mathematics

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Detecting Extreme Values with Order Statistics in Samples from Continuous Distributions

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Received: 17 December 2019; Accepted: 4 February 2020; Published: 8 February 2020

Abstract: In the subject of statistics for engineering, physics, computer science, chemistry, and earth sciences, one of the sampling challenges is the accuracy, or, in other words, how representative the sample is of the population from which it was drawn. A series of statistics were developed to measure the departure between the population (theoretical) and the sample (observed) distributions. Another connected issue is the presence of extreme values—possible observations that may have been wrongly collected—which do not belong to the population selected for study. By subjecting those two issues to study, we hereby propose a new statistic for assessing the quality of sampling intended to be used for any continuous distribution. Depending on the sample size, the proposed statistic is operational for known distributions (with a known probability density function) and provides the risk of being in error while assuming that a certain sample has been drawn from a population. A strategy for sample analysis, by analyzing the information about quality of the sampling provided by the order statistics in use, is proposed. A case study was conducted assessing the quality of sampling for ten cases, the latter being used to provide a pattern analysis of the statistics.

Keywords: probability computing; Monte Carlo simulation; order statistics; extreme values; outliers

MSC: 62G30; 62G32; 62H10; 65C60

1. Introduction

Under the assumption that a sample of size n, was drawn from a certain population ($x_1, ..., x_n \in X$) with a known distribution (with known probability density function, PDF) but with unknown parameters (in number of m, $\{\pi_1, ..., \pi_m\}$), there are alternatives available in order to assess the quality of sampling.

One category of alternatives sees the sample as a whole—and in this case, a series of statistics was developed to measure the agreement between a theoretical (in the population) and observed (of the sample) distribution. This approach is actually a reversed engineering of the sampling distribution, providing a likelihood for observing the sample as drawn from the population. To do this for any continuous distribution, the problem is translated into the probability space by the use of a cumulative distribution function (CDF).

Formally, if $\text{PDF}(x;(\pi_j)_{1\le j\le m})$ takes values on a domain D, then CDF is defined by Equation (1) and $\{p_1, ..., p_n\}$ defined by Equation (2) is the series of cumulative probabilities associated with the drawings from the sample.

$$\text{CDF}(x;(\pi_j)_{1\le j\le m}) = \int_{inf(D)}^{x} \text{PDF}(t;(\pi_j)_{1\le j\le m})dt \tag{1}$$

$$\{p_1, ..., p_n\} = \text{CDF}(\{x_1, ..., x_n\};(\pi_j)_{1\le j\le m}). \tag{2}$$

CDF is always a bijective (and invertible; let InvCDF be its inverse, Equation (3)) function.

$$x = \mathrm{InvCDF}(p; (\pi_j)_{1 \le j \le m}). \tag{3}$$

The series of cumulative probabilities $\{p_1, \ldots, p_n\}$, independently of the distribution (PDF) of the population (X) subjected to the analysis, have a known domain ($0 \le p_i \le 1$ for all $1 \le i \le n$) belonging to the continuous uniform distribution ($p_1, \ldots, p_n \in \mathrm{U}(0,1)$). In the sorted cumulative probabilities ($\{q_1, \ldots, q_n\}$ defined by Equation (4)), sorting defines an order relationship ($0 \le q_1 \le \ldots \le q_n \le 1$).

$$\{q_1, \ldots, q_n\} = \mathrm{SORT}(\{p_1, \ldots, p_n\}; \text{"ascending"}). \tag{4}$$

If the order of drawing in sample ($\{x_1, \ldots, x_n\}$) and of appearance in the series of associated CDF ($\{p_1, \ldots, p_n\}$) is not relevant (e.g., the elements in those sets are indistinguishable), the order relationship defined by Equation (4) makes them ($\{q_1, \ldots, q_n\}$) distinguishable (the order being relevant).

A series of order statistics (OS) were developed (to operate on ordered cumulative probabilities $\{q_1, \ldots, q_n\}$) and they may be used to assess the quality of sampling for the sample taken as a whole (Equations (5)–(10) below): Cramér–von Mises ($CM_{Statistic}$ in Equation (5), see [1,2]), Watson U2 ($WU_{Statistic}$ in Equation (6), see [3]), Kolmogorov–Smirnov ($KS_{Statistic}$ in Equation (7), see [4–6]), Kuiper V ($KV_{Statistic}$ in Equation (8), see [7]), Anderson–Darling ($AD_{Statistic}$ in Equation (9), see [8,9]), and H1 ($H1_{Statistic}$ in Equation (10), see [10]).

$$CM_{Statistic} = \frac{1}{12n} + \sum_{i=1}^{n} \left(\frac{2i-1}{2n} - q_i \right)^2 \tag{5}$$

$$WU_{Statistic} = CM_{Statistic} + \left(\frac{1}{2} - \frac{1}{n} \sum_{i=1}^{n} q_i \right)^2 \tag{6}$$

$$KS_{Statistic} = \sqrt{n} \cdot \max_{1 \le i \le n} \left(q_i - \frac{i-1}{n}, \frac{i}{n} - q_i \right) \tag{7}$$

$$KV_{Statistic} = \sqrt{n} \cdot \left(\max_{1 \le i \le n} \left(q_i - \frac{i-1}{n} \right) + \max_{1 \le i \le n} \left(\frac{i}{n} - q_i \right) \right) \tag{8}$$

$$AD_{Statistic} = -n - \frac{1}{n} \sum_{i=1}^{n} (2i-1) \ln\bigl(q_i (1 - q_{n-i}) \bigr) \tag{9}$$

$$H1_{Statistic} = -\sum_{i=1}^{n} q_i \ln(q_i) - \sum_{i=1}^{n} (1 - q_i) \ln(1 - q_i). \tag{10}$$

Recent uses of those statistics include [11] (CM), [12] (WU), [13] (KS), [14] (AD), and [15] (H1). Any of the above given test statistics are to be used, providing a risk of being in error for the assumption (or a likelihood to observe) that the sample ($\{x_1, \ldots, x_n\}$) was drawn from the population (X). Usually this risk of being in error is obtained from Monte Carlo simulations (see [16]) applied on the statistic in question and, in some of the fortunate cases, there is also a closed-form expression (or at least, an analytic expression) for CDF of the statistic available as well. In the less fortunate cases, only 'critical values' (values of the statistic for certain risks of being in error) for the statistic are available.

The other alternative in assessing the quality of sampling refers to an individual observation in the sample, specifically the less likely one (having associated q_1 or q_n with the notations given in Equation (4)). The test statistic is $g1$ [15], given in Equation (11).

$$g1_{Statistic} = \max_{1 \le i \le n} |p_i - 0.5|. \tag{11}$$

It should be noted that 'taken as a whole' refers to the way in which the information contained in the sample is processed in order to provide the outcome. In this scenario ('as a whole'), the entirety of the information contained in the sample is used. As it can be observed in Equations (5)–(10), each formula uses all values of sorted probabilities ($\{q_1, ..., q_n\}$) associated with the values ($\{x_1, ..., x_n\}$) contained in the sample, while, as it can be observed in Equation (11), only the extreme value ($\max(\{q_1, ..., q_n\})$ or $\min(\{q_1, ..., q_n\})$) is used; therefore, one may say that only an individual observation (the extremum portion of the sample) yields the statistical outcome.

The statistic defined by Equation (11) no longer requires cumulative probabilities to be sorted; one only needs to find the most departed probability from 0.5—see Equation (11)—or, alternatively, to find the smallest (one having associated q_1 defined by Equation (4)) and the largest (one having associated q_n defined by Equation (4)), and to find which deviates from 0.5 the most ($g1_{Statistic} = \max\{|q_1 - 0.5|, |q_n - 0.5|\}$).

We hereby propose a hybrid alternative, a test statistic (let us call it *TS*) intended to be used in assessing the quality of sampling for the sample, which is mainly based on the less likely observation in the sample, Equation (12).

$$TS_{Statistic} = \frac{\max\limits_{1 \le i \le n} |p_i - 0.5|}{\sum\limits_{1 \le i \le n} |p_i - 0.5|}. \tag{12}$$

The aim of this paper is to characterize the newly proposed test statistic (*TS*) and to analyze its peculiarities. Unlike the test statistics assessing the quality of sampling for the sample taken as a whole (Equations (5)–(10), and like the test statistic assessing the quality of sampling based on the less likely observation of the sample, Equation (11), the proposed statistic, Equation (12), does not require that the values or their associated probabilities ($\{p_1, ..., p_n\}$) be sorted (as $\{q_1, ..., q_n\}$); since (like the $g1$ statistic) it uses the extreme value from the sample, one can still consider it a sort of *OS* [17]. When dealing with extreme values, the newly proposed statistic, Equation (12), is a much more natural construction of a statistic than the ones previously reported in the literature, Equations (5)–(10), since its value is fed mainly from the extreme value in the sample (see the *max* function in Equation (12)). Later, it will be given a pattern analysis, revealing that it belongs to a distinct group of statistics that are more sensitive to the presence of extreme values. A strategy of using the pool of *OS* (Equations (5)–(12)) including *TS* in the context of dealing with extreme values is given, and the probability patterns provided by the statistics are analyzed.

The rest of the paper is organized as follows. The general strategy of sampling a CDF from an *OS* and the method of combining probabilities from independent tests are given in Section 2, while the analytical formula for the proposed statistic is given in Section 3.1, and computation issues and proof of fact results are given in Section 3.2. Its approximation with other functions is given in Section 3.3. Combining its calculated risk of being in error with the risks from other statistics is given in Section 3.4, while discussion of the results is continued with a cluster analysis in Section 3.5, and in connection with other approaches in Section 3.6. The paper also includes an appendix of the source codes for two programs and accompanying Supplementary Material.

2. Material and Method

2.1. Addressing the Computation of CDF for OS(s)

A method of constructing the observed distribution of the $g1$ statistic, Equation (11), has already been reported elsewhere [15]. A method of constructing the observed distribution of the Anderson–Darling (*AD*) statistic, Equation (9), has already been reported elsewhere [17]; the method for constructing the observed distribution of any *OS* via Monte Carlo (MC) simulation, Equations (5)–(12), is described here and it is used for *TS*, Equation (12).

Let us take a sample size of n. The MC simulation needs to generate a large number of samples (let the number of samples be m) drawn from uniform continuous distribution ($\{p_1, ..., p_n\}$ in

Equation (2)). To ensure a good quality MC simulation, simply using a random number generator is not good enough. The next step (Equations (10)–(12) do not require this) is to sort the probabilities to arrive at $\{q_1, ..., q_n\}$ from Equation (4) and to calculate an OS (an order statistic) associated with each sample. Finally, this series of sample statistics ($\{OS_1, ..., OS_w\}$ in Figure 1) must be sorted in order to arrive at the population emulated distribution. Then, a series of evenly spaced points (from 0 to 1000 in Figure 1) corresponding to fixed probabilities (from $\text{InvCDF}_0 = 0$ to $\text{InvCDF}_{1000} = 1$ in Figure 1) is to be used saving the (OS statistic, its observed CDF probability) pairs (Figure 1).

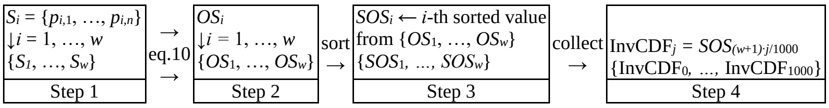

Figure 1. The four steps to arrive at the observed CDF of *OS*.

The main idea is how to generate a good pool of random samples from a uniform $\text{U}(0, 1)$ distribution. Imagine a (pseudo) random number generator, *Rand*, is available, which generates numbers from a uniform $\text{U}(0, 1)$ distribution, from a $[0, 1)$ interval; such an engine is available in many types of software and in most cases, it is based on Mersenne Twister [18]. What if we have to extract a sample of size $n = 2$? If we split in two the $[0, 1)$ interval (then into $[0, 0.5)$ and $[0.5, 1)$) then for two values (let us say $v1$ and $v2$), the contingency of the cases is illustrated in Figure 2.

$\in[0, 1)$	v_1		v_2		v_1v_2				v_1+v_2		
$\in[0, 0.5)$	0	1	0	1	00	01	10	11	0	1	2
occurrence	50%	50%	50%	50%	25%	25%	25%	25%	25%	50%	25%

Figure 2. Contingency of two consecutive drawings from $[0, 1)$.

According to the design given in Figure 2, for 4 (=22) drawings of two numbers ($v1$ and $v2$) from the [0, 1) interval, a better uniform extraction ($v1v2$, 'distinguishable') is ("00") to extract first ($v1$) from [0, 0.5) and second ($v2$) from [0, 0.5), then ("01") to extract first ($v1$) from [0, 0.5) and second ($v2$) from [0.5, 1), then ("10") to extract first ($v1$) from [0, 0.5) and second ($v2$) from [0.5, 1), and finally ("11") to extract first ($v1$) from [0.5, 1) and second ($v2$) from [0.5, 1).

An even better alternative is to do only 3 (=2 + 1) drawings ($v1 + v2$, 'undistinguishable'), which is ("0") to extract both from [0, 0.5), then "1") to extract one (let us say first) from [0, 0.5), and another (let us say second) from [0.5, 1), and finally, ("2") to extract both from [0.5, 1) and to keep a record for their occurrences (1, 2, 1), as well. For n numbers (Figure 3), it can be from [0, 0.5) from 0 to n of them, with their occurrences being accounted for.

$\lvert\{v_i, v_i \in [0, 0.5), 1 \le i \le n\}\rvert$	0	…	j	…	n
Occurrence	1	…	$n!/((n-j)!\cdot j!)$	…	1

Figure 3. Contingency of n consecutive drawings from $[0, 1)$.

According to the formula given in Figure 3, for n numbers to be drawn from [0, 1), a multiple of $n + 1$ drawings must be made in order to maintain the uniformity of distribution (w from Figure 1 becomes $n + 1$). In each of those drawings, we actually only pick one of n (random) numbers (from the [0, 1) interval) as independent. In the $(j + 1)$-th drawing, the first j of them are to be from [0, 0.5), while the rest are to be from [0.5, 1). The algorithm implementing this strategy is given as Algorithm 1.

Algorithm 1 is ready to be used to calculate any OS (including the TS first reported here). For each sample drawn from the $\text{U}(0, 1)$ distribution (the array v in Algorithm 1), the output of it (the array u and its associated frequencies $n!/j!/(n - j)!$) can be modified to produce less information and operations (Algorithm 2). Calculation of the OS (OSj output value in Algorithm 2) can be made to any precision, but for storing the result, a *single* data type (4 bytes) is enough (providing seven significant digits as the precision of the observed CDF of the OS). Along with a *byte* data type (j output value in Algorithm 2) to store each sampled OS, 5 bytes of memory is required, and the calculation of

$n!/(n-j)!/j!$ can be made at a later time, or can be tabulated in a separate array, ready to be used at a later time.

