

EXACT P-VALUES OF SAVAGE TEST STATISTIC

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ABSTRACT

In recent years, the use of software for the calculation of statistical tests has become widespread. For many nonparametric tests, a number of statistical programs calculate significance levels based on algorithms appropriate for large samples only. In scientific experiments, small samples are common. This requires the use of the exact statistical test. This paper presents a simple but logical method of obtaining unconditional exact permutation distribution for test statistics involving small samples. The exact critical values for the savage test statistic are generated and the probability of a type I error is exactly α .

Keywords: Monte Carlo sampling, Permutation test, p-value, Rank order statistic, Savage test

INTRODUCTION

The use of the asymptotic test with small sample sizes usually yields an incorrect p-value, and may therefore lead to a false acceptance or rejection of the null hypothesis. Application of the asymptotic test when the sample size is smaller than the allowable sample size for the particular test statistic can lead to a wrong decision. In an attempt to avoid these wrong decisions, an algorithm for obtaining exact permutation distribution is presented with the Savage test as the principal focus. The Savage test involves the null hypothesis that there is no difference in spread, which is tested against the two-tailed alternative that there is a difference in variability.

There are two approaches to a permutation test viz; conditional and unconditional approaches. In the unconditional exact permutation approach, row and column totals are not fixed as it is done in the conditional exact permutation approach. Computational time for a permutation test is highly prohibitive even with very fast processor speed of available personal computers. Hall and Tajvidi (2002) described the permutation test as unattractive because of the large number of permutations required and therefore suggested other alternatives such as the bootstrap technique without replacement. Good (2000) only considered the tails of permutation distribution and presented steps that could lead to a permutation test.

According to the survey on permutation sampling procedures carried out by Opdyke (2003), three procedures in SAS v8.2: PROC NPARIWAY, PROC MULTTEST, and PROC PLAN, one procedure in Cytel's Proc StatXact v5.0: PROC TWOSAMPL can be used to perform two-sample nonparametric permutation tests. All of these procedures can perform conventional Monte Carlo sampling without replacement within a sample but none can avoid the possibility of drawing the same sample more than once. Considering this associated difficulty in obtaining the distinct and exhaustive permutations coupled with the prohibitive runtimes, the algorithm presented in this paper ensures that a complete and systematic enumeration of the permutations is carried out.

Mundry and Fischer (1998) observed that for many parametric and nonparametric tests, some of the statistical programs available calculate significance levels based on algorithms appropriate for large samples only. The asymptotic version of a nonparametric test with small sample sizes usually yields an incorrect p-value, and may lead to a false acceptance or rejection of the null hypothesis. Mundry and Fischer (1998) reported their earlier findings, where they examined the results of nonparametric tests with small sample sizes published in some issues of "Animal Behaviour" and found that in more than half of the articles examined, the asymptotic tests had apparently been inappropriately used and incorrect p-values had been presented.

MATERIALS AND METHODS

Permutation tests provide exact p-values for Savage test, especially when complete enumeration is possible. A discussion on the properties of permutation tests can be found in Good (2000) and Pesarin (2001). The problem with permutation tests has been high computational demands, viz; space and time complexities. Sampling from the permutation sample space rather than carrying out complete enumeration of all possible distinct rearrangements is what most of the avail-

able permutation procedures do (Opdyke 2003). Several approaches have been suggested as alternatives to the computationally intensive unconditional exact permutation approach. For example, Fisher (1935) and Agresti (1992) give a discussion on exact conditional permutation distribution. Also Efron (1979), Hall and Tajvidi (2002), Efron and Tibshirani (1993), Opdyke (2003) have discussed the Monte Carlo approaches.

The purpose of this paper is to provide exact p-values of the Savage test statistic for positive random variables. This therefore ensures that the probability of making a Type I error is exactly α . This paper also provides computer algorithms for achieving the unconditional exact distribution of the Savage test statistic. Contrary to what Fahoome (2002) noted that when $\alpha = 0.05$, sample size should exceed 10 for the large sample approximation to be adopted for the Savage test, the p-values for $\max(m, n) \leq 10$ for the Savage test are generated in this work. The unconditional permutation approach is employed in obtaining these exact p-values.

