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HYPERADMISSIBILITY OF ESTIMATORS FOR FINITE POPULATIONS

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1. Introduction. This note deals with a point arising from the recently published paper of Hanurav (1968). Defining the notion of hyperadmissibility for estimators for finite populations, Hanurav proves that (i) if the sampling design is a non-unicluster design, then the Horvitz Thomson estimator (H-T estimator for short) for the population total is the unique unbiased and hyperadmissible estimator, in the class of all polynomial estimators; he further claims to prove that (ii) if the sampling design is a unicluster design there is always a class of unbiased hyperadmissible estimators. Hanurav has also expressed the conjecture that his result (i) is probably true for the entire class of unbiased estimators of the population total.

We show that (ii) is false; for any unicluster design which has three or more clusters, the H–T estimator is the unique hyperadmissible estimator. Thus for obtaining a unique hyperadmissible estimator, the restraint on the sampling design of non-uniclusterness is not the correct one. A revised condition if formulated, and it is shown that if the sampling design satisfies this revised condition, then the H–T estimator is (as conjectured by Hanurav), the unique hyperadmissible estimator in the entire class of all unbiased estimators of the population total.

The revised restraint on the sampling design is a mild one, which would be satisfied for most designs—whether unicluster or non-unicluster—met with in practical work. For the remaining cases of non-unicluster designs, which do not satisfy the revised condition, Hanurav's result (i) continues to apply, but even in these cases, the restriction to polynomial estimators is unnecessary, and the result remains valid if the class of estimators is restricted only by requiring that the estimators should be continuous functions of the variate values at the single point at which all the variate values vanish.

2. Notation. For convenience we use the same notation and definitions as Hanurav. For ready reference the notation and the relevant definitions are briefly reproduced here. The population $\mathscr{U}$ consists of distinct units $U_1, U_2, \cdots, U_N$. A sample s is a finite, ordered, sequence of units, not necessarily distinct, drawn from $\mathscr{U}$. S is the set of all possible samples s. A sampling design P (or more briefly a design) is determined by defining a probability P on S. P_s denotes the probability of the sample s when the sampling design is P. $\mathscr{Y}$ is a real variable defined on $\mathscr{U}$ which takes the value Y_i on U_i, $i = 1, 2, \cdots, N$. Y denotes the population total of the $\mathscr{Y}$-values, i.e.

(1) $$Y = \sum_{i=1}^{i=N} Y_i$$

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