Algorithm 1: Balancing the drawings from uniform $U(0,1)$ distribution.

```
Input data: n ($2 \leq$ n, integer)
Steps:
  For i from 1 to n do v[i] ← Rand
  For j from 0 to n do
    For i from 1 to j do u[i] ← v[i]/2
    For i from j+1 to n do u[i] ← v[i]/2+1/2
    occ ← n!/j!/(n-j)!
    Output u[1], ..., u[n], occ
  EndFor
Output data: (n+1) samples (u) of sample size (n) and their occurrences (occ)
```

Algorithm 2: Sampling an order statistic (*OS*).

```
Input data: n ($2 \leq$ n, integer)
Steps:
  For i from 1 to n do v[i] ← Rand
  For j from 0 to n do
    For i from 1 to j do u[i] ← v[i]/2
    For i from j+1 to n do u[i] ← v[i]/2+1/2
    OSj ← any Equations (5)–(12) with $p_1$ ←u[1], ..., $p_n$ ←u[n]
    Output OSj, j
  EndFor
Output data: (n+1) OS and their occurrences
```

As given in Algorithm 2, each use of the algorithm sampling *OS* will produce two associated arrays: *OSj* (*single* data type) and *j* (*byte* data type); each of them with $n+1$ values. Running the algorithm $r0$ times will require $5 \cdot (n+1) \cdot r0$ bytes for storage of the results and will produce $(n+1) \cdot r0$ *OS*s, ready to be sorted (see Figure 1). With a large amount of internal memory (such as 64 GB when running on a 16/24 cores 64 bit computers), a single process can dynamically address very large arrays and thus can provide a good quality, sampled *OS*. To do this, some implementation tricks are needed (see Table 1).

Table 1. Software implementation peculiarities of MC simulation.

Constant/Variable/Type Value	Meaning
stt ← record v:single; c:byte; end	(OSj, j) pair from Algorithm 2 stored in 5 bytes
mem ← 12,800,000,000	in bytes, 5*mem ← 64Gb, hardware limit
buf ← 1,000,000	the size of a static buffer of data (5*buf bytes)
stst ← array[0..buf-1]of stt	static buffer of data
dyst ← array of stst	dynamic array of buffers
lvl ← 1000	*lvl* + 1: number of points in the grid (see Figure 1)

Depending on the value of the sample size (n), the number of repetitions ($r2$) for sampling of *OS*, using Algorithm 2, from $r0 \leftarrow mem/(n+1)$ runs, is $r2 \leftarrow r0 \cdot (n+1)$, while the length ($sts$) of the variable (CDF*st*) storing the dynamic array (*dyst*) from Table 1 is $sts \leftarrow 1 + r2/buf$. After sorting the *OS*s (of *sttype*, see Table 1; total number of $r2$) another trick is to extract a sample series at evenly spaced probabilities from it (from InvCDF_0 to InvCDF_{1000} in Figure 1). For each pair in the sample (*lvli* varying from 0 to *lvl* = 1000 in Table 1), a value of the *OS* is extracted from CDF*st* array (which contains ordered

OS values and frequencies indexed from 0 to $r2-1$), while the MC-simulated population size is $r0 \cdot 2^n$. A program implementing this strategy is available upon request (*project_OS.pas*).

The associated objective (with any statistic) is to obtain its CDF and thus, by evaluating the CDF for the statistical value obtained from the sample, Equations (5)–(12), to associate a likelihood for the sampling. Please note that only in the lucky cases is it possible to do this; in the general case, only critical values (values corresponding to certain risks of being in error) or approximation formulas are available (see for instance [1–3,5,7–9]). When a closed form or an approximation formula is assessed against the observed values from an MC simulation (such as the one given in Table 1), a measure of the departure such as the standard error (SE) indicates the degree of agreement between the two. If a series of evenly spaced points ($lvl+1$ points indexed from 0 to lvl in Table 1) is used, then a standard error of the agreement for inner points of it (from 1 to $lvl-1$, see Equation (13)) is safe to be computed (where p_i stands for the observed probability while $\hat{p}_i$ for the estimated one).

$$SE = \sqrt{\frac{SS}{lvl-1}}, \quad SS = \sum_{i=1}^{lvl-1} (p_i - \hat{p}_i)^2. \tag{13}$$

In the case of $lvl+1$, evenly spaced points in the interval $[0,1]$ in the context of MC simulation (as the one given in Table 1) providing the values of OS statistic in those points (see Figure 1), the observed cumulative probability should (and is) taken as $p_i = i/lvl$, while $\hat{p}_i$ is to be (and were) taken from any closed form or approximation formula for the CDF statistic (labeled $\hat{p}$) as $\hat{p}_i = \hat{p}(\text{InvCDF}_i)$, where InvCDF_i are the values collected by the strategy given in Figure 1 operating on the values provided by Algorithm 2. Before giving a closed form for CDF of *TS* (Equation (12)) and proposing approximation formulas, other theoretical considerations are needed.

2.2. Further Theoretical Considerations Required for the Study

When the PDF is known, it does not necessarily imply that its statistical parameters ($(\pi_j)_{1\leq j\leq m}$ in Equations (1)–(3)) are known, and here, a complex problem of estimating the parameters of the population distribution from the sample (it then uses the same information as the one used to assess the quality of sampling) or from something else (and then it does not use the same information as the one used to assess the quality of sampling) can be (re)opened, but this matter is outside the scope of this paper.

The estimation of distribution parameters $(\pi_j)_{1\leq j\leq m}$ for the data is, generally, biased by the presence of extreme values in the data, and thus, identifying the outliers along with the estimation of parameters for the distribution is a difficult task operating on two statistical hypotheses. Under this state of facts, the use of a hybrid statistic, such as the proposed one in Equation (12), seems justified. However, since the practical use of the proposed statistics almost always requires estimation of the population parameters (and in the examples given below, as well), a certain perspective on estimation methods is required.

Assuming that the parameters are obtained using the maximum likelihood estimation method (MLE, Equation (14); see [19]), one could say that the uncertainty accompanying this estimation is propagated to the process of detecting the outliers. With a series of τ statistics ($\tau = 6$ for Equations (5)–(10) and $\tau = 8$ for Equations (5)–(12)) assessing independently the risk of being in error (let be $\alpha_1, ..., \alpha_\tau$ those risks), assuming that the sample was drawn from the population, the unlikeliness of the event (α_{FCS} in Equation (15) below) can be ascertained safely by using a modified form of Fisher's "combining probability from independent tests" method (FCS, see [10,20,21]; Equation (15)), where $\text{CDF}_{\chi^2}(x;\tau)$ is the CDF of χ^2 distribution with τ degrees of freedom.

$$\max\Big(\prod_{1\leq i\leq n} \text{PDF}(x_i;(\pi_j)_{1\leq j\leq m})\Big) \rightarrow \min\Big(\sum_{1\leq j\leq m} \ln\big(\text{PDF}(x_i;(\pi_j)_{1\leq j\leq m})\big)\Big) \tag{14}$$

$$FCS = -\ln\Big(\prod_{1\le k\le\tau}\alpha_k\Big), \alpha_{FCS} = 1-\mathrm{CDF}_{\chi^2}(FCS;\tau). \tag{15}$$

Two known symmetrical distributions were used (PDF, see Equation (1)) to express the relative deviation from the observed distribution: Gauss ($G2$ in Equation (16)) and generalized Gauss–Laplace (GL in Equation (17)), where (in both Equations (16) and (17)) $z = (x-\mu)/\sigma$.

$$G2(x;\mu,\sigma) = (2\pi)^{-1/2}\sigma^{-1}e^{-z^2/2} \tag{16}$$

$$GL(x;\mu,\sigma,\kappa) = \frac{c_1}{\sigma}e^{-|c_0 z|^\kappa}, c_0 = \left(\frac{\Gamma(3/\kappa)}{\Gamma(1/\kappa)}\right)^{1/2}, c_1 = \frac{\kappa c_0}{2\Gamma(1/\kappa)}. \tag{17}$$

The distributions given in Equations (16) and (17) will be later used to approximate the CDF of TS as well as in the case studies of using the order statistics. For a sum ($x \leftarrow p_1+...+p_n$ in Equation (18)) of uniformly distributed ($p_1,...,p_n \in U(0,1)$) deviates (as $\{p_1,...,p_n\}$ in Equation (2)) the literature reports the Irwin–Hall distribution [22,23]. The $\mathrm{CDF}_{IH}(x;n)$ is:

$$\mathrm{CDF}_{IH}(x;n) = \sum_{k=0}^{\lfloor x\rfloor}(-1)^k\frac{(x-k)^n}{k!(n-k)!}. \tag{18}$$

3. Results and Discussion

3.1. The Analytical Formula of CDF for *TS*

The CDF of TS depends (only) on the sample size (n), e.g., $\mathrm{CDF}_{TS}(x;n)$. As the proposed equation, Equation (12), resembles (as an inverse of) a sum of normal deviates, we expected that the CDF_{TS} will also be connected with the Irwin–Hall distribution, Equation (18). Indeed, the conducted study has shown that the inverse ($y \leftarrow 1/x$) of the variable (x) following the TS follows a distribution ($1/TS$) of which the CDF is given in Equation (19). Please note that the similarity between Equations (18) and (19) is not totally coincidental; $1/TS$ (see Equation (12)) is more or less a sum of uniform distributed deviates divided by the highest one. Also, for any positive arbitrary generated series, its ascending (x) and descending ($1/x$) sorts are complementary. With the proper substitution, $\mathrm{CDF}_{1/TS}(y;n)$ can be expressed as a function of CDF_{IH}—see Equation (20).

$$\mathrm{CDF}_{1/TS}(y;n) = \sum_{k=0}^{\lfloor n-y\rfloor}(-1)^k\frac{(n-y-k)^{n-1}}{k!(n-1-k)!} \tag{19}$$

$$\mathrm{CDF}_{1/TS}(y;n) = \mathrm{CDF}_{IH}(n-y;n-1). \tag{20}$$

Unfortunately, the formulas, Equation (18) to Equation (20), are not appropriate for large n and p ($p = \mathrm{CDF}_{1/TS}(y;n)$ from Equation (19)), due to the error propagated from a large number of numerical operations (see further Table 2 in Section 3.2). Therefore, for $p > 0.5$, a similar expression providing the value for $\alpha = 1-p$ is more suitable. It is possible to use a closed analytical formula for $\alpha = 1-\mathrm{CDF}_{1/TS}(y;n)$ as well, Equation (21). Equation (21) resembles the Irwin–Hall distribution even more closely than Equation (20)—see Equation (22).

$$1-\mathrm{CDF}_{1/TS}(y;n) = \sum_{k=0}^{\lfloor y\rfloor-1}(-1)^k\frac{(y-1-k)^n}{k!(n-1-k)!} \tag{21}$$

$$1-\mathrm{CDF}_{1/TS}(y;n) = \mathrm{CDF}_{IH}(y-1;n-1). \tag{22}$$

For consistency in the following notations, one should remember the definition of CDF, see Equation (1), and then we mark the connection between notations in terms of the analytical expressions of the functions, Equation (23):

$$\begin{aligned}\mathrm{CDF}_{TS}(x;n)=1–\mathrm{CDF}_{1/TS}(1/x;n), \mathrm{CDF}_{TS}(1/x;n)=1-\mathrm{CDF}_{1/TS}(x;n),\\ \text{since } \mathrm{InvCDF}_{TS}(p;n)\cdot\mathrm{InvCDF}_{1/TS}(p;n)=1.\end{aligned} \tag{23}$$

One should notice (Equation (1); Equation (23)) that the infimum for the domain of $1/TS$ (1) is the supremum for the domain of TS (1) and the supremum (n) for the domain of $1/TS$ is the infimum (1/n) for the domain of TS. Also, TS has the median ($p = \alpha = 0.5$) at $2/(n+1)$, while $1/TS$ has the median (which is also the mean and mode) at $(n+1)/2$. The distribution of $1/TS$ is symmetrical.

For $n = 2$, the $p = \mathrm{CDF}_{1/TS}(y;n)$ is linear ($y + p = 2$), while for $n = 3$, it is a mixture of two square functions: $2p = (3-y)^2$, for $p \leq 0.5$ (and $y \geq 2$), and $2p + (y-1)^2 = 1$ for $p \geq 0.5$ (and $x \leq 2$). With the increase of n, the number of mixed polynomials of increasing degree defining its expression increases. Therefore, it has no way to provide an analytical expression for InvCDF of $1/TS$, not even for certain p values (such as 'critical' analytical functions).

The distribution of $1/TS$ can be further characterized by its central moments (Mean μ, Variance σ^2, Skewness γ_1, and Kurtosis κ in Equation (24)), which are closely connected with the Irwin–Hall distribution.

$$\text{For } 1/TS(y;n)\text{: } \mu=(n+1)/2;\ \sigma^2=(n-1)/12, \gamma_1=0; \kappa=3-6/(5n-5). \tag{24}$$

3.2. Computations for the CDF of TS and Its Analytical Formula

Before we proceed in providing the simulation results, some computational issues must be addressed. Any of the formulas provided for CDF of TS (Equations (19) and (21); or Equations (20) and (22) both connected with Equation (18)), will provide almost exact calculations as long as computations with the formulas are conducted with an engine or package that performs the operations with rational numbers to an infinite precision (such as is available in the Mathematica software [24]), when also the value of y ($y \leftarrow 1/x$, of floating point type) is converted to a rounded, rational number. Otherwise, with increasing n, the evaluation of CDF for TS using either Equation (19) to Equation (22) carries huge computational errors (see the alternating sign of the terms in the sums of Equations (18), (19), and (21)). In order to account for those computational errors (and to reduce their magnitude) an alternate formula for the CDF of TS is proposed (Algorithm 3), combining the formulas from Equations (19) and (21), and reducing the number of summed terms.

