

**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)`

Add additional drug concentration data stored in `v2`  
`pkcollapse tvar v1 v2, id(idvar)`

As above, but use trapezoidal rule for calculating AUC  
`pkcollapse tvar v1 v2, id(idvar) trapezoid`

As above, and increase the number of data points used to estimate  $AUC_{0,\infty}$  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 [if] , id(id_var) [options]
```

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

\**id(id\_var)* is required.

<i>measures</i>	Description
<i>auc</i>	area under the concentration-time curve ( $AUC_{0,\infty}$ )
<i>aucline</i>	area under the concentration-time curve from 0 to $\infty$ using a linear extension
<i>aucexp</i>	area under the concentration-time curve from 0 to $\infty$ using an exponential extension
<i>auclog</i>	area under the log-concentration-time curve extended with a linear fit
<i>half</i>	half-life of the drug
<i>ke</i>	elimination rate
<i>cmax</i>	maximum concentration
<i>tmax</i>	time at last concentration
<i>tomc</i>	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 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  $AUC_{0,\infty}$ . 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

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

`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/r15/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
	<i>(output omitted)</i>				
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
	<i>(output omitted)</i>				
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