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Subset Selection of ε- Better Exponential Populations under Heteroscedasticity

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Abstract: Suppose we have $k(\geq 2)$independent processes/populations/sources/ treatments such that the data from i^{th} treatment follow two-parameter exponential distribution with location parameter μ_i and scale parameter θ_i, denoted $E(\mu_i,\theta_i)$, $i=1,\ldots,k$. The location parameters $\mu_1,\ldots,\mu_k$ and scale parameters $\theta_1,\ldots,\theta_k$ are unknown and possibly unequal. Let $\underline{\delta}=(\mu_1,\ldots,\mu_k,\theta_1,\ldots\theta_k)\in R^k\times R_+^k=\Omega$ and $\mu_{[k]}=max_{1\leq i\leq k}\mu_i$. For a given $\varepsilon_1>0$, we define a set of good populations as $G=\{i:\mu_i\geq\mu_{[k]}-\varepsilon_1\}$. In this paper two-stage and one-stage subset selection procedures have been proposed to select a subset, say S, of k populations which contains G with a pre-specified probability P^*, i.e., $P_{\underline{\delta}}=(G\subseteq S|\text{under the proposed procedure})\geq P^*\forall\underline{\delta}\in\Omega)$. The related simultaneous confidence intervals for $\mu_{[k]}-\mu_i, i=1,\ldots,k$ and $\mu_{[j]}-\mu_{[i]}, i\neq j=1,\ldots,k$, have been derived. A subset selection procedure is also proposed which controls the probability of omitting a "good" treatment or selecting a "bad" treatment at $1-P^*$ by considering a set $B=\{i:\mu_i\leq\mu_{[k]}-\varepsilon_2\}$ of bad treatments, where $\varepsilon_2>\varepsilon_1$.The implementation of proposed procedure is demonstrated through a real life data.

Keywords: Best treatment; Multiple comparisons; Probability of Correct Selection; Subset Selection.

1 Introduction

The observations from i^{th} treatment or population are assumed to follow two-parameter exponential distribution,denoted by $E(\mu_i,\theta_i)$, with probability distribution function (pdf)

$$f(\mu_i,\theta_i)=\frac{1}{\theta_i}e^{-\left(\frac{x-\mu_i}{\theta_i}\right)},x>\mu_i,i=1,\ldots,k.$$

Here $\mu_1,\cdots,\mu_k$ are unknown location parameters and $\theta_1,\ldots,\theta_k$ are unknown and possibly unequal scale parameters.The ordered values of location parameters are denoted by $\mu_{[1]}\leq,\ldots,\leq\mu_{[k]}$. The two-parameter exponential distribution finds applications in queuing, reliability, medical sciences and epidemiological studies. The location parameter of the exponential distribution is the so-called threshold value and the scale parameter is the expected value in addition to the threshold value. In queuing theory, exponential distribution is used to model the time elapsed between successive customer arrivals at the terminal and in reliability it is being used to model the failure time of electronic components. In dose-response experiment, the exponential distribution is used to model the effective duration of a drug with location parameter as guaranteed effective duration. For detailed discussions and applications of the exponential distribution, we refer to Bain and Engelhardt [1], Johnson et al. [2], Lawless and Singhal [3] and Zelen [4].

It is of frequent interest in life testing problems to identify good ones among the k two parameter exponential distributions. Lehmann [5] made a remark that a population may be considered good if it does not fall too much below the best one. For a given $\varepsilon>0$, we define a set of good populations as $G=\{i:\mu_i\geq\mu_{[k]}-\varepsilon\}$. We want to select a subset $S\subseteq\{1,\ldots,k\}$ which contains the set G of "good" populations with large location parameters. The cardinality $|S|$ of S depends on the sample values. Bechhofer [6] proposed indifference zone approach for selecting a population with the largest location parameter from k normal populations under the assumption of common variance. Later Gupta [7] [8]

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proposed subset selection procedure to select a subset of given populations which contains the best with a pre-specified probability. Gupta and Sobel [9] considered a population good if its mean satisfies $\mu_i \geq \mu_0$, where μ_0 is a known or unknown location parameter of a control population. Gill and Sharma [10], Gill et al. [11] and Lam [12] considered the problem of selecting a subset which includes all the good populations under different probability settings.