Algorithm 3: Avoiding computational errors for *TS*.

```
Input data: n (n ≥ 2, integer), x (1 ≤ x ≤ 1/n, real number, double precision)
  $y \leftarrow 1/x$; //$p_{1/TS} \leftarrow$ Equation (19), $\alpha_{1/TS} \leftarrow$ Equation (21)
if y <(n+1)/2
  $p \leftarrow \sum_{k=0}^{\lfloor y\rfloor-1}(-1)^k\frac{(y-1-k)^n}{k!(n-1-k)!}$ ; $\alpha \leftarrow 1-p$
else if y >(n+1)/2
  $\alpha \leftarrow \sum_{k=0}^{\lfloor n-y\rfloor}(-1)^k\frac{(n-y-k)^{n-1}}{k!(n-1-k)!}$ ; $p \leftarrow 1-\alpha$
else
  $\alpha \leftarrow 0.5$ ; $p \leftarrow 0.5$
Output data: $\alpha=\alpha_{1/TS}=p_{TS} \leftarrow \mathrm{CDF}_{TS}(x;n)$ and $p=p_{1/TS}=\alpha_{TS} \leftarrow 1-p_{TS}$
```

Table 2 contains the sums of the residuals ($SS = \sum_{i=1}^{999}(p_i - \hat{p}_i)^2$ in Equation (13), $lvl = 1000$) of the agreement between the observed CDF of *TS* ($p_i = i/1000$, for i from 1 to 999) and the calculated CDF of *TS* (the $\hat{p}_i$ values are calculated using Algorithm 3 from $x_i = \text{InvCDF}(i/1000; n)$ for i from 1 to 999) for some values of the sample size (n). To prove the previous given statements, Table 2 provides the square sums of residuals computed using three alternate formulas (from Equation (20) and from Equation (22), along with the ones from Algorithm 3).

Table 2. Square sums of residuals calculated in double precision (IEEE 754 binary64, 64 bits).

n	p_i Calculated with Equation (19)	p_i Calculated with Equation (21)	p_i Calculated with Algorithm 4
34	$3.0601572482628 \times 10^{-8}$	$3.0601603616294 \times 10^{-8}$	$3.0601364353173 \times 10^{-8}$
35	$6.0059397209079 \times 10^{-8}$	$6.0057955311142 \times 10^{-8}$	$6.0057052975471 \times 10^{-8}$
36	$1.1567997676343 \times 10^{-8}$	$1.1572997605838 \times 10^{-8}$	$1.1567370749831 \times 10^{-8}$
37	$8.9214456109544 \times 10^{-8}$	$8.9215230398577 \times 10^{-8}$	$8.9213063043724 \times 10^{-8}$
38	$1.1684682533384 \times 10^{-8}$	$1.1681544866285 \times 10^{-8}$	$1.1677646550768 \times 10^{-8}$
39	$1.2101651325053 \times 10^{-8}$	$1.2181659126285 \times 10^{-8}$	$1.2100378665608 \times 10^{-8}$
40	$1.1041708665520 \times 10^{-7}$	$1.1043952711846 \times 10^{-7}$	$1.1036003349029 \times 10^{-7}$
41	$7.2871410520319 \times 10^{-8}$	$7.2755412302319 \times 10^{-8}$	$7.2487977100103 \times 10^{-8}$
42	$1.9483807018501 \times 10^{-8}$	$1.9626447735907 \times 10^{-8}$	$1.9273186509959 \times 10^{-8}$
43	$3.1128379331196 \times 10^{-8}$	$1.7088238120170 \times 10^{-8}$	$1.3899520242290 \times 10^{-8}$
44	$8.7810761126831 \times 10^{-8}$	$3.8671367222236 \times 10^{-8}$	$1.0878689813951 \times 10^{-8}$
45	$1.1914784602127 \times 10^{-7}$	$3.1416715528555 \times 10^{-7}$	$5.8339481916925 \times 10^{-8}$
46	$2.0770754629042 \times 10^{-6}$	$1.2401177918843 \times 10^{-6}$	$4.4594953399233 \times 10^{-8}$
47	$5.0816356972050 \times 10^{-7}$	$4.1644326761832 \times 10^{-7}$	$1.8942487765410 \times 10^{-8}$
48	$1.5504732794049 \times 10^{-6}$	$5.5760558048026 \times 10^{-6}$	$5.7292512517324 \times 10^{-8}$
49	$1.1594466754136 \times 10^{-5}$	$6.4164330856396 \times 10^{-6}$	$1.7286761495408 \times 10^{-7}$
50	$1.0902858025759 \times 10^{-5}$	$8.0190771776360 \times 10^{-6}$	$8.5891058550425 \times 10^{-8}$
51	$6.4572577668164 \times 10^{-6}$	$1.6023753568028 \times 10^{-4}$	$1.9676739380922 \times 10^{-8}$
52	$1.0080944275181 \times 10^{-4}$	$9.1080176774820 \times 10^{-5}$	$1.0359121739272 \times 10^{-7}$
53	$9.3219609856284 \times 10^{-4}$	$2.7347575817507 \times 10^{-4}$	$1.5873847007230 \times 10^{-8}$
54	$4.8555844748161 \times 10^{-4}$	$1.6086902937472 \times 10^{-3}$	$9.2930071189138 \times 10^{-9}$
55	$6.2446720485774 \times 10^{-4}$	$1.6579954395873 \times 10^{-3}$	$1.2848119194342 \times 10^{-7}$

In red: computing affected digits.

As given in Table 2, the computational errors by using either Equation (20) (or Equation (19)) and Equation (22) (or Equation (21)) until n = 34 are reasonably low, while from n = 42, they become significant. As can be seen (red values in Table 2), double precision alone cannot cope with the large number of computations, especially as the terms in the sums are constantly changing their signs (see $(-1)^k$ in Equations (19) and (21)).

The computational errors using Algorithm 3 are reasonably low for the whole domain of the simulated CDF of *TS* (with n from 2 to 55), but the combined formula (Algorithm 3) is expected to lose its precision for large n values, and therefore, a solution to safely compute (CDF for IH, *TS* and $1/TS$) is to operate with rational numbers.

One other alternative is to use GNU GMP (Multiple Precision Arithmetic Library [25]). The calculations are the same (Algorithm 3); the only difference is the way in which the temporary variables are declared (instead of *double*, the variables become *mpf_t* initialized later with a desired precision).

For convenience, the FreePascal [26] implementation for CDF of the Irwin–Hall distribution (Equation (18), called in the context of evaluating the CDF of *TS* in Equations (20) and (22)) is given as Algorithm 4.

Algorithm 4: FreePascal implementation for calculating the CDF of *IH*.

```
Input data: n (integer), x (real number, double precision);
  var k,i: integer; //integer enough for n < 32,768
  var z,y: mpf_t; //double or extended instead of mpf_t
Begin //CDF for Irwin–Hall distribution
  mpf_set_default_prec(128); //or bigger,256,512,...
  mpf_init(y); mpf_init(z); //y := 0.0;
  for k := trunc(x) downto 0 do begin //main loop
    If(k mod 2 = 0) // z := 1.0 or z := −1.0;
      then mpf_set_si(z,1) //z := 1.0;
      else mpf_set_si(z,-1); //z := -1.0;
    for i := n − k downto 1 do z := z*(x − k)/i;
    for i := k downto 1 do z := z*(x− k)/i;
    y := y + z;
  end;
  pIH_gmp := mpf_get_d(y); mpf_clear(z); mpf_clear(y);
End;
Output data: p (real number, double precision)
```

In Algorithm 4, the changes made to a classical code running without GNU GMP floating point arithmetic functions are written in blue color. For convenience, the combined formula (Algorithm 3) trick for avoiding the computation errors can be implemented with the code given as Algorithm 4 at the call level, Equation (25). If `pIH(x:double; n:integer):double` returns the value from Algorithm 4, then $pg1$, as given in Equation (25), safely returns the combined formula (Algorithm 3) with (or without) GNU GMP.

$$pg1 \leftarrow \begin{cases} 1-pIH(n-1, n-1/x), & \text{if } x(n+1) < 2. \\ pIH(n-1, 1/x-1), & \text{otherwise.} \end{cases} \tag{25}$$

Regarding Table 2, Algorithm 4 listed data, from $n = 2$ to $n = 55$, the calculation of the residuals were made with *double* (64 bits), *extended* (FreePascal 80 bits), and *mpf_t*-128 bits (GNU GMP). The sum of residuals (for all n from 2 to 55) differs from *double* to *extended* with less than 10^{-11} and the same for *mpf_t* with 128 bits, which safely provides confidence in the results provided in Table 2 for the combined formula (last column, Algorithm 4). The deviates for agreement in the calculation of CDF for TS are statistically characterized by SE (Equation (13)), *min*, and *max* in Table 3.

The SE of agreement (Table 3) between the expected value and the observed one (Algorithm 4, Equation (12), Table 1) of the $\text{CDF}_{1/TS}(x; n)$ is safely below the resolution for the grid of observing points ($lvl^{-1} = 10^{-3}$ in Table 1; $SE \leq 1.2 \times 10^{-5}$ in Table 3; two orders of magnitude). By using Algorithm 4, Figures 4–7 depict the shapes of $\text{CDF}_{TS}(x; n)$, $\text{CDF}_{1/TS}(x; n)$, $\text{InvCDF}_{TS}(x; n)$, and $\text{InvCDF}_{1/TS}(x; n)$ for n from 2 to 20.

Finally, for the domain of the simulated CDF of the TS population for n from 2 to 54, the error in the odd points of the grid (for $1000 \cdot p$ from 1 to 999 with a step of 2) is depicted in Figure 8 (the calculations of theoretical CDF for TS made with *gmpfloat* at a precision of at least 256 bits). As can be observed in Figure 8, the difference between p and $\hat{p}$ is rarely larger than 10^{-5} and never larger than 3×10^{-5} (the boundary of the representation in Figure 8) for n ranging from 2 to 54.

Table 3. Descriptive for the agreement in the calculation of the CDF of TS (Equation (12) vs. Algorithm 4).

n	SE	$minep$	$maxep$	n	SE	$minep$	$maxep$	n	SE	$minep$	$maxep$
2	3.0×10^{-6}	-2.1×10^{-6}	1.8×10^{-6}	20	5.4×10^{-6}	-4.1×10^{-6}	3.9×10^{-6}	38	3.4×10^{-6}	-7.3×10^{-6}	6.1×10^{-6}
3	3.2×10^{-6}	-2.4×10^{-6}	2.7×10^{-6}	21	3.0×10^{-6}	-4.5×10^{-6}	4.1×10^{-6}	39	3.5×10^{-6}	-7.3×10^{-6}	6.4×10^{-6}
4	3.5×10^{-6}	-2.3×10^{-6}	2.7×10^{-6}	22	6.3×10^{-6}	-4.8×10^{-6}	4.0×10^{-6}	40	1.1×10^{-5}	-7.2×10^{-6}	5.5×10^{-6}
5	4.2×10^{-6}	-2.8×10^{-6}	2.2×10^{-6}	23	5.6×10^{-6}	-5.6×10^{-6}	4.6×10^{-6}	41	8.5×10^{-6}	-7.2×10^{-6}	7.4×10^{-6}
6	2.8×10^{-6}	-3.2×10^{-6}	2.4×10^{-6}	24	4.0×10^{-6}	-6.4×10^{-6}	4.6×10^{-6}	42	4.4×10^{-6}	-7.0×10^{-6}	7.8×10^{-6}
7	4.4×10^{-6}	-3.3×10^{-6}	3.1×10^{-6}	25	4.1×10^{-6}	-6.3×10^{-6}	4.5×10^{-6}	43	3.7×10^{-6}	-6.5×10^{-6}	6.9×10^{-6}
8	3.5×10^{-6}	-3.7×10^{-6}	2.6×10^{-6}	26	1.2×10^{-5}	-6.2×10^{-6}	5.1×10^{-6}	44	3.3×10^{-6}	-6.1×10^{-6}	7.0×10^{-6}
9	3.7×10^{-6}	-3.9×10^{-6}	2.2×10^{-6}	27	1.2×10^{-5}	-6.3×10^{-6}	4.9×10^{-6}	45	7.6×10^{-6}	-6.1×10^{-6}	6.8×10^{-6}
10	4.5×10^{-6}	-3.7×10^{-6}	2.9×10^{-6}	28	7.8×10^{-6}	-6.3×10^{-6}	5.1×10^{-6}	46	6.7×10^{-6}	-6.1×10^{-6}	6.9×10^{-6}
11	5.7×10^{-6}	-3.7×10^{-6}	2.7×10^{-6}	29	7.2×10^{-6}	-6.6×10^{-6}	5.4×10^{-6}	47	4.4×10^{-6}	-6.2×10^{-6}	7.3×10^{-6}
12	7.6×10^{-6}	-3.9×10^{-6}	2.5×10^{-6}	30	3.5×10^{-6}	-6.3×10^{-6}	5.7×10^{-6}	48	7.6×10^{-6}	-6.2×10^{-6}	8.0×10^{-6}
13	5.2×10^{-6}	-3.8×10^{-6}	3.0×10^{-6}	31	4.1×10^{-6}	-6.2×10^{-6}	5.0×10^{-6}	49	1.3×10^{-5}	-6.3×10^{-6}	7.8×10^{-6}
14	5.6×10^{-6}	-4.3×10^{-6}	3.2×10^{-6}	32	5.2×10^{-6}	-6.0×10^{-6}	4.9×10^{-6}	50	9.3×10^{-6}	-6.0×10^{-6}	7.0×10^{-6}
15	1.0×10^{-5}	-3.8×10^{-6}	3.5×10^{-6}	33	3.5×10^{-6}	-6.0×10^{-6}	4.5×10^{-6}	51	4.4×10^{-6}	-6.4×10^{-6}	7.0×10^{-6}
16	6.9×10^{-6}	-3.9×10^{-6}	3.6×10^{-6}	34	5.5×10^{-6}	-6.6×10^{-6}	4.3×10^{-6}	52	1.0×10^{-5}	-6.4×10^{-6}	6.4×10^{-6}
17	8.4×10^{-6}	-4.2×10^{-6}	3.5×10^{-6}	35	7.8×10^{-6}	-6.3×10^{-6}	5.2×10^{-6}	53	4.0×10^{-6}	-6.1×10^{-6}	6.1×10^{-6}
18	5.1×10^{-6}	-4.1×10^{-6}	4.1×10^{-6}	36	3.4×10^{-6}	-6.7×10^{-6}	5.7×10^{-6}	54	3.1×10^{-6}	-6.4×10^{-6}	6.7×10^{-6}
19	5.4×10^{-6}	-4.2×10^{-6}	4.4×10^{-6}	37	9.4×10^{-6}	-6.8×10^{-6}	6.4×10^{-6}	55	1.1×10^{-5}	-6.7×10^{-6}	7.1×10^{-6}

$minep = min(p_i - \hat{p}_i),\ maxep = max(p_i - \hat{p}_i).$

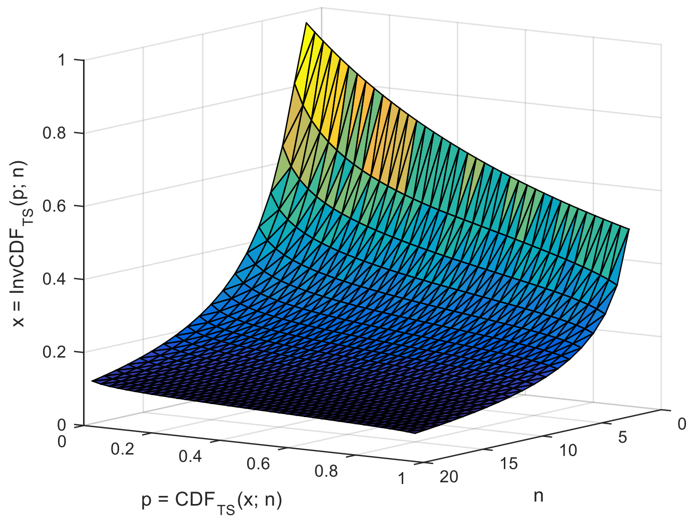

Figure 4. InvCDF$_{TS}(x; n)$ for n = 2 to 20.

