

**cvpermute()** — Obtain all permutations

Syntax Diagnostics	Description Also see	Remarks and examples	Conformability
-----------------------	-------------------------	----------------------	----------------

## Syntax

```

info = cvpermutesetup(real colvector  $V$  [, real scalar unique ])
real colvector cvpermute(info)

```

where *info* should be declared *transmorphic*.

## Description

`cvpermute()` returns all permutations of the values of column vector  $V$ , one at a time. If  $V = (1\ 2\ 3)$ , there are six permutations and they are  $(1\ 2\ 3)$ ,  $(1\ 3\ 2)$ ,  $(2\ 1\ 3)$ ,  $(2\ 3\ 1)$ ,  $(3\ 1\ 2)$ , and  $(3\ 2\ 1)$ . If  $V = (1\ 2\ 1)$ , there are three permutations and they are  $(1\ 1\ 2)$ ,  $(1\ 2\ 1)$ , and  $(2\ 1\ 1)$ .

Vector  $V$  is specified by calling `cvpermutesetup()`,

```
info = cvpermutesetup( $V$ )
```

*info* holds information that is needed by `cvpermute()` and it is *info*, not  $V$ , that is passed to `cvpermute()`. To obtain the permutations, repeated calls are made to `cvpermute()` until it returns  $J(0,1,..)$ :

```

info = cvpermutesetup( $V$ )
while (( $p$ =cvpermute(info)) != J(0,1,..)) {
    ...  $p$  ...
}

```

Column vector  $p$  will contain a permutation of  $V$ .

`cvpermutesetup()` may be specified with one or two arguments:

```

info = cvpermutesetup( $V$ )

info = cvpermutesetup( $V$ , unique)

```

*unique* is usually not specified. If *unique* is specified, it should be 0 or 1. Not specifying *unique* is equivalent to specifying *unique* = 0. Specifying *unique* = 1 states that the elements of  $V$  are unique or, at least, are to be treated that way.

When the arguments of  $V$  are unique—for instance,  $V = (1\ 2\ 3)$ —specifying *unique* = 1 will make `cvpermute()` run faster. The same permutations will be returned, although usually in a different order.

When the arguments of  $V$  are not unique—for instance,  $V = (1\ 2\ 1)$ —specifying *unique* = 1 will make `cvpermute()` treat them as if they were unique. With *unique* = 0, there are three permutations of  $(1\ 2\ 1)$ . With *unique* = 1, there are six permutations, just as there are with  $(1\ 2\ 3)$ .

## Remarks and examples

[stata.com](http://stata.com)

### ▷ Example 1

You have the following data:

v1	v2
22	29
17	33
21	26
20	32
16	35

You wish to do an exact permutation test for the correlation between  $v1$  and  $v2$ .

That is, you wish to (1) calculate the correlation between  $v1$  and  $v2$ —call that value  $r$ —and then (2) calculate the correlation between  $v1$  and  $v2$  for all permutations of  $v1$ , and count how many times the result is more extreme than  $r$ .

For the first step,

```
: X = (22, 29 \
>      17, 33 \
>      21, 26 \
>      20, 32 \
>      16, 35)
:
: correlation(X)
[symmetric]
           1           2
1          1
2    -.8468554653          1
```

The correlation is  $-.846855$ . For the second step,

```
: V1 = X[,1]
: V2 = X[,2]
: num = den = 0
: info = cvpermutesetup(V1)
: while ((V1=cvpermute(info)) != J(0,1,.)) {
>     rho = correlation((V1,V2))[2,1]
>     if (rho<=-.846 | rho>=.846) num++
>     den++
> }
: (num, den, num/den)
           1           2           3
1          13          120    .1083333333
```

Of the 120 permutations, 13 (10.8%) were outside .846855 or  $-.846855$ .

◀

## ▷ Example 2

You now wish to do the same thing but using the Spearman rank-correlation coefficient. Mata has no function that will calculate that, but Stata has a command that does—see [R] [spearman](#)—so we will use the Stata command as our subroutine.

This time, we will assume that the data have been loaded into a Stata dataset:

```
. list
```

	var1	var2
1.	22	29
2.	17	33
3.	21	26
4.	20	32
5.	16	35

For the first step,

```
. spearman var1 var2
Number of obs =      5
Spearman's rho =    -0.9000
Test of Ho: var1 and var2 are independent
Prob > |t| =      0.0374
```

For the second step,

```
. mata
----- mata (type end to exit) -----
: V1 = st_data(., "var1")
: info = cvpermutsetup(V1)
: num = den = 0
: while ((V1=cvpermute(info)) != J(0,1,.)) {
>   st_store(., "var1", V1)
>   stata("quietly spearman var1 var2")
>   rho = st_numscalar("r(rho)")
>   if (rho<=-.9 | rho>=.9) num++
>   den++
> }
: (num, den, num/den)
      1          2          3
1  2          120    .016666667
```

Only two of the permutations resulted in a rank correlation of at least .9 in magnitude.

In the code above, we obtained the rank correlation from `r(rho)` which, we learned from [R] [spearman](#), is where `spearman` stores it.

Also note how we replaced the contents of `var1` by using `st_store()`. Our code leaves the dataset changed and so could be improved.

◀

## Conformability

`cvpermutesetup(V, unique)`:

*V*:  $n \times 1$   
*unique*:  $1 \times 1$  (optional)  
*result*:  $1 \times L$

`cvpermute(info)`:

*info*:  $1 \times L$   
*result*:  $n \times 1$  or  $0 \times 1$

where

$$L = \begin{cases} 3 & \text{if } n = 0 \\ 4 & \text{if } n = 1 \\ (n + 3)(n + 2)/2 - 6 & \text{otherwise} \end{cases}$$

The value of  $L$  is not important except that the *info* vector returned by `cvpermutesetup()` and then passed to `cvpermute()` consumes memory. For instance,

$n$	$L$	Total memory ( $8 * L$ )
5	22	176 bytes
10	72	576
50	1,372	10,560
100	5,247	41,976
1,000	502,497	4,019,976

## Diagnostics

`cvpermute()` returns `J(0, 1, .)` when there are no more permutations.

## Also see

[M-4] [statistical](#) — Statistical functions