These authors defined a set G of good populations and selected a subset S such that $P(G \subseteq S) \geq P^*$ regardless of the true configuration of parameters of underlying populations. Desu [13] defined the population π_i as "bad" if $\mu_i < \mu_{[k]} - \varepsilon$ where $\varepsilon \geq 0$ and proposed a subset selection procedure satisfying $P(S \subseteq B^c) \geq P^*$, regardless of true parametric configuration, where $B^c = \{i : \mu_i \geq \mu_{[k]} - \varepsilon\}$. Lam's [12] procedure is dual to that considered by Desu [13] .Laan [14] discussed some efficiency results of subset selection procedures for ε-best populations. Laan [15] also discussed subset selection of an almost best treatment. All the afore said procedures proposed for location parameters assumed the equality of the scale parameters. In the recent past, Wu and Yu [16] proposed two-stage as well as one-stage procedures for selecting all good populations in terms of means when the variances are unknown and possibly unequal in the normal setting.In this article we will propose two-stage and one–stage subset selection procedures for selecting a subset S of the k populations which contain the set G with probability at least P^* regardless true configuration when the scale parameters $\theta_1, \ldots, \theta_k$ are unknown and possible unequal. The layout of the article is as follows:

The two-stage procedure for selecting a subset S such that $P_{\underline{\delta}}(G \subseteq S) \geq P^* \forall \delta \in \Omega$ and the related simultaneous confidence intervals for $\mu_{[k]} - \mu_i, i = 1, \ldots, k$ and $\mu_{[j]} - \mu_{[i]}, i \neq j = 1, \ldots, k$, are proposed in Sec. 2. In practical situations if the additional samples for the second stage sampling are not available due to the experimental budget shortage or other constraints of experiment, a one-stage procedure is proposed in Sec. 3. In Sec. 4, we propose a subset selection which of controls the probability of selecting a bad population and omitting the good population. Finally, the proposed two-stage and one-stage procedures are implemented through a real life example in Sec. 5.

2 Two-Stage Procedure

Take an initial sample $X_{i1}, \ldots, X_{im}$ of size $m(\geq 2)$ from $\pi_i, i = 1, \ldots, k$. Let $Y_i = min(X_{i1}, \ldots, X_{im})$ and $S_i = \sum_{j=1}^{m} (X_{ij} - Y_i)/(m-1)$, be maximum likelihood estimators (MLE) and minimum variance unbiased estimator (MVUE)of μ_i and θ_i respectively, $i = 1, \ldots, k$. The random variables $m(Y_i - \mu_i)/\theta_i$ and $2(m-1)S_i/\theta_i$ are distributed independently as $E(0,1)$ and chi-square with $2m-2$ df, respectively, $i = 1, \ldots, k$.

The ordered values of $Y's$ are denoted by $Y_{[1]} \leq, \ldots, \leq Y_{[k]}$. In case of ties, the indices can be chosen in any manner so long as the above relation is satisfied. Given a fixed constant $c > 0$, to be chosen to control (to be discussed later) the confidence length of the parameter $\mu_{[k]}$ or $\mu_{[1]}$, the overall sample size N_i from population π_i for the two-stage procedure is given by

$$N_i = max\left\{m, \left[\frac{S_i}{c}\right] + 1\right\}, \qquad i = 1, \ldots, k,$$

where $[x]$ denotes the largest integer contained in x. When $N_i > m$, take $N_i - m$ additional observations $X_{i,m+1}, \ldots, X_{i,N_i}$ from π_i and so that the total random sample from π_i will be $X_{i1}, \ldots, X_{im}, X_{i,m+1}, \ldots, X_{i,N_i}$. Let

$$\widetilde{X}_{i,N_i} = \widetilde{X}_i = \begin{cases} min(Y_i, X_{i,m+1}, \ldots, X_{i,N_i}), & \text{when } N_i > m \\ Y_i, & \text{when } N_i = m \end{cases}$$

$i = 1, \ldots, k$, be the minimum value of the combined sample. It can be noted that $V_i = N_i(\widetilde{X}_{i,N_i} - \mu_i)/\theta_i$ and $2(m-1)S_i/\theta_i$ are stochastically independently distributed as standard exponential, i.e. $E(0,1)$ and a chi-square with $2m-2$ df, respectively. Thus $V_i^* = N_i(\widetilde{X}_{i,N_i} - \mu_i)/S_i$ follows F distribution with $(2, 2m-2)$ df,$i = 1, \ldots, k$.

