

permute — Monte Carlo permutation tests

Syntax Remarks and examples	Menu Stored results	Description References	Options Also see
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Syntax

Compute permutation test

```
permute permvar exp_list [, options] : command
```

Report saved results

```
permute [varlist] [using filename] [, display_options]
```

<i>options</i>	Description
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Main

<u>r</u> eps(#)	perform # random permutations; default is reps(100)
<u>l</u> eft <u>r</u> ight	compute one-sided <i>p</i> -values; default is two-sided

Options

<u>s</u> trata(<i>varlist</i>)	permute within strata
<u>s</u> aving(<i>filename</i> , ...)	save results to <i>filename</i> ; save statistics in double precision; save results to <i>filename</i> every # replications

Reporting

<u>l</u> evel(#)	set confidence level; default is level(95)
<u>n</u> oheader	suppress table header
<u>n</u> olegend	suppress table legend
<u>v</u> erbose	display full table legend
<u>n</u> odrop	do not drop observations
<u>n</u> odots	suppress replication dots
<u>n</u> oisily	display any output from <i>command</i>
<u>t</u> race	trace <i>command</i>
<u>t</u> itle(<i>text</i>)	use <i>text</i> as title for permutation results

Advanced

<u>e</u> ps(#)	numerical tolerance; seldom used
<u>n</u> owarn	do not warn when e(sample) is not set
<u>f</u> orce	do not check for <i>weights</i> or <i>svy</i> commands; seldom used
<u>r</u> eject(<i>exp</i>)	identify invalid results
<u>s</u> eed(#)	set random-number seed to #

weights are not allowed in *command*.

<i>display_options</i>	Description
<u>l</u> eft <u>r</u> ight	compute one-sided p -values; default is two-sided
<u>l</u> evel(#)	set confidence level; default is level(95)
<u>n</u> oheader	suppress table header
<u>n</u> olegend	suppress table legend
<u>v</u> erbose	display full table legend
<u>t</u> itle(<i>text</i>)	use <i>text</i> as title for results
<u>e</u> ps(#)	numerical tolerance; seldom used

exp_list contains (name: *elist*)
elist
eexp

elist contains *newvar* = (*exp*)
(*exp*)

eexp is *specname*
[*eqno*]*specname*

specname is _b
_b []
_se
_se []

eqno is ##
name

exp is a standard Stata expression; see [U] 13 Functions and expressions.

Distinguish between [], which are to be typed, and [], which indicate optional arguments.

Menu

Statistics > Resampling > Permutation tests

Description

`permute` estimates p -values for permutation tests on the basis of Monte Carlo simulations. Typing

```
. permute permvar exp_list, reps(#): command
```

randomly permutes the values in *permvar* # times, each time executing *command* and collecting the associated values from the expression in *exp_list*.

These p -value estimates can be one-sided: $\Pr(T^* \leq T)$ or $\Pr(T^* \geq T)$. The default is two-sided: $\Pr(|T^*| \geq |T|)$. Here T^* denotes the value of the statistic from a randomly permuted dataset, and T denotes the statistic as computed on the original data.

permvar identifies the variable whose observed values will be randomly permuted.

command defines the statistical command to be executed. Most Stata commands and user-written programs can be used with `permute`, as long as they follow standard Stata syntax; see [U] 11 Language syntax. The `by` prefix may not be part of *command*.

exp_list specifies the statistics to be collected from the execution of *command*.

`permute` may be used for replaying results, but this feature is appropriate only when a dataset generated by `permute` is currently in memory or is identified by the `using` option. The variables specified in *varlist* in this context must be present in the respective dataset.

Options

Main

`reps(#)` specifies the number of random permutations to perform. The default is 100.

`left` or `right` requests that one-sided p -values be computed. If `left` is specified, an estimate of $\Pr(T^* \leq T)$ is produced, where T^* is the test statistic and T is its observed value. If `right` is specified, an estimate of $\Pr(T^* \geq T)$ is produced. By default, two-sided p -values are computed; that is, $\Pr(|T^*| \geq |T|)$ is estimated.

Options

`strata(varlist)` specifies that the permutations be performed within each stratum defined by the values of *varlist*.

`saving(filename [, suboptions])` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

`double` specifies that the results for each replication be saved as `doubles`, meaning 8-byte reals. By default, they are saved as `floats`, meaning 4-byte reals.

`every(#)` specifies that results are to be written to disk every *#*th replication. `every()` should be specified only in conjunction with `saving()` when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] [postfile](#).

