Title

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pkcollapse — Generate pharmacokinetic measurement dataset

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Description

`pkcollapse` generates new variables with the pharmacokinetic summary measures of interest.

`pkcollapse` is one of the pk commands. Please read [R] **pk** before reading this entry.

Quick start

Single concentration, `v1`, measured over time, `tvar`, for patients identified by `idvar`

```
pkcollapse tvar v1, id(idvar)
```

Same as above, but add additional drug concentration data stored in `v2`

```
pkcollapse tvar v1 v2, id(idvar)
```

Same as above, but use trapezoidal rule for calculating area under the concentration–time curve ($\text{AUC}_{0,t_{\max}}$)

```
pkcollapse tvar v1 v2, id(idvar) trapezoid
```

Same as above, and increase the number of data points used to estimate $\text{AUC}_{0,\infty}$ to 10

```
pkcollapse tvar v1 v2, id(idvar) trapezoid fit(10)
```

Retain variables `v3` and `v4` when collapsing dataset

```
pkcollapse tvar v1 v2, id(idvar) keep(v3 v4)
```

Menu

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Syntax

```
pkcollapse time concentration [concentration [...]] [if] , id(id_var) [options]
```

options	Description
Main	
* `id(`*id_var*`)`	subject ID variable
`stat(`*measures*`)`	create specified *measures*; default is all
`trapezoid`	use trapezoidal rule; default is cubic splines
`fit(#)`	use # points to estimate $\text{AUC}_{0,\infty}$; default is `fit(3)`
`keep(`*varlist*`)`	keep variables in *varlist*
`force`	force collapse
`nodots`	suppress dots during calculation

* `id(`*id_var*`)` is required.

measures	Description
`auc`	$\text{AUC}_{0,t_{\max}}$
`aucline`	$\text{AUC}_{0,\infty}$ using a linear extension
`aucexp`	$\text{AUC}_{0,\infty}$ using an exponential extension
`auclog`	area under the concentration–time curve from 0 to ∞ extended with a linear fit to log concentration
`half`	half-life of the drug
`ke`	elimination rate
`cmax`	maximum concentration
`tmax`	time at last concentration
`tomc`	time of maximum concentration

Options

Main

`id(`*id_var*`)` is required and specifies the variable that contains the subject ID over which `pkcollapse` is to operate.

`stat(`*measures*`)` specifies the measures to be generated. The default is to generate all the measures.

`trapezoid` tells Stata to use the trapezoidal rule when calculating the $\text{AUC}_{0,t_{\max}}$. The default is to use cubic splines, which give better results for most functions. When the curve is irregular, `trapezoid` may give better results.

`fit(#)` specifies the number of points to use in estimating the $\text{AUC}_{0,\infty}$. The default is `fit(3)`, the last three points. This number should be viewed as a minimum; the appropriate number of points will depend on your data.

`keep(`*varlist*`)` specifies the variables to be kept during the collapse. Variables not specified with the `keep()` option will be dropped. When `keep()` is specified, the kept variables are checked to ensure that all values of the variables are the same within *id_var*.

`force` forces the collapse, even when values of the `keep()` variables differ within *id_var*.

`nodots` suppresses the display of dots during calculation.

Remarks and examples

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pkcollapse generates all the summary pharmacokinetic measures.

▷ Example 1

We demonstrate the use of pkcollapse with pkdata.dta described in example 2 of [R] **pk**. We have drug concentration data on 16 subjects. Each subject is measured at 13 time points over a 32-hour period. Some of the records are as follows:

```
. use https://www.stata-press.com/data/r18/pkdata
(Fictional drug concentration data)
. list, sep(0)
```

	id	seq	time	conc1	conc2
1.	1	1	0	0	0
2.	1	1	.5	3.073403	3.712592
3.	1	1	1	5.188444	6.230602
4.	1	1	1.5	5.898577	7.885944
5.	1	1	2	5.096378	9.241735
6.	1	1	3	6.094085	13.10507
			(*output omitted*)		
14.	2	1	0	0	0
15.	2	1	.5	2.48462	.9209593
16.	2	1	1	4.883569	5.925818
17.	2	1	1.5	7.253442	8.710549
18.	2	1	2	5.849345	10.90552
19.	2	1	3	6.761085	8.429898
			(*output omitted*)		
207.	16	2	24	4.673281	6.059818
208.	16	2	32	3.487347	5.213639

Although pksumm allows us to view all the pharmacokinetic measures, we can create a dataset with the measures by using pkcollapse.

```
. pkcollapse time conc1 conc2, id(id) stat(auc) keep(seq)
..............................
. list, sep(8) abbrev(10)
```

	id	seq	auc_conc1	auc_conc2
1.	1	1	150.9643	218.5551
2.	2	1	146.7606	133.3201
3.	3	1	160.6548	126.0635
4.	4	1	157.8622	96.17461
5.	5	1	133.6957	188.9038
6.	6	1	160.639	223.6922
7.	7	1	131.2604	104.0139
8.	8	1	168.5186	237.8962
9.	9	2	137.0627	139.7382
10.	10	2	153.4038	202.3942
11.	11	2	163.4593	136.7848
12.	12	2	146.0462	104.5191
13.	13	2	158.1457	165.8654
14.	14	2	147.1977	139.235
15.	15	2	164.9988	166.2391
16.	16	2	145.3823	158.5146

The resulting dataset contains one observation per subject and is in wide format. If we want to use `pkcross` or `pkequiv`, we must transform these data to long format with the `pkshape` command, which we do in example 2 of [R] **pk**.

◁

Methods and formulas

The statistics generated by `pkcollapse` are described in [R] **pkexamine**.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data