For given $\varepsilon > 0$, let $G = \{i : \mu_i \geq \mu_{[k]} - \varepsilon\}$ be a set of all good populations and the goal of the experimenter is to select a subset S of the given k populations which includes all populations in G. Thus, a correct selection will occur if $G \subseteq S$ with a pre-specified probability, say P^*, where the size of the selected subset is not restricted. In the following theorem we propose a subset selection procedure which meets the required goal when the scale parameters $\theta_1, \ldots, \theta_k$ are unknown and possibly unequal.

Theorem 2.1. Define $G = \{i : \mu_i \geq \mu_{[k]} - \varepsilon\}$ and $B = \left\{max_{1 \leq i \leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) - min_{1 \leq i \leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) \leq q\right\}$, where for a given $P^* \in (0,1)$ the constant $q = q(k, P^*)$ is choosen such that $P(B) \geq P^*$. Then the selection procedure which selects the subset $S = \{i : \widetilde{X}_i \geq \widetilde{X}_{[k]} - \varepsilon - qc\}$ satisfies the probability requirement $P(G \subseteq S) \geq P^*$.

Proof. Let $\mu_{(i)}$ (μ_i) be the parameter associated with $\widetilde{X}_{[i]}$ $(\widetilde{X}_i), i = 1, \ldots, k$. Now

$$B = \left\{max_{1 \leq i \leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) - min_{1 \leq i \leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) \leq q\right\}$$

By the choice of q, $P(B) \geq P^*$ for all parametric configuration of $\mu's$. In order to prove $P(G \subseteq S) \geq P^*$, it is sufficient to show that $B \subseteq (G \subseteq S)$. Now

$$\begin{aligned} B &= \left\{ max_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) - min_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) \leq q, i = 1,\ldots,k \right\} \\ &= \{\widetilde{X}_i \geq \widetilde{X}_{[k]} - (\mu_{(k)} - \mu_i) - qc, i = 1,\ldots,k\} \\ &\subseteq \{\widetilde{X}_i \geq \widetilde{X}_{[k]} - (\mu_{[k]} - \mu_i) - qc, i = 1,\ldots,k\} \quad (\because \mu_{[k]} \geq \mu_{(k)}) \\ &\subseteq \{\widetilde{X}_i \geq \widetilde{X}_{[k]} - \varepsilon - qc, i = 1,\ldots,k\} \quad (\because \mu_i \geq \mu_{[k]} - \varepsilon) \end{aligned}$$

This proves the theorem.

Theorem 2.2. For given $P^*(0 < P^* < 1)$ if $P(B) \geq P^*$, then $q = q(k, P^*) = F^{-1}_{2,2m-2}(P^*)^{\frac{1}{k}}$, where $F_{2,2m-2}$ is an F statistic with $(2, 2m-2)$ df.
In order to prove this theorem we will use the following lemma due to Kharrati-Kopaei [17].

Lemma 1. If X and Y are two non-negative random variables, a, b and d are three positive constants, then $[aX \geq bY - bd] \supseteq [Y \leq d]$.

Proof of theorem 2.2. Let $S_{(k)}$ and $N_{(k)}$ be the quantities assiciated with $\widetilde{X}_{[k]}$. Now

$$\begin{aligned} P(B) &= P\left\{ max_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) - min_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) \leq q \right\} \\ &= P\{(\widetilde{X}_i - \mu_i) \geq max_{1\leq i\leq k}(\widetilde{X}_i - \mu_i) - qc, i = 1,\ldots,k\} \\ &= P\{(\widetilde{X}_i - \mu_i) \geq (\widetilde{X}_{[k]} - \mu_{(k)}) - qc, i = 1,\ldots,k\} \\ &= P\left(\frac{S_i}{N_i}V_i^* \geq \frac{S_{(k)}}{N_{(k)}}V^*_{[k]} - qc, i = 1,\ldots,k\right) \\ &\geq P\left(\frac{S_i}{N_i}V_i^* \geq \frac{S_{(k)}}{N_{(k)}}V^*_{[k]} - q\frac{S_{(k)}}{N_{(k)}}, i = 1,\ldots,k\right). \end{aligned} \tag{2.1}$$

