Title

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pkcollapse — Generate pharmacokinetic measurement dataset

Syntax

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

Menu

Statistics > Epidemiology and related > Other > 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.

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 AUC. 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 keep variables are checked to ensure that all values of the variables are the same within *id_var*.

`force` forces the collapse, even when the values of the `keep()` variables are different within the *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 the data described in [R] **pk**. We have drug concentration data on 15 subjects. Each subject is measured at 13 time points over a 32-hour period. Some of the records are

```
. use http://www.stata-press.com/data/r13/pkdata
. list, sep(0)
```

	id	seq	time	concA	concB
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.	20	2	24	4.673281	6.059818
208.	20	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 concA concB, id(id) stat(auc) keep(seq)
.............................
. list, sep(8) abbrev(10)
```

	id	seq	auc_concA	auc_concB
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.	7	1	160.639	223.6922
7.	8	1	131.2604	104.0139
8.	9	1	168.5186	237.8962
9.	10	2	137.0627	139.7382
10.	12	2	153.4038	202.3942
11.	13	2	163.4593	136.7848
12.	14	2	146.0462	104.5191
13.	15	2	158.1457	165.8654
14.	18	2	147.1977	139.235
15.	19	2	164.9988	166.2391
16.	20	2	145.3823	158.5146

The resulting dataset, which we will call pkdata2, contains 1 observation per subject. This dataset is in wide format. If we want to use pkcross or pkequiv, we must transform these data to long format, which we do in the last example of [R] **pkshape**.

◁

Methods and formulas

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

Also see

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