Exact versus Asymptotic Test Procedures

Almost all statistical tests are based on the same idea, viz; (i) formulate the null and alternative hypotheses, (ii) choose a level of significance, (iii) calculate the test statistic and (iv) compare the calculated test statistic with a critical value.

If the value of the test statistic is smaller or larger than the critical value, the null hypothesis can be accepted or rejected, depending on the test applied. The critical values are usually determined by obtaining the most extreme 5% (say) of the theoretical frequency distribution of the test statistic. When the sample size is small, the exact probability of obtaining the calculated value of the test statistic or any less likely value has to be determined. The sum of these probabilities is the exact p-value of the test statistic. The calculated values of the test statistic are compared with the tabulated critical values. This procedure, based on the calculation of the exact probability of a given test statistic, is called exact testing proce-

dure (Siegel and Castellan, 1988). With large sample size, the frequency distribution of a test statistic is often asymptotically a normal or a chi-square distribution. The p-value is obtained by transforming the test statistic as required by the large sample approximation of the test statistic and looking up the transformed value in a table of standard normal distribution (Z) or chi-square values (χ^2).

The Savage test

The Savage test does not assume that location remains the same. It is assumed that differences in scale cause a difference in location. The samples are assumed to be drawn from continuous distributions (Hajek, 1969). The null hypothesis is that there is no difference in spread, which is tested against the two-tailed alternative that there is a difference in variability. Savage scores are powerful for comparing scale differences in exponential distributions or location shifts in extreme value distributions.

Let Sample 1 be x_1, x_2, \dots, x_m and let Sample 2 be y_1, y_2, \dots, y_n . The combined samples are ordered, keeping track of sample membership. Let R_i be the rank for x_i . The test statistic is computed for either sample. The test statistic is

$$S = \sum_{i=1}^m a(R_i)$$

where

$$a(i) = \sum_{j=N+1-i}^N \frac{1}{j} \quad N = m + n$$

For large sample sizes the following normal approximation may be used, that is,

$$Z = \frac{S - n}{\sqrt{\frac{mn}{N-1} \left(1 - \frac{1}{N} \sum_{j=1}^N \frac{1}{j} \right)}}$$

Z is compared with the critical value from the standard normal distribution.

Methodology

The p-value of a test statistic represents the probability of obtaining values of the test statistic that are equal to or greater than the observed test statistic when considering the right-tail of the distribution of the test statistic. For the continuous case, find the area under the curve of the theoretical distribution of the test statistic in the direction of the alternative hypothesis. For the discrete case, add up the probabilities of events occurring in the direction of the alternative hypothesis that occur at and after the observed value of the test statistic.

If the experiment to be analyzed is made up of small or sparse data, large sample procedures for statistical inference are not appropriate (Senchaudhuri *et al*, 1995; Siegel and Castellan, 1988). In this paper, consideration is given to the special case of $2 \times n$ tables with row and column totals allowed to vary with each permutation. This is the unconditional exact permutation approach which involves all the possible permutations rather than the constrained or conditional exact permutation approach of fixing row and column totals (Agresti, 1992). The tails of permutation distribution can also be considered in order to arrive at p-values without actually carrying out complete enumeration required for the permutation test. This approach has no precise model for the tail of the distribution from which data are drawn (Hall and Weissman, 1997).

Let p_1, p_2, \dots, p_n be a set of all distinct permutations of the ranks of the data set in the experiment. The permutation test procedure for the Savage test is as follows:

Permutation test procedure

1. Rank the combined observed original data set of the experiment as required by the Savage test statistic.
2. Compute the observed value of the Savage test statistic ($S_I = t_0$).
3. Obtain a distinct permutation p_i , of the ranks in Step 1.

