

MULTIPLE RANDOM START SYSTEMATIC SAMPLING: AN EMPIRICAL STUDY

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I. INTRODUCTION

Suppose we are interested in estimating the population total Y of a population with an intrinsic ordering $Y(1), Y(2), \dots, Y(k), \dots, Y(N)$, based on a sample size n . For simplicity, throughout the paper we will assume that $N=nk$, where n is the desired sample size and k is the sampling interval. Several systematic sampling designs with similar sampling fraction can be compared based on the "true" variance of the estimate and the MSE of the variance estimate. A single random start systematic sample of n elements is drawn by selecting one element at random from the first k elements and thereafter selecting every k^{th} element. Single random start (SRS) systematic sampling is widely used in major surveys and national censuses, mainly due to its administrative benefits. The major liability associated with this sampling procedure is that the variance of the estimate can not be unbiasedly estimated from the sample itself. It is natural to compare SRS systematic sampling with possible competitors within its family. Let now consider a procedure which appears to have been suggested by J. Tukey[1].

Select a simple random sample of size h (without replacement) from the first kh elements and then every kh^{th} element following those that were initially selected. Using this procedure a sample of size n is selected. This sampling procedure is evidently equivalent to drawing a simple random sample of size h from the kh clusters $C_j, j = 1, 2, \dots, kh$. It, therefore, follows that this procedure yields an unbiased estimate of the variance from the sample at the cost of some (perhaps negligible) increase in the "true" variance of the estimates. For the 1980 Decennial Census, single random start systematic sampling was used. The variance estimation method recommended and used was the random groups method, using 25 systematic subsamples. A major problem with the random group variance estimator (and other resampling methods like Jackknife) is that the bias is relatively large for a large number of census data items. Furthermore, the bias is generally the major component of the total MSE of the random groups variance estimator[2,3].

In this paper, we examined the alternative of using MRS systematic sampling as a way of reducing the bias of the census variance estimates.

One hundred and twenty 1980 tracts comprised the empirical study population. These tracts were contained in 16 counties (in 7 states) with a high concentration of minorities[4]. The geo-

graphic level for which estimates were produced is defined as the 1980 tract. Housing units within each tract were divided into all possible systematic samples for $(h=1,2,\dots,10)$ for a 1-in-6 systematic sampling design. Two basic sampling designs were simulated, single random start ($h=1$) and multiple random start ($h=2,3,\dots,10$) systematic sampling. The variance estimation procedure was independently performed for each tract and for each sample.

2. STUDY POPULATION

A study population consisting of counties with minority race concentration was generated. This study population was comprised of counties which have at least 16 percent nonwhite and 6 percent Hispanic or 11 percent Black and 6 percent Hispanic. A total of 153 counties and 22 percent of the 1980 U.S. population were included in the study population. A two-stage sampling scheme was designed to select a sample of 120 census tracts, which constitute the unit of analysis in this study.

2.1. Source of Data and Characteristics

The source of data for this study was the 1980 100-Percent Edited Detail File. From this data file, a tract population was created using the 100-percent housing unit records within the sample tracts. The relative increase in the true variance of the estimate resulting from the use of MRS systematic sampling is a function of the homogeneity (autocorrelation) between "neighbors" in the geographic area of interest. Homogeneity is a function of distance, it is reasonable to expect that the closer two units the more alike they will be. Therefore, we decided to use 100-percent data because using sample data (units are farther apart, lower autocorrelation) would have created a bias against single random start systematic sampling. If sample data had been used then the autocorrelation would have been decreased introducing a bias in favor of MRS[1]. Estimates were produced at the tract level for several 100-percent data items, such as (1) counts by race/Hispanic origin, (2) marital status, (3) rent/value, (4) tenure, and (5) substituted persons (as a proxy for small size data items).

