pkcollapse — Generate pharmacokinetic measurement dataset

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)
```

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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

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/r19/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
			(*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