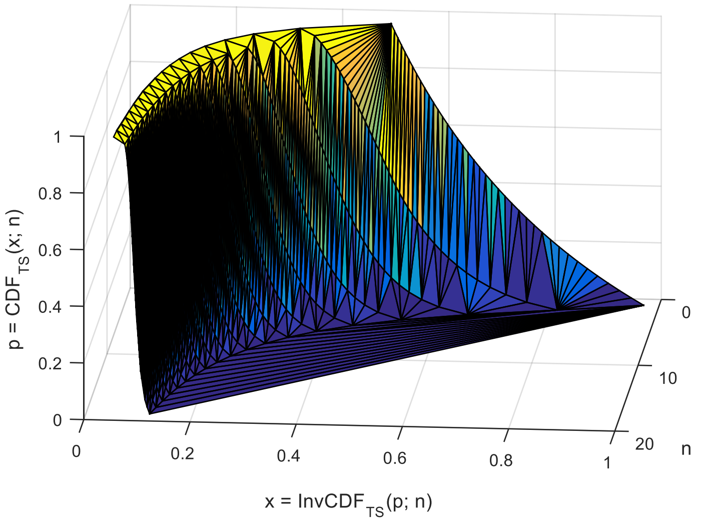

Figure 5. CDF$_{TS}(x; n)$ for n = 2 to 20.

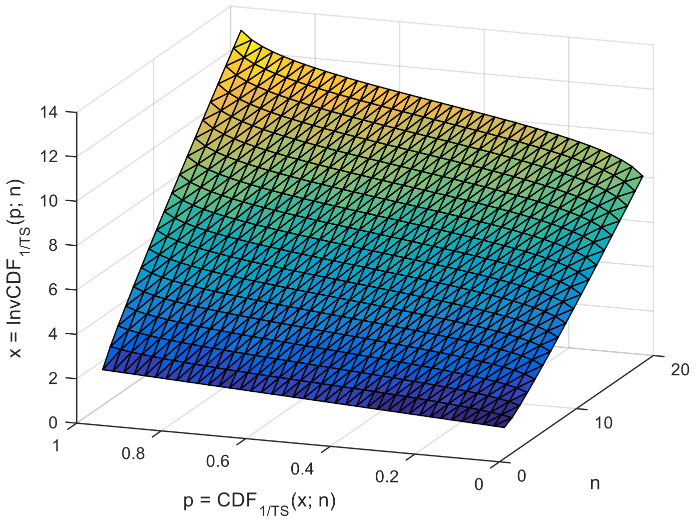

Figure 6. InvCDF$_{1/TS}(x; n)$ for n = 2 to 20.

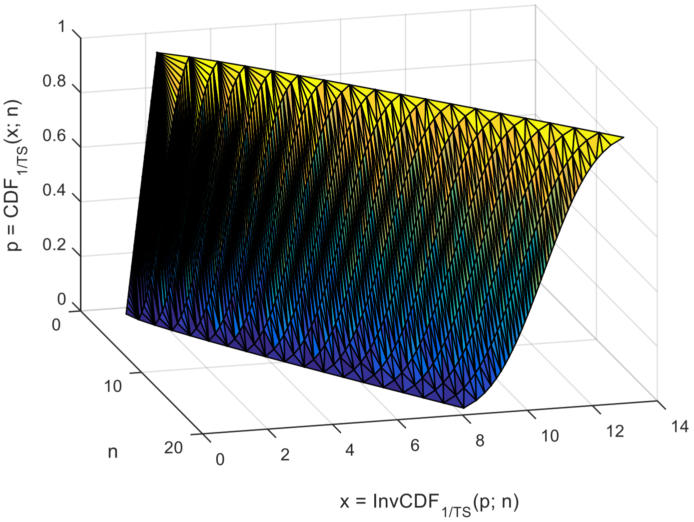

Figure 7. $\mathrm{CDF}_{1/TS}(x;n)$ for n = 2 to 20.

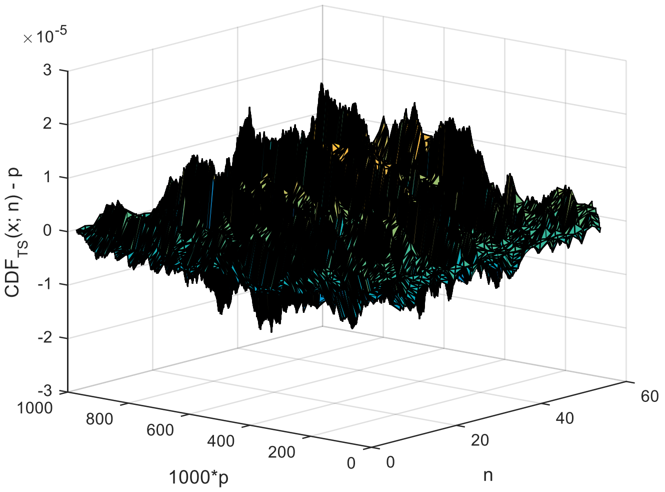

Figure 8. Agreement estimating CDF_{TS} for n = 2...54 and $1000p$ = 1...999 with a step of 2.

Based on the provided results, one may say that there is no error in saying that Equations (19) and (21) are complements (see Equation (23) as well) of the CDF of *TS* given as Equation (12). As long as the calculations (of either Equations (19) and (21)) are conducted using rational numbers, either formula provides the most accurate result. The remaining concerns are how large those numbers can be (e.g., the range of n). This is limited only by the amount of memory available and how precise the calculations are. This reaches the maximum defined by the measurement of data precision, and finally, the resolutions are provided, which are given by the precision of converting (if necessary) the *TS* value given by Equation (12) from float to rational. Either way, some applications prefer approximate formulas, which are easier to calculate, and are considered common knowledge for interpreting the results. For those reasons, the next section describes approximation formulas.

3.3. Approximations of CDF of TS with Known Functions

Considering, once again, Equation (24), for sufficiently large n, the distribution of $1/TS$ is approximately normal (Equation (26). For normal Gauss distribution, see Equation (16)).

$$\mathrm{PDF}_{1/TS}(y;n)\xrightarrow{n\to\infty}\mathrm{PDF}_{G2}((n+1)/2;\sqrt{(n-1)/12}). \qquad (26)$$

Even better (than Equation (26)), for large values of n, a generalized Gauss–Laplace distribution (see Equation (17)) can be used to approximate the $1/TS$ statistic. Furthermore, for those looking for critical values of the TS statistic, the approximation of the $1/TS$ statistic to a generalized Gauss–Laplace distribution may provide safe critical values for large n. One way to derive the parameters of the generalized Gauss–Laplace distribution approximating the $1/TS$ statistic is by connecting the kurtosis and skewness of the two (Equation (27)).

$$Ku(\beta)=\frac{\Gamma(\frac{5}{\beta})\Gamma(\frac{1}{\beta})}{\Gamma(\frac{3}{\beta})\Gamma(\frac{3}{\beta})}\to\beta=Ku^{-1}\left(3-\frac{6}{5n-5}\right),\ \alpha=\sqrt{\frac{n-1}{12}\frac{\Gamma(1/\beta)}{\Gamma(3/\beta)}}. \tag{27}$$

With α and β given by Equation (27) and $\mu = (n+1)/2$ (Equation (24)), the PDF of the generalized Gauss–Laplace distribution (Equation (17)), which approximates $1/TS$ (for large n), is given in Equation (28).

$$\mathrm{PDF}_{GL}(x;\mu,\alpha,\beta) = \frac{\beta}{2\alpha\Gamma(1/\beta)}e^{-\left(\frac{|x-\mu|}{\alpha}\right)^{\beta}}. \tag{28}$$

The errors of approximation (with Equation (29)) of $p_i = \mathrm{CDF}_{1/TS}$ (from Algorithm 3) with $\hat{p}_i = \mathrm{CDF}_{GL}$ (from Equations (27) and 28) are depicted in Figure 9 using a grid of 52×999 points for $n = 50...101$ and $p = 0.001...0.999$.

$$SE=\sqrt{\sum_{i=1}^{999}\frac{(p_i-\hat{p}_i)^2}{999}},\ p_i=\frac{i}{10^3},\ \hat{p}_i = \mathrm{CDF}_{GL}(\mathrm{InvCDF}_{1/TS}(p_i;n);\alpha,\beta). \tag{29}$$

As can be observed in Figure 9, the confidence in approximation of $1/TS$ with the GL increases with the sample size (n), but the increase is less than linear. The tendency is to approximately linearly decrease with an exponential increase.

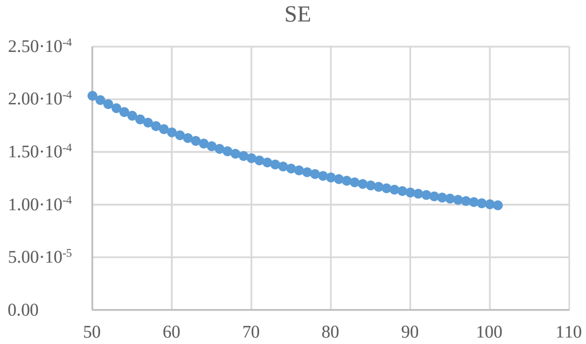

Figure 9. Standard errors (SE) as function of sample size (n) for the approximation of $1/TS$ with GL (Equation (29)).

The calculation of CDF for $1/TS$ is a little tricky, as anticipated previously (see Section 3.2). To avoid the computation errors in the calculation of CDF_{TS}, a combined formula is more appropriate (Algorithms 3 and 4). With $p_{1/TS} \leftarrow \mathrm{CDF}_{1/TS}(y;n)$ and $\alpha_{1/TS} \leftarrow 1-\mathrm{CDF}_{1/TS}(y;n)$, depending on the value of y ($y \leftarrow 1/x$, where x is the sample statistic of TS, Equation (12)), only one (from α and p, where $\alpha + p = 1$) is suitable for a precise calculation.

An important remark at this point is that $(n+1)/2$ is the median, mean, and mode for $1/TS$ (see Section 3.1). Indeed, any symbolic calculation with either of the formulas from Equation (19) to Equation (22) will provide that $\mathrm{CDF}_{1/TS}((n+1)/2;n) = 0.5$, or, expressed with InvCDF, $\mathrm{InvCDF}_{1/TS}(0.5;n) = (n+1)/2$.

3.4. The Use of CDF for TS to Measure the Departure between an Observed Distribution and a Theoretical One

With any of Equations (5)–(12), a likelihood to observe an observed sample can be ascertained. One may ask which statistic is to be trusted. The answer is, at the same time, none and all, as the problem of fitting the data to a certain distribution involves the estimation of the distribution's parameters—such as using MLE, Equation (14). In this process of estimation, there is an intrinsic variability that cannot be ascertained by one statistic alone. This is the reason that calculating the risk of being in error from a battery of statistics is necessary, Equation (15).

Also, one may say that the $g1$ statistic (Equation (11)) is not associated with the sample, but to its extreme value(s), while others may say the opposite. Again, the truth is that both are right, as in certain cases, samples containing outliers are considered not appropriate for the analysis [27], and in those cases, there are exactly two modes of action: to reject the sample or to remove the outlier(s). Figure 10 gives the proposed strategy of assessing the samples using order statistics.

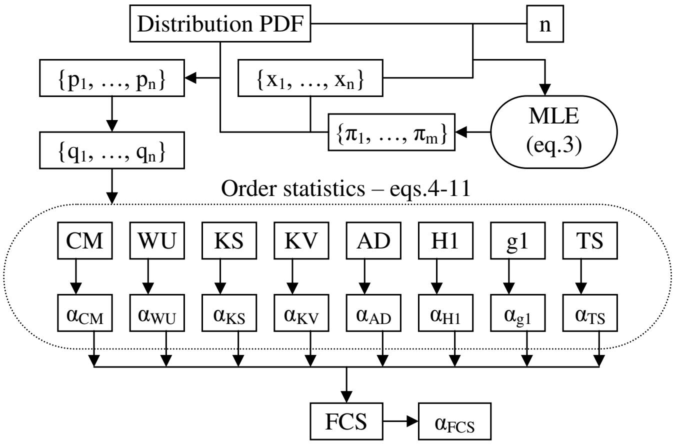

Figure 10. Using the order statistics to measure the likelihood of sampling.

As other authors have noted, in nonparametric problems, it is known that order statistics, i.e., the ordered set of values in a random sample from least to greatest, play a fundamental role. 'A considerable amount of new statistical inference theory can be established from order statistics assuming nothing stronger than continuity of the cumulative distribution function of the population' as [28] noted, a statement that is perfectly valid today.

In the following case studies, the values of the sample statistics were calculated with Equations (5)–(10) ($AD, KS, CM, KV, WU, H1$; see also Figure 10), while the risks of being in error—associated with the values of sample statistics ($\alpha_{Statistic}$ for those)—were calculated with the program developed and posted online available at http://l.academicdirect.org/Statistics/tests. The $g1_{Statistic}$ (Equation (11)) and α_{g1} were calculated as given in [15], while the $TS_{Statistic}$ (Equation (12)) was calculated with Algorithm 4. For FCS and α_{FCS}, Equation (15) was used.

Case study 1.

Data: "Example 1" in [29]; Distribution: Gauss (Equation (16)); Sample size: $n = 10$; Population parameters (MLE, Equation (14)): $\mu = 575.2$; $\sigma = 8.256$; Order statistics analysis is given in Table 4. Conclusion: at $\alpha = 5\%$ risk of being in error, the sample does not have an outlier ($\alpha_{g1} = 11.2\%$) but it is a bad drawing from normal (Gauss) distribution, with less than the imposed level ($\alpha = 5\%$) likelihood to appear from a random draw ($\alpha_{FCS} = 4.5\%$).

Table 4. Order statistics analysis for case studies 1 to 10.