2.2. Sample Size Determination

From the beginning it was decided that the Friedman test, or the Thompson-Willke's nonparametric multiple comparison test was to be used to evaluate the different systematic sampling designs. The basic idea of the Friedman test is

that the difference between the rank sums is a result of the difference between the (sampling designs) treatments. Despite the lower efficiency of the Friedman test, it is very useful and a versatile technique. Independence between each tract was assumed. Basically, the Friedman test was implemented in this study as follows. The systematic sampling designs were first ranked by the magnitude of various statistics (e.g., the MSE or the variance) within each tract. Then, a rank sum was obtained for each systematic sampling design by adding the ranks over all tracts.

The Friedman test statistics is a function of

k - the total number of sampling design to be compared,

v - the total number of tracts,

\bar{R}_i - the average rank of the i^{th} sampling design, and

\bar{R}_j - the average rank of the j^{th} sampling design.

The Friedman test statistic follows a chi-square distribution with $k-1$ degrees of freedom. To determine how large the sample of tracts should be so that under the null hypothesis of no difference among the treatments the probability is $(1-\alpha)$ that all absolute values of D_{ij} , the absolute pairwise mean rank difference, will not exceed a constant d , we determined v such that

$$P \left[\begin{matrix} \text{All} \\ H_0 \text{ is} \end{matrix} \mid \bar{R}_i - \bar{R}_j \leq d \right] = 1 - \alpha \dots (1)$$

$$d = q_{k,\infty}^{\alpha} \left[\frac{k(k+1)}{12v} \right]^{1/2} \dots (2)$$

where $q_{k,\infty}^{\alpha}$ is the upper α percentile point of the studentized range statistic. For $d = 1.25$ and $\alpha = 0.05$, $v = 120$.

2.3. Sample Selection [5]

A two-stage stratified systematic sampling design was used to select the sample of tracts. Prior to the first stage sampling, the study population (153 counties with minority concentration) was stratified on (1) Count of Blacks, (2) 1982 Unemployed, and (3) Final number of 1980 weighting areas[2]. The population of counties was systematically sampled at the rate of 1-in-10. For the second stage (selection of tracts within sample counties) there was a minimum size requirement for tracts. Contiguous tracts were collapsed, if necessary, such that the number of housing units was at least 800. Finally, an equal probability sample 120 tracts were systematically selected from within the 16 counties initially selected to be in the sample.

3. VARIANCE ESTIMATORS

We begin the discussion of variance estimators with a description of MRS systematic sampling. Define h as the desired number of random starts and $m=n/h$ is the size of each of the kh systematic clusters ($N=mhk$).

A simple random sample of h integers is selected from the integers $1, 2, \dots, kh$ with $k=6$. If integer i is selected, then, the i^{th} systematic sample (cluster) consists of the population elements $i^{\text{th}}, (i+kh)^{\text{th}}, (i+2kh)^{\text{th}}, \dots, (i+(m-1)kh)^{\text{th}}$. The population was divided into kh (i.e., $k=6$; $h=2$ to $h=10$) systematic samples. The structure of the kh systematic samples from the population is as follows.

Y_1	Y_{1+kh}	Y_{1+2kh}	\dots	$Y_{1+(m-1)kh}$
Y_2	Y_{2+kh}	Y_{2+2kh}	\dots	$Y_{2+(m-1)kh}$
\vdots	\vdots	\vdots	\dots	\vdots
\vdots	\vdots	\vdots	\dots	\vdots
Y_i	Y_{i+kh}	Y_{i+2kh}	\dots	$Y_{i+(m-1)kh}$
\vdots	\vdots	\vdots	\dots	\vdots
\vdots	\vdots	\vdots	\dots	\vdots
Y_{kh}	Y_{2kh}	Y_{3kh}	\dots	Y_{mkh}

Therefore, for $h=5$, the population will be divided into 30 systematic samples or clusters. Five integers are randomly selected from 1 to 30, then the systematic samples associated with the random integers are selected to be in the systematic sample. Thus, the sample size is $5m=5(n/5)=n=N/k$, the desired sample size.

