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A TEST OF HOMOGENEITY BASED ON MAXIMUM LIKELIHOOD ESTIMATES

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A sample is said to be homogeneous, if all its elements are drawn from the same population, otherwise heterogeneous. It is self-evident that there is no sense in estimating the parameters of an assumed distribution from heterogeneous samples. Considering the fact that samples of fatigue test data are frequently composed of elements drawn from two or even three populations, it is an important rule, frequently violated, to start statistical analyses of a given sample by stating whether it is homogeneous or not.

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A simple test based on the alternative maximum likelihood estimates of the complete sample and of the sample more or less truncated is presented.

FOREWORD

The research work reported herein was conducted by Prof. Dr. Waloddi Weibull, Avenue d'Albigny, 9 bis, 74000 Annecy, France, under USAF Contract No. F44620-73-C-0066. This contract, which was initiated under Project No. 7351, "Metallic Materials", Task 735106, "Behavior of Metals", was administered by the European Office of Aerospace Research. The work was monitored by the Metals and Ceramics Division, Air Force Materials Laboratory, Air Force Systems Command, Wright-Patterson Air Force Base, Ohio 45433, under the direction of Mr. W. J. Trapp, AFML/LL.

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1. INTRODUCTION

A sample is said to be homogeneous, if all its elements are drawn from the same population, otherwise heterogeneous. It is self-evident that there is no sense in trying to estimate the parameters of an assumed distribution function from heterogeneous samples. Considering the fact that samples of fatigue test data are quite frequently composed of elements drawn from two or even three different populations, it is an important rule, frequently violated, to start the statistical analysis of a given set of test data by stating whether the underlying samples are homogeneous or not.

The chi-square test has been used for such investigations, but this test requires very large samples. The present test is quite simple, and it is not restricted with regard to the size of the sample.

2. THE PRINCIPLE OF THE TEST

Consider a sample of size N with its elements $x_1,\ldots,x_N$ rearranged in ascending order of magnitude. If all these order statistics belong to the same population, and the unknown parameters are estimated by use of a reliable method, say, the maximum likelihood method, applied alternatively to the complete sample and to (N - 1) of its elements, for instance, by excluding the largest order statistic x_N, then no *significant differences between the two* sets of estimates will be expected. If a significant difference appears, then it may be concluded that the value x_N does not belong to the same population as the main part of the other (N - 1) order statistics.

Let $F(x,m,\beta,\mu)$ be the distribution function of the population and let $f(x,m,\beta,\mu)$ be the density function of a single value drawn from it, where m, β, and μ are parameters.

Following formulae presented by Sarhan and Greenberg (1), the density function of the joint distribution of the first k order statistics, which will be called the likelihood equation of the k-truncated sample and denoted by L_k, is given by

$$L_k = \frac{N!}{(N-k)!} \{1 - F(x_k)\}^{N-k} \cdot f(x_1) \ldots f(x_k) \tag{1}$$

which for k = N takes the form

$$L_N = (N!)\ f(x_1)\ldots f(x_N) \tag{2}$$

The present test now consists in computing the particular set of estimates $(\hat{m},\hat{\beta},\hat{\mu})$, which maximizes the likelihood equations L_N and L_{N-1}, possibly also L_{N-2}, etc., and stating whether there are significant differences between the alternative sets of estimates. The term "significant" will be defined in the sequel.

The further calculations will be applied to the Weibull distribution.

3. APPLICATIONS TO THE WEIBULL DISTRIBUTION

3.1 General Formulas

In this particular case, we have

$$P = F(x,m,\beta,\mu) = 1 - e^{-(x-\mu)^m/\beta^m} \qquad (3)$$

and

$$f(x,m,\beta,\mu) = (m/\beta^m)(x-\mu)^{m-1} \cdot e^{-(x-\mu)^m/\beta^m} \qquad (4)$$

Introducing (4) into (1), we have

$$L_k = \frac{N!}{(N-k)!} (m^k/\beta^{km}) ((x_1 - \mu)\ldots(x_k - \mu))^{m-1} \cdot \\ \cdot e^{-((x_1 - \mu)^m + \ldots + (N-k+1)(x_k - \mu)^m)} \qquad (5)$$

and

$$\ln L_k = \ln \frac{N!}{(N-k)!} + k(\ln m) - km (\ln\beta) + (m-1)(\ln (x_1 - \mu) + \ldots \\ + \ln(x_k - \mu)) - ((x_1 - \mu)^m + \ldots + (N-k+1)(x_k - \mu)^m)/\beta^m \qquad (6)$$