4. Compute the Savage test statistic S_I for permutation p_i in Step 3, $S_i = S(p_i)$.
5. Repeat Steps 3 and 4 for $i=2(1)n$.
6. Construct an empirical cumulative distribution for S .

$$p_0 = \hat{p}(S \leq S_i) = \frac{1}{\eta} \sum_{i=1}^{\eta} \phi(t_0 - S_i)$$

where $\phi(t_0 - S_i) = 1$, if $t_0 \geq S_i$, and $\phi(t_0 - S_i) = 0$ if $t_0 < S_i$.

7. Under the empirical distribution, if $p_0 \leq \alpha$, reject the null hypothesis.

Under H_0 , each distinct permutation of ranks is obtained, the value of S determined for each one, and the null distribution obtained by counting the number of times each value of S occurs.

A 2-sample experiment with m and n as the sizes of Sample 1 and Sample 2 respectively has

$$\frac{(m+n)!}{m!n!} = \frac{N!}{m!n!}$$

possible permutations of the N variates of the two samples with each occurring with the probability

$$\left(\frac{N!}{m!n!} \right)^{-1}$$

The difficulty in permutation test lies in obtaining all the distinct arrangements of the results of a given experiment, that is, Step 3 of the permutation procedure. For example, a two-sample experiment with 16 variates in Sample 1 and 14 variates in Sample 2 requires 145,422,675 permutations. When a complete enumeration of all the possible permutations is achieved, p-values can be computed. Permutation test requires very few assumptions as a nonparametric procedure,

the sufficient condition for a permutation test to be exact and unbiased against shifts in the direction of higher values is the exchangeability of the observations in the combined sample (Good, 2000).

Illustrative implementation

An illustrative implementation of the systematic way of obtaining all the possible permutations of the N variates now follows:

Let $m = 3$ and $n = 4$ variates, i.e.

$$\begin{pmatrix} x_{11} & x_{21} \\ x_{12} & x_{22} \\ x_{13} & x_{23} \\ & x_{24} \end{pmatrix} \text{ We expect to have } \frac{7!}{3!4!} = 35$$

distinct permutations for an exhaustive enumeration. Thus:

Stage 1

$$\begin{pmatrix} x_{11} & x_{21} \\ x_{12} & x_{22} \\ x_{13} & x_{23} \\ & x_{24} \end{pmatrix} \text{ original arrangement of the data of the experiment.}$$

$$\begin{pmatrix} 3 \\ 0 \end{pmatrix} \begin{pmatrix} 4 \\ 0 \end{pmatrix} = 1 \text{ Permutation (original arrangement of the data of the experiment).}$$

Stage 2

$$x_{11} \leftarrow x_{2i} \quad i = 1(1)4 \quad (4 \text{ permutations})$$

$$x_{12} \leftarrow x_{2i} \quad i = 1(1)4 \quad (4 \text{ permutations})$$

$$x_{13} \leftarrow x_{2i} \quad i = 1(1)4 \quad (4 \text{ permutations})$$

$$\begin{pmatrix} 3 \\ 1 \end{pmatrix} \begin{pmatrix} 4 \\ 1 \end{pmatrix} = 12 \text{ Permutations (using one variate from first sample)}$$

Stage 3

$$\begin{pmatrix} x_{1s} \\ x_{1t} \end{pmatrix} \leftarrow \begin{pmatrix} x_{2i} \\ x_{2j} \end{pmatrix}; s \neq t, i \neq j$$

$$\binom{3}{2} \binom{4}{2} = 18 \text{ Permutations (using two variates from first sample)}$$

$$X_N = \begin{pmatrix} 1 & m + 1 \\ 2 & m + 2 \\ 3 & m + 3 \\ \vdots & \vdots \\ m & m + n \end{pmatrix}$$

where $m \neq n$ for unequal sample sizes. This initial arrangement is what is permuted and the Savage statistic is computed for each permutation, leading to the construction of the distribution of the Savage test statistic.