Case	Parameter	AD	KS	CM	KV	WU	$H1$	$g1$	TS	FCS
1	*Statistic*	1.137	1.110	0.206	1.715	0.182	5.266	0.494	4.961	15.80
	$\alpha_{Statistic}$	0.288	0.132	0.259	0.028	0.049	0.343	0.112	0.270	0.045
2	*Statistic*	0.348	0.549	0.042	0.934	0.039	7.974	0.496	6.653	6.463
	$\alpha_{Statistic}$	0.894	0.884	0.927	0.814	0.844	0.264	0.109	0.107	0.596
3	*Statistic*	0.617	0.630	0.092	1.140	0.082	4.859	0.471	5.785	4.627
	$\alpha_{Statistic}$	0.619	0.742	0.635	0.486	0.401	0.609	0.451	0.627	0.797
4	*Statistic*	0.793	0.827	0.144	1.368	0.129	3.993	0.482	4.292	8.954
	$\alpha_{Statistic}$	0.482	0.420	0.414	0.190	0.154	0.524	0.255	0.395	0.346
5	*Statistic*	0.440	0.486	0.049	0.954	0.047	104.2	0.500	103.2	5.879
	$\alpha_{Statistic}$	0.810	0.963	0.884	0.850	0.742	0.359	0.034	0.533	0.661
6	*Statistic*	0.565	0.707	0.083	1.144	0.061	83.32	0.499	82.17	5.641
	$\alpha_{Statistic}$	0.683	0.675	0.673	0.578	0.580	0.455	0.247	0.305	0.687
7	*Statistic*	1.031	1.052	0.170	1.662	0.149	52.66	0.494	51.00	11.24
	$\alpha_{Statistic}$	0.320	0.202	0.333	0.067	0.106	0.471	0.729	0.249	0.188
8	*Statistic*	0.996	0.771	0.132	1.375	0.127	22.201	0.460	27.95	5.933
	$\alpha_{Statistic}$	0.322	0.556	0.451	0.248	0.162	0.853	0.980	0.978	0.655
9	*Statistic*	0.398	0.576	0.058	1.031	0.051	31.236	0.489	32.04	2.692
	$\alpha_{Statistic}$	0.853	0.869	0.828	0.728	0.694	0.577	0.746	0.507	0.952
10	*Statistic*	0.670	0.646	0.092	1.170	0.085	11.92	0.460	14.66	3.549
	$\alpha_{Statistic}$	0.583	0.753	0.627	0.488	0.373	0.747	0.874	0.879	0.895

Case study 2.

Data: "Example 3" in [29]; Distribution: Gauss (Equation (16)); Sample size: $n = 15$; Population parameters (MLE, Equation (14)): $\mu = 0.018$; $\sigma = 0.532$; Order statistics analysis is given in Table 4. Conclusion: at $\alpha = 5\%$ risk of being in error, the sample does not have an outlier ($\alpha_{g1} = 10.9\%$) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level ($\alpha = 5\%$) likelihood to appear from a random draw ($\alpha_{FCS} = 59.6\%$).

Case study 3.

Data: "Example 4" in [29]; Distribution: Gauss (Equation (16)); Sample size: $n = 10$; Population parameters (MLE, Equation (14)): $\mu = 3.406$; $\sigma = 0.732$; Order statistics analysis is given in Table 4. Conclusion: at $\alpha = 5\%$ risk of being in error, the sample does not have an outlier ($\alpha_{g1} = 45.1\%$) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level ($\alpha = 5\%$) likelihood to appear from a random draw ($\alpha_{FCS} = 79.7\%$).

Case study 4.

Data: "Example 5" in [29]; Distribution: Gauss (Equation (16)); Sample size: $n = 8$; Population parameters (MLE, Equation (14)): $\mu = 4715$; $\sigma = 140.8$; Order statistics analysis is given in Table 4. Conclusion: at $\alpha = 5\%$ risk of being in error, the sample does not have an outlier ($\alpha_{g1} = 25.5\%$) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level ($\alpha = 5\%$) likelihood to appear from a random draw ($\alpha_{FCS} = 34.6\%$).

Case study 5.

Data: "Table 4" in [15]; Distribution: Gauss (Equation (16)); Sample size: $n = 206$; Population parameters (MLE, Equation (14)): $\mu = 6.481$; $\sigma = 0.829$; Order statistics analysis is given in Table 4. Conclusion: at $\alpha = 5\%$ risk of being in error, the sample have an outlier ($\alpha_{g1} = 3.4\%$) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level (α = 5%) likelihood to appear from a random draw (α_{FCS} = 66.1%).

Case study 6.

Data: "Table 1, Column 1" in [30]; Distribution: Gauss (Equation (16)); Sample size: n = 166; Population parameters (MLE, Equation (14)): $\mu = -0.348$; $\sigma = 1.8015$; Order statistics analysis is given in Table 4. Conclusion: at α = 5% risk of being in error, the sample does not have an outlier (α_{g1} = 24.7%) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level (α = 5%) likelihood to appear from a random draw (α_{FCS} = 68.7%).

Case study 7.

Data: "Table 1, Set BBB" in [31]; Distribution: Gauss (Equation (16)); Sample size: n = 105; Population parameters (MLE, Equation (14)): $\mu = -0.094$; $\sigma = 0.762$; Order statistics analysis is given in Table 4. Conclusion: at α = 5% risk of being in error, the sample does not have an outlier (α_{g1} = 72.9%) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level (α = 5%) likelihood to appear from a random draw (α_{FCS} = 18.8%).

Case study 8.

Data: "Table 1, Set SASCAII" in [31]; Distribution: Gauss (Equation (16)); Sample size: n = 47; Population parameters (MLE, Equation (14)): $\mu = 1.749$; $\sigma = 0.505$; Order statistics analysis is given in Table 4. Conclusion: at α = 5% risk of being in error, the sample does not have an outlier (α_{g1} = 98.0%) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level (α = 5%) likelihood to appear from a random draw (α_{FCS} = 65.5%).

Case study 9.

Data: "Table 1, Set TaxoIA" in [31]; Distribution: Gauss (Equation (16)); Sample size: n = 63; Population parameters (MLE, Equation (14)): $\mu = 0.744$; $\sigma = 0.670$; Order statistics analysis is given in Table 4. Conclusion: at α = 5% risk of being in error, the sample does not have an outlier (α_{g1} = 74.6%) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level (α = 5%) likelihood to appear from a random draw (α_{FCS} = 95.2%).

Case study 10.

Data: "Table 1, Set ERBAT" in [31]; Distribution: Gauss (Equation (16)); Sample size: n = 25; Population parameters (MLE, Equation (14)): $\mu = 0.379$; $\sigma = 1.357$; Order statistics analysis is given in Table 4. Conclusion: at α = 5% risk of being in error, the sample does not have an outlier (α_{g1} = 87.9%) and it is a good drawing from normal (Gauss) distribution, with more than the imposed level (α = 5%) likelihood to appear from a random draw (α_{FCS} = 89.5%).

3.5. The Patterns in the Order Statistics

A cluster analysis on the risks of being in error, provided by the series of order statistics on the case studies considered in this study, may reveal a series of peculiarities (Figures 11 and 12). The analysis given here is based on the series of the above given case studies in order to illustrate similarities (and not to provide a 'gold standard' as in [32] or in [33]).

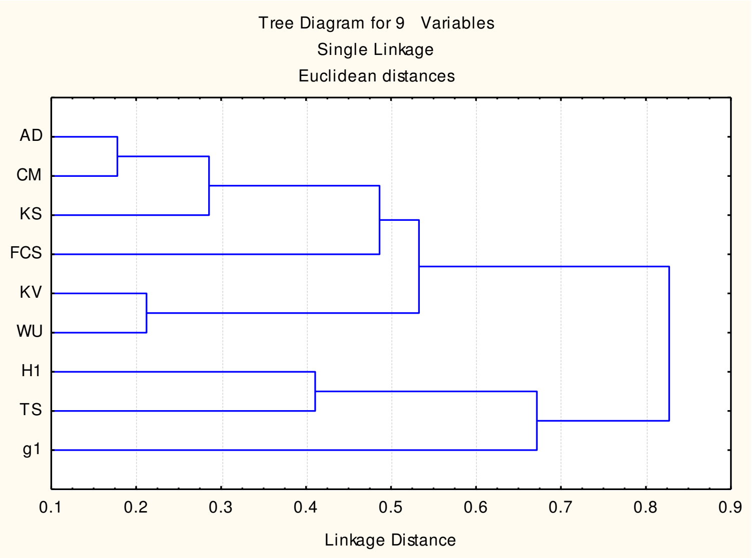

Figure 11. Euclidian distances between the risks being in error provided by the order statistics.

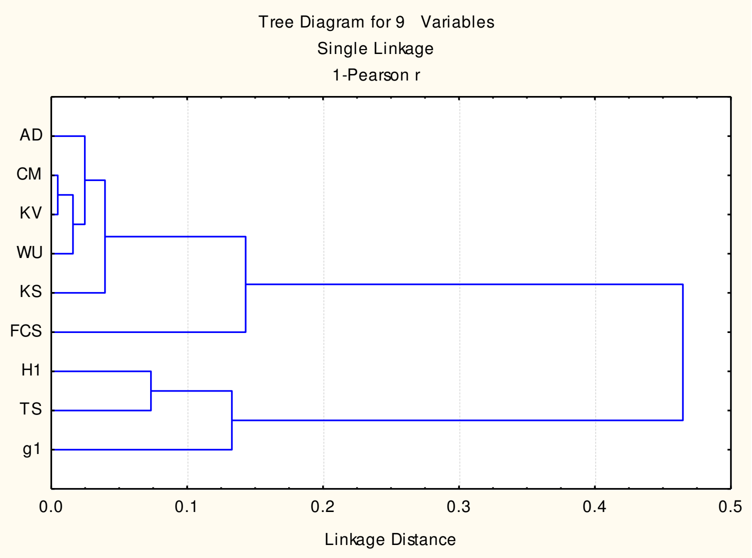

Figure 12. Pearson disagreement between the risks being in error provided by the order statistics.

Both clustering methods illustrated in Figures 11 and 12 reveal two distinct groups of statistics: {AD, CM, KV, WU, KS} and {H1, TS, g1}. The combined test FCS is also attracted (as expected) to the largest group. When looking at single Euclidean distances (Figure 11) of the largest group, two other associations should be noticed {AD, CM, KS} and {KV, WU}, suggesting that those groups carry similar information, but when looking at the Pearson disagreements (Figure 12), we must notice that the subgroups are changed {CM, KV, WU}, {AD}, and {KS}, with no hint of an association with their calculation formulas (Equations (5)–(9)); therefore, their independence should not be dismissed. The second group {H1, TS, g1} is more stable, maintaining the same clustering pattern of the group ({H1, TS}, {g1} in Figure 12).

Taking into account that the g1 test (Equation (11)) was specifically designed to account for outliers suggests that the H1 and TS tests are more sensitive to the outliers than other statistics, and therefore, when the outliers (or just the presence of extreme values) are the main concern in the sampling, it is strongly suggested to use those tests. The H1 statistic is a Shannon entropy formula applied in the probability space of the sample. When accounting for this aspect in the reasoning, the rassociation of the H1 with TS suggests that TS is a sort of entropic measure (max-entropy, to be more exact [34], a limit case of generalized Rényi's entropy [35]). Again, the g1 statistic is alone in this entropic group, suggesting that it carries a unique fingerprint about the sample—specifically, about its extreme value (see Equation (11))—while the others account for the context (the rest of the sampled values, Equations (10) and (12)).

Regarding the newly proposed statistic (TS), from the given case studies, the fact that it belongs to the {H1, TS, g1} group strongly suggests that it is more susceptible to the presence of outliers (such as g1, purely defined for this task, and unlike the well known statistics defined by Equations (5)–(9)).

Moreover, one may ask that, if based on the risks being in error provided by the statistics from case studies 1 to 10, some peculiarity about TS or another statistic involved in this study could be revealed. An alternative is to ask if the values of risks can be considered to be belonging to the same population or not, and for this, the K-sample Anderson–Darling test can be invoked [36]. With the series of probabilities, there are actually $2^9 - 1 - 9 = 502$ tests to be conducted (for each subgroup of 2, 3, 4, 5, 6, 7, 8, and 9 statistics picked from nine possible choices) and for each of them, the answer is same: At the 5% risk of being in error, it cannot be rejected that the groups (of statistics) were selected from identical populations (of statistics), so, overall, any of those statistics perform the same.

The proposed method may find its uses in testing symmetry [37], as a homogeneity test [38] and, of course, in the process of detecting outliers [39].

3.6. Another Rank Order Statics Method and Other Approaches

The series of rank order statistics included in this study, Equations (5)–(11), covers the most known rank order statistics reported to date. However, when considering a new order statistic not included there, the use of it in the context of combining methods, Equation (15), only increases the degrees of freedom τ, while the design of using (Figure 10) is changed accordingly.

It should be noted that the proposed approach is intended to be used for small sample sizes, when no statistic alone is capable of high precision and high trueness. With the increasing sample size, all statistics should converge to the same risk of being in error and present other alternatives, such as the superstatistical approach [40]. In the same context, each of the drawings included in the sample are supposed to be independent. In the presence of correlated data (such as correlated in time), again, other approaches, such as the one communicated in [41], are more suited.

4. Conclusions

A new test statistic to be used to measure the agreement between continuous theoretical distributions and samples drawn from *TS* was proposed. The analytical formula of the *TS* cumulative distribution function was obtained. The comparative study against other order statistics revealed that the newly proposed statistic carries distinct information regarding the quality of the sampling. A combined probability formula from a battery of statistics is suggested as a more accurate measure for the quality of the sampling. Therefore Equation (15) combining the probabilities (the risks of being in error) from Equation (5) to Equation (12) is recommended anytime when extreme values are suspected being outliers in samples from continuous distributions.

Supplementary Materials: The following are available online at http://www.mdpi.com/2227-7390/8/2/216/s1. The source code for sampling order statistics (file named OS.pas) and source code evaluation of the CDF of *TS* with Algorithm 4 (file named TS.pas file) are available upon request. The k-Sample Anderson–Darling test(s) on risks of being in error from the case studies 1 to 10 is given as a supplementary file.

Funding: This research received no external funding.

