

Package: CaseCohortCoxSurvival (via r-universe)

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Description Cox model inference for relative hazard and covariate-specific pure risk estimated from stratified and unstratified case-cohort data as described in Etievant, L., Gail, M.H. (2023) <[arXiv:2304.03396](https://arxiv.org/abs/2304.03396)>.

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CaseCohortCoxSurvival-package

Case-Cohort Cox Survival Inference

Description

This package uses case-cohort data to estimate log-relative hazard, baseline hazards at each unique event time, cumulative baseline hazard in a given time interval and pure risk on the time interval and for a given covariate profile, under the Cox model. For the corresponding variance estimation, it relies on influence functions and follows the complete variance decomposition, to enable correct analysis of case-cohort data with and without stratification, weight calibration or missing phase-two covariate data.

Details

The package provides functions implementing the methods described in Etievant and Gail (2023). More precisely, it includes

- a main driver function, `caseCohortCoxSurvival`.
- one function, `estimatePureRisk`, to estimate pure risks and the corresponding variances with additional covariate profiles.
- three functions, `estimation`, `estimation.CumBH` and `estimation.PR`, for parameters estimation.
- four functions, `influences`, `influences.RH`, `influences.CumBH` and `influences.PR`, for influence functions derivation when estimation is with design or calibrated weights and from a case-cohort consisting of the subcohort and cases not in the subcohort (i.e., case-cohort obtained from two phases of sampling).

- four functions, `influences.missingdata`, `influences.RH.missingdata`, `influences.CumBH.missingdata` and `influences.PR.missingdata`, for influence functions derivation when estimation is with design weights and from a case-cohort when covariate information was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling).
- two functions, `variance` and `variance.missingdata`, for variance estimation following complete variance decomposition (with design or calibrated weights and without missing phase-two data, or with design weights and missing phase-two covariate data).
- one function, `robustvariance`, for robust variance estimation.
- one function, `auxiliary.construction`, to compute the auxiliary variables proposed by Breslow et al. (Stat. Biosci., 2009), Breslow and Lumley (IMS, 2013), and Shin et al. (Biometrics, 2020),.
- one function, `calibration`, for weight calibration.
- one function, `estimation.weights.phase3`, for estimating the phase-three weights.

Author(s)

Lola Etievant, Mitchell H. Gail

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

auxiliary.construction

auxiliary.construction

Description

Creates the auxiliary variables proposed by Breslow et al. (Stat. Biosci., 2009), Breslow and Lumley (IMS, 2013), and proposed by Shin et al. (Biometrics, 2020).

Usage

```
auxiliary.construction(mod, Tau1=NULL, Tau2=NULL, method="Breslow",
                      time.on.study=NULL, casecohort=NULL)
```

Arguments

<code>mod</code>	A cox model object, result of function <code>coxph</code> run on the cohort data with imputed covariate values.
<code>Tau1</code>	Left bound of the time interval considered for the cumulative baseline hazard. Default is the first event time.
<code>Tau2</code>	Right bound of the time interval considered for the cumulative baseline hazard. Default is the last event time.

method	"Breslow", "Breslow2013" or "Shin" to specify the algorithm to construct the auxiliary variables. The default is "Breslow".
time.on.study	Total follow-up time in [Tau1, Tau2]. Required for method = "Shin".
casecohort	Data frame containing the casecohort data. It must include columns "weights" containing the design weights and "id" as an id variable. Required for method = "Shin".

Details

Construction of the auxiliary variables can follow Breslow et al. (2009), Breslow and Lumley (2013), or Shin et al. (2020) (method). It relies on predictions of the phase-two covariates for all members of the cohort. The auxiliary variables are given by (i) the influences for the log-relative hazard parameters estimated from the Cox model with imputed cohort data; (ii) the influences for the cumulative baseline parameter estimated from the Cox model with imputed cohort data; (iii) the products of total follow-up time (on the time interval for which pure risk is to be estimated) with the estimated relative hazard for the imputed cohort data, where the log-relative hazard parameters are estimated from the Cox model with case-cohort data and weights calibrated with (i). When method = Breslow, calibration of the design weights is against (i), as proposed by Breslow et al. (2009) to improve efficiency of case-cohort estimates of relative hazard. When method = Breslow2013, calibration of the design weights is against (i) and (ii), as proposed by Breslow and Lumley (2013) to also improve efficiency of case-cohort estimates of cumulative baseline hazard. When method = Shin, calibration is against (i) and (iii), as proposed by Shin et al. (2020) to improve efficiency of relative hazard and pure risk estimates under the nested case-control design. See also Section 4.1 in Etievant and Gail (2023).

