Title

lccsm -- Longitudinal and survival modelling in a case-control design

Syntax

lccsm [*survivalvar*] [*timevar*] [*longitvar*] [*varlist*] [, options]

options	Description
Main	
detail	display additional statistics
notrend	suppresses trend based calculations
novar	suppresses covaraiate variance calculations
order(#)	specifies the order of the polynomial function in the longitudinal model
gentrend(*newvar*)	create trend variable name *newvar*
gentrvar(*newvar*)	create variance variable name *newvar*
global	use global measures of mean and variance in the survival model; defaults are time-dependent
match(*matchvarlist*)	match cases and controls on analysis time and specified categorical variables; default is to match on analysis time only
number(#)	matches each case with # controls; default is **number(1)**

Description

lccsm fits a two-stage survival model to longitudinal data with a time-to-event outcome. A stage 1 longitudinal mixed effects model is specified for a time-dependent covariate. Best linear unbiased (empirical Bayes) predictions of the underlying covariate trend are then obtained. Time-dependent (non-global) estimates of covariate variance are also calculated with the option of adjusting for the underlying covariate trend. In the second stage, a nested case-control study dataset is generated from the cohort-study dataset by sampling controls from the risk sets. For each case, the controls are chosen randomly from those members of the cohort who are at risk at the event time of the case. The resulting dataset is then analysed as a matched case-control study with odds ratios estimating the corresponding rate-ratio parameters in a proportional hazards model for the cohort study. Randomness in the matching is obtained using Stata's runiform() function. To ensure that the sample is random, the user should set the random-number seed; see **[R] set seed**.

Options

Main

detail specifies that additional information from the fitting of the longitudinal model (stage 1) be displayed with the output from the survival model (stage 2). The default is to only display the stage 2 survival model output.

notrend specifies suppression of the trend based calculations for the longitudinal covariate. The original (supplied) covariate values are used directly in the survival model rather than the estimates of underlying trend, and the covariate variance is calculated directly.

order(#) specifies the number of terms in the fitted polynomial function of time in the longitudinal part of the model (stage 1).

gentrend(*newvar*) creates a new longitudinal variable (called *newvar*) in the original (supplied) data set containing predicted values for the underlying trend at each time point.

gentrvar(*newvar*) creates a new longitudinal variable (called *newvar*) in the original (supplied) data set containing trend adjusted values for the time-dependent covariate variance at each time point.

match(*matchvarlist*) specifies variables for matching controls to cases. When match() is not specified, cases and controls are matched with respect to time only. If match(matchvarlist) is specified, the cases will also be matched by matchvarlist.

number(#) specifies the number of controls to draw for each case. The default is 1, even though this is not a sensible choice.

Remarks

For detailed information on the routine, see...

Example

```
. lccsm stroke bp baseage

. lccsm stroke bp baseage, order(2) match(numvisits)
```