Stage 4

$$\begin{pmatrix} x_{1s} \\ x_{1t} \\ x_{1u} \end{pmatrix} \leftarrow \begin{pmatrix} x_{2i} \\ x_{2j} \\ x_{2k} \end{pmatrix}; s \neq t \neq u, i \neq j \neq k$$

$$\binom{3}{3} \binom{4}{3} = 4 \text{ Permutations (exchange samples, i.e., three variates)}$$

$$\text{Total} = \binom{3}{0} \binom{4}{0} + \binom{3}{1} \binom{4}{1} + \binom{3}{2} \binom{4}{2} + \binom{3}{3} \binom{4}{3} = 35$$

Continuing in the above manner, the number of permutations for a 2-sample experiment can be written as

$$\sum_{i=0}^{\min(m,n)} \binom{m}{i} \binom{n}{i} \text{ permutations, because } \binom{m}{n} = 0$$

for $n > m$. For more details, see Odiase and Ogbonmwan (2005).

The Savage test statistic is a function of ranks. Therefore, in formulating the computer algorithm for the unconditional exact permutation distribution, a consideration is given to rank order statistics. First obtain any arbitrary arrangement of the ranks of the observations in an experiment. Any such arrangement of ranks can be used for a full enumeration of all the distinct permutations of the ranks of the experiment. For convenience, take a simple case as the initial arrangement of ranks such that

Algorithm for exact p-values of Savage test statistic

In Algorithm(SAVAGE), X is the arrangement or configuration of ranks. The test statistic handles a two-sample problem, where K is the sample size. The algorithm for the generation of the distribution of the Savage test statistic for different sample sizes now follows (Odiase and Ogbonmwan, 2005) for more details.

Algorithm (SAVAGE)

- 1: **for** I←1,N **do**
- 2: SAV_I←0
- 3: n₁←N-I+1
- 4: **for** J← n₁,N **do**
- 5: SAV_I←SAV_I+1/j
- 6: **end for**
- 7: **end for**
- 8: **for** J₁←1,K **do**
- 9: RANK←X_{J₁,1}
- 10: I₁←2
- 11: **for** J₂←1,K **do**
- 12: X_{J₁,1}←X_{J₂,I₁}
- 13: X_{J₂,I₁}←RANK
- 14: Compute statistic and restore original values of X
- 15: **end for**
- 16: **end for**
- 17: **for** I←1,K-1 **do**

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18: RANK1←XI,1
19: for J←I+1,K do
20:   RANK2←XJ,1
21:   L←2
22:   for I1←1,K do
23:     for L1←L,2 do
24:       if L←L1 then
25:         T←I1+1
26:       else
27:         T←1
28:       end if
29:       for J1←T,K do
30:         XI,1←XI1,L
31:         XI1,L←RANK1
32:         X(J,1)←XJ1,L1
33:         X(J1,L1)←RANK2
34: Compute statistic and restore original values
    of X
35:   end for
36: end for
37: end for
38: end for
39: end for
40: for I←1,K-2 do
41:   RANK1←XI,1
42:   for J←I+1,K-1 do
43:     RANK2←XJ,1
44:     for M←J+1,K do
45:       RANK3←XM,1
46:       L←2
47:       for I1←1,k do
48:         for L1←L,2 do
49:           if L←L1 then
50:             T←I1+1
51:           else
52:             T←1
53:           end if
54:           for J1←T,K do
55:             for L2←L1,2 do
56:               if L1←L2 then
57:                 T1←J1+1
58:               else
59:                 T1←1
60:               end if
61:             for J2←T1,K do
62:               XI,1←XI1,L
63:               XI1,L←RANK1
64:               XJ,1←XJ1,L1
65:               XJ1,L1←RANK2
66:               XM,1←XJ2,L2
67:               XJ2,L2←RANK3
68:               TS←0
69:               for CC2←1,K do
70:                 TS←TS+SAVx(cc@,8)
71:               end for
72:               Restore original values of X
73:               CHECK←0
74:               for C0←1,COUNT1 do
75:                 if SAVAGEC0←TS then
76:                   FREQC0←FREQC0+1
77:                   CHECK←1
78:                 end if
79:               end for
80:               if CHECK←0 then
81:                 COUNT1←COUNT1+1
82:                 SAVAGECOUNT1←TS
83:                 FREQCOUNT1←1
84:               end if
85:               Compute pdf of test statistic
86:             end for
87:           end for
88:         end for
89:       end for
90:     end for
91:   end for
92: end for
93: end for

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The Algorithm(SAVAGE) was implemented in Intel Visual FORTRAN. The p-values generated from the distinct permutations for the Savage test statistic are presented in Tables 1 and 2. The algorithm can be extended to any sample size.

