. Also here, the asymptotic behavior of the bias is in line with that expected from the theoretical developments, as it decreases with increasing sample size. Loss of information in the conditional estimator is discernable but small.

The results are presented in Tables 13-18.

**Table 9:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples where we continued to N = 2n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	2.0033	.00166	0.02001	1.72613	2.2805
50	2	2.0067	.00332	0.01004	1.81065	2.2027
250	2	2.0001	.00003	0.00200	1.91241	2.0877
500	2	2.0000	.00002	0.00100	1.93805	2.0620
5000	2	2.0000	.00001	0.00010	1.98041	2.0196
25	4	4.0025	.00061	0.02001	3.72526	4.2796
50	4	4.0057	.00144	0.01003	3.80974	4.2017
250	4	4.0001	.00002	0.00200	3.91241	4.0877
500	4	4.0000	.00001	0.00100	3.93805	4.0620
5000	4	4.0000	.00000	0.00010	3.98041	4.0196
25	10	10.0003	.00002	0.02000	9.72306	10.2774
50	10	10.0001	.00000	0.01000	9.80405	10.1961
250	10	10.0001	.00001	0.00200	9.91241	10.0877
500	10	10.0000	.00000	0.00100	9.93805	10.0620
5000	10	10.0000	.00000	0.00010	9.98041	10.0196

**Table 10:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	2.0069	0.00687	0.02560	1.69777	2.3160
50	2	2.0195	0.01951	0.01182	1.81170	2.2273
25	4	4.0196	0.01961	0.02318	3.72629	4.3129
50	4	4.0423	0.04227	0.01206	3.84389	4.2406
25	10	10.0527	0.05272	0.02295	9.77448	10.3310

**Table 11:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples where we stopped at N = n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.98129	0.01871	0.04029	1.58970	2.3729
50	2	1.95747	0.04253	0.02062	1.68994	2.2250
25	4	3.97558	0.02442	0.04035	3.58500	4.3662
50	4	3.88135	0.11865	0.02860	3.64853	4.1142
25	10	9.97511	0.02489	0.04062	9.58309	10.3671

**Table 12:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples where we continued to N = 2n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	2.0166	0.01661	0.02035	1.73890	2.2943
50	2	2.0309	0.03089	0.01104	1.83403	2.2277
25	4	4.0266	0.02664	0.02080	3.74884	4.3044
50	4	4.0490	0.04901	0.01250	3.85207	4.2459
25	10	10.0531	0.05308	0.02289	9.77537	10.3308

**Table 13:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9997	.00014	0.02904	1.67065	2.3288
50	2	2.0001	.00007	0.01452	1.76743	2.2329
250	2	1.9999	.00005	0.00291	1.89581	2.1040
500	2	2.0000	.00001	0.00145	1.92638	2.0736
5000	2	2.0000	.00001	0.00015	1.97675	2.0233
25	4	3.9998	.00006	0.02888	3.67160	4.3279
50	4	4.0001	.00002	0.01444	3.76801	4.2322
250	4	4.0001	.00002	0.00289	3.89630	4.1038
500	4	4.0000	.00001	0.00144	3.92663	4.0734
5000	4	4.0000	.00000	0.00014	3.97681	4.0232
25	10	9.9997	.00003	0.02841	9.67427	10.3252
50	10	10.0001	.00001	0.01421	9.76993	10.2303
250	10	10.0001	.00001	0.00284	9.89715	10.1030
500	10	10.0000	.00000	0.00142	9.92723	10.0728
5000	10	10.0000	.00000	0.00014	9.97700	10.0230

**Table 14:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples where we stopped at N = n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	2.0005	.00026	0.0200	1.72333	2.2777
50	2	2.0002	.00009	0.0100	1.80418	2.1962
250	2	2.0001	.00006	0.0020	1.91246	2.0878
500	2	2.0001	.00002	0.0010	1.93807	2.0620
5000	2	2.0000	.00000	0.0001	1.98041	2.0196
25	4	4.0003	.00007	0.0200	3.72309	4.2775
50	4	4.0001	.00003	0.0100	3.80412	4.1961
250	4	4.0001	.00001	0.0020	3.91240	4.0877
500	4	4.0000	.00001	0.0010	3.93806	4.0620
5000	4	4.0000	.00000	0.0001	3.98041	4.0196
25	10	10.0004	.00004	0.0200	9.72320	10.2776
50	10	10.0002	.00002	0.0100	9.80421	10.1962
250	10	10.0001	.00001	0.0020	9.91240	10.0877
500	10	10.0000	.00000	0.0010	9.93805	10.0620
5000	10	10.0000	.00000	0.0001	9.98041	10.0196