The inequality (2.1) follows from the fact that $N_i \geq S_i/c$ or $c \geq S_i/N_i, i = 1,\ldots,k$.

$$\begin{aligned} &= E_{S_1,\ldots,S_k} P\left(\frac{s_i}{N_i}V_i^* \geq \frac{s_{(k)}}{N_{(k)}}V^*_{[k]} - q\frac{s_{(k)}}{N_{(k)}}, i = 1,\ldots,k\right) \\ &\geq P\left(V_{[k]} \leq q\right) \\ &= P(max(V_1^*,\ldots,V_k^*) \leq q) \\ &= P(F_{2,2m-2} \leq q)^k \end{aligned} \tag{2.2}$$

By equality above expression to P^*, we get $q = q(k, P^*) = F^{-1}_{2,2m-2}(P^*)^{\frac{1}{k}}$.
The (2.2) inequality follows by using the above lemma with $a = \left(\frac{S_i}{N_i}\right)$, $b = \left(\frac{s_{(k)}}{N_{(k)}}\right)$, $X = V_i^*$ and $d = q$.

Remark. When the unequal scale parameters are known, the unbiased estimator S_i of θ_i is replaced by θ_i throughout Theorem 2.2 and the statistics V_i^* which is distributed as a F distribution with $(2, 2m-2)$ df is replaced by the statistics V_i^* which is distributed as a standard exponential distribution. Therefore, $q = q(k, P^*) = -ln\left(1 - P^{*\frac{1}{k}}\right)$ when scale parameters are known.

The result that all good populations have been included in the selected subset can be strengthened by giving simultaneous confidence intervals for the parameters $\alpha_i = \mu_{[k]} - \mu_i, i = 1,\ldots,k$, without decreasing the nominal confidence level P^*. The result can be summarized in the following theorem.

Theorem 2.3. Assume that the assumptions of theorem 2.1 hold. Then
$P\left(G \subseteq S, (\widetilde{X}_{[k]} - \widetilde{X}_i - qc)^+ \leq \mu_{[k]} - \mu_i \leq (max_{j\neq i}(\widetilde{X}_j - \widetilde{X}_i) + qc)^+, i = 1,\ldots,k\right) \geq P^*$, where $A^+ = max(A, 0)$.

Proof. In Theorem 2.1, we have already proved that $B \subseteq (G \subseteq S)$. Thus, it is sufficient to show that

$$B \subseteq \left((\widetilde{X}_{[k]} - \widetilde{X}_i - qc)^+ \leq \mu_{[k]} - \mu_i \leq (max_{j \neq i}(\widetilde{X}_j - \widetilde{X}_i) + qc)^+, i = 1, \ldots, k \right)$$

In terms of above notations ($\mu_{(i)}$ associated with $\widetilde{X}_{[i]}$ and $\mu_{[k]}$ with $\widetilde{X}_{(k)}$) and by definition of event B, we have $\frac{\widetilde{X}_i - \mu_i}{c} - \frac{\widetilde{X}_{(k)} - \mu_{[k]}}{c} \leq q; i = 1, \ldots, k$. Hence

$$\mu_{[k]} - \mu_i \leq \widetilde{X}_{(k)} - \widetilde{X}_i + qc, i \neq k.$$

This implies that , $\mu_{[k]} - \mu_i \leq (max_{j \neq i}(\widetilde{X}_j - \widetilde{X}_i) + qc)^+, i = 1, \ldots, k$ (2.3)

On the other hand, under the event E, we have $\frac{\widetilde{X}_{[k]} - \mu_{(k)}}{c} - \frac{\widetilde{X}_i - \mu_i}{c} \leq q; i = 1, \ldots, k$. Hence $\mu_{(k)} - \mu_i \geq \widetilde{X}_{[k]} - \widetilde{X}_i - qc, \forall i$. Since $\mu_{[k]} \geq \mu_{(k)}$, thus

$$\mu_{[k]} - \mu_i \geq \left(\widetilde{X}_{[k]} - \widetilde{X}_i - qc \right)^+ ; i = 1, \ldots, k. \tag{2.4}$$

Then (2.3) and (2.4) completes the proof of the theorem.

From the proof of Theorem 2.3 we have the following theorem to give the pairwise comparison of the ranked parameters $\mu_{[i]} - \mu_{[j]}$.