RESULTS

The unconditional permutation algorithm described so far was implemented for a two-sample

problem with sample sizes m and n . Tables 1 and 2 present the exact permutation critical values for the Savage test statistic, while the values in parentheses are those obtained through other parametric approaches in Hajek (1969).

The idea of formulating and implementing the methodology for the exact permutation paradigm is to obtain the exact distribution of a test statistic. It is the exact distribution of a test statistic

that guarantees that the probability of a type I error is exactly α . R. A. Fisher compiled by hand 32,768 permutations of Charles Darwin's data on heights of self and cross fertilized plants (Ludbrook and Dudley, 1998). Fisher examined the data at 5% level of significance thus: the null hypothesis of no significant difference in the means of the two samples is rejected under the t-distribution (p-value = 0.0497) while it is accepted under the exact permutation distribution

Table 1: Lower critical values S_α for the Savage test statistic

$$S = \sum_{i=1}^m \sum_{j=N-R_i+1}^N \frac{1}{j} ; \alpha' = P(S \leq S_\alpha), 5 \leq m = n \leq 10$$

(If $\alpha' \leq \alpha$, then $S_\alpha = S_\alpha^{\geq}$; if $\alpha' > \alpha$, then $S_\alpha = S_\alpha^{>}$)

α		0.001		0.0025		0.005		0.01	
m	n	S_α	α'	S_α	α'	S_α	α'	S_α	α'
5	5					1.7718	0.0040	2.1385	0.0119
6	6	2.0807	0.0011	2.2474	0.0022	2.5153 (2.50)	0.0054 (0.0054)	2.7153 (2.70)	0.0097 (0.0097)
7	7	2.6570	0.0009	2.9347	0.0026	3.1256 (3.12)	0.0050 (0.0050)	3.3847 (3.38)	0.0099 (0.0099)
8	8	3.2669	0.0010	3.5169	0.0025	3.7697 (3.77)	0.0050 (0.0051)	4.0569 (4.05)	0.0100 (0.0099)
9	9	3.8514	0.0010	4.1607	0.0025	4.4250 (4.43)	0.0050 (0.0050)	4.7536 (4.76)	0.0100 (0.0100)
10	10	4.4650	0.0010	4.8095	0.0025	5.1109 (5.11)	0.0050 (0.0050)	5.4666 (5.46)	0.0100 (0.0100)

α		0.025		0.05		0.1	
m	n	S_α	α'	S_α	α'	S_α	α'
5	5	2.3885	0.0238	2.7218	0.0516	3.1341	0.1032
6	6	3.0764 (3.07)	0.0249 (0.0249)	3.4518 (3.44)	0.0498 (0.0498)	3.9129	0.0996
7	7	3.7942 (3.78)	0.0251 (0.0248)	4.2148 (4.20)	0.0501 (0.0495)	4.7288	0.0999
8	8	4.5292 (4.52)	0.0250 (0.0249)	4.9848 (4.98)	0.0500 (0.0500)	5.5669	0.1000
9	9	5.2736 (5.28)	0.0250 (0.0249)	5.7762 (5.78)	0.0500 (0.0497)	6.4100	0.1000
10	10	6.0375 (6.03)	0.0250 (0.0249)	6.5801 (6.57)	0.0500 (0.0497)	7.2594	0.1000

The values in parentheses are those presented in Table XI of Hajek (1969)

Table 2: Upper critical values S_α for the Savage test statistic

$$S = \sum_{i=1}^m \sum_{j=N-R_i+1}^N \frac{1}{j} ; \alpha' = P(S \leq S_\alpha), 5 \leq m = n \leq 10$$

