Package 'cchs'

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Type Package

Title Cox Model for Case-Cohort Data with Stratified
Subcohort-Selection

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Description Contains a function, also called cchs, that calculates Estimator III of Bor-
gan et al (2000), Exposure-stratified Case-cohort Designs. This estimator is for fitting a Cox pro-
portional hazards model to data from a case-cohort study where the subcohort was se-
lected by stratified simple random sampling.

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R topics documented:

| cchs | *Cox model for case–cohort data with stratified subcohort-selection* |

Description

cchs fits a Cox proportional-hazards regression model to case-cohort data where the subcohort was selected by stratified simple random sampling. It uses Estimator III of Borgan et al (2000).

Usage

```
cchs(formula, data=sys.parent(), inSubcohort, stratum,
samplingFractions, cohortStratumSizes, precision=NULL,
swap=TRUE, dropNeverAtRiskRows=TRUE, dropSubcohEventsDfbeta=FALSE,
adjustSampFracIfAnyNAs=FALSE, keepAllCoxphElements=FALSE,
verbose=FALSE, coxphControl, ...)
```

Arguments

formula	An object of class [formula](#) that specifies the terms in the model. The left-hand side must be a [Surv](#) object. The special terms cluster and strata are not allowed.
data	A data-frame or environment that contains the variables used in the formula. The variables named in inSubcohort, stratum, samplingFractions, and cohortStratumSizes will be looked for first in data, if that is a data-frame, and then in the environment that cchs was called from.
inSubcohort	A vector of logical variables that shows whether each observation/row is in the subcohort (TRUE) or not (FALSE).
stratum	A vector that defines the strata within which the subcohort was selected. Each element of stratum corresponds to one observation/row in the data. The elements can be character strings, integers, or any other type of variable that can be converted to a [factor](#).
samplingFractions, cohortStratumSizes	
	samplingFractions is a vector of the sampling fractions in the different strata, and cohortStratumSizes is a vector of the sizes of the strata in the full cohort. Exactly one of these must be given. There are two possible forms for the vector: if it has names, then these must all be distinct and include the names of the strata (and if one value of stratum is "France", then samplingFraction["France"] should be the sampling fraction for that stratum); if it does not have names, then it must have one element for each observation/row in the data.
precision	For example, if the times were recorded to the nearest day but are stored as numbers of years, then precision should be 1/365.25. If there are no tied event-times, then it makes no difference what precision is. If there are tied event-times and precision is a number, then the tied event-times will be slightly changed before the estimator is calculated. If there are tied event-times and precision is NULL (meaning unspecified), then the estimator cannot be calculated and an error will be thrown.

swap	If this is FALSE then the swapping will be omitted (in the formula for Estimator III in Borgan et al 2000, the randomly selected observation/row will not be removed). This is only intended to be used for testing or development.

dropNeverAtRiskRows

If this is TRUE, observations/rows whose at-risk periods do not include any of the event-times will be dropped just before cchs internally calls [coxph](). These observations/rows make no difference to the regression coefficients produced by coxph, but they do affect the dfbeta residuals (see Langholz & Jiao 2007) and therefore the variance-estimates, because coxph calculates the dfbeta residuals using an approximation.

dropSubcohEventsDfbeta

If this is FALSE, which is the default, the dfbeta residuals and therefore the variance-estimates will be calculated exactly as described by Borgan et al (2000). If it is TRUE, they will be calculated as described by Langholz & Jiao (2007) (see "There is a slight approximation ..." in section 2.4).

adjustSampFracIfAnyNAs

If this is true, and if any observations are dropped because of missing data (NAs), then the sampling fractions will be recalculated using the numbers of observations after those observations are dropped.

keepAllCoxphElements

If this is TRUE, then the object returned by cchs will contain elements such as loglik and linear.predictors from the object that was produced by cchs's internal call to [coxph](). These are not likely to be relevant or correct, since cchs manipulates and changes the dataset in many ways before passing it to coxph. (For a list of the elements produced by coxph, see [coxph.object]().)

verbose	If this is TRUE, detailed information about the internal manipulations and calculations will be displayed.

coxphControl, ...

