Description	Quick start	Menu	Syntax
Options	Remarks and examples	Methods and formulas	Also see

Description

pksumm obtains summary measures based on the first four moments from the empirical distribution of each pharmacokinetic measurement and tests the null hypothesis that the distribution of that measurement is normally distributed.

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

Quick start

Table of pharmacokinetic measures for concentrations y at times tvar for patients identified by idvar

    pksumm idvar tvar y

Add a histogram of $\text{AUC}_{0,t_{\max}}$ values

    pksumm idvar tvar y, graph

Same as above

    pksumm idvar tvar y, graph stat(auc)

Same as above, but plot AUC calculated from 0 to ∞ using a linear extension

    pksumm idvar tvar y, graph stat(aucline)

Same as above, but use 10 bins for the histogram

    pksumm idvar tvar y, graph stat(aucline) bins(10)

Menu

Statistics > Epidemiology and related > Other > Summarize pharmacokinetic data

Syntax

> pksumm *id time concentration* [*if*] [*in*] [, *options*]

options	Description
Main	
trapezoid	use trapezoidal rule to calculate $\text{AUC}_{0,t_{\max}}$; default is cubic splines
fit(#)	use # points to estimate $\text{AUC}_{0,\infty}$; default is fit(3)
notimechk	do not check whether follow-up time for all subjects is the same
nodots	suppress the dots during calculation
graph	graph the distribution of *statistic*
stat(*statistic*)	graph the specified statistic; default is stat(auc)
Histogram, Density plots, Y axis, X axis, Titles, Legend, Overall	
histogram_options	any option other than by() documented in [R] **histogram**

statistic	Description
auc	area under the concentration–time curve ($\text{AUC}_{0,t_{\max}}$); the default
aucline	AUC from 0 to ∞ using a linear extension
aucexp	AUC from 0 to ∞ 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

trapezoid specifies that the trapezoidal rule be used to calculate the $\text{AUC}_{0,t_{\max}}$. The default is cubic splines, which give better results for most situations. When the curve is irregular, the trapezoidal rule may give better results.

fit(#) specifies the number of points, counting back from the last time measurement, to use in fitting the extension to estimate the $\text{AUC}_{0,\infty}$. The default is fit(3), the last three points. This default should be viewed as a minimum; the appropriate number of points will depend on the data.

notimechk suppresses the check that the follow-up time for all subjects is the same. By default, pksumm expects the maximum follow-up time to be equal for all subjects.

nodots suppresses the progress dots during calculation. By default, a dot (a period) is displayed for every call to calculate the pharmacokinetic measures.

graph requests a graph of the distribution of the statistic specified with stat().

stat(*statistic*) specifies the statistic that pksumm should graph. The default is stat(auc). If the graph option is not also specified, then this option is ignored.

> Histogram, Density plots, Y axis, X axis, Titles, Legend, Overall

histogram_options are any of the options documented in [R] **histogram**, excluding by(). For pksumm, fraction is the default, not density.

Remarks and examples

pksumm produces summary statistics for the distribution of nine common pharmacokinetic measurements. If there are more than eight subjects, pksumm also computes a test for normality on each measurement. The nine measurements summarized by pksumm are listed above and are described in *Methods and formulas* of [R] **pkexamine**.

▷ Example 1

We demonstrate the use of pksumm on a variation of the data described in [R] **pk**. We have drug concentration data on 15 subjects, each measured at 13 time points over a 32-hour period. A few of the records are as follows:

```
. use https://www.stata-press.com/data/r19/pksumm
. list, sep(0)
```

	id	time	conc
1.	1	0	0
2.	1	.5	3.073403
3.	1	1	5.188444
4.	1	1.5	5.898577
5.	1	2	5.096378
6.	1	3	6.094085
	(output omitted)		
183.	15	0	0
184.	15	.5	3.86493
185.	15	1	6.432444
186.	15	1.5	6.969195
187.	15	2	6.307024
188.	15	3	6.509584
189.	15	4	6.555091
190.	15	6	7.318319
191.	15	8	5.329813
192.	15	12	5.411624
193.	15	16	3.891397
194.	15	24	5.167516
195.	15	32	2.649686

