**pksumm — Summarize pharmacokinetic data**

**Syntax**

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

**options**

```
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**

```
  auc              area under the concentration-time curve (AUC₀,∞); 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

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_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...
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
                      | 150.74  |  150.96   |  123.07     |  -0.26     |  2.10       |  0.69
          auc      | 408.30  |  214.17   |  188856.87  |   2.57     |  8.93       |  0.00
          aucline  | 691.68  |  297.08   |  762679.94  |   2.56     |  8.87       |  0.00
          aucexp   | 688.98  |  297.67   |  797237.24  |   2.59     |  9.02       |  0.00
          auclog   |   94.84 |   29.39   |   18722.13  |   2.26     |   7.37      |  0.00
          half     |   0.02  |   0.02    |    0.00     |   0.89     |   3.70      |  0.09
          ke        |   7.36  |   7.42    |   0.42      |  -0.60     |   2.56      |  0.44
          cmax     |   3.47  |   3.00    |    7.62     |   2.17     |   7.18      |  0.00
          tomc     |  32.00  |  32.00    |    0.00     |     .      |     .       |     .
          tmax     |          |          |            |          |            |     .
```

For the 15 subjects, the mean $\text{AUC}_{0,t_{\text{max}}}$ 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 $\chi^2$ 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 $\text{AUC}_{0,t_{\text{max}}}$ by specifying the `graph` option.
. `pksumm` id time conc, graph bin(20)

Summary statistics for the pharmacokinetic measures

<table>
<thead>
<tr>
<th>Measure</th>
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<th>Median</th>
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Graph, by default, plots $\text{AUC}_{0,t_{\text{max}}}$. 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)

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Methods and formulas

The $\chi^2$ test for normality is conducted with \texttt{sktest}; see \texttt{R sktest} for more information on the test of normality.

The statistics reported by \texttt{pksumm} are identical to those reported by \texttt{summarize} and \texttt{sktest}; see \texttt{R summarize} and \texttt{R sktest}.

Also see

\texttt{[R pk] — Pharmacokinetic (biopharmaceutical) data}