Assume simple inflation estimation, then

$$\hat{Y}_i = \sum_{j=1}^{n_i} Y_{ij}, \quad \text{for single random start systematic sampling,} \dots (3)$$

and

$$\hat{Y}_{MRS|h} = 6 \sum_{p=1}^h Y_p [Y_p = \sum_{j=1}^m Y_{pj}; p=1, 2, \dots, 6h] \quad \text{for MRS,} \dots (4)$$

where

- Y_{ij} - Value of the characteristic for the j^{th} unit in the i^{th} cluster,
- n_i - Cluster size (SRS),
- m - Cluster size (MRS), and
- Y_p - p^{th} systematic sample total.

3.1. Single Random Start Systematic Sampling

The random group variance estimator was used to estimate the variance of the population total estimate. Each sample unit was systematically designated into one of 25 mutually exclusive random groups or subsamples.

The true variance of the population total estimate and the expected value of the random groups variance estimate for a given characteristic and tract were determined. The bias and the true var-

iance of the random groups variance estimate were calculated and finally the MSE was calculated.

3.2. Variance Estimators for MRS Systematic Sampling

The true variance of the population total estimate for each MRS systematic sampling design (i.e., $h=2,3,\dots,10$) was determined for each tract and characteristic as follows.

$$\text{Var}(\hat{Y}_{MRh}) = \frac{30h}{6h-1} \left[\sum_{p=1}^{6h} \left[Y_p - \frac{1}{6h} \sum_{p=1}^{6h} Y_p \right]^2 \right] \quad (5)$$

3.2.1 Unbiased Variance Estimator

An unbiased estimate of the variance of the population total estimate was determined as follows.

$$v_\ell(\hat{Y}_{MRh}) = \frac{30h}{h-1} \sum_{p=1}^h \left[Y_p - \frac{1}{h} \sum_{p=1}^h Y_p \right]^2; \quad (6)$$

$\ell=1,2,\dots,J$ and $h=2,3,\dots,10$.

The number of all possible samples (variance estimates) for a given h is given by

$$J = \binom{6h}{h}.$$

The true variance of the variance estimate for MRS systematic sampling is defined by the following expression.

$$\begin{aligned} & \text{Var} \left[v(\hat{Y}_{MRh}) \right] \\ &= \frac{1}{J} \sum_{\ell=1}^J \left[v_\ell(\hat{Y}_{MRh}) - \text{Var}(\hat{Y}_{MRh}) \right]^2 \quad (7) \end{aligned}$$

It is obvious that the cost of calculating the "true" variance of the variance estimate (for large h) becomes prohibitive very fast. As h increases J increases without limit.

For $h=3,4,\dots,10$, the "true" variance was estimated based on a simple random sample with replacement (size 200) from the population of all possible samples, for $h=2$, $J=66$, therefore, we calculated the true variance of the variance estimate.

Assuming that $v_\ell(\hat{Y}_{MRh})$ is normally distributed (μ, σ^2) , the above sample size provides an estimate of the "true" variance with a 10 percent coefficient of variation. Substitute J by 200 in (7) to get the desired unbiased estimate of the "true" variance.

3.2.2. Biased Variance Estimator

The variance estimator described in the previous section may have high variance since it is a function of a small number of sample systematic clusters which are the sampling units under this sample design. Thus, we decided to con-

sider an alternative variance estimator which could have some bias but less variance. This rationale led us to consider a random groups variance estimator for a MRS systematic sampling design. The number of random groups (g) was defined as a function of h . The original plan was to use the same number of random groups (10) for all the MRS designs. However, there was a concern with the relative difference in random group size. In order to avoid (perhaps) biasing the variance estimate unnecessarily, we defined the number of random groups as a function of the number of random starts in such a way that the number of units per random group was about the same[7].

a. A variable number of random groups were used; a minimum of 3 (for $8 \leq h \leq 10$) and a maximum of 12 (for $h=2$). In this way the maximum number of replicates was 30 ($h=10$) and the minimum 24 ($h=2$). For $3 \leq h \leq 9$, the number of replicates was between 24 and 27, inclusive with a minimum size of 4 units/replicate and a maximum of 6 units/replicate.