We can use pksumm to view the summary statistics for all the pharmacokinetic parameters.

```
. pksumm id time conc
..............

Summary statistics for the pharmacokinetic measures
                                            Number of observations =    15
    Measure  |    Mean     Median    Variance  Skewness   Kurtosis   p-value

        auc  |   150.74    150.96      123.07     -0.26       2.10      0.69
    aucline  |   408.30    214.17   188856.87      2.57       8.93      0.00
     aucexp  |   691.68    297.08   762679.94      2.56       8.87      0.00
     auclog  |   688.98    297.67   797237.24      2.59       9.02      0.00
       half  |    94.84     29.39    18722.13      2.26       7.37      0.00
         ke  |     0.02      0.02        0.00      0.89       3.70      0.09
       cmax  |     7.36      7.42        0.42     -0.60       2.56      0.44
       tomc  |     3.47      3.00        7.62      2.17       7.18      0.00
       tmax  |    32.00     32.00        0.00         .          .         .
```
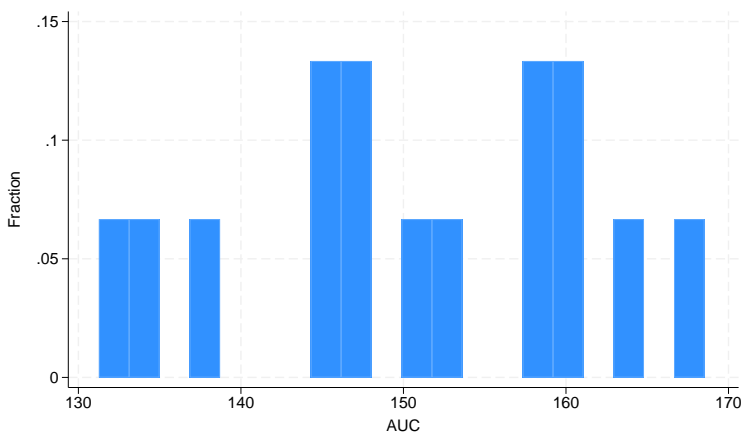
For the 15 subjects, the mean $\mathrm{AUC}_{0,t_{\max}}$ is 150.74, and $\sigma^2 = 123.07$. The skewness of -0.26 indicates that the distribution is slightly skewed left. The p-value of 0.69 for the χ^2 test of normality indicates that we cannot reject the null hypothesis that the distribution is normal.

If we were to consider any of the three variants of the $\mathrm{AUC}_{0,\infty}$, we would see that there is huge variability and that the distribution is heavily skewed. A skewness different from 0 and a kurtosis different from 3 are expected because the distribution of the $\mathrm{AUC}_{0,\infty}$ is not normal.

We now graph the distribution of $\mathrm{AUC}_{0,t_{\max}}$ by specifying the graph option.

```
. pksumm id time conc, graph bins(20)
..............

Summary statistics for the pharmacokinetic measures
                                            Number of observations =    15
    Measure  |    Mean     Median    Variance  Skewness   Kurtosis   p-value

        auc  |   150.74    150.96      123.07     -0.26       2.10      0.69
    aucline  |   408.30    214.17   188856.87      2.57       8.93      0.00
     aucexp  |   691.68    297.08   762679.94      2.56       8.87      0.00
     auclog  |   688.98    297.67   797237.24      2.59       9.02      0.00
       half  |    94.84     29.39    18722.13      2.26       7.37      0.00
         ke  |     0.02      0.02        0.00      0.89       3.70      0.09
       cmax  |     7.36      7.42        0.42     -0.60       2.56      0.44
       tomc  |     3.47      3.00        7.62      2.17       7.18      0.00
       tmax  |    32.00     32.00        0.00         .          .         .
```
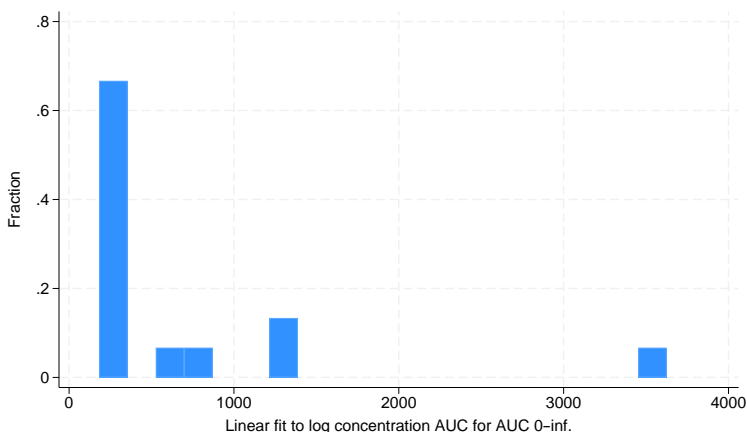
graph, by default, plots $\text{AUC}_{0,t_{\max}}$. To plot a graph of one of the other pharmacokinetic measurements, we need to specify the stat() option. For example, we can ask Stata to produce a plot of the $\text{AUC}_{0,\infty}$ using the log extension:

```
. pksumm id time conc, stat(auclog) graph bins(20)
..............
Summary statistics for the pharmacokinetic measures
```

| | | | | Number of observations = | | 15 |
Measure	Mean	Median	Variance	Skewness	Kurtosis	p-value
auc	150.74	150.96	123.07	-0.26	2.10	0.69
aucline	408.30	214.17	188856.87	2.57	8.93	0.00
aucexp	691.68	297.08	762679.94	2.56	8.87	0.00
auclog	688.98	297.67	797237.24	2.59	9.02	0.00
half	94.84	29.39	18722.13	2.26	7.37	0.00
ke	0.02	0.02	0.00	0.89	3.70	0.09
cmax	7.36	7.42	0.42	-0.60	2.56	0.44
tomc	3.47	3.00	7.62	2.17	7.18	0.00
tmax	32.00	32.00	0.00	.	.	.

Linear fit to log concentration AUC for AUC 0–inf.

◁

Methods and formulas

The χ^2 test for normality is conducted with sktest; see [R] **sktest** for more information on the test of normality.

The statistics reported by pksumm are identical to those reported by summarize and sktest; see [R] **summarize** and [R] **sktest**.

Also see

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