**Table 15:** Estimates were obtained by maximizing the joint likelihood and averaging was done over estimates from all the simulated samples where we continued to N = 2n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9994	.00031	0.03291	1.64807	2.3507
50	2	2.0001	.00006	0.01646	1.75168	2.2486
250	2	1.9998	.00009	0.00330	1.88866	2.1110
500	2	2.0000	.00002	0.00165	1.92137	2.0786
5000	2	2.0000	.00001	0.00016	1.97518	2.0249
25	4	3.9995	.00012	0.03287	3.64846	4.3506
50	4	4.0001	.00002	0.01643	3.75188	4.2483
250	4	4.0001	.00002	0.00328	3.88910	4.1111
500	4	4.0000	.00000	0.00164	3.92154	4.0785
5000	4	4.0000	.00000	0.00016	3.97521	4.0248
25	10	9.9994	.00006	0.03265	9.64959	10.3492
50	10	10.0001	.00001	0.01634	9.75262	10.2475
250	10	10.0001	.00001	0.00327	9.88944	10.1107
500	10	10.0000	.00000	0.00163	9.92178	10.0783
5000	10	10.0000	.00000	0.00016	9.97529	10.0248

**Table 16:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples; n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9997	.00031	0.02904	1.67061	2.3288
50	2	2.0001	.00010	0.01454	1.76728	2.2329
250	2	2.0000	.00000	0.00290	1.89594	2.1041
500	2	2.0001	.00006	0.00713	1.85669	2.1434
5000	2	2.0000	.00001	0.00015	1.97675	2.0233
25	4	4.0000	.00004	0.02888	3.67186	4.3282
50	4	4.0001	.00013	0.01445	3.76798	4.2323
250	4	4.0000	.00000	0.00289	3.89622	4.1038
500	4	4.0001	.00005	0.00144	3.92666	4.0734
5000	4	4.0000	.00001	0.00014	3.97681	4.0232
25	10	10.0000	.00004	0.02841	9.67458	10.3255
50	10	10.0001	.00010	0.01422	9.76984	10.2304
250	10	10.0000	.00002	0.00284	9.89709	10.1029
500	10	10.0001	.00005	0.00142	9.92726	10.0728
5000	10	10.0000	.00001	0.00014	9.97700	10.0230

**Table 17:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples where we stopped at N = n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	1.9988	.00118	0.04000	1.60682	2.3908
50	2	1.9999	.00006	0.02000	1.72276	2.2771
250	2	1.9999	.00007	0.00400	1.87597	2.1239
500	2	2.0000	.00002	0.01001	1.82802	2.1720
5000	2	2.0000	.00003	0.00020	1.97232	2.0278
25	4	3.9995	.00055	0.04000	3.60745	4.3915
50	4	4.0002	.00017	0.02000	3.72298	4.2774
250	4	3.9998	.00016	0.00400	3.87588	4.1238
500	4	4.0000	.00003	0.00200	3.91238	4.0877
5000	4	4.0000	.00003	0.00020	3.97231	4.0278
25	10	9.9993	.00068	0.04000	9.60732	10.3913
50	10	10.0001	.00012	0.02000	9.72293	10.2773
250	10	9.9999	.00014	0.00400	9.87590	10.1238
500	10	10.0000	.00003	0.00200	9.91238	10.0877
5000	10	10.0000	.00004	0.00020	9.97232	10.0278

**Table 18:** Estimates were obtained by maximizing the conditional likelihood and averaging was done over estimates from all the simulated samples where we continued to N = 2n, n is the sample size generated at a particular stage,  $\mu$  is the true mean,  $\hat{\mu}$  is the average estimated mean, Rel. bias= $|(\mu - \hat{\mu})|/\mu$ , 'MSE' is the mean square error and 'lower' and 'upper' are the lower and upper confidence interval limits respectively, obtained as  $\hat{\mu} \pm 1.96\hat{\sigma}$ .

n	$\mu$	$\widehat{\mu}$	Rel. bias	MSE	lower	upper
25	2	2.0004	.00041	0.02000	1.72322	2.2776
50	2	2.0002	.00023	0.01000	1.80423	2.1962
250	2	2.0001	.00006	0.00200	1.91241	2.0877
500	2	2.0001	.00009	0.00515	1.87638	2.1238
5000	2	2.0000	.00000	0.00010	1.98040	2.0196
25	4	4.0005	.00051	0.02000	3.72332	4.2777
50	4	4.0001	.00011	0.01000	3.80411	4.1961
250	4	4.0001	.00013	0.00200	3.91247	4.0878
500	4	4.0001	.00006	0.00100	3.93808	4.0620
5000	4	4.0000	.00000	0.00010	3.98040	4.0196
25	10	10.0006	.00057	0.02000	9.72338	10.2778
50	10	10.0001	.00008	0.01000	9.80408	10.1961
250	10	10.0001	.00013	0.00200	9.91248	10.0878
500	10	10.0001	.00006	0.00100	9.93808	10.0620
5000	10	10.0000	.00000	0.00010	9.98040	10.0196