Let h be the number of random starts,

g be the number of random groups/systematic sample,

t be the random group size, and

Y_{pji} be the value of the characteristic for the i^{th} unit in the j^{th} random group in the p^{th} systematic sample.

Then, the j -th random group total in the p -th systematic sample is defined as

$$Y_{pj} = \sum_{i=1}^t Y_{pji}$$

The biased estimate of the true variance of the population total estimate for each MRS systematic sampling design was determined for each characteristic and sample within tract using the following formula:

$$\begin{aligned} & v_\ell(\hat{Y}_{MRh}) \\ &= k(k-1) \frac{hg}{hg-1} \sum_{p=1}^h \sum_{j=1}^g \left\{ Y_{pj} - \frac{1}{hg} \sum_{p=1}^h \sum_{j=1}^g Y_{pj} \right\}^2 \quad (8) \end{aligned}$$

The true variance of the variance estimate is given by

$$\begin{aligned} & \text{Var} \left[v_\ell(\hat{Y}_{MRh}) \right] \\ &= \frac{1}{J} \sum_{\ell=1}^J \left[v_\ell(\hat{Y}_{MRh}) - \frac{1}{J} \sum_{\ell=1}^J v_\ell(\hat{Y}_{MRh}) \right]^2 \quad (9) \end{aligned}$$

Again, for $h \geq 3$, it was not feasible to compute the true variance of the variance estimate, therefore, it was estimated using the same methodology described in Section 3.2.1.

b. The bias of the proposed variance estimate was calculated as follows [6].

$$\text{Bias} \left[v_{\ell} (\hat{Y}_{MRh}) \right] = \frac{30h^2gt(g-1)}{hg-1} S_w^2 + \left[\frac{30h(h-1)}{hg-1} - 30h \right] S_{\beta}^2 \quad (10)$$

where

$$S_w^2 = \frac{1}{6h(m-1)} \sum_{p=1}^{6h} \sum_{j=1}^g \sum_{i=1}^t \quad (11)$$

$$\left[Y_{pji} - \frac{1}{gt} \sum_{j=1}^g \sum_{i=1}^t Y_{pji} \right]^2$$

$$S_{\beta}^2 = \frac{1}{6h-1} \sum_{p=1}^{6h} \left[Y_p - \frac{1}{6h} \sum_{p=1}^{6h} Y_p \right]^2 \quad (12)$$

c. An estimate of the MSE of the Variance Estimator was calculated adding (9) and the square of (10)

Note that for $h=3$ to 10, the MSE is an estimate with a 10 percent coefficient of variation for the variance component.

4. SUMMARY OF THE TEST RESULTS

The objective of the nonparametric analysis was to screen the data for significant trends. The quantitative analysis was performed to assess the magnitude of the differences detected between the sampling schemes.

4.1. Unbiased Variance Estimator

We compared the MRS sampling schemes with SRS systematic sampling in terms of the "true" variance of the unbiased variance estimator and the MSE of the random groups variance estimator, respectively. The summary data shown in Table 1.A indicate that the null hypothesis of no difference among the sampling designs was rejected for all but characteristics 9 and 10. The random groups variance estimator ($h=1$ or SRS) yielded a large number of data items having a significant low mean rank. For 12 out of the 23 characteristics, the mean rank was below 4 and it did not exceed 6 for any of the remainder 9 characteristics. As h increases ($h \geq 2$) the mean ranks generally decreases. The use of 2 random starts ($h=2$) resulted consistently in significantly high mean ranks. For 16 out of the 23 characteristics, the mean rank was above 6 and no characteristic has a mean rank smaller than 5. For 14 out of the 23 characteristics, $h=10$

(excluding $h=1$) resulted in the lowest mean rank. From the data, it can be seen that the variability between the mean ranks for $h=6$ to $h=10$ is almost negligible. However, this observation does not apply to $1 \leq h \leq 5$.