Acknowledgments: The following software were used during the research and writing the paper: Lazarus (freeware) were used to compile the 64bit executable for Monte Carlo sampling (using the parametrization given in Table 1). The executable was compiled to work for a 64GB multi-core workstation and were used so. Mathcad (v.14, licensed) were used to check the validity for some of the equations given (Equations (19)–(22), (24), (26), (27)), and to do the MLE estimates (implementing Equation (14) with first order derivatives and results given in Section 3.4 as Case studies 1 to 10). Matlab (v.8.5.0, licensed) was used to obtain Figures 4–8. Wolfram Mathematica (v.12.0, licensed) was used to check (iteratively) the formulas given for $1/TS$ (Equations (19) and 21))

and to provide the data for Figure 8. FreePascal (with GNU GMP, freeware) were used to assess numerically the agreement for TS statistic (Tables 2 and 3, Figure 8). StatSoft Statistica (v.7, licensed) was used to obtain Figures 11 and 12.

Conflicts of Interest: The author declares no conflict of interest.

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Supplementary information: kS-AD test on risks being in error from case studies 1 to 10

(http://l.academicdirect.org/Statistics/tests/kS-AD/ with "Case_Statistics.txt" input data)

Compute k-sample Anderson-Darling test.

Refs:

- Scholz FW, Stephens MA. 1987. K-sample Anderson-Darling Tests. Journal of the American Statistical Association 82:918-924.
- Department of Defense Handbook. 2002. Composite Materials Handbook. Volume 1. Polymer Matrix Composites Guidelines for Characterization of Structural Materials. Chapter 8. Statistical Methods. 8.3.2.2 The k-sample Anderson-Darling test, MIL-HDBK-17-1F.

Name Table:

Grp\Obs	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	Cnt
AD	0.288	0.894	0.619	0.482	0.81	0.683	0.32	0.322	0.853	0.583	10
KS	0.132	0.884	0.742	0.42	0.963	0.675	0.202	0.556	0.869	0.753	10
CM	0.259	0.927	0.635	0.414	0.884	0.673	0.333	0.451	0.828	0.627	10
KV	0.028	0.814	0.486	0.19	0.85	0.578	0.067	0.248	0.728	0.488	10
WU	0.049	0.844	0.401	0.154	0.742	0.58	0.106	0.162	0.694	0.373	10
H1	0.343	0.264	0.609	0.524	0.359	0.455	0.471	0.853	0.577	0.747	10
g1	0.112	0.109	0.451	0.255	0.034	0.247	0.729	0.98	0.746	0.874	10
TS	0.27	0.107	0.627	0.395	0.533	0.305	0.249	0.978	0.507	0.879	10
FCS	0.045	0.596	0.797	0.346	0.661	0.687	0.188	0.655	0.952	0.895	10

Here X are split into it's components.

X=(AD, KS, CM, KV, WU, H1, g1, TS, FCS)

Nr	X's	G.S	kAD	cAD	c/k	Groups	Interpretation
1	000000011	2	0.8946	2.3653	2.64	TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
2	000000101	2	0.5426	2.3653	4.36	g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
3	000000110	2	0.5793	2.3653	4.08	g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
4	000000111	3	0.6768	1.9672	2.91	g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
5	000001001	2	1.1767	2.3653	2.01	H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
6	000001010	2	0.7073	2.3653	3.34	H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
7	000001011	3	0.9044	1.9672	2.18	H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
8	000001100	2	1.6960	2.3653	1.39	H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
9	000001101	3	1.1149	1.9672	1.76	H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
10	000001110	3	0.9726	1.9672	2.02	H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
11	000001111	4	0.9136	1.7831	1.95	H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
12	000010001	2	1.0046	2.3653	2.35	WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
13	000010010	2	0.6654	2.3653	3.55	WU, TS	Cannot be rejected that the groups were selected from *identical populations*.

14	000010011	3	0.8476	1.9672	2.32	WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
15	000010100	2	0.4233	2.3653	5.59	WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
16	000010101	3	0.6289	1.9672	3.13	WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
17	000010110	3	0.5246	1.9672	3.75	WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
18	000010111	4	0.6628	1.7831	2.69	WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
19	000011000	2	1.0621	2.3653	2.23	WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
20	000011001	3	1.1048	1.9672	1.78	WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
21	000011010	3	0.8378	1.9672	2.35	WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
22	000011011	4	0.9223	1.7831	1.93	WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
23	000011100	3	0.9940	1.9672	1.98	WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
24	000011101	4	0.9405	1.7831	1.90	WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
25	000011110	4	0.8097	1.7831	2.20	WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
26	000011111	5	0.8432	1.6727	1.98	WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
27	000100001	2	0.7643	2.3653	3.09	KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
28	000100010	2	0.6654	2.3653	3.55	KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
29	000100011	3	0.7586	1.9672	2.59	KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
30	000100100	2	0.3981	2.3653	5.94	KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
31	000100101	3	0.5486	1.9672	3.59	KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
32	000100110	3	0.5166	1.9672	3.81	KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
33	000100111	4	0.6193	1.7831	2.88	KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
34	000101000	2	0.8991	2.3653	2.63	KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
35	000101001	3	0.9436	1.9672	2.08	KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
36	000101010	3	0.7841	1.9672	2.51	KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
37	000101011	4	0.8402	1.7831	2.12	KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
38	000101100	3	0.9327	1.9672	2.11	KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.

39	000101101	4	0.8659	1.7831	2.06	KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
40	000101110	4	0.7791	1.7831	2.29	KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
41	000101111	5	0.7970	1.6727	2.10	KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
42	000110000	2	0.2655	2.3653	8.91	KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
43	000110001	3	0.6977	1.9672	2.82	KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
44	000110010	3	0.5244	1.9672	3.75	KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
45	000110011	4	0.7003	1.7831	2.55	KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
46	000110100	3	0.3802	1.9672	5.17	KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
47	000110101	4	0.5564	1.7831	3.20	KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
48	000110110	4	0.4747	1.7831	3.76	KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
49	000110111	5	0.5987	1.6727	2.79	KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
50	000111000	3	0.6771	1.9672	2.91	KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
51	000111001	4	0.8591	1.7831	2.08	KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
52	000111010	4	0.6987	1.7831	2.55	KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
53	000111011	5	0.7991	1.6727	2.09	KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
54	000111100	4	0.7361	1.7831	2.42	KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
55	000111101	5	0.7829	1.6727	2.14	KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
56	000111110	5	0.6884	1.6727	2.43	KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
57	000111111	6	0.7471	1.5976	2.14	KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
58	001000001	2	0.3497	2.3653	6.76	CM, FCS	Cannot be rejected that the groups were selected from *identical populations*.
59	001000010	2	1.0316	2.3653	2.29	CM, TS	Cannot be rejected that the groups were selected from *identical populations*.
60	001000011	3	0.7386	1.9672	2.66	CM, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
61	001000100	2	1.4738	2.3653	1.60	CM, g1	Cannot be rejected that the groups were selected from *identical populations*.
62	001000101	3	0.7847	1.9672	2.51	CM, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
63	001000110	3	1.0166	1.9672	1.94	CM, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.

64	001000111	4	0.8023	1.7831	2.22	CM, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
65	001001000	2	0.8008	2.3653	2.95	CM, H1	Cannot be rejected that the groups were selected from *identical populations*.
66	001001001	3	0.7663	1.9672	2.57	CM, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
67	001001010	3	0.8677	1.9672	2.27	CM, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
68	001001011	4	0.8086	1.7831	2.21	CM, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
69	001001100	3	1.4526	1.9672	1.35	CM, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
70	001001101	4	1.0341	1.7831	1.72	CM, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
71	001001110	4	1.0851	1.7831	1.64	CM, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
72	001001111	5	0.9287	1.6727	1.80	CM, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
73	001010000	2	1.5974	2.3653	1.48	CM, WU	Cannot be rejected that the groups were selected from *identical populations*.
74	001010001	3	0.9655	1.9672	2.04	CM, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
75	001010010	3	1.0875	1.9672	1.81	CM, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
76	001010011	4	0.9048	1.7831	1.97	CM, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
77	001010100	3	1.0572	1.9672	1.86	CM, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
78	001010101	4	0.8393	1.7831	2.12	CM, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
79	001010110	4	0.8992	1.7831	1.98	CM, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
80	001010111	5	0.8146	1.6727	2.05	CM, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
81	001011000	3	1.2735	1.9672	1.54	CM, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
82	001011001	4	1.0277	1.7831	1.73	CM, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
83	001011010	4	1.0265	1.7831	1.74	CM, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
84	001011011	5	0.9375	1.6727	1.78	CM, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
85	001011100	4	1.1571	1.7831	1.54	CM, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
86	001011101	5	0.9889	1.6727	1.69	CM, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
87	001011110	5	0.9842	1.6727	1.70	CM, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
88	001011111	6	0.9117	1.5976	1.75	CM, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.

89	001100000	2	1.2600	2.3653	1.88	CM, KV	Cannot be rejected that the groups were selected from *identical populations*.
90	001100001	3	0.7504	1.9672	2.62	CM, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
91	001100010	3	0.9784	1.9672	2.01	CM, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
92	001100011	4	0.7965	1.7831	2.24	CM, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
93	001100100	3	0.9423	1.9672	2.09	CM, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
94	001100101	4	0.7384	1.7831	2.41	CM, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
95	001100110	4	0.8421	1.7831	2.12	CM, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
96	001100111	5	0.7529	1.6727	2.22	CM, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
97	001101000	3	1.1032	1.9672	1.78	CM, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
98	001101001	4	0.8788	1.7831	2.03	CM, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
99	001101010	4	0.9437	1.7831	1.89	CM, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
100	001101011	5	0.8494	1.6727	1.97	CM, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
101	001101100	4	1.0714	1.7831	1.66	CM, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
102	001101101	5	0.9070	1.6727	1.84	CM, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
103	001101110	5	0.9333	1.6727	1.79	CM, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
104	001101111	6	0.8567	1.5976	1.86	CM, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
105	001110000	3	0.9963	1.9672	1.97	CM, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
106	001110001	4	0.8364	1.7831	2.13	CM, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
107	001110010	4	0.8735	1.7831	2.04	CM, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
108	001110011	5	0.8153	1.6727	2.05	CM, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
109	001110100	4	0.8171	1.7831	2.18	CM, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
110	001110101	5	0.7480	1.6727	2.24	CM, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
111	001110110	5	0.7698	1.6727	2.17	CM, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
112	001110111	6	0.7449	1.5976	2.14	CM, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
113	001111000	4	1.0020	1.7831	1.78	CM, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.

114	001111001	5	0.9128	1.6727	1.83	CM, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
115	001111010	5	0.8984	1.6727	1.86	CM, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
116	001111011	6	0.8646	1.5976	1.85	CM, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
117	001111100	5	0.9405	1.6727	1.78	CM, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
118	001111101	6	0.8731	1.5976	1.83	CM, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
119	001111110	6	0.8613	1.5976	1.85	CM, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
120	001111111	7	0.8333	1.5423	1.85	CM, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
121	010000001	2	0.2591	2.3653	9.13	KS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
122	010000010	2	0.9833	2.3653	2.41	KS, TS	Cannot be rejected that the groups were selected from *identical populations*.
123	010000011	3	0.7109	1.9672	2.77	KS, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
124	010000100	2	0.9355	2.3653	2.53	KS, g1	Cannot be rejected that the groups were selected from *identical populations*.
125	010000101	3	0.5888	1.9672	3.34	KS, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
126	010000110	3	0.8387	1.9672	2.35	KS, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
127	010000111	4	0.7057	1.7831	2.53	KS, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
128	010001000	2	1.3360	2.3653	1.77	KS, H1	Cannot be rejected that the groups were selected from *identical populations*.
129	010001001	3	0.8737	1.9672	2.25	KS, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
130	010001010	3	0.9816	1.9672	2.00	KS, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
131	010001011	4	0.8560	1.7831	2.08	KS, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
132	010001100	3	1.3410	1.9672	1.47	KS, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
133	010001101	4	0.9775	1.7831	1.82	KS, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
134	010001110	4	1.0334	1.7831	1.73	KS, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
135	010001111	5	0.8959	1.6727	1.87	KS, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
136	010010000	2	1.7279	2.3653	1.37	KS, WU	Cannot be rejected that the groups were selected from *identical populations*.
137	010010001	3	0.9776	1.9672	2.01	KS, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
138	010010010	3	1.1333	1.9672	1.74	KS, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.

139	010010011	4	0.9138	1.7831	1.95	KS, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
140	010010100	3	0.9650	1.9672	2.04	KS, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
141	010010101	4	0.7777	1.7831	2.29	KS, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
142	010010110	4	0.8547	1.7831	2.09	KS, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
143	010010111	5	0.7790	1.6727	2.15	KS, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
144	010011000	3	1.4615	1.9672	1.35	KS, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
145	010011001	4	1.0987	1.7831	1.62	KS, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
146	010011010	4	1.1124	1.7831	1.60	KS, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
147	010011011	5	0.9789	1.6727	1.71	KS, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
148	010011100	4	1.1645	1.7831	1.53	KS, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
149	010011101	5	0.9831	1.6727	1.70	KS, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
150	010011110	5	0.9876	1.6727	1.69	KS, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
151	010011111	6	0.9078	1.5976	1.76	KS, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
152	010100000	2	1.2145	2.3653	1.95	KS, KV	Cannot be rejected that the groups were selected from *identical populations*.
153	010100001	3	0.7207	1.9672	2.73	KS, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
154	010100010	3	0.9569	1.9672	2.06	KS, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
155	010100011	4	0.7802	1.7831	2.29	KS, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
156	010100100	3	0.7959	1.9672	2.47	KS, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
157	010100101	4	0.6539	1.7831	2.73	KS, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
158	010100110	4	0.7673	1.7831	2.32	KS, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
159	010100111	5	0.7017	1.6727	2.38	KS, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
160	010101000	3	1.2125	1.9672	1.62	KS, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
161	010101001	4	0.9237	1.7831	1.93	KS, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
162	010101010	4	0.9881	1.7831	1.80	KS, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
163	010101011	5	0.8729	1.6727	1.92	KS, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.

164	010101100	4	1.0454	1.7831	1.71	KS, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
165	010101101	5	0.8849	1.6727	1.89	KS, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
166	010101110	5	0.9153	1.6727	1.83	KS, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
167	010101111	6	0.8410	1.5976	1.90	KS, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
168	010110000	3	1.1037	1.9672	1.78	KS, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
169	010110001	4	0.8648	1.7831	2.06	KS, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
170	010110010	4	0.9174	1.7831	1.94	KS, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
171	010110011	5	0.8306	1.6727	2.01	KS, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
172	010110100	4	0.7956	1.7831	2.24	KS, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
173	010110101	5	0.7235	1.6727	2.31	KS, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
174	010110110	5	0.7553	1.6727	2.21	KS, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
175	010110111	6	0.7283	1.5976	2.19	KS, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
176	010111000	4	1.1328	1.7831	1.57	KS, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
177	010111001	5	0.9701	1.6727	1.72	KS, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
178	010111010	5	0.9637	1.6727	1.74	KS, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
179	010111011	6	0.8993	1.5976	1.78	KS, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
180	010111100	5	0.9643	1.6727	1.73	KS, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
181	010111101	6	0.8795	1.5976	1.82	KS, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
182	010111110	6	0.8737	1.5976	1.83	KS, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
183	010111111	7	0.8366	1.5423	1.84	KS, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
184	011000000	2	0.4621	2.3653	5.12	KS, CM	Cannot be rejected that the groups were selected from *identical populations*.
185	011000001	3	0.3400	1.9672	5.79	KS, CM, FCS	Cannot be rejected that the groups were selected from *identical populations*.
186	011000010	3	0.8104	1.9672	2.43	KS, CM, TS	Cannot be rejected that the groups were selected from *identical populations*.
187	011000011	4	0.6463	1.7831	2.76	KS, CM, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
188	011000100	3	0.9983	1.9672	1.97	KS, CM, g1	Cannot be rejected that the groups were selected from *identical populations*.