Theorem 2.4. The conclusion in the Theorem 2.3 can be strengthened by adding the statements

$$\widetilde{X}_{[i]} - \widetilde{X}_{[j]} - qc \leq \mu_{[i]} - \mu_{[j]} \leq \widetilde{X}_{[i]} - \widetilde{X}_{[j]} + qc; i, j = 1, \ldots k$$

without decreasing the probability P^*.

Remark 2. Let $k = 4, m = 10$, $P^* = 0.95$ we can find $q = q(k, P^*) = F^{-1}_{2,18}(0.95)^{\frac{1}{4}} = 5.614$. Suppose that the width of the pairwise confidence interval, proposed in Theorem 2.4, is specified to be $L = 2.5$. Then the value of $c = L/2q = 2.5/(2(5.614)) = 0.222657$ which can be used in (2.1) to determine the required total sample size N_i, $i = 1, \ldots, k$.

3 One-Stage Selection Procedure

In some practical situations the additional sample for the second stage may not be available due to the experimental budget shortage or other factors in an experiment. The two-stage selection procedure, proposed in section 2 cannot be used when the scale parameters are unknown and possibly unequal. In this case we proposed one-stage selection procedure as follows:

Take a one-stage sample $X_{i1}, \ldots, X_{im}$ of size $m(\geq 2)$ from $\pi_i, i = 1, \ldots, k$. Let $Y_i = min(X_{i1}, \ldots, X_{im})$ and $S_i = \sum_{j=1}^{m} (X_{ij} - Y_i)/(m-1)$ and let $c^* = max_{1 \leq i \leq k}(S_i/m)$. Now define an event E, as $E = \left\{ max_{1 \leq i \leq k} \left(\frac{Y_i - \mu_i}{c^*} \right) - min_{1 \leq i \leq k} \left(\frac{Y_i - \mu_i}{c^*} \right) \leq q \right\}$. Now, we can have the following four Theorems for one-stage procedure which one analogous to Theorems 2.1-2.4 used in two-stage procedure.

Theorem 3.1. Let $G = \{i : \mu_i \geq \mu_{[k]} - \varepsilon\}$ and $E = \left\{ max_{1 \leq i \leq k} \left(\frac{Y_i - \mu_i}{c^*} \right) - min_{1 \leq i \leq k} \left(\frac{Y_i - \mu_i}{c^*} \right) \leq q \right\}$, where $q = q(k, P^*)$ is to be choosen such that $P(E) \geq P^*$. If we propose a selection procedure $S = \{i : \widetilde{X}_i \geq \widetilde{X}_{[k]} - \varepsilon - qc^*\}$. Then $P(G \subseteq S) \geq P^*$.

Theorem 3.2. For given $P^*(0 < P^* < 1)$
$P \left(max_{1 \leq i \leq k} \left(\frac{Y_i - \mu_i}{c^*} \right) - min_{1 \leq i \leq k} \left(\frac{Y_i - \mu_i}{c^*} \right) \leq q \right) \geq P^*$ if $q = q(k, P^*) = F^{-1}_{2,2m-2}(P^*)^{\frac{1}{k}}$.

Theorem 3.3. Assume that the assumptions of theorem 3.1 hold. Then
$P \left(G \subseteq S, (\widetilde{X}_{[k]} - \widetilde{X}_i - qc^*)^+ \leq \mu_{[k]} - \mu_i \leq (max_{j \neq i}(\widetilde{X}_j - \widetilde{X}_i) + qc^*)^+, i = 1, \ldots, k \right) \geq P^*$, where $A^+ = max(A, 0)$.

Theorem 3.4. The conclusion in the Theorem 3.3 can be strengthened by adding the statements

$$\widetilde{X}_{[i]} - \widetilde{X}_{[j]} - qc^* \leq \mu_{[i]} - \mu_{[j]} \leq \widetilde{X}_{[i]} - \widetilde{X}_{[j]} + qc^*; i, j = 1, \ldots k$$

without decreasing the probability P^*.

4 Controlling Both Types of Error

An experimenter can commit the following two types of errors in a subset selection procedure :

1.Not including a "good population" in the selected subset or
2.Including a "bad population" in the selected subset.