Following Etievant and Gail (2023), in function `caseCohortCoxSurvival` we only provide calibration of the design weight as proposed by Breslow et al. (2009) or Shin et al. (2020).

Value

A.RH.Breslow: matrix with the influences on the log-relative hazard, estimated from the cohort with imputed phase-two covariate values for method = "Breslow" and method = "Breslow2013".

A.CumBH.Breslow: matrix with the influences on the cumulative baseline hazard in [Tau1, Tau2], estimated from the cohort with imputed phase-two covariate values for method = "Breslow2013".

A.RH.Shin: matrix with the influences on the log-relative hazard, estimated from the cohort with imputed phase-two covariate values for method = "Shin".

A.PR.Shin: matrix with the products of total follow-up times in [Tau1, Tau2] and estimated relative hazards, estimated from the cohort with imputed phase-two covariate values for method = "Shin".

References

Breslow, N.E. and Lumley, T. (2013). Semiparametric models and two-phase samples: Applications to Cox regression. From Probability to Statistics and Back: High-Dimensional Models and Processes, 9, 65-78.

Breslow, N.E., Lumley, T., Ballantyne, C.M., Chambless, L.E. and Kulich, M. (2009). Improved Horvitz- Thompson Estimation of Model Parameters from Two-phase Stratified Samples: Applications in Epidemiology. Statistics in Biosciences, 1, 32-49.

Shin Y.E., Pfeiffer R.M., Graubard B.I., Gail M.H. (2020) Weight calibration to improve the efficiency of pure risk estimates from case-control samples nested in a cohort. *Biometrics*, 76, 1087-1097

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[calibration](#), [influences](#), [influences.RH](#), [influences.CumBH](#) and [influences.PR](#).

Examples

```
data(dataexample, package="CaseCohortCoxSurvival")

cohort <- dataexample$cohort
Tau1 <- 0
Tau2 <- 8

# Running the coxph model on the imputed cohort data
mod.imputedcohort <- coxph(Surv(times, status) ~ X1.pred + X2.pred + X3.pred,
  data = cohort, robust = TRUE)

# method = Breslow
ret <- auxiliary.construction(mod.imputedcohort)
# print auxiliary variables based on the log-relative hazard influences
ret$A.RH.Breslow[1:5,]

# Example for method = Shin, variables names must match with fitted model
casecohort <- dataexample$casecohort
casecohort[, "X1.pred"] <- casecohort[, "X1"]
casecohort[, "X2.pred"] <- casecohort[, "X2"]
casecohort[, "X3.pred"] <- casecohort[, "X3"]

time.on.study <- pmax(pmin(Tau2, cohort$times) - Tau1, 0)
ret <- auxiliary.construction(mod.imputedcohort, method="Shin",
  time.on.study=time.on.study, casecohort=casecohort)
ret$A.PR.Shin[1:5]
```

calibration

calibration

Description

Calibrates the design weights using the raking procedure.

Usage

```
calibration(A.phase2, design.weights, total, eta0 = NULL, niter.max = NULL,
  epsilon.stop = NULL)
```

Arguments

<code>A.phase2</code>	matrix with the values of the q auxiliary variables to be used for the calibration of the weights in the case-cohort (phase-two data).
<code>design.weights</code>	design weights to be calibrated.
<code>total</code>	vector of length q with un-weighted auxiliary variable totals in the whole cohort.
<code>eta0</code>	vector of length q with initial values for η (the Lagrangian multipliers), to be used as seed in the iterative procedure. Default is $(0, \dots, 0)$.
<code>niter.max</code>	maximum number of iterations for the iterative optimization algorithm. Default is 10^4 iterations.
<code>epsilon.stop</code>	threshold for the difference between the estimated weighted total and the total in the whole cohort. If this difference is less than the value of <code>epsilon.stop</code> , no more iterations will be performed. Default is 10^{-10} .