189	011000101	4	0.6832	1.7831	2.61	KS, CM, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
190	011000110	4	0.9182	1.7831	1.94	KS, CM, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
191	011000111	5	0.7520	1.6727	2.22	KS, CM, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
192	011001000	3	0.8558	1.9672	2.30	KS, CM, H1	Cannot be rejected that the groups were selected from *identical populations*.
193	011001001	4	0.6949	1.7831	2.57	KS, CM, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
194	011001010	4	0.8687	1.7831	2.05	KS, CM, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
195	011001011	5	0.7695	1.6727	2.17	KS, CM, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
196	011001100	4	1.1885	1.7831	1.50	KS, CM, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
197	011001101	5	0.9187	1.6727	1.82	KS, CM, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
198	011001110	5	1.0218	1.6727	1.64	KS, CM, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
199	011001111	6	0.8814	1.5976	1.81	KS, CM, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
200	011010000	3	1.2659	1.9672	1.55	KS, CM, WU	Cannot be rejected that the groups were selected from *identical populations*.
201	011010001	4	0.8859	1.7831	2.01	KS, CM, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
202	011010010	4	1.0791	1.7831	1.65	KS, CM, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
203	011010011	5	0.8850	1.6727	1.89	KS, CM, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
204	011010100	4	1.0449	1.7831	1.71	KS, CM, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
205	011010101	5	0.8390	1.6727	1.99	KS, CM, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
206	011010110	5	0.9513	1.6727	1.76	KS, CM, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
207	011010111	6	0.8337	1.5976	1.92	KS, CM, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
208	011011000	4	1.2276	1.7831	1.45	KS, CM, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
209	011011001	5	0.9867	1.6727	1.70	KS, CM, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
210	011011010	5	1.0686	1.6727	1.57	KS, CM, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
211	011011011	6	0.9374	1.5976	1.70	KS, CM, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
212	011011100	5	1.1438	1.6727	1.46	KS, CM, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
213	011011101	6	0.9720	1.5976	1.64	KS, CM, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.

214	011011110	6	1.0217	1.5976	1.56	KS, CM, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
215	011011111	7	0.9214	1.5423	1.67	KS, CM, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
216	011100000	3	0.9643	1.9672	2.04	KS, CM, KV	Cannot be rejected that the groups were selected from *identical populations*.
217	011100001	4	0.6842	1.7831	2.61	KS, CM, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
218	011100010	4	0.9297	1.7831	1.92	KS, CM, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
219	011100011	5	0.7637	1.6727	2.19	KS, CM, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
220	011100100	4	0.9005	1.7831	1.98	KS, CM, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
221	011100101	5	0.7252	1.6727	2.31	KS, CM, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
222	011100110	5	0.8640	1.6727	1.94	KS, CM, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
223	011100111	6	0.7568	1.5976	2.11	KS, CM, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
224	011101000	4	1.0382	1.7831	1.72	KS, CM, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
225	011101001	5	0.8380	1.6727	2.00	KS, CM, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
226	011101010	5	0.9571	1.6727	1.75	KS, CM, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
227	011101011	6	0.8392	1.5976	1.90	KS, CM, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
228	011101100	5	1.0361	1.6727	1.61	KS, CM, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
229	011101101	6	0.8800	1.5976	1.82	KS, CM, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
230	011101110	6	0.9500	1.5976	1.68	KS, CM, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
231	011101111	7	0.8554	1.5423	1.80	KS, CM, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
232	011110000	4	1.0626	1.7831	1.68	KS, CM, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
233	011110001	5	0.8602	1.6727	1.94	KS, CM, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
234	011110010	5	0.9635	1.6727	1.74	KS, CM, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
235	011110011	6	0.8495	1.5976	1.88	KS, CM, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
236	011110100	5	0.9116	1.6727	1.83	KS, CM, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
237	011110101	6	0.7960	1.5976	2.01	KS, CM, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
238	011110110	6	0.8632	1.5976	1.85	KS, CM, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.

239	011110111	7	0.7931	1.5423	1.94	KS, CM, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
240	011111000	5	1.0847	1.6727	1.54	KS, CM, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
241	011111001	6	0.9380	1.5976	1.70	KS, CM, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
242	011111010	6	0.9846	1.5976	1.62	KS, CM, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
243	011111011	7	0.8994	1.5423	1.71	KS, CM, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
244	011111100	6	1.0055	1.5976	1.59	KS, CM, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
245	011111101	7	0.9023	1.5423	1.71	KS, CM, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
246	011111110	7	0.9328	1.5423	1.65	KS, CM, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
247	011111111	8	0.8694	1.4996	1.72	KS, CM, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
248	100000001	2	0.5242	2.3653	4.51	AD, FCS	Cannot be rejected that the groups were selected from *identical populations*.
249	100000010	2	0.9563	2.3653	2.47	AD, TS	Cannot be rejected that the groups were selected from *identical populations*.
250	100000011	3	0.7639	1.9672	2.58	AD, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
251	100000100	2	1.5151	2.3653	1.56	AD, g1	Cannot be rejected that the groups were selected from *identical populations*.
252	100000101	3	0.8532	1.9672	2.31	AD, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
253	100000110	3	0.9883	1.9672	1.99	AD, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
254	100000111	4	0.8159	1.7831	2.19	AD, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
255	100001000	2	0.7064	2.3653	3.35	AD, H1	Cannot be rejected that the groups were selected from *identical populations*.
256	100001001	3	0.8209	1.9672	2.40	AD, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
257	100001010	3	0.8104	1.9672	2.43	AD, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
258	100001011	4	0.8146	1.7831	2.19	AD, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
259	100001100	3	1.4355	1.9672	1.37	AD, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
260	100001101	4	1.0611	1.7831	1.68	AD, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
261	100001110	4	1.0551	1.7831	1.69	AD, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
262	100001111	5	0.9313	1.6727	1.80	AD, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
263	100010000	2	1.3830	2.3653	1.71	AD, WU	Cannot be rejected that the groups were selected from *identical populations*.

264	100010001	3	0.9702	1.9672	2.03	AD, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
265	100010010	3	0.9757	1.9672	2.02	AD, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
266	100010011	4	0.8831	1.7831	2.02	AD, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
267	100010100	3	1.0025	1.9672	1.96	AD, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
268	100010101	4	0.8443	1.7831	2.11	AD, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
269	100010110	4	0.8496	1.7831	2.10	AD, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
270	100010111	5	0.8038	1.6727	2.08	AD, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
271	100011000	3	1.1570	1.9672	1.70	AD, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
272	100011001	4	1.0248	1.7831	1.74	AD, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
273	100011010	4	0.9523	1.7831	1.87	AD, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
274	100011011	5	0.9191	1.6727	1.82	AD, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
275	100011100	4	1.1113	1.7831	1.60	AD, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
276	100011101	5	0.9863	1.6727	1.70	AD, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
277	100011110	5	0.9438	1.6727	1.77	AD, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
278	100011111	6	0.9000	1.5976	1.78	AD, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
279	100100000	2	1.1947	2.3653	1.98	AD, KV	Cannot be rejected that the groups were selected from *identical populations*.
280	100100001	3	0.8072	1.9672	2.44	AD, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
281	100100010	3	0.9139	1.9672	2.15	AD, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
282	100100011	4	0.7993	1.7831	2.23	AD, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
283	100100100	3	0.9357	1.9672	2.10	AD, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
284	100100101	4	0.7686	1.7831	2.32	AD, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
285	100100110	4	0.8160	1.7831	2.19	AD, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
286	100100111	5	0.7567	1.6727	2.21	AD, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
287	100101000	3	1.0358	1.9672	1.90	AD, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
288	100101001	4	0.9016	1.7831	1.98	AD, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.

289	100101010	4	0.8930	1.7831	2.00	AD, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
290	100101011	5	0.8456	1.6727	1.98	AD, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
291	100101100	4	1.0497	1.7831	1.70	AD, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
292	100101101	5	0.9195	1.6727	1.82	AD, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
293	100101110	5	0.9070	1.6727	1.84	AD, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
294	100101111	6	0.8548	1.5976	1.87	AD, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
295	100110000	3	0.9008	1.9672	2.18	AD, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
296	100110001	4	0.8380	1.7831	2.13	AD, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
297	100110010	4	0.8037	1.7831	2.22	AD, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
298	100110011	5	0.7980	1.6727	2.10	AD, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
299	100110100	4	0.7781	1.7831	2.29	AD, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
300	100110101	5	0.7481	1.6727	2.24	AD, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
301	100110110	5	0.7327	1.6727	2.28	AD, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
302	100110111	6	0.7348	1.5976	2.17	AD, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
303	100111000	4	0.9271	1.7831	1.92	AD, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
304	100111001	5	0.9089	1.6727	1.84	AD, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
305	100111010	5	0.8440	1.6727	1.98	AD, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
306	100111011	6	0.8488	1.5976	1.88	AD, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
307	100111100	5	0.9048	1.6727	1.85	AD, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
308	100111101	6	0.8688	1.5976	1.84	AD, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
309	100111110	6	0.8288	1.5976	1.93	AD, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
310	100111111	7	0.8224	1.5423	1.88	AD, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
311	101000000	2	0.2825	2.3653	8.37	AD, CM	Cannot be rejected that the groups were selected from *identical populations*.
312	101000001	3	0.3989	1.9672	4.93	AD, CM, FCS	Cannot be rejected that the groups were selected from *identical populations*.
313	101000010	3	0.7821	1.9672	2.52	AD, CM, TS	Cannot be rejected that the groups were selected from *identical populations*.

314	101000011	4	0.6635	1.7831	2.69	AD, CM, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
315	101000100	3	1.2331	1.9672	1.60	AD, CM, g1	Cannot be rejected that the groups were selected from *identical populations*.
316	101000101	4	0.8267	1.7831	2.16	AD, CM, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
317	101000110	4	1.0106	1.7831	1.76	AD, CM, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
318	101000111	5	0.8242	1.6727	2.03	AD, CM, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
319	101001000	3	0.5803	1.9672	3.39	AD, CM, H1	Cannot be rejected that the groups were selected from *identical populations*.
320	101001001	4	0.6459	1.7831	2.76	AD, CM, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
321	101001010	4	0.7706	1.7831	2.31	AD, CM, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
322	101001011	5	0.7360	1.6727	2.27	AD, CM, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
323	101001100	4	1.2576	1.7831	1.42	AD, CM, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
324	101001101	5	0.9741	1.6727	1.72	AD, CM, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
325	101001110	5	1.0457	1.6727	1.60	AD, CM, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
326	101001111	6	0.9083	1.5976	1.76	AD, CM, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
327	101010000	3	1.1589	1.9672	1.70	AD, CM, WU	Cannot be rejected that the groups were selected from *identical populations*.
328	101010001	4	0.8763	1.7831	2.03	AD, CM, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
329	101010010	4	1.0055	1.7831	1.77	AD, CM, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
330	101010011	5	0.8657	1.6727	1.93	AD, CM, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
331	101010100	4	1.0760	1.7831	1.66	AD, CM, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
332	101010101	5	0.8827	1.6727	1.89	AD, CM, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
333	101010110	5	0.9562	1.6727	1.75	AD, CM, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
334	101010111	6	0.8534	1.5976	1.87	AD, CM, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
335	101011000	4	1.0917	1.7831	1.63	AD, CM, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
336	101011001	5	0.9383	1.6727	1.78	AD, CM, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
337	101011010	5	0.9782	1.6727	1.71	AD, CM, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
338	101011011	6	0.8967	1.5976	1.78	AD, CM, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.

339	101011100	5	1.1231	1.6727	1.49	AD, CM, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
340	101011101	6	0.9770	1.5976	1.64	AD, CM, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
341	101011110	6	0.9993	1.5976	1.60	AD, CM, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
342	101011111	7	0.9182	1.5423	1.68	AD, CM, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
343	101100000	3	0.9831	1.9672	2.00	AD, CM, KV	Cannot be rejected that the groups were selected from *identical populations*.
344	101100001	4	0.7261	1.7831	2.46	AD, CM, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
345	101100010	4	0.9198	1.7831	1.94	AD, CM, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
346	101100011	5	0.7766	1.6727	2.15	AD, CM, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
347	101100100	4	0.9880	1.7831	1.80	AD, CM, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
348	101100101	5	0.8000	1.6727	2.09	AD, CM, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
349	101100110	5	0.9038	1.6727	1.85	AD, CM, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
350	101100111	6	0.7978	1.5976	2.00	AD, CM, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
351	101101000	4	0.9740	1.7831	1.83	AD, CM, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
352	101101001	5	0.8230	1.6727	2.03	AD, CM, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
353	101101010	5	0.9092	1.6727	1.84	AD, CM, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
354	101101011	6	0.8216	1.5976	1.94	AD, CM, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
355	101101100	5	1.0529	1.6727	1.59	AD, CM, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
356	101101101	6	0.9073	1.5976	1.76	AD, CM, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
357	101101110	6	0.9529	1.5976	1.68	AD, CM, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
358	101101111	7	0.8685	1.5423	1.78	AD, CM, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
359	101110000	4	0.9793	1.7831	1.82	AD, CM, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
360	101110001	5	0.8434	1.6727	1.98	AD, CM, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
361	101110010	5	0.9038	1.6727	1.85	AD, CM, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
362	101110011	6	0.8293	1.5976	1.93	AD, CM, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
363	101110100	5	0.9107	1.6727	1.84	AD, CM, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.

