<div style="border:1px solid black; padding:10px;">

cluster utility — List, rename, use, and drop cluster analyses

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Description

These `cluster` utility commands allow you to view and manipulate the cluster objects that you have created. See [MV] **cluster** for an overview of cluster analysis and for the available `cluster` commands. If you want even more control over your cluster objects, or if you are programming new cluster subprograms, more `cluster` programmer utilities are available; see [MV] **cluster programming utilities** for details.

The `cluster dir` command provides a directory-style listing of all the currently defined clusters. `cluster list` provides a detailed listing of the specified clusters or of all current clusters if no cluster names are specified. The default action is to list all the information attached to the clusters. You may limit the type of information listed by specifying particular options.

The `cluster drop` command removes the named clusters. The keyword `_all` specifies that all current cluster analyses be dropped.

Stata cluster analyses are referred to by name. Many `cluster` commands default to using the most recently defined cluster analysis if no cluster name is provided. The `cluster use` command sets the specified cluster analysis as the most recently executed cluster analysis, so that, by default, this cluster analysis will be used if the cluster name is omitted from many of the `cluster` commands. You may use the * and ? name-matching characters to shorten the typing of cluster names; see **[U] 11.2 Abbreviation rules**.

`cluster rename` allows you to rename a cluster analysis without changing any of the variable names attached to the cluster analysis. The `cluster renamevar` command, on the other hand, allows you to rename the variables attached to a cluster analysis and to update the cluster object with the new variable names. Do not use the `rename` command (see [D] **rename**) to rename variables attached to a cluster analysis because this would invalidate the cluster object. Use the `cluster renamevar` command instead.

Menu

cluster list

Statistics > Multivariate analysis > Cluster analysis > Postclustering > Detailed listing of clusters

cluster drop

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cluster rename

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Syntax

Directory-style listing of currently defined clusters

> cluster dir

Detailed listing of clusters

> cluster list [*clnamelist*] [, *list_options*]

Drop cluster analyses

> cluster drop { *clnamelist* | _all }

Mark a cluster analysis as the most recent one

> cluster use *clname*

Rename a cluster

> cluster rename *oldclname newclname*

Rename variables attached to a cluster

> cluster renamevar *oldvarname newvar* [, name(*clname*)]

> cluster renamevar *oldstub newstub* , prefix [name(*clname*)]

list_options	Description
Options	
notes	list cluster notes
type	list cluster analysis type
method	list cluster analysis method
dissimilarity	list cluster analysis dissimilarity measure
similarity	list cluster analysis similarity measure
vars	list variable names attached to the cluster analysis
chars	list any characteristics attached to the cluster analysis
other	list any "other" information
all	list all items and information attached to the cluster; the default

all does not appear in the dialog box.

Options for cluster list

Options

notes specifies that cluster notes be listed.

type specifies that the type of cluster analysis be listed.

method specifies that the cluster analysis method be listed.

dissimilarity specifies that the dissimilarity measure be listed.

similarity specifies that the similarity measure be listed.

vars specifies that the variables attached to the clusters be listed.

chars specifies that any Stata characteristics attached to the clusters be listed.

other specifies that information attached to the clusters under the heading "other" be listed.

The following option is available with cluster list but is not shown in the dialog box:

all, the default, specifies that all items and information attached to the cluster(s) be listed. You may
   instead pick among the notes, type, method, dissimilarity, similarity, vars, chars, and
   other options to limit what is presented.

Options for cluster renamevar

name(*clname*) indicates the cluster analysis within which the variable renaming is to take place. If
   name() is not specified, the most recently performed cluster analysis (or the one specified by cluster
   use) will be used.

prefix specifies that all variables attached to the cluster analysis that have *oldstub* as the beginning of
   their name be renamed, with *newstub* replacing *oldstub*.