Details

Calibration matches the weighted total of the auxiliary variables in the case-cohort (with calibrated weights), to the un-weighted auxiliary variables total in the whole cohort. In other words, it solves in $\eta \sum_{j=1}^J \sum_{i=1}^{n^{(j)}} \{\xi_{i,j} w_{i,j} \exp(\eta' A_{i,j}) A_{i,j} - A_{i,j}\} = 0$, with $\xi_{i,j}$ the sampling indicator and $w_{i,j}$ the design weight of individual i in stratum j , and with $\sum_{j=1}^J \sum_{i=1}^{n^{(j)}} A_{i,j}$ the total in the whole cohort. See Section 4.1 and Web Appendix D.1 in Etievant and Gail (2023). The Newton Raphson method is used to solve the optimization problem. In the end, the calibrated weights of the case-cohort individuals are given by $w_{i,j} \exp(\hat{\eta}' A_{i,j})$, and $\sum_{j=1}^J \sum_{i=1}^{n^{(j)}} \{\xi_{i,j} w_{i,j} \exp(\hat{\eta}' A_{i,j}) A_{i,j}\}$ gives the estimated total.

Value

`eta.hat`: vector of length q with final η values.

`calibrated.weights`: vector with the calibrated weights for the individuals in the case-cohort (phase-two data), computed from `design.weights`, `A.phase2` and `eta.hat`.

`estimated.total`: vector with the estimated totals, computed from the `calibrated.weights` and `A.phase2`.

References

Deville, J.C. and Sarndal, C.E. (1992). Calibration Estimators in Survey Sampling. *Journal of the American Statistical Association*, 87, 376-382.

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[auxiliary.construction](#), [influences](#), [influences.RH](#), [influences.CumBH](#) and [influences.PR](#).

Examples

```

data(dataexample, package="CaseCohortCoxSurvival")

casecohort <- dataexample$casecohort # a stratified case-cohort
A <- dataexample$A # matrix with auxiliary variables values in the cohort
indiv.phase2 <- casecohort$id
q <- ncol(A)
total <- colSums(A)
A.phase2 <- A[indiv.phase2,]
calib <- calibration(A.phase2 = A[indiv.phase2,], design.weights = casecohort$weights,
                    total = total, eta0 = rep(0, q), niter.max = 10^3, epsilon.stop = 10^(-10))
# print calibrated weights
#calib$calibrated.weights

```

caseCohortCoxSurvival *Parameter estimation and variance for case-cohort analyses under the Cox model*

Description

Function for estimating parameters (log-relative hazard, baseline hazards, cumulative baseline hazard, pure risks) and their variance (robust or the one accounting for sampling features) from cohort or case-cohort data, under the Cox model.

Usage

```

caseCohortCoxSurvival(data, status, time,
                      cox.phase1=NULL, cox.phase2=NULL, other.covars=NULL,
                      strata=NULL, weights.phase2=NULL, calibrated=FALSE,
                      subcohort=NULL, subcohort.strata.counts=NULL,
                      predict=TRUE, predicted.cox.phase2=NULL,
                      predictors.cox.phase2=NULL,
                      aux.vars=NULL, aux.method="Shin",
                      phase3=NULL, strata.phase3=NULL,
                      weights.phase3=NULL, weights.phase3.type="both",
                      Tau1=NULL, Tau2=NULL, x=NULL,
                      weights.op=NULL, print=1)

```

Arguments

data	Data frame containing the cohort and all variables needed for the analysis.
status	Column name in data giving the case status for each individual in the cohort. This variable must be coded as 0 for non-cases and 1 for cases.
time	Column name(s) in data giving the time to event for each individual in the case-cohort. One variable is required for a time-on-study time scale, two variables for age-scale, with the first variable as the start age and second as the end age.