4.2. Biased Variance Estimator

MRS systematic sampling was compared to SRS systematic sampling based upon the MSE of the biased variance estimate. The summary data presented in Table B indicate that the null hypothesis was rejected for all but 5 characteristics, these are characteristics 2, 9, 10, 22, and 23. SRS systematic sampling ($h=1$) ranks consistently higher than MRS with $h=9$ or $h=10$. MRS with $h=10$ resulted in the lowest mean rank for 11 out of the 23 characteristics and for 13 characteristics the mean rank for MRS with $h=2$ is generally higher than for the other designs.

4.3. Pairwise Comparison Test

For those characteristics for which the null hypothesis of no difference between the sampling schemes was rejected we conducted a pairwise comparison test. The test is based upon the absolute mean rank difference for any pair. The null hypothesis of no difference between the two sampling designs is rejected if the difference exceeds 1.24 ($q_{k,\infty}$). The analysis showed a (unbiased variance estimate) statistical significant difference between SRS systematic sampling and the MRS sampling designs with small h , however, with $h \geq 9$, the null hypothesis was not rejected for about 70 percent (28 out of 46) of the cases. For the MRS systematic sampling schemes defined by $7 \leq h \leq 10$, the differences were found to be not statistically significant for about 83 percent of the cases involving combinations of these designs. The analysis for the biased estimate indicates, statistical significant difference between SRS systematic sampling and MRS systematic sampling with $8 \leq h \leq 10$ for most of the characteristics (14 out of the 18 characteristics). Again, the differences between MRS systematic sampling designs defined by $7 \leq h \leq 10$ were found to be not statistically significant for over 90 percent of the cases.

4.4. Quantitative Analysis

For those characteristics and pairs of sampling designs for which the null hypothesis of no difference was rejected, we conducted a quantitative analysis as follows. For each pair, the ratio of the mean square errors was calculated for each characteristic and tract, the denominator of the ratio being the MSE of the variance estimate of the design defined by the largest h value. For each characteristic the distribution of these ratios was created and the median was determined. Our analysis indicates that for the unbiased variance estimator the MSE of the random

groups variance estimator (SRS) is a small fraction (in many cases less than 0.5) of the MSE of the variance estimator for MRS for at least 50 percent of the tracts. For MRS with $7 \leq h \leq 10$, the median ratios were close to 1 indicating no real difference between these designs with respect to the MSE of the variance estimate. For the biased variance estimate, the MSE of the random groups variance estimator (SRS) is usually larger than the MSE of the variance estimator for MRS for at least 50 percent of the tracts with the only exception of $h=2$. With the exception of characteristic 14 the MSE of SRS is at least 1.5 times (as high as 3.4) the MSE of MRS for at least half of the tracts. These data suggest that greater reductions in the MSE of the variance estimate are achieved by using 8 or more random starts.

4.5. Autocorrelation and True Variance of the Estimate - Additional Research

For each tract and each characteristic, the correlation, ρ , of neighboring elements will be computed as follows[8].

Let N be the number of HU's in the tract or tract size.

For housing unit data,

$$X_j = \begin{cases} 1 & \text{if the } j^{\text{th}} \text{ HU in a given} \\ & \text{tract has the character-} \\ & \text{istic of interest} \\ 0 & \text{otherwise} \end{cases}$$

and for population characteristics,

X_j = value of the characteristic for the j^{th} HU,

$$\bar{X} = \frac{1}{N} \sum_{j=1}^N X_j$$

Then the correlation ρ is

$$\rho = \frac{C_1}{C_0} \quad \text{where}$$

$$C_1 = \frac{1}{N-1} \sum_{j=1}^{N-1} (X_j - \bar{X})(X_{j+1} - \bar{X})$$

$$C_0 = \frac{1}{N-1} \sum_{j=1}^N (X_j - \bar{X})^2$$

If the correlation ρ , of neighboring elements for the variable being measured is high, then the more random starts, the higher the true variance of estimates due to the increased likelihood of neighbors being in sample. Theoretically, the more random starts, the higher the increase in the true variance of the estimate for a given amount of autocorrelation. This relationship will be examined.