(If $\alpha' \leq \alpha$, then $S'_\alpha = S_\alpha^{\geq}$; if $\alpha' > \alpha$, then $S'_\alpha = S_\alpha^{>}$)

α		0.001		0.0025		0.005		0.01	
m	n	S_α	α'	S_α	α'	S_α	α'	S_α	α'
5	5					8.2282	0.0040	7.8615	0.0119
6	6	9.9193	0.0011	9.7526	0.0022	9.4847 (9.58)	0.0054 (0.0054)	9.2847 (9.28)	0.0097 (0.0097)
7	7	11.3431	0.0009	11.0653	0.0026	10.8744 (10.87)	0.0050 (0.0050)	10.6153 (10.61)	0.0099 (0.0099)
8	8	12.7331	0.0010	12.4831	0.0025	12.2303 (12.23)	0.0050 (0.0051)	11.9431 (11.95)	0.0100 (0.0099)
9	9	14.1486	0.0010	13.8393	0.0025	13.5750 (13.60)	0.0050 (0.0050)	13.2464 (13.27)	0.0100 (0.0100)
10	10	15.2324	0.0010	15.0158	0.0025	14.7797 (14.89)	0.0050 (0.0050)	14.4675 (14.54)	0.0100 (0.0100)

α		0.025		0.05		0.1	
m	n	S_α	α'	S_α	α'	S_α	α'
5	5	7.6115	0.0238	7.2782	0.0516	6.8659	0.1032
6	6	8.9236 (8.91)	0.0249 (0.0249)	8.5482 (8.54)	0.0498 (0.0498)	8.0871	0.0996
7	7	10.2058 (10.21)	0.0251 (0.0248)	9.7852 (9.79)	0.0501 (0.0495)	9.2712	0.0999
8	8	11.4708 (11.48)	0.0250 (0.0249)	11.0152 (11.02)	0.0500 (0.0500)	10.4331	0.1000
9	9	12.7264 (12.75)	0.0250 (0.0249)	12.2238 (12.25)	0.0500 (0.0498)	11.5900	0.1000
10	10	13.9284 (13.97)	0.0250 (0.0249)	13.4009 (13.43)	0.0500 (0.0497)	12.7288	0.1000

The values in parentheses are those presented in Table X of Hajek (1969)

(p-value = 0.0527). Fisher concluded by noting that permutation test can therefore serve as an independent check on the classical methods in common use.

Looking at Tables 1 and 2, there are some entries in the table that will lead to opposite decisions for a given null hypothesis when the exact permutation and Hajek (1969) values are used. For example, p-values for $\alpha = 0.05$ when $m = n = 7, 9, 10$ could lead to contradictory decisions when

the given values of Savage test statistic in the tables are actually the observed values of the test statistic.

The permutation critical values provided in this paper expose the danger in using asymptotic or parametric distributions to analyze small data sets when the exact functional form of the distribution is not explicitly known. This becomes more obvious when the experiment leads to a p-value close to the threshold level of significance.

CONCLUSION

The p-value obtained through unconditional exact permutation are reliable and exact (Agresti, 1992; Good, 2000). Obtaining exact p-values through unconditional permutation has remained elusive because of computational difficulties.

In this paper, a straight forward approach has been adopted in obtaining exact p-values for Savage test through a careful enumeration of distinct permutations of the ranks of the observations for an experiment. The permutation algorithm presented in this paper beats the limitations and difficulties experienced by other authors which probably led them to providing p-values via other simpler methods which do not truly provide exact p-values. With this algorithm, the p-values for Savage test statistic can be accurately generated, thereby ensuring that the probability of making a Type I error is exactly α .

In comparison with Tables X and XI of Hajek (1969) for the p-values of Savage test statistic, it is clear that the probability of a Type I error is not exactly α for some of the entries in Tables X and XI of Hajek (1969). The actual exact critical values are the results presented in this paper.

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