<code>cox.phase1</code>	Column name(s) in data giving the Cox model covariates measured on the entire cohort. See covariates and prediction in details.
<code>cox.phase2</code>	Column name(s) in data giving the Cox model covariates measured only on phase-two individuals. See covariates and prediction in details.
<code>other.covars</code>	Column name(s) in data giving other covariates measured on the entire cohort that might be useful, alone or in combination with <code>cox.phase1</code> , if predicted values of the phase-two covariates (<code>cox.phase2</code>) need to be obtained on the whole cohort for the weight calibration.
<code>strata</code>	NULL or column name in data with the stratum value for each individual in the cohort. The number of strata used for the sampling of the subcohort equals the number of different stratum values. For example, a stratum variable might take values 0,1,2,3 or 4. The default is NULL.
<code>weights.phase2</code>	NULL or column name in data giving the phase-two design weights for each individual in the cohort. For a whole cohort analysis (see <code>subcohort</code> below), weights are not used in the <code>coxph</code> call. If NULL but <code>subcohort</code> is not NULL, <code>subcohort.strata.counts</code> will be used to estimate <code>weights.phase2</code> . The default is NULL.
<code>calibrated</code>	TRUE or FALSE to calibrate the weights. Calibrated weights will be computed using the function <code>calibration</code> . If TRUE, then <code>phase3</code> (below) will be set to NULL. See calibration in details. The default is FALSE.
<code>subcohort</code>	NULL or column name in data giving the indicators of membership in the subcohort. The indicators are 1 if the individual belongs to the subcohort and 0 otherwise. Some cases might be in the subcohort and others not. If NULL, then a whole cohort analysis will be performed. The default is NULL.
<code>subcohort.strata.counts</code>	NULL or a list of the number of individuals sampled into the subcohort from each stratum of strata. The names in the list must be the strata values and the length of the list must be equal to the number of strata. If NULL, then the count for each stratum is estimated by the number of subcohort individuals in each stratum. The default is NULL.
<code>predict</code>	TRUE or FALSE to predict the phase-two covariates using <code>predictors.cox.phase2</code> . This option is not used if <code>calibrated=FALSE</code> . If <code>calibrated=TRUE</code> , <code>aux.vars=NULL</code> and <code>predict=FALSE</code> , then <code>predicted.cox.phase2</code> must be specified. See covariates and prediction in details. This option is only used when <code>calibrated=TRUE</code> , <code>aux.vars=NULL</code> and <code>predicted.cox.phase2=NULL</code> . The default is TRUE.
<code>predicted.cox.phase2</code>	NULL or a named list giving the predicted values of the phase-two covariates (<code>cox.phase2</code>) on the whole cohort. For example, if the phase-two covariates are X1 and X2, then the list is of the form <code>list(X1=X1.pred, X2=X2.pred)</code> , where <code>X1.pred</code> and <code>X2.pred</code> are the predictions of X1 and X2 respectively. This option is only used when <code>calibrated=TRUE</code> and <code>aux.vars=NULL</code> . If <code>calibrated=TRUE</code> , <code>aux.vars=NULL</code> and <code>predict=FALSE</code> , then <code>predicted.cox.phase2</code> must be specified and must not contain missing values. The default is NULL.
<code>predictors.cox.phase2</code>	NULL, a vector, or a list specifying the columns in data to use as predictor variables for obtaining the predicted values on the whole cohort for the phase-two