Our analysis of the distribution, of the true variance of the estimates, suggest that there is a significant (not in statistical sense) increase in the true variance of the estimate when MRS with $h \geq 3$ is compared to SRS systematic sampling, suggesting high autocorrelation values. The data indicate that for MRS with $h \geq 5$, the (changes) increases in the true variance are independent from h . This was a very surprising finding since the true variance of the estimate is supposed to increase as the number of random starts increases. We will examine this in conjunction with the autocorrelation measure. The increase in the true variance of the estimate is in the order of 60 percent, averaging across characteristics. For instance, for characteristic 1, when SRS systematic sampling is compared to MRS with $h=7$, the increase in the true variance of the estimate is 59 percent. For other comparisons the percent increases are significantly higher (as high as 120 percent).

5. CONCLUSION

The findings of this research indicate that we can improve the mean square error of the random groups variance estimator through the use of MRS systematic sampling. However, in order to realize any gains in the MSE of the variance estimator, the true variance of the estimate is significantly increased. In other words, the reduction in the MSE of the variance estimate is accompanied by a significant increase in the true variance of the estimate. We do not think that the reduction in the MSE of the variance estimate is worth the increase in the true variance of the estimate. Contrary to suggestions in previous research on this topic[1], when the statistician has a choice between systematic sampling (and random groups variance estimation) and MRS systematic sampling (and unbiased estimation of the variance), he/she should use the former. Results of this research suggest that MRS is superior (in the sense of variance of the variance estimate) to SRS systematic sampling if biased estimation of variance is used.

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Table A: **Friedman Test Mean Ranks for the MRS Systematic Sampling Designs (Unbiased Variance Est.) Mean Ranks - Values of h**

Char	1	2	3	4	5	6	7	8	9	10	Cases	Chi-Sq.	DF	Signif
1	2.33	9.22	7.92	6.63	6.36	5.54	5.22	4.15	4.03	3.60	120	515.935	9	0.000
2	4.58	7.94	6.48	6.13	4.92	5.48	5.35	4.95	4.64	4.52	120	137.618	9	0.000
3	4.32	7.85	6.67	5.87	5.27	5.46	5.17	5.05	4.70	4.65	120	132.831	9	0.000
4	2.47	9.17	8.07	6.78	6.19	5.60	5.08	4.25	3.90	3.48	120	519.464	9	0.000
5	2.07	9.19	7.92	6.86	6.52	5.45	5.02	4.20	4.14	3.63	120	541.738	9	0.000
6	1.93	9.22	8.32	6.85	6.25	5.72	5.06	4.32	3.86	3.47	120	594.011	9	0.000
7	2.58	9.24	8.12	6.59	6.55	5.88	5.02	3.97	3.80	3.24	120	554.556	9	0.000
8	5.66	5.02	4.56	5.17	5.36	5.20	5.67	6.09	6.02	6.25	120	33.845	9	0.000
9	5.40	5.48	5.03	4.95	5.40	5.32	5.75	5.96	5.85	5.83	120	14.169	9	0.116
10	5.43	5.47	5.14	5.33	5.25	5.23	5.50	5.95	6.01	5.70	120	10.622	9	0.303
11	5.44	5.60	4.67	5.02	5.55	5.20	5.64	6.10	5.68	6.09	120	23.244	9	0.006
12	2.59	8.87	7.52	6.66	6.45	5.22	5.54	4.09	4.19	3.87	120	426.035	9	0.000
13	3.27	8.37	7.57	6.65	6.02	5.19	4.53	4.69	4.50	4.21	120	306.669	9	0.000
14	4.44	7.45	6.63	6.04	5.96	5.48	5.00	4.65	4.85	4.51	120	119.295	9	0.000
15	3.13	9.09	7.72	6.45	6.29	5.41	4.59	4.52	3.86	3.94	120	417.180	9	0.000
16	2.44	8.81	7.56	6.65	6.53	4.95	5.13	4.49	4.34	4.10	120	414.813	9	0.000
17	2.55	8.87	7.46	6.73	6.50	5.12	5.16	4.58	4.17	3.86	120	418.225	9	0.000
18	5.51	5.59	4.66	5.25	5.03	5.36	5.76	5.82	5.60	6.42	120	26.750	9	0.002
19	4.54	6.93	6.18	5.28	5.49	5.27	5.50	5.08	5.30	5.40	120	49.203	9	0.000
20	3.81	8.32	7.35	6.38	6.03	4.98	5.51	4.63	4.15	3.84	120	273.864	9	0.000
21	3.09	8.96	7.71	6.76	5.94	5.33	4.66	4.47	4.50	3.57	120	404.611	9	0.000
22	4.93	6.99	5.74	5.50	5.31	5.21	5.29	5.17	5.38	5.47	120	37.728	9	0.000
23	5.16	6.88	5.78	5.32	5.15	5.03	5.20	5.34	5.68	5.46	94	26.770	9	0.002