Remarks and examples

▷ Example 1

   We demonstrate these cluster utility commands by beginning with four already-defined cluster anal-
yses. The dir and list subcommands provide listings of the cluster analyses.

```
. cluster dir
bcx3kmed
ayz5kmeans
abc_clink
xyz_slink
. cluster list xyz_slink
xyz_slink  (type: hierarchical,  method: single,  dissimilarity: L2)
      vars: xyz_slink_id (id variable)
            xyz_slink_ord (order variable)
            xyz_slink_hgt (height variable)
     other: cmd: cluster singlelinkage x y z, name(xyz_slink)
            varlist: x y z
            range: 0 .
```

```
. cluster list
bcx3kmed  (type: partition,  method: kmedians,  dissimilarity: L2)
      vars: bcx3kmed (group variable)
     other: cmd: cluster kmedians b c x, k(3) name(bcx3kmed)
            varlist: b c x
            k: 3
            start: krandom
            range: 0 .
ayz5kmeans  (type: partition,  method: kmeans,  dissimilarity: L2)
      vars: ayz5kmeans (group variable)
     other: cmd: cluster kmeans a y z, k(5) name(ayz5kmeans)
            varlist: a y z
            k: 5
            start: krandom
            range: 0 .
abc_clink  (type: hierarchical,  method: complete,  dissimilarity: L2)
      vars: abc_clink_id (id variable)
            abc_clink_ord (order variable)
            abc_clink_hgt (height variable)
     other: cmd: cluster completelinkage a b c, name(abc_clink)
            varlist: a b c
            range: 0 .
xyz_slink  (type: hierarchical,  method: single,  dissimilarity: L2)
      vars: xyz_slink_id (id variable)
            xyz_slink_ord (order variable)
            xyz_slink_hgt (height variable)
     other: cmd: cluster singlelinkage x y z, name(xyz_slink)
            varlist: x y z
            range: 0 .

. cluster list a*, vars
ayz5kmeans
      vars: ayz5kmeans (group variable)
abc_clink
      vars: abc_clink_id (id variable)
            abc_clink_ord (order variable)
            abc_clink_hgt (height variable)
```

`cluster dir` listed the names of the four currently defined cluster analyses. `cluster list` followed by the name of one of the cluster analyses listed the information attached to that cluster analysis. The `cluster list` command, without an argument, listed the information for all currently defined cluster analyses. We demonstrated the `vars` option of `cluster list` to show that we can restrict the information that is listed. Notice also the use of `a*` as the cluster name. The `*` here indicates that any ending is allowed. For these four cluster analyses, Stata matches the names `ayz5kmeans` and `abc_clink`.

We now demonstrate the use of the `renamevar` subcommand.

```
. cluster renamevar ayz5kmeans g5km
variable ayz5kmeans not found in bcx3kmed
r(198);
. cluster renamevar ayz5kmeans g5km, name(ayz5kmeans)
. cluster list ayz5kmeans
ayz5kmeans  (type: partition,  method: kmeans,  dissimilarity: L2)
      vars: g5km (group variable)
     other: cmd: cluster kmeans a y z, k(5) name(ayz5kmeans)
            varlist: a y z
            k: 5
            start: krandom
            range: 0 .
```

The first use of cluster renamevar failed because we did not specify which cluster object to use (with the name() option), and the most recent cluster object, bcx3kmed, was not the appropriate one. After specifying the name() option with the appropriate cluster name, the renamevar subcommand changed the name as shown in the cluster list command that followed.

The cluster use command sets a particular cluster object as the default. We show this in conjunction with the prefix option of the renamevar subcommand.

```
. cluster use ayz5kmeans
. cluster renamevar g grp, prefix
. cluster renamevar xyz_slink_ wrk, prefix name(xyz*)
. cluster list ayz* xyz*
ayz5kmeans  (type: partition,  method: kmeans,  dissimilarity: L2)
       vars: grp5km (group variable)
      other: cmd: cluster kmeans a y z, k(5) name(ayz5kmeans)
             varlist: a y z
             k: 5
             start: krandom
             range: 0 .
xyz_slink  (type: hierarchical,  method: single,  dissimilarity: L2)
       vars: wrkid (id variable)
             wrkord (order variable)
             wrkhgt (height variable)
      other: cmd: cluster singlelinkage x y z, name(xyz_slink)
             varlist: x y z
             range: 0 .
```

The cluster use command placed ayz5kmeans as the current cluster object. The cluster renamevar command that followed capitalized on this placement by leaving off the name() option. The prefix option allowed us to change the variable names, as demonstrated in the cluster list of the two changed cluster objects.

cluster rename changes the name of cluster objects. cluster drop allows us to drop some of or all the cluster objects.

```
. cluster rename xyz_slink bob
. cluster rename ayz* sam
. cluster list, type method vars
sam  (type: partition,  method: kmeans)
       vars: grp5km (group variable)
bob  (type: hierarchical,  method: single)
       vars: wrkid (id variable)
             wrkord (order variable)
             wrkhgt (height variable)
bcx3kmed  (type: partition,  method: kmedians)
       vars: bcx3kmed (group variable)
abc_clink  (type: hierarchical,  method: complete)
       vars: abc_clink_id (id variable)
             abc_clink_ord (order variable)
             abc_clink_hgt (height variable)
. cluster drop bcx3kmed abc_clink
. cluster dir
sam
bob
. cluster drop _all
. cluster dir
```

We used options with `cluster list` to limit what was presented. The `_all` keyword with `cluster drop` removed all currently defined cluster objects.

◁

Also see

[MV] **cluster** — Introduction to cluster-analysis commands

[MV] **cluster notes** — Cluster analysis notes

[MV] **cluster programming utilities** — Cluster-analysis programming utilities

[MV] **clustermat** — Introduction to clustermat commands

[D] **notes** — Place notes in data

[P] **char** — Characteristics