	<p>covariates (cox.phase2). A list allows for different proxy variables to be used for the different phase-two covariates. The selected predictor variables must be from among cox.phase1 and other.covars. See examples and covariates and prediction in details. If NULL, then the phase-two covariates will be predicted using cox.phase1 and other.covars. If NULL, cox.phase1=NULL and other.covars=NULL, then the calibrated analysis will not be performed. This option is only used when calibrated=TRUE, aux.vars=NULL, predicted.cox.phase2=NULL and predict=TRUE. The default is NULL.</p>
aux.vars	<p>NULL or column name(s) in data giving the auxiliary variables for each individual in the cohort. This option is only used when calibrated=TRUE. If NULL, then auxiliary variables will be constructed using method Breslow or Shin and predicted values on the whole cohort for the phase-two covariates (see aux.method, predict, predicted.cox.phase2 and predictors.cox.phase2). aux.vars must not contain missing values. The default is NULL.</p>
aux.method	<p>"Breslow", or "Shin" to specify the algorithm to construct the auxiliary variables. This option is only used if aux.vars=NULL and calibrated=TRUE. The default is "Shin".</p>
phase3	<p>NULL or column name in data giving the indicators of membership in the in the phase-three sample. The indicators are 1 if the individual belongs to the phase-three sample and 0 otherwise. All individuals in the phase-three sample must also belong to the phase-two sample. This option is not used if calibrated=TRUE. The default is NULL.</p>
strata.phase3	<p>NULL or column name in data giving the phase-three stratification for each individual in phase-two. The number of strata used for the third phase of sampling equals the number of different stratum values. The default is NULL.</p>
weights.phase3	<p>NULL or column name in data giving the phase-three design weights for each individual in phase-two. If NULL but phase3 is not NULL, then phase3 and subcohort will be used to estimate weights.phase3 (see details in estimation.weights.phase3). The default is NULL.</p>
weights.phase3.type	<p>One of NULL, "design", "estimated", or "both" to specify whether the phase-three weights are design weights (known), or to be estimated. The variance estimation differs for estimated and design weights. If set to "both", then both variance estimates will be computed. If not NULL, then only the first letter is matched for this option. The default is "both".</p>
Tau1	<p>NULL or left bound of the time interval considered for the cumulative baseline hazard and the pure risk. If NULL, then the first event time is used.</p>
Tau2	<p>NULL or right bound of the time interval considered for the cumulative baseline hazard and the pure risk. If NULL, then the last event time is used.</p>
x	<p>Data frame containing cox.phase1 and cox.phase2 variables for which pure risk is estimated. The default is NULL so that no pure risk estimates will be computed.</p>
weights.op	<p>NULL or a list of options for calibration of phase-two design weights or estimating phase-three design weights. The available options are niter.max, and epsilon.stop (see calibration or estimation.weights.phase3). The default is NULL.</p>

`print` 0-3 to print information as the analysis is performed. The larger the value, the more information will be printed. To not print any information, set `print = 0`. The default is 1.

Details

The different scenarios covered by the function are:

- 1) Whole cohort (`subcohort = NULL`)

- 2) (stratified) case-cohort (= stratified phase-two sample with no missing covariate data)
 - a. With design weights (`subcohort, strata, calibrated = FALSE`)
 - b. With calibrated weights and proxies to predict phase-two covariates and the auxiliary variables (`subcohort, strata, calibrated=TRUE, predict=TRUE, predictors.cox.phase2, aux.method`)
 - c. With calibrated weights and externally supplied predicted values of phase-two covariates (`calibrated=TRUE, strata, predict=FALSE, predicted.cox.phase2`)

- 3) (unstratified) case-cohort (= unstratified phase-two sample with no missing covariate data)
 - a. With design weights (`subcohort, strata=NULL, calibrated=FALSE`)
 - b. With calibrated weights and proxies to predict phase-two covariates and obtain the auxiliary variables (`subcohort, strata=NULL, calibrated=TRUE, predict=TRUE, predictors.cox.phase2, aux.method`)
 - c. With calibrated weights and externally supplied predicted values of phase-two covariates (`calibrated=TRUE, strata=NULL, predict=FALSE, predicted.cox.phase2`)