`replace` specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [R] [level](#).

`noheader` suppresses display of the table header. This option implies the `nolegend` option.

`nolegend` suppresses display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

`verbose` requests that the full table legend be displayed. By default, coefficients and standard errors are not displayed.

`nodrop` prevents `permute` from dropping observations outside the `if` and `in` qualifiers. `nodrop` will also cause `permute` to ignore the contents of `e(sample)` if it exists as a result of running *command*. By default, `permute` temporarily drops out-of-sample observations.

`nodots` suppresses display of the replication dots. By default, one dot character is displayed for each successful replication. A red ‘x’ is displayed if `command` returns an error or if one of the values in `exp_list` is missing.

`noisily` requests that any output from `command` be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of `command` to be displayed. This option implies the `noisily` option.

`title(text)` specifies a title to be displayed above the table of permutation results; the default title is Monte Carlo permutation results.

Advanced

`eps(#)` specifies the numerical tolerance for testing $|T^*| \geq |T|$, $T^* \leq T$, or $T^* \geq T$. These are considered true if, respectively, $|T^*| \geq |T| - \#$, $T^* \leq T + \#$, or $T^* \geq T - \#$. The default is `1e-7`. You will not have to specify `eps()` under normal circumstances.

`nowarn` suppresses the printing of a warning message when `command` does not set `e(sample)`.

`force` suppresses the restriction that `command` may not specify weights or be a `svy` command. `permute` is not suited for weighted estimation, thus `permute` should not be used with weights or `svy`. `permute` reports an error when it encounters weights or `svy` in `command` if the `force` option is not specified. This is a seldom used option, so use it only if you know what you are doing!

`reject(exp)` identifies an expression that indicates when results should be rejected. When `exp` is true, the resulting values are reset to missing values.

`seed(#)` sets the random-number seed. Specifying this option is equivalent to typing the following command prior to calling `permute`:

```
. set seed #
```

Remarks and examples

stata.com

Permutation tests determine the significance of the observed value of a test statistic in light of rearranging the order (permuting) of the observed values of a variable.

► Example 1: A simple two-sample test

Suppose that we conducted an experiment to determine the effect of a treatment on the development of cells. Further suppose that we are restricted to six experimental units because of the extreme cost of the experiment. Thus three units are to be given a placebo, and three units are given the treatment. The measurement is the number of newly developed healthy cells. The following listing gives the hypothetical data, along with some summary statistics.

```
. input y treatment
      y treatment
1. 7 0
2. 9 0
3. 11 0
4. 10 1
5. 12 1
6. 14 1
7. end
. sort treatment
```

```
. summarize y
      Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----+-----+-----+-----+-----
           y |         6     10.5   2.428992         7     14
. by treatment: summarize y
```

```
-> treatment = 0
      Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----+-----+-----+-----+-----
           y |         3         9         2         7     11
```

```
-> treatment = 1
      Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----+-----+-----+-----+-----
           y |         3     12         2     10     14
```

Clearly, there are more cells in the treatment group than in the placebo group, but a statistical test is needed to conclude that the treatment does affect the development of cells. If the sum of the treatment measures is our test statistic, we can use `permute` to determine the probability of observing 36 or more cells, given the observed data and assuming that there is no effect due to the treatment.

```
. set seed 1234
. permute y sum=r(sum), saving(permdish) right nodrop nowarn: sum y if treatment
(running summarize on estimation sample)
Permutation replications (100)
-----|-----|-----|-----|-----|-----|-----
..... 1 ..... 2 ..... 3 ..... 4 ..... 5 ..... 50
..... 100
Monte Carlo permutation results      Number of obs   =      6
      command: summarize y if treatment
      sum: r(sum)
      permute var: y
```

T	T(obs)	c	n	p=c/n	SE(p)	[95% Conf. Interval]
sum	36	10	100	0.1000	0.0300	.0490047 .1762226

Note: confidence interval is with respect to p=c/n.
 Note: c = #{T >= T(obs)}

We see that 10 of the 100 randomly permuted datasets yielded sums from the treatment group larger than or equal to the observed sum of 36. Thus the evidence is not strong enough, at the 5% level, to reject the null hypothesis that there is no effect of the treatment.