Table B: **(Biased variance estimate) Mean Ranks - Values of h**

Char	1	2	3	4	5	6	7	8	9	10	Cases	Chi-Sq.	DF	Signif
1	7.07	6.73	6.15	6.19	5.84	5.22	4.63	4.93	4.51	3.73	120	134.355	9	0.000
2	5.41	6.04	5.85	5.87	5.64	5.45	5.55	5.00	4.95	5.25	120	15.715	9	0.073
3	5.90	6.02	5.95	5.97	5.22	5.72	5.11	5.55	4.52	5.03	120	30.307	9	0.000
4	7.09	7.25	6.25	6.17	5.83	5.22	4.59	4.92	4.10	3.58	120	178.434	9	0.000
5	7.82	6.63	6.62	6.07	5.84	5.17	4.72	4.50	4.25	3.39	120	210.334	9	0.000
6	7.22	6.92	5.86	6.46	5.59	5.41	4.71	4.92	4.34	3.57	120	157.820	9	0.000
7	7.52	6.73	6.15	5.85	5.84	5.35	4.50	4.84	4.23	4.00	120	152.270	9	0.000
8	5.58	4.43	5.19	5.81	5.44	5.39	5.69	5.89	5.78	5.80	120	22.468	9	0.008
9	5.31	4.63	5.34	5.46	5.73	5.40	5.71	5.84	5.68	5.90	120	16.087	9	0.065
10	5.64	4.89	5.45	5.63	5.42	5.38	5.62	5.91	5.63	5.45	120	8.364	9	0.498
11	5.70	4.56	5.14	5.58	5.65	5.32	5.84	5.80	5.50	5.90	120	19.500	9	0.021
12	5.97	7.31	6.91	6.61	5.52	5.36	4.63	4.63	4.46	3.59	120	170.164	9	0.000
13	5.91	7.14	6.54	6.54	5.69	5.35	5.18	4.60	4.35	3.70	120	137.840	9	0.000
14	5.67	7.69	6.91	6.67	5.91	5.00	5.40	4.03	3.88	3.83	120	211.387	9	0.000
15	6.14	6.52	6.52	6.09	5.64	5.49	4.72	5.05	4.44	4.40	120	78.940	9	0.000
16	5.46	7.43	7.03	6.95	6.01	5.47	4.56	4.37	4.13	3.59	120	211.059	9	0.000
17	5.60	7.26	6.96	6.68	5.75	5.75	4.74	4.43	3.98	3.85	120	177.219	9	0.000
18	5.59	4.70	5.27	6.02	5.28	5.52	5.68	5.52	5.27	6.15	120	19.848	9	0.019
19	5.69	5.72	6.29	5.77	5.36	5.60	5.15	5.24	4.82	5.35	120	19.309	9	0.023
20	5.79	6.67	6.37	6.47	5.59	5.06	5.37	5.24	4.14	4.30	120	88.464	9	0.000
21	5.74	6.89	6.89	6.05	5.78	5.50	4.79	4.68	4.78	3.90	120	112.316	9	0.000
22	5.48	5.27	5.54	5.73	5.82	5.18	5.36	5.48	5.66	5.47	120	4.708	9	0.859
23	5.81	4.66	5.39	5.84	5.82	5.37	5.45	5.36	5.71	5.60	94	11.540	9	0.240