- 4) Case-cohort (= phase-three sample, because of missing covariate information in phase-two data, with stratified or unstratified phase-two sampling)
 - a. With known phase-three design weights (`subcohort, strata, phase3, strata.phase3, weights.phase3.type="design"`)
 - b. With estimated phase-three design weights (`subcohort, strata, phase3, strata.phase3, weights.phase3.type="estimated"`)

covariates and prediction

Prediction of phase-two covariates is performed when `calibrated = TRUE, predict = TRUE, aux.vars = NULL` and `predicted.cox.phase2 = NULL`. If `predictors.cox.phase2 = NULL`, all the covariates measured on the entire cohort will be used for the prediction (see `cox.phase1` and `other.covars`). Prediction of phase-two covariates is performed by linear regression for a continuous variable, logistic regression for a binary variable and the function `multinom` for a categorical variable. Dummy variables should not be used for categorical covariates, because independent logistic (or linear) regressions will be performed using the dummy variables. Alternatively, predicted values of phase-two covariates on the whole cohort can be specified with `predicted.cox.phase2`.

calibration

Calibrating the design weights against some informative auxiliary variables, measured on all cohort members, can increase efficiency. When `calibrated = TRUE`, the user can either provide the auxiliary variables (`aux.vars`), or let the driver function build the auxiliary variables (`aux.method`). Construction of the auxiliary variables follows Breslow et al. (2009) or Shin et al. (2020) (see `aux.method`), and relies on predictions of the phase-two covariates for all members of the cohort

(see covariates and prediction above). The auxiliary variables are given by (i) the influences for the log-relative hazard parameters estimated from the Cox model with imputed cohort data; and (ii) the products of total follow-up time (on the time interval for which pure risk is to be estimated) with the estimated relative hazard for the imputed cohort data, where the log-relative hazard parameters are estimated from the Cox model with case-cohort data and weights calibrated with (i). When `aux.method = Breslow`, calibration of the design weights is against (i), as proposed by Breslow et al. (2009) to improve efficiency of case-cohort estimates of relative hazard. When `aux.method = Shin`, calibration is against (i) and (ii), as proposed by Shin et al. (2020) to improve efficiency of relative hazard and pure risk estimates under the nested case-control design.

Note

If `subcohort = NULL`, then a whole cohort analysis will be run and only robust variance estimates will be computed.

Value

A list with class `casecohortcoxsurv` containing:

- `beta` Estimated log-relative hazard estimates
- `Lambda0` Cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$
- `beta.var` Influence-based variance estimate for `beta`
- `Lambda0.var` Influence-based variance estimate for `Lambda0`
- `beta.var.estimated` Influence-based variance estimate for `beta` with estimated phase-three weights
- `Lambda0.var.estimated` Influence-based variance estimate for `Lambda0` with estimated phase-three weights
- `beta.var.design` Influence-based variance estimate for `beta` with design phase-three weights
- `Lambda0.var.design` Influence-based variance estimate for `Lambda0` with design phase-three weights
- `beta.robustvar` Robust variance estimate for `beta`
- `Lambda0.robustvar` Robust variance estimate for `Lambda0`
- `beta.robustvar.estimated` Robust variance estimate for `beta` with estimated phase-three weights
- `Lambda0.robustvar.estimated` Robust variance estimate for `Lambda0` with estimated phase-three weights
- `beta.robustvar.design` Robust variance estimate for `beta` with design phase-three weights
- `Lambda0.robustvar.design` Robust variance estimate for `Lambda0` with design phase-three weights
- `Pi.var` Matrix of pure risk estimates in $[\text{Tau1}, \text{Tau2}]$ and variance estimates
- `Pi.var.estimated` Matrix of pure risk estimates in $[\text{Tau1}, \text{Tau2}]$ and variance estimates with estimated phase-three weights
- `Pi.var.design` Matrix of pure risk estimates in $[\text{Tau1}, \text{Tau2}]$ and variance estimates with design phase-three weights
- `coxph.fit` Return object from `coxph` of the model fit

- `changed.times` Matrix of original and new event times for individuals who had their event times changed due to ties. Will be NULL if event times were not changed.
- `args` List containing the values of the input arguments (except `data`)
- `risk.obj` List containing objects needed to compute pure risk estimates and variances for a different set of data

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

Shin Y.E., Pfeiffer R.M., Graubard B.I., Gail M.H. (2020) Weight calibration to improve the efficiency of pure risk estimates from case-control samples nested in a cohort. *Biometrics*, 76, 1087-1097

Breslow, N.E., Lumley, T., Ballantyne, C.M., Chambless, L.E. and Kulich, M. (2009). Improved Horvitz-Thompson Estimation of Model Parameters from Two-phase Stratified Samples: Applications in Epidemiology. *Statistics in Biosciences*, 1, 32-49.