These are optional arguments to control the working of coxph when it is called internally by cchs. If coxphControl is supplied then it must be a list produced by [coxph.control](), and if "..." arguments are supplied then it must be possible to pass them to coxph.control.

Details

In a case–cohort study, the dataset consists only of the cases (the participants who have an event) and the participants who are in the subcohort, which is a randomly selected subset of the cohort. In a stratified case–cohort study, the subcohort is selected by stratified simple random sampling. This means that the cohort is divided into strata, and from each stratum a proportion of the participants equal to that stratum's sampling fraction is selected to be in the subcohort (and within each stratum, each participant is selected with equal probability). For more on stratified case–cohort studies see any of the references listed below.

cchs fits a Cox proportional-hazards regression model to data from a stratified case–cohort study, using the time-fixed version of Estimator III from Borgan et al (2000). Estimators I and II from Borgan et al (2000) are available by using [cch]() with the options method="I.Borgan" and method="II.Borgan", but only Estimator III is score-unbiased, which is the main desirable criterion. The data must be in the usual form where each row corresponds to one observation (that is, one participant). cchs works

by manipulating the data in various ways, then passing it to [coxph](#) (which is suitable for fitting a Cox model to data from a cohort study), and finally making corrections to the variance-estimates. It is planned that a vignette will be produced and this will contain more detail.

For normal use, the logical (boolean) arguments should have their default values. cchs performs a complete-case analysis, meaning that rows will be dropped if they contain NAs in any of the variables that appear in the model, including inside the Surv(), or in inSubcohort or stratum. NAs are not allowed in samplingFractions or cohortStratumSizes, unless that vector has names and any of those names are not equal to values of stratum, in which case the corresponding elements can be NA.

cchs does not normally give replicable results, because the swapping and the small changes to tied event-times are random (see swap and precision in the Argument section). To get exactly the same results every time, use [set.seed](#) with a fixed seed just before calling cchs.

Value

An S3 object of class cchs. This is a list that contains the following elements:

coefficients	The vector of coefficients.
var	The variance matrix of the coefficients.
iter	The number of iterations used by [coxph](#).
n	The number of observations (that is, rows), that were used in the call to coxph.
nevent	The number of events (also called failures).
call	The call that was used to create the cchs object (an object of mode [call](#)).
coeffsTable	A summary of the main numerical output. This is a matrix that contains the hazard ratios, 95% confidence intervals for them, *p*-values for the Wald tests, log hazard ratios (which are the coefficients in the Cox model), and standard errors of the log hazard ratios.
nEachStatus	A vector with three elements: the numbers of subcohort non-cases, subcohort cases, and non-subcohort cases. The sum of these is n.
nStrata	The number of strata that appear in the data.
message	A message about observations that have been dropped because of NAs and event-times that have been changed to deal with ties, if either of these happened.

If keepAllCoxphElements is TRUE, then the cchs object will also contain the other elements listed under [coxph.object](#).

References

Borgan, Ø., Langholz, B., Samuelsen S.O., Goldstein, L., Pogoda, J. (2000). Exposure stratified case–cohort designs. *Lifetime Data Analysis* **6** (1), 39–58. link

Cologne, J., Preston, D.L., Imai, K., Misumi, M., Yoshida, K., Hayashi, T., Nakachi, K. (2012). Conventional case–cohort design and analysis for studies of interaction. *International Journal of Epidemiology* **41** (4), 1174–1186. link

Langholz, B., Jiao, J. (2007). Computational methods for case–cohort studies. *Computational Statistics and Data Analysis* **51** (8), 3737–3748. link

See Also

cch, which can calculate Estimators I and II from Borgan et al (2000), coxph, which cchs uses internally, and coxph.control, a container for certain parameters that are passed to coxph. These are all in the **survival** package.

cchsData, an example dataset that cchs can be used on.