For given ε_1 and ε_2 $(\varepsilon_2 > \varepsilon_1 > 0)$ the treatment populationis π_i called "good" if $\mu_i \geq \mu_{[k]} - \varepsilon_1$ and "bad" if $\mu_i \leq \mu_{[k]} - \varepsilon_2, i = 1,\ldots,k-1$. Define two subsets of k treatments as $G_{\varepsilon_1} = \{i : \mu_i \geq \mu_{[k]} - \varepsilon_1, i = 1,\ldots,k\}$ and $B_{\varepsilon_2} = \{i : \mu_i < \mu_{[k]} - \varepsilon_2, i = 1,\ldots,k\}$ which are labeled as subsets of good and bad populations, respectively. Now the aim of the experimenter is to control both types of errors and also wants to select a subset S of k treatment populations satisfying the requirement $(G_{\varepsilon_1} \subseteq S) \subset B^c_{\varepsilon_2}$ with a high probability, where $B^c_{\varepsilon_2}$ is the complement of B_{ε_2}. In the following theorem we propose a two stage subset selection procedure which meets the above goal with probability greater than or equal to P^*.

Theorem (5.1). Let $G_{\varepsilon_1} = \{i : \mu_i \geq \mu_{[k]} - \varepsilon_1, i = 1,\ldots,k\}$ and $B_{\varepsilon_2} = \{i : \mu_i < \mu_{[k]} - \varepsilon_2, i = 1,\ldots,k\}$ where $\varepsilon_2 > \varepsilon_1$ and $\varepsilon_i > 0, i = 1,2$. Let t be a constant satisfying $\frac{\varepsilon_2}{c} - q > t \geq q + \frac{\varepsilon_1}{c}$. If we select the subset $S = \{i : \widetilde{X}_i \geq \widetilde{X}_{[k]} - tc\}$. The total sample size for either two-stage or one-stage procedure is determined as $n_i = max\left\{m+1, \left[\frac{S_i}{c}\right]+1\right\}$, where c satisfies $c < \dfrac{\varepsilon_2 - \varepsilon_1}{2q}$. Then $P\left(G_{\varepsilon_1} \subseteq S \subset B^c_{\varepsilon_2}\right) \geq P^*$.

Proof: We know that

$$E = \left\{ max_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) - min_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) \leq q \right\}$$
$$\subset \left\{ max_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) - min_{1\leq i\leq k}\left(\frac{\widetilde{X}_i - \mu_i}{c}\right) \leq t - \frac{\varepsilon_1}{c} \right\} \qquad \left(\because t \geq q + \frac{\varepsilon_1}{c}\right) \tag{5.1}$$

The event in the right hand of (5.1) is contained in the event $(G_{\varepsilon_1} \subseteq S_U)$. Therefore,

$$(G_{\varepsilon_1} \subseteq S) \supset E. \tag{5.2}$$

Also,

$$\left(S \subseteq B^c_{\varepsilon_2}\right) = \{\widetilde{X}_i > \widetilde{X}_{[k]} - tc', \mu_i > \mu_{[k]} - \varepsilon_2, i = 1,\ldots,k\}$$
$$\supset \left\{ \frac{\widetilde{X}_{(k)} - \mu_{(k)}}{c'} - \frac{\widetilde{X}_i - \mu_i}{c'} < t - \frac{\mu_{(k)} - \mu_i}{c'}, \mu_{[k]} - \mu_i < \varepsilon_2, i = 1,\ldots,k \right\}$$
$$\supset \left\{ \frac{\widetilde{X}_{(k)} - \mu_{(k)}}{c'} - \frac{\widetilde{X}_i - \mu_i}{c'} < t - \frac{\varepsilon_2}{c'}, i = 1,\ldots,k \right\}$$
$$\supset \left\{ \frac{\widetilde{X}_{(k)} - \mu_{(k)}}{c'} - \frac{\widetilde{X}_i - \mu_i}{c'} < q, i = 1,\ldots,k \right\} \supset E \qquad \left(\because \left[t - \frac{\varepsilon_2}{c'} > q\right]\right) \tag{5.3}$$

Thus, from (5.2) and (5.3), we get $\left(G_{\varepsilon_1} \subseteq S \subset B^c_{\varepsilon_2}\right) \supset E$.
Therefore $P^* = P(E) \leq P\left(G_{\varepsilon_1} \subseteq S \subset B^c_{\varepsilon_2}\right)$.
This completes the proof of the theorem.