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

data <- dataexample.missingdata$cohort
cov1 <- "X1"
cov2 <- c("X2", "X3")

# Whole cohort, get pure risk estimate for every individual's profile in the cohort
# Only robust variance estimates are computed for a whole cohort analysis.
caseCohortCoxSurvival(data, "status", "times", cox.phase1 = cov1, x = data)

# Stratified case-cohort analysis with missing covariate information in
# phase-two data, with phase-three strata
caseCohortCoxSurvival(data, "status", "times", cox.phase1 = cov1,
                      cov.phase2 = cov2, strata = "W", subcohort = "subcohort",
                      phase3 = "phase3", strata.phase3 = "W3")

data(dataexample, package="CaseCohortCoxSurvival")

data <- dataexample$cohort
cov2 <- c("X1", "X2", "X3")

# Stratified case-cohort (phase-two) analysis with weight calibration and default
# proxies to predict the phase-two covariates.
caseCohortCoxSurvival(data, "status", "times", cox.phase2 = cov2, strata = "W",
                      subcohort = "subcohort", calibrated = TRUE)

# Stratified case-cohort (phase-two) analysis with weight calibration specifying
# a different set of proxy variables to predict each phase-two covariate.
```

```

caseCohortCoxSurvival(data, "status", "times", cox.phase2 = cov2,
                      strata = "W", subcohort = "subcohort", calibrated = TRUE,
                      predictors.cox.phase2 = list(X1 = c("X1.proxy"),
                                                  X2 = c("X1.proxy", "X2.proxy", "W"), X3 = c("X1.proxy", "X3.proxy")))

# Stratified case-cohort (phase-two) analysis with weight calibration, get pure
# risk estimate for one given covariate profile.
caseCohortCoxSurvival(data, "status", "times", cox.phase2 = cov2,
                      strata = "W", subcohort = "subcohort", calibrated = TRUE,
                      predictors.cox.phase2=list(X1 = c("X1.proxy"),
                                                  X2 = c("X1.proxy", "X2.proxy", "W"), X3 = c("X1.proxy", "X3.proxy")),
                      x = list(X1 = 1, X2 = 1, X3 = 0.6), Tau1 = 0, Tau2 = 8)

# Set the correct sampling counts in phase-two for each level of strata.
# The strata variable W has levels 0-3.
caseCohortCoxSurvival(data, "status", "times", cox.phase2 = cov2,
                      subcohort = "subcohort", calibrated = TRUE, strata = "W",
                      subcohort.strata.counts = list("0"=129, "1"=313, "2"=308, "3"=311))

```

dataexample

Data for examples

Description

Simulated cohort, case-cohort and set of auxiliary variables for examples. The case-cohort is a stratified phase-two sample with no missing covariate data.

Examples

```

data(dataexample, package="CaseCohortCoxSurvival")

# Display some of the data
dataexample$cohort[1:5, ]

dataexample$A[1:5, ] # auxiliary variable values in the cohort

```

dataexample.missingdata

Data for examples with missing data

Description

Simulated cohort and case-cohort for examples. The case-cohort is a stratified phase-three sample, because of missing covariate information in the stratified phase-two data.

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

# Display some of the data
dataexample.missingdata$cohort[1:5, ]
```

estimatePureRisk	<i>estimatePureRisk</i>
------------------	-------------------------

Description

Computes pure risk estimates and variances for new covariate values.

Usage

```
estimatePureRisk(obj, x)
```

Arguments

obj	Return object from caseCohortCoxSurvival .
x	Data frame or a list containing values of the covariates that were used when caseCohortCoxSurvival was called, and for which the pure risk is to be estimated.

