Title

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pksumm — Summarize pharmacokinetic data

Syntax

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

options	Description
Main	
`trapezoid`	use trapezoidal rule to calculate AUC; default is cubic splines
`fit(#)`	use # points to estimate AUC; 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 ($AUC_{0,\infty}$); the default
`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 > Summarize pharmacokinetic data

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.

Options

Main

`trapezoid` specifies that the trapezoidal rule be used to calculate the AUC. 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 $AUC_{0,\infty}$. 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 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 specified, 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

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`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

```
. use http://www.stata-press.com/data/r13/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 $\text{AUC}_{0,t_{\max}}$ 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 $\text{AUC}_{0,\infty}$, 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 $\text{AUC}_{0,\infty}$ is not normal.

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

```
. pksumm id time conc, graph bin(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
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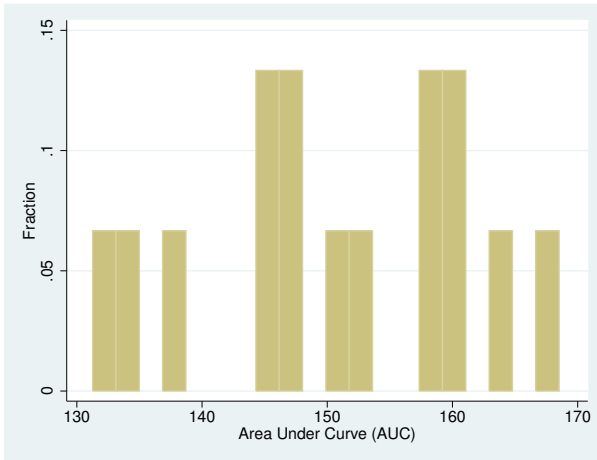
tomc	3.47	3.00	7.62	2.17	7.18	0.00
tmax	32.00	32.00	0.00	.	.	.



`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 bin(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
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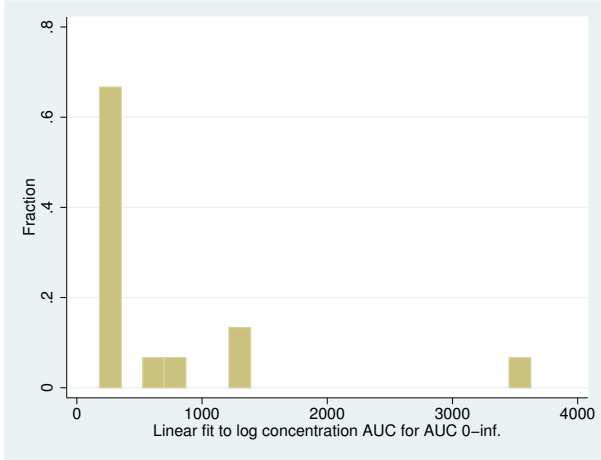
ke	0.02	0.02	0.00	0.89	3.70	0.09
cmax	7.36	7.42	0.42	-0.60	2.56	0.44
tomc	3.47	3.00	7.62	2.17	7.18	0.00
tmax	32.00	32.00	0.00	.	.	.



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