Example. The data set, given in Wu and Wu [18] and Wu et al. [19], representing the duration of remission achieved by four drugs used in the treatment of leukemia are taken. The initial sample size $m = 20$ from each population representing duration of remission by four drugs and reproduced below in Table 1. The authors have shown the exponentiality of data with unequal scale parameters.

Let $m = 20$ be the common initial sample size in the first stage, from each of the four drugs. For $k = 4$ and $P^* = 0.90(0.95)$, the value of $q = 4.0239(4.9045)$. Let $L = 1.1309(1.3783)$ then we have $c = L/(2q) = 1.1309/(2*4.0239) = 0.14052$ $(c = L/(2q) = 1.3783/(2*4.9045) = 0.14051)$ for $P^* = 0.90(0.95)$. We use c to determine the total sample size for two stages and end up with total sample sizes as $N_1 = 20$, $N_2 = 30$, $N_3 = 20$, $N_4 = 24$ from respective populations. Using the same initial sample size $m = 20$ and additional sample sizes asobtained by Wu and Wu [18] are proposed below in Table 2.

Table 1: Duration of remission by four drugs data

Drug 1	Drug 2	Drug 3	Drug 4
1.034	2.214	4.158	5.115
2.344	4.976	4.025	4.498
1.266	8.154	5.17	4.617
1.563	2.686	11.909	4.651
1.169	2.271	4.912	4.533
4.118	3.139	4.629	4.513
1.013	2.214	3.955	7.641
1.509	4.48	6.735	5.971
1.109	8.847	3.14	12.13
1.965	2.239	12.446	4.699
5.136	3.473	8.777	4.914
1.533	2.761	6.321	17.169
1.716	2.833	3.256	5.497
2.778	2.381	8.25	11.332
2.546	3.548	3.759	18.922
2.626	2.414	5.205	13.712
3.413	2.832	3.071	6.309
1.929	5.551	3.147	10.086
2.061	3.376	9.773	9.293
2.951	2.968	10.218	11.787

Table 2: Statistics and Critical Constants

Statistics	Drug 1	Drug 2	Drug 3	Drug 4
N_i	20	30	20	24
$\widetilde{X}_i$	1.013	4.498	2.214	3.064
S_i	1.238	4.075	1.53	3.233

From Theorem 2.1, our proposed subset selection procedure is $S = \left\{i : \widetilde{X}_i \geq 4.4980 - \varepsilon - 4.0239(0.14052)\right\}$ = $\left\{i : \widetilde{X}_i \geq 3.932562 - \varepsilon\right\}$ and $S = \left\{i : \widetilde{X}_i \geq 4.4980 - \varepsilon - 4.9045(0.14051)\right\}$ =$\left\{i : \widetilde{X}_i \geq 3.808869 - \varepsilon\right\}$ for $P^* = 0.90, 0.95$, respectively. The selected subset rule and selected subset of populations are listed in Table 3 for $P* = 0.90, 0.95$ and ε=0.5, 1, 1.5, 2, 2.5.

From Theorem 2.3, we can construct the 90%, 95% simultaneous confidence intervals of given by $\mu_{[k]} - \mu_i, i = 1,2,3,4$ given by

P*	$\mu_{[k]} - \mu_1$	$\mu_{[k]} - \mu_2$	$\mu_{[k]} - \mu_3$	$\mu_{[k]} - \mu_4$
0.90	(2.91955, 4.05045)	(0,0)	(1.71855, 2.84945)	(0.86855, 1.99945)
0.95	(2.79585, 4.17415)	(0,0)	(1.59485, 2.97315)	(0.74485, 2.12315)

From Theorem 2.4, we can construct the 90%, 95% simultaneous confidence intervals of the ranked parameters as follows:

P^*	0.90	0.95
$\mu_{[4]} - \mu_{[3]}$	(0.28455, 1.41545)	(0.16085, 1.53915)
$\mu_{[4]} - \mu_{[2]}$	(-1.99945, -0.86855)	(-2.12315, -0.74485)
$\mu_{[4]} - \mu_{[1]}$	(1.48555, 2.61645)	(1.36185, 2.74015)
$\mu_{[3]} - \mu_{[2]}$	(-2.84945, -1.71855)	(-2.97315, -1.59485)
$\mu_{[3]} - \mu_{[1]}$	(0.63555, 1.76645)	(0.51185, 1.89015)
$\mu_{[2]} - \mu_{[1]}$	(2.91955, 4.05045)	(2.79585, 4.17415)