364	101110101	6	0.8154	1.5976	1.96	AD, CM, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
365	101110110	6	0.8546	1.5976	1.87	AD, CM, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
366	101110111	7	0.8004	1.5423	1.93	AD, CM, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
367	101111000	5	0.9833	1.6727	1.70	AD, CM, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
368	101111001	6	0.8978	1.5976	1.78	AD, CM, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
369	101111010	6	0.9134	1.5976	1.75	AD, CM, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
370	101111011	7	0.8649	1.5423	1.78	AD, CM, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
371	101111100	6	0.9758	1.5976	1.64	AD, CM, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
372	101111101	7	0.8975	1.5423	1.72	AD, CM, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
373	101111110	7	0.9069	1.5423	1.70	AD, CM, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
374	101111111	8	0.8612	1.4996	1.74	AD, CM, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
375	110000000	2	0.4570	2.3653	5.18	AD, KS	Cannot be rejected that the groups were selected from *identical populations*.
376	110000001	3	0.3930	1.9672	5.01	AD, KS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
377	110000010	3	0.7765	1.9672	2.53	AD, KS, TS	Cannot be rejected that the groups were selected from *identical populations*.
378	110000011	4	0.6554	1.7831	2.72	AD, KS, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
379	110000100	3	1.0110	1.9672	1.95	AD, KS, g1	Cannot be rejected that the groups were selected from *identical populations*.
380	110000101	4	0.7164	1.7831	2.49	AD, KS, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
381	110000110	4	0.9038	1.7831	1.97	AD, KS, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
382	110000111	5	0.7595	1.6727	2.20	AD, KS, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
383	110001000	3	0.8382	1.9672	2.35	AD, KS, H1	Cannot be rejected that the groups were selected from *identical populations*.
384	110001001	4	0.7190	1.7831	2.48	AD, KS, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
385	110001010	4	0.8413	1.7831	2.12	AD, KS, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
386	110001011	5	0.7717	1.6727	2.17	AD, KS, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
387	110001100	4	1.1840	1.7831	1.51	AD, KS, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
388	110001101	5	0.9348	1.6727	1.79	AD, KS, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.

389	110001110	5	1.0059	1.6727	1.66	AD, KS, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
390	110001111	6	0.8832	1.5976	1.81	AD, KS, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
391	110010000	3	1.1898	1.9672	1.65	AD, KS, WU	Cannot be rejected that the groups were selected from *identical populations*.
392	110010001	4	0.8806	1.7831	2.02	AD, KS, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
393	110010010	4	1.0220	1.7831	1.74	AD, KS, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
394	110010011	5	0.8694	1.6727	1.92	AD, KS, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
395	110010100	4	1.0159	1.7831	1.76	AD, KS, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
396	110010101	5	0.8398	1.6727	1.99	AD, KS, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
397	110010110	5	0.9211	1.6727	1.82	AD, KS, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
398	110010111	6	0.8255	1.5976	1.94	AD, KS, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
399	110011000	4	1.1794	1.7831	1.51	AD, KS, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
400	110011001	5	0.9812	1.6727	1.70	AD, KS, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
401	110011010	5	1.0272	1.6727	1.63	AD, KS, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
402	110011011	6	0.9242	1.5976	1.73	AD, KS, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
403	110011100	5	1.1190	1.6727	1.49	AD, KS, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
404	110011101	6	0.9696	1.5976	1.65	AD, KS, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
405	110011110	6	0.9962	1.5976	1.60	AD, KS, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
406	110011111	7	0.9129	1.5423	1.69	AD, KS, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
407	110100000	3	0.9465	1.9672	2.08	AD, KS, KV	Cannot be rejected that the groups were selected from *identical populations*.
408	110100001	4	0.7080	1.7831	2.52	AD, KS, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
409	110100010	4	0.8991	1.7831	1.98	AD, KS, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
410	110100011	5	0.7642	1.6727	2.19	AD, KS, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
411	110100100	4	0.8986	1.7831	1.98	AD, KS, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
412	110100101	5	0.7425	1.6727	2.25	AD, KS, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
413	110100110	5	0.8493	1.6727	1.97	AD, KS, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.

414	110100111	6	0.7591	1.5976	2.10	AD, KS, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
415	110101000	4	1.0185	1.7831	1.75	AD, KS, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
416	110101001	5	0.8497	1.6727	1.97	AD, KS, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
417	110101010	5	0.9314	1.6727	1.80	AD, KS, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
418	110101011	6	0.8367	1.5976	1.91	AD, KS, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
419	110101100	5	1.0275	1.6727	1.63	AD, KS, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
420	110101101	6	0.8885	1.5976	1.80	AD, KS, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
421	110101110	6	0.9348	1.5976	1.71	AD, KS, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
422	110101111	7	0.8544	1.5423	1.81	AD, KS, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
423	110110000	4	1.0173	1.7831	1.75	AD, KS, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
424	110110001	5	0.8559	1.6727	1.95	AD, KS, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
425	110110010	5	0.9229	1.6727	1.81	AD, KS, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
426	110110011	6	0.8366	1.5976	1.91	AD, KS, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
427	110110100	5	0.8891	1.6727	1.88	AD, KS, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
428	110110101	6	0.7947	1.5976	2.01	AD, KS, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
429	110110110	6	0.8391	1.5976	1.90	AD, KS, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
430	110110111	7	0.7853	1.5423	1.96	AD, KS, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
431	110111000	5	1.0501	1.6727	1.59	AD, KS, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
432	110111001	6	0.9329	1.5976	1.71	AD, KS, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
433	110111010	6	0.9521	1.5976	1.68	AD, KS, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
434	110111011	7	0.8879	1.5423	1.74	AD, KS, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
435	110111100	6	0.9850	1.5976	1.62	AD, KS, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
436	110111101	7	0.8990	1.5423	1.72	AD, KS, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
437	110111110	7	0.9115	1.5423	1.69	AD, KS, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
438	110111111	8	0.8614	1.4996	1.74	AD, KS, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.

439	111000000	3	0.4171	1.9672	4.72	AD, KS, CM	Cannot be rejected that the groups were selected from *identical populations*.
440	111000001	4	0.3802	1.7831	4.69	AD, KS, CM, FCS	Cannot be rejected that the groups were selected from *identical populations*.
441	111000010	4	0.6905	1.7831	2.58	AD, KS, CM, TS	Cannot be rejected that the groups were selected from *identical populations*.
442	111000011	5	0.6043	1.6727	2.77	AD, KS, CM, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
443	111000100	4	0.9474	1.7831	1.88	AD, KS, CM, g1	Cannot be rejected that the groups were selected from *identical populations*.
444	111000101	5	0.7164	1.6727	2.33	AD, KS, CM, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
445	111000110	5	0.8979	1.6727	1.86	AD, KS, CM, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
446	111000111	6	0.7601	1.5976	2.10	AD, KS, CM, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
447	111001000	4	0.6768	1.7831	2.63	AD, KS, CM, H1	Cannot be rejected that the groups were selected from *identical populations*.
448	111001001	5	0.6177	1.6727	2.71	AD, KS, CM, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
449	111001010	5	0.7651	1.6727	2.19	AD, KS, CM, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
450	111001011	6	0.7077	1.5976	2.26	AD, KS, CM, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
451	111001100	5	1.0735	1.6727	1.56	AD, KS, CM, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
452	111001101	6	0.8769	1.5976	1.82	AD, KS, CM, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
453	111001110	6	0.9723	1.5976	1.64	AD, KS, CM, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
454	111001111	7	0.8567	1.5423	1.80	AD, KS, CM, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
455	111010000	4	1.0210	1.7831	1.75	AD, KS, CM, WU	Cannot be rejected that the groups were selected from *identical populations*.
456	111010001	5	0.8105	1.6727	2.06	AD, KS, CM, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.
457	111010010	5	0.9687	1.6727	1.73	AD, KS, CM, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
458	111010011	6	0.8340	1.5976	1.92	AD, KS, CM, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
459	111010100	5	1.0092	1.6727	1.66	AD, KS, CM, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
460	111010101	6	0.8458	1.5976	1.89	AD, KS, CM, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
461	111010110	6	0.9462	1.5976	1.69	AD, KS, CM, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
462	111010111	7	0.8406	1.5423	1.83	AD, KS, CM, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
463	111011000	5	1.0507	1.6727	1.59	AD, KS, CM, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.

464	111011001	6	0.8992	1.5976	1.78	AD, KS, CM, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
465	111011010	6	0.9814	1.5976	1.63	AD, KS, CM, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
466	111011011	7	0.8833	1.5423	1.75	AD, KS, CM, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
467	111011100	6	1.0806	1.5976	1.48	AD, KS, CM, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
468	111011101	7	0.9435	1.5423	1.63	AD, KS, CM, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
469	111011110	7	0.9972	1.5423	1.55	AD, KS, CM, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
470	111011111	8	0.9079	1.4996	1.65	AD, KS, CM, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
471	111100000	4	0.8329	1.7831	2.14	AD, KS, CM, KV	Cannot be rejected that the groups were selected from *identical populations*.
472	111100001	5	0.6626	1.6727	2.52	AD, KS, CM, KV, FCS	Cannot be rejected that the groups were selected from *identical populations*.
473	111100010	5	0.8575	1.6727	1.95	AD, KS, CM, KV, TS	Cannot be rejected that the groups were selected from *identical populations*.
474	111100011	6	0.7361	1.5976	2.17	AD, KS, CM, KV, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
475	111100100	5	0.9020	1.6727	1.85	AD, KS, CM, KV, g1	Cannot be rejected that the groups were selected from *identical populations*.
476	111100101	6	0.7541	1.5976	2.12	AD, KS, CM, KV, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
477	111100110	6	0.8746	1.5976	1.83	AD, KS, CM, KV, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
478	111100111	7	0.7748	1.5423	1.99	AD, KS, CM, KV, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
479	111101000	5	0.9146	1.6727	1.83	AD, KS, CM, KV, H1	Cannot be rejected that the groups were selected from *identical populations*.
480	111101001	6	0.7822	1.5976	2.04	AD, KS, CM, KV, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
481	111101010	6	0.8925	1.5976	1.79	AD, KS, CM, KV, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
482	111101011	7	0.8010	1.5423	1.93	AD, KS, CM, KV, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
483	111101100	6	0.9950	1.5976	1.61	AD, KS, CM, KV, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
484	111101101	7	0.8665	1.5423	1.78	AD, KS, CM, KV, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
485	111101110	7	0.9363	1.5423	1.65	AD, KS, CM, KV, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
486	111101111	8	0.8501	1.4996	1.76	AD, KS, CM, KV, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
487	111110000	5	0.9724	1.6727	1.72	AD, KS, CM, KV, WU	Cannot be rejected that the groups were selected from *identical populations*.
488	111110001	6	0.8305	1.5976	1.92	AD, KS, CM, KV, WU, FCS	Cannot be rejected that the groups were selected from *identical populations*.

489	111110010	6	0.9260	1.5976	1.73	AD, KS, CM, KV, WU, TS	Cannot be rejected that the groups were selected from *identical populations*.
490	111110011	7	0.8322	1.5423	1.85	AD, KS, CM, KV, WU, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
491	111110100	6	0.9244	1.5976	1.73	AD, KS, CM, KV, WU, g1	Cannot be rejected that the groups were selected from *identical populations*.
492	111110101	7	0.8193	1.5423	1.88	AD, KS, CM, KV, WU, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
493	111110110	7	0.8853	1.5423	1.74	AD, KS, CM, KV, WU, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
494	111110111	8	0.8141	1.4996	1.84	AD, KS, CM, KV, WU, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
495	111111000	6	1.0046	1.5976	1.59	AD, KS, CM, KV, WU, H1	Cannot be rejected that the groups were selected from *identical populations*.
496	111111001	7	0.8957	1.5423	1.72	AD, KS, CM, KV, WU, H1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
497	111111010	7	0.9477	1.5423	1.63	AD, KS, CM, KV, WU, H1, TS	Cannot be rejected that the groups were selected from *identical populations*.
498	111111011	8	0.8750	1.4996	1.71	AD, KS, CM, KV, WU, H1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.
499	111111100	7	0.9906	1.5423	1.56	AD, KS, CM, KV, WU, H1, g1	Cannot be rejected that the groups were selected from *identical populations*.
500	111111101	8	0.8991	1.4996	1.67	AD, KS, CM, KV, WU, H1, g1, FCS	Cannot be rejected that the groups were selected from *identical populations*.
501	111111110	8	0.9354	1.4996	1.60	AD, KS, CM, KV, WU, H1, g1, TS	Cannot be rejected that the groups were selected from *identical populations*.
502	111111111	9	0.8731	1.4653	1.68	AD, KS, CM, KV, WU, H1, g1, TS, FCS	Cannot be rejected that the groups were selected from *identical populations*.

Algorithm:

- Let $(X_{i,j}; i=1..k)$ be k groups (samples) of independent observations; let $(n_i; i=1..k)$ be the sizes of the samples;
- Let $n=S(n_i; i=1..k)$ be the total number of observations;
- Let dn be the number of distinct values from $(X_{i,j})$; note that dn is less (tied observations) or equal (no tied observations) to n;
- Let $(z_j; j=1..dn)$ be the distinct values from $(X_{i,j})$; let $(h_j; j=1..dn)$ be numbers of ties corresponding to $(z_j; j=1..dn)$ from $(X_{i,j})$;
- Let $H_j = S(h_m; m=1..(j-1)) + h_j/2$; let $F_{i,j}$ be the number of values from i-th group similarly with H;
- kAD statistic is:
    - $kAD = S(S(V_{i,j}; j=1..dn)/n_i; i=1..k)*(n-1)/n^2/(k-1)$,
    - $V_{i,j} = h_j*(n*F_{i,j}-n_iH_j)^2/(H_j*(n-H_j)-n*h_j/4)$;
- cAD critical value (5% significance level) is
    - $cAD = 1 + s_n*(1.645 + 0.678*(k-1)^{-0.5} - 0.362*(k-1)^{-1})$,
    - $s_n^2 = 2*(a*n^3 + b*n^2 + c*n + d)*(n-1)^{-1}*(n-2)^{-1}(n-3)^{-1}(k-1)^{-2}$,
    - $a = (2*g-3)*(k-1) + (5-3*g)*w$,
    - $b = (g-2)*k^2 + 4*t*k + (g-7*t-2)*w - 4*t + 2*g - 3$,
    - $c = (3*t+g-1)*k^2 + (2*t-2*g+3)*k + (t-3)*w + 2*t$,
    - $d = (t+3)*k^2 - 2*t*k$,
    - $w = S(n_i^{-1}; i=1..k)$,
    - $t = S(i^{-1}; i=1..(n-1))$,
    - $g = S(S((n-i)^{-1}j^{-1}; j=(i+1)..(n-1)); i=1..(n-2))$;
- If cAD < kAD Then (with a 5% risk being in error) "The groups were drawn from different populations";
- Else the hypothesis that whe groups were selected from identical populations is not rejected and the data can be considered unstructured with respect of the random fixed effect in question.