Because of the small size of this experiment, we could have calculated the exact permutation *p*-value from all possible permutations. There are six units, but we want the sum of the treatment units. Thus there are $\binom{6}{3} = 20$ permutation sums from the possible unique permutations.

```

7 + 9 + 10 = 26   7 + 10 + 12 = 29   9 + 10 + 11 = 30   9 + 12 + 14 = 35
7 + 9 + 11 = 27   7 + 10 + 14 = 31   9 + 10 + 12 = 31   10 + 11 + 12 = 33
7 + 9 + 12 = 28   7 + 11 + 12 = 30   9 + 10 + 14 = 33   10 + 11 + 14 = 35
7 + 9 + 14 = 30   7 + 11 + 14 = 32   9 + 11 + 12 = 32   10 + 12 + 14 = 36
7 + 10 + 11 = 28  7 + 12 + 14 = 33   9 + 11 + 14 = 34   11 + 12 + 14 = 37

```

Two of the 20 permutation sums are greater than or equal to 36. Thus the exact p -value for this permutation test is 0.1. Tied values will decrease the number of unique permutations.

When the `saving()` option is supplied, `permute` saves the values of the permutation statistic to the indicated file, in our case, `permdish.dta`. This file can be used to replay the result of `permute`. The `level()` option controls the confidence level of the confidence interval for the permutation p -value. This confidence interval is calculated using `cii` with the reported `n` (number of nonmissing replications) and `c` (the counter for events of significance).

```

. permute using permdish, level(80)
Monte Carlo permutation results                Number of obs   =           6
      command: summarize y if treatment
             sum: r(sum)
      permute var: y

```

T	T(obs)	c	n	p=c/n	SE(p)	[80% Conf. Interval]
sum	36	10	100	0.1000	0.0300	.0631113 .1498826

Note: confidence interval is with respect to $p=c/n$.

Note: $c = \#\{|T| \geq |T(\text{obs})|\}$

◀

► Example 2: Permutation tests with ANOVA

Consider some fictional data from a randomized complete-block design in which we wish to determine the significance of five treatments.

```

. use http://www.stata-press.com/data/r13/permute1, clear
. list y treatment in 1/10, abbrev(10)

```

	y	treatment
1.	4.407557	1
2.	5.693386	1
3.	7.099699	1
4.	3.12132	1
5.	5.242648	1
6.	4.280349	2
7.	4.508785	2
8.	4.079967	2
9.	5.904368	2
10.	3.010556	2

These data may be analyzed using `anova`.

```
. anova y treatment subject
```

	Number of obs =	50	R-squared =	0.3544	
	Root MSE =	.914159	Adj R-squared =	0.1213	
Source	Partial SS	df	MS	F	Prob > F
Model	16.5182188	13	1.27063221	1.52	0.1574
treatment	13.0226706	9	1.44696341	1.73	0.1174
subject	3.49554813	4	.873887032	1.05	0.3973
Residual	30.0847503	36	.835687509		
Total	46.6029691	49	.951081002		

Suppose that we want to compute the significance of the F statistic for `treatment` by using `permute`. All we need to do is write a short program that will save the result of this statistic for `permute` to use. For example,

```
program panova, rclass
  version 13
  args response fac_intrst fac_other
  anova 'response' 'fac_intrst' 'fac_other'
  return scalar Fmodel = e(F)
  test 'fac_intrst'
  return scalar F = r(F)
end
```

Now in `panova`, `test` saves the F statistic for the factor of interest in `r(F)`. This is different from `e(F)`, which is the overall model F statistic for the model fit by `anova` that `panova` saves in `r(Fmodel)`. In the following example, we use the `strata()` option so that the treatments are randomly rearranged within each subject. It should not be too surprising that the estimated p -values are equal for this example, because the two F statistics are equivalent when controlling for differences between subjects. However, we would not expect to always get the same p -values every time we reran `permute`.

```
. set seed 1234
. permute treatment treatmentF=r(F) modelF=e(F), reps(1000) strata(subject)
> saving(permanova) nodots: panova y treatment subject
Monte Carlo permutation results
Number of strata = 5 Number of obs = 50
command: panova y treatment subject
treatmentF: r(F)
modelF: e(F)
permute var: treatment
```

T	T(obs)	c	n	p=c/n	SE(p)	[95% Conf. Interval]
treatmentF	1.731465	118	1000	0.1180	0.0102	.0986525 .1396277
modelF	1.520463	118	1000	0.1180	0.0102	.0986525 .1396277

Note: confidence intervals are with respect to $p=c/n$.