Examples

```
# Analyze the relation between survival and three covariates in cchsData.
# The times are stored as years but were recorded to the nearest month, so
# precision has to be 1/12. The selection of the subcohort was stratified
# according to two strata, defined by cchsData$localHistol, and the sampling
# fractions are stored in cchsData$sampFrac.

cchs(Surv(time, isCase) ~ stage + centralLabHistol + ageAtDiagnosis,
     data=cchsData, inSubcohort=inSubcohort, stratum=localHistol,
     samplingFractions=sampFrac, precision=1/12)
```

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cchsData   *Data from a case–cohort study with stratified subcohort-selection*

Description

A case–cohort dataset where the subcohort was selected by stratified simple random sampling. This is an artificial dataset that was made from nwtco, a real dataset from the National Wilms Tumor Study (NWTS). It is designed for demonstrating the use of cchs.

Format

id	An ID number.
localHistol	Result of the histology from the local institution.
centralLabHistol	Result of the histology from the central laboratory.
stage	Stage of the cancer (I, II, III, or IV).
study	The study (NWTS-3 or NWTS-4). For details see this NWTS webpage.
isCase	Indicator for whether this participant had a relapse or not.
time	Number of days from diagnosis of Wilms tumor to relapse or censoring.
ageAtDiagnosis	Age in years at diagnosis of Wilms tumor.
sampFrac	The sampling fraction for the stratum that contains this participant.

Details

The nwtco data is from two clinical trials but can be regarded as cohort data. cchsData can be created from it by running the code in the Source section below, which is partly based on the Examples from the cch help page. Two strata are used for the subcohort-selection, correspond-

ing to the two values of `localHistol`. The sampling fraction is 5% for the stratum defined by `localHistol="favorable"` and 20% for the stratum defined by `localHistol="unfavorable"`. After the subcohort is selected, the sampling fractions are recalculated using the exact integer numbers of participants in the subcohort and the full cohort.

Source

```
# Starting with nwtco, rename variables, convert some to factors, drop
# in.subcohort (which is used elsewhere for a different simulated dataset), etc.
library(survival, quietly=TRUE)
cchsData <- data.frame(
   id = nwtco$seqno,
   localHistol = factor(nwtco$instit, labels=c("favorable", "unfavorable")),
  centralLabHistol = factor(nwtco$histol, labels=c("favorable", "unfavorable")),
   stage = factor(nwtco$stage, labels=c("I", "II", "III", "IV")),
   study = factor(nwtco$study, labels=c("NWTS-3", "NWTS-4")),
   isCase = as.logical(nwtco$rel),
   time = nwtco$edrel,
   ageAtDiagnosis = nwtco$age / 12  # nwtco$age is in months
)

# Define the intended sampling fractions for the two strata.
samplingFractions <- c(favorable=0.05, unfavorable=0.2)

# Select participants/rows to be in the subcohort by stratified simple random
# sampling.
cchsData$inSubcohort <- rep(FALSE, nrow(cchsData))
set.seed(1)
for (stratumName in levels(cchsData$localHistol)) {
   inThisStratum <- cchsData$localHistol == stratumName
   stratumSubcohortSize <-
         round(samplingFractions[stratumName] * sum(inThisStratum))
   rowsToSetTrue <- sample(which(inThisStratum), size=stratumSubcohortSize)
   cchsData$inSubcohort[rowsToSetTrue] <- TRUE
}

# Change the sampling fractions to their exact values.
stratumSubcohortSizes <- table(cchsData$localHistol[cchsData$inSubcohort])
stratumCohortSizes <- table(cchsData$localHistol)
samplingFractions <- stratumSubcohortSizes / stratumCohortSizes
samplingFractions <- c(samplingFractions)  # make it a vector, not a table

# Keep only the cases and the subcohort.
cchsData <- cchsData[cchsData$isCase | cchsData$inSubcohort,]

# Put the sampling fraction in each row of the data-frame.
cchsData$sampFrac <-
      samplingFractions[match(cchsData$localHistol, names(samplingFractions))]
```

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