Table 3: Subset of selected good populations

ε	0.5	1.0	1.5	2.0	2.5
			P^*=0.90		
$\widetilde{X}_i \geq$	3.43255	2.93255	2.43255	1.93255	1.43255
Selected subset	(2)	(2,3)	(2,3)	(2,3,4)	(2,3,4)
			P^*=0.95		
$\widetilde{X}_i \geq$	3.30885	2.80885	2.30885	1.80885	1.30885
Selected subset	(2)	(2,3)	(2,3)	(2,3,4)	(2,3,4)

Table 4: Statistics

Statistics	Drug 1	Drug 2	Drug 3	Drug 4
N_i	20	20	20	20
$\widetilde{X}_i$	1.013	4.498	2.214	3.071
S_i	1.238	4.075	1.53	3.233

For the one-stage procedure, we use the sample size $N_i = 20, i = 1,2,3,4$ and the value of $c^* = max_{1\leq i\leq k}(S_i/m) = 0.20375$, we have the immediate statistics given in Table 4. From Theorem 3.1, our proposed subset selection procedure is $S = \left\{i : \widetilde{X}_i \geq 4.4980 - \varepsilon - 4.0239(0.20375)\right\} = \left\{i : \widetilde{X}_i \geq 3.67813 - \varepsilon\right\}$ and $S = \left\{i : \widetilde{X}_i \geq 4.4980 - \varepsilon - 4.9045(0.20375)\right\} = \left\{i : \widetilde{X}_i \geq 3.498708 - \varepsilon\right\}$ for $P^* = 0.90, 0.95$, respectively. The selected subset rule and selected subset of populations are listed in Table 5 for $P^* = 0.90, 0.95$ and $\varepsilon = 0.5, 1, 1.5, 2, 2.5$.

From Theorem 3.3, we can construct the 90%, 95% simultaneous confidence intervals of $\mu_{[k]} - \mu_i, i = 1,2,3,4$ given by

P*	$\mu_{[k]} - \mu_1$	$\mu_{[k]} - \mu_2$	$\mu_{[k]} - \mu_3$	$\mu_{[k]} - \mu_4$
0.90	(2.665125, 4.304875)	(0,0)	(1.464125, 3.103875)	(0.6071254, 2.2468746)
0.95	(2.485717, 4.484283)	(0,0)	(1.284717, 3.283283)	(0.4277165, 2.4262835)

From Theorem 3.4, we can construct the 90%, 95% simultaneous confidence intervals of the ranked parameters as follows:

P^*	0.90	0.95
$\mu_{[4]} - \mu_{[3]}$	(0.03712541, 1.67687459)	(-0.1422835, 1.8562835)
$\mu_{[4]} - \mu_{[2]}$	(-2.2468746, -0.6071254)	(-2.4262835, -0.4277165)
$\mu_{[4]} - \mu_{[1]}$	(1.238125, 2.877875)	(1.058717, 3.057283)
$\mu_{[3]} - \mu_{[2]}$	(-3.103875, -1.464125)	(-3.283283, -1.284717)
$\mu_{[3]} - \mu_{[1]}$	(0.3811254, 2.0208746)	(0.2017165, 2.2002835)
$\mu_{[2]} - \mu_{[1]}$	(2.665125, 4.304875)	(2.485717, 4.484283)

Table 5: Subset of selected good populations

ε	0.5	1.0	1.5	2.0	2.5
			P^*=0.90		
$\widetilde{X}_i \geq$	3.17813	2.67813	2.17813	1.67813	1.17813
Selected subset	(2)	(2,3)	(2,3,4)	(2,3,4)	(2,3,4)
			P^*=0.95		
$\widetilde{X}_i \geq$	2.99872	2.49872	1.99872	1.49872	0.99872
Selected subset	(2,3)	(2,3)	(2,3,4)	(2,3,4)	(1,2,3,4)

Comparing selected subset size for one stage and two stage procedure given in Table 3 and Table 5, we can see that for both the procedures the last values for ε include more populations than the initial one for $P^* = 0.90, 0.95$.

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Conflict of interest

The authors declare that they have no conflict of interest.

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