Note: `c = #{|T| >= |T(obs)|}`

▷ Example 3: Wilcoxon rank-sum test

As a final example, let's consider estimating the p -value of the Z statistic returned by `ranksum`. Suppose that we collected data from some experiment: `y` is some measure we took on 17 individuals, and `group` identifies the group that an individual belongs to.

```
. use http://www.stata-press.com/data/r13/permute2
. list
```

	group	y
1.	1	6
2.	1	11
3.	1	20
4.	1	2
5.	1	9
6.	1	5
7.	0	2
8.	0	1
9.	0	6
10.	0	0
11.	0	2
12.	0	3
13.	0	3
14.	0	12
15.	0	4
16.	0	1
17.	0	5

Next we analyze the data using `ranksum` and notice that the observed value of the test statistic (stored as `r(z)`) is -2.02 with an approximate p -value of 0.0434.

```
. ranksum y, by(group)
Two-sample Wilcoxon rank-sum (Mann-Whitney) test
```

group	obs	rank sum	expected
0	11	79	99
1	6	74	54
combined	17	153	153

```

unadjusted variance      99.00
adjustment for ties      -0.97
-----
adjusted variance        98.03
Ho: y(group==0) = y(group==1)
      z = -2.020
      Prob > |z| = 0.0434
```

The observed value of the rank-sum statistic is 79, with an expected value (under the null hypothesis of no group effect) of 99. There are 17 observations, so the permutation distribution contains $\binom{17}{6} = 12,376$ possible values of the rank-sum statistic if we ignore ties. With ties, we have fewer possible values but still too many to want to count them. Thus we use `permute` with 10,000 replications and see that the Monte Carlo permutation test agrees with the result of the test based on the normal approximation.


```

. set seed 18385766
. permute y z=r(z), reps(10000) nowarn nodots: ranksum y, by(group)
Monte Carlo permutation results          Number of obs   =          17
      command:  ranksum y, by(group)
              z:  r(z)
permute var:  y

```

T	T(obs)	c	n	p=c/n	SE(p)	[95% Conf. Interval]
z	-2.020002	468	10000	0.0468	0.0021	.0427429 .0511236

Note: confidence interval is with respect to $p=c/n$.

Note: $c = \#\{|T| \geq |T(\text{obs})|\}$

◀

For an application of a permutation test to a problem in epidemiology, see [Hayes and Moulton \(2009, 190–193\)](#).

□ Technical note

`permute` reports confidence intervals for p to emphasize that it is based on the binomial estimator for proportions. When the variability implied by the confidence interval makes conclusions difficult, you may increase the number of replications to determine more precisely the significance of the test statistic of interest. In other words, the value of p from `permute` will converge to the true permutation p -value as the number of replications gets arbitrarily large. □

Stored results

`permute` stores the following in `r()`:

Scalars

<code>r(N)</code>	sample size	<code>r(k_exp)</code>	number of standard expressions
<code>r(N_reps)</code>	number of requested replications	<code>r(k_eexp)</code>	number of <code>_b/_se</code> expressions
<code>r(level)</code>	confidence level		

Macros

<code>r(cmd)</code>	<code>permute</code>	<code>r(left)</code>	left or empty
<code>r(command)</code>	<i>command</i> following colon	<code>r(right)</code>	right or empty
<code>r(permvvar)</code>	permutation variable	<code>r(seed)</code>	initial random-number seed
<code>r(title)</code>	title in output	<code>r(event)</code>	$T \leq T(\text{obs}), T \geq T(\text{obs}),$ or $ T \leq T(\text{obs}) $
<code>r(exp#)</code>	#th expression		

Matrices

<code>r(b)</code>	observed statistics	<code>r(p)</code>	observed proportions
<code>r(c)</code>	count when <code>r(event)</code> is true	<code>r(se)</code>	standard errors of observed proportions
<code>r(reps)</code>	number of nonmissing results	<code>r(ci)</code>	confidence intervals of observed proportions

References

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- Hayes, R. J., and L. H. Moulton. 2009. *Cluster Randomised Trials*. Boca Raton, FL: Chapman & Hall/CRC.
- Kaiser, J. 2007. *An exact and a Monte Carlo proposal to the Fisher–Pitman permutation tests for paired replicates and for independent samples*. *Stata Journal* 7: 402–412.

Kaiser, J., and M. G. Lacy. 2009. A general-purpose method for two-group randomization tests. *Stata Journal* 9: 70–85.

Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **jackknife** — Jackknife estimation

[R] **simulate** — Monte Carlo simulations