From the condition $\partial L_k/\partial\beta = 0$, we obtain

$$\beta^m = ((x_1 - \mu)^m + \ldots + (N - k + 1)(x_k - \mu)^m)/k \qquad (7)$$

Introducing (7) into (5) we have, neglecting factors depending only on N and k,

$$L_k = \frac{m^k (x_1 - \mu) \ldots (x_k - \mu))^{m-1}}{((x_1 - \mu)^m + \ldots + (N - k + 1)(x_k - \mu)^m)^k} \tag{8}$$

which for k = N takes the form

$$L_N = \frac{m^k ((x_1 - \mu) \ldots (x_N - \mu))^{m-1}}{((x_1 - \mu)^m + \ldots + (x_N - \mu)^m)^N} \tag{9}$$

The unknown parameters m and μ may be estimated by equating to zero the partial derivatives of L_k, that is

$$\partial L_k / \partial m = 0, \qquad \partial L_k / \partial \mu = 0 \tag{10}$$

3.2 Criteria for Significant Differences

3.2.1 Parameter μ known

Without loss of generality, we may put $\mu = 0$ and equation (8) then takes the form

$$L_k = \frac{m^k (x_1 \ldots x_k)^{m-1}}{x_1{}^m + \ldots + (N - k + 1) x_k)^k} \tag{11}$$

and

$$\ln L_k = k(\ln m) + (m - 1)(\ln x_1 + \ldots + \ln x_k) - k\ln (x_1{}^m + \ldots + (N - k + 1) x_k{}^m) \tag{12}$$

The likelihood L_k will be maximized by the particular value $\hat{m}$ which satisfies the equation

$$\partial \ln L_k / \partial m = 0 \tag{13}$$

that is,

$$\frac{x_1^{\hat{m}}(\ln x_1^{\hat{m}}) + \ldots + (N-k+1)x_k^{\hat{m}}(\ln x_k^{\hat{m}})}{x_1^{\hat{m}} + \ldots + (N-k+1)x_k^{\hat{m}}} - \frac{\ln x_1^{\hat{m}} + \ldots + \ln x_k^{\hat{m}}}{k} = 1 \qquad (14)$$

The sampling distribution of the estimate $\hat{m}$ may be determined by generating a large number of random samples from the actual population and computing the corresponding values of $\hat{m}$ for each of them by use of equation (14). Observing that the probability P in equation (3) is uniformly distributed over the interval (0,1), the elements x_i of a sample from a Weibull population with the parameters (m_o, β_o) is obtained by taking a sample of random sampling numbers $r_i(0,1)$ and computing x_i from

$$x_i = \beta_o(-\ln(1 - r_i))^{1/m_o} \qquad (15)$$

Introducing (15) into (14), the parameter β_o disappears and $x_i^{\hat{m}}$ will be replaced by

$$x_i^{\hat{m}} = (-\ln(1 - r_i))^{\hat{m}/m_o} \qquad (16)$$

which implies that the sampling distribution of $\hat{m}/m_o$ is, for any given value of k, parameter-free and thus uniquely given for each combination of N and k.

Denoting the estimate of m for k = N by $\hat{m}_1$, for k = N - 1 by $\hat{m}_2$, for k = N - 2 by $\hat{m}_3$, etc., it can be concluded that the quotients $\hat{m}_1/\hat{m}_2$, $\hat{m}_2/\hat{m}_3$, etc., have sampling distributions which are independent of the true population parameter m_o and uniquely given for each sample size N.

From these distributions, quotients $\hat{m}_1/\hat{m}_2$, $\hat{m}_2/\hat{m}_3$, corresponding to preassigned levels of significance, say, 2% or 5%, will be determined. The hypothesis of homogeneity will be rejected for samples yielding larger quotients.

3.2.2 All Parameters Unknown

If none of the parameters is known, it has been found convenient to estimate the parameters by computing the values of L_k or L_N in equations (8) and (9) for an appropriate set of pairs (m,u) and to select that particular pair (m,μ) which yields the largest value of L_k or L_N.

The computer program 6/73 has been written for computing L_N. Observing that

$$0 \leq \mu \leq x_1 \tag{17}$$

this program computes the eleven values of m which maximize L_N for

$$\mu = x_1(i/10) \;, \qquad i = 0(1)10 \tag{18}$$

and corresponding values of $\log L_N$ and $= x_o$.

The computing time of this procedure is about one second for sample size N = 10 with the computer IBM 360, M/75.

This program will now be extended to produce the same set of data for k = N - 1, N - 2, etc., and to present the eleven quotients $\hat{m}_1/\hat{m}_2$, etc. In cases where all the quotients are larger than the assigned levels of significance, the hypothesis of homogeneity will be rejected. If some of the quotients have acceptable values, the decision depends on the location of these values. If they are far from the place of maximum likelihood, they will motivate a rejection. If not, the hypothesis may be accepted or examined by other tests.

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