Value

A list containing:

- var Matrix of pure risk estimates in [Tau1, Tau2] and variance estimates
- var.estimated Matrix of pure risk estimates in [Tau1, Tau2] and variance estimates when the phase-three weights are estimated
- var.design Matrix of pure risk estimates in [Tau1, Tau2] and variance estimates when the phase-three weights are known

Depending on the analysis run, some of the above objects will be NULL.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[caseCohortCoxSurvival](#)

Examples

```

data(dataexample, package="CaseCohortCoxSurvival")

data <- dataexample$cohort

obj <- caseCohortCoxSurvival(data, "status", "times", cox.phase2 = c("X1", "X2", "X3"),
                             subcohort = "subcohort", Tau1 = 0, Tau2 = 8)

# get pure risk estimate for every individual's profile in the cohort
ret <- estimatePureRisk(obj, data)

# get pure risk estimate for one given covariate profile
ret <- estimatePureRisk(obj, list(X1 = 1, X2 = 2, X3 = 3))

```

estimation

estimation

Description

Estimates the log-relative hazard, baseline hazards at each unique event time, cumulative baseline hazard in a given time interval [Tau1, Tau2] and pure risk in [Tau1, Tau2] and for a given covariate profile x .

Usage

```

estimation(mod, Tau1 = NULL, Tau2 = NULL, x = NULL, missing.data = NULL,
           riskmat.phase2 = NULL, dNt.phase2 = NULL, status.phase2 = NULL)

```

Arguments

<code>mod</code>	a Cox model object, result of function <code>coxph</code> .
<code>Tau1</code>	left bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the first event time.
<code>Tau2</code>	right bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the last event time.
<code>x</code>	vector of length p , specifying the covariate profile considered for the pure risk. Default is $(0, \dots, 0)$.
<code>missing.data</code>	was data on the p covariates missing for certain individuals in the phase-two data (i.e., was a third phase of sampling performed)? If <code>missing.data = TRUE</code> , the arguments below need to be provided. Default is <code>FALSE</code> .
<code>riskmat.phase2</code>	at risk matrix for the phase-two data at all of the case event times, even those with missing covariate data. Needs to be provided if <code>missing.data = TRUE</code> .
<code>dNt.phase2</code>	counting process matrix for failures in the phase-two data. Needs to be provided if <code>missing.data = TRUE</code> and <code>status.phase2 = NULL</code> .
<code>status.phase2</code>	vector indicating the case status in the phase-two data. Needs to be provided if <code>missing.data = TRUE</code> and <code>dNt.phase2 = NULL</code> .

Details

estimation returns the log-relative hazard estimates provided by mod, and estimates the baseline hazard point mass at any event time non-parametrically.

estimation works for estimation from a case-cohort with design weights or calibrated weights, when the case-cohort consists of the subcohort and cases not in the subcohort (i.e., case-cohort obtained from two phases of sampling), as well as with design weights when covariate data was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling).

Value

beta.hat: vector of length p with log-relative hazard estimates.

lambda0.t.hat: vector with baseline hazards estimates at each unique event time.

Lambda0.Tau1Tau2.hat: cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

Pi.x.Tau1Tau2.hat: pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

References

Breslow, N. (1974). Covariance Analysis of Censored Survival Data. *Biometrics*, 30, 89-99.

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation.CumBH](#), [estimation.PR](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), and [influences.PR.missingdata](#).

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")
cohort      <- dataexample.missingdata$cohort # a simulated cohort
casecohort <- dataexample.missingdata$casecohort # a simulated stratified case-cohort
riskmat.phase2 <- dataexample.missingdata$riskmat.phase2
dNt.phase2    <- dataexample.missingdata$dNt.phase2

Tau1 <- 0 # given time interval for the pure risk
Tau2 <- 8
x     <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the whole cohort

mod.cohort <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = cohort,
  robust = TRUE)
estimation.cohort <- estimation(mod = mod.cohort, Tau1 = Tau1, Tau2 = Tau2,
  x = x)

# print the vector with log-relative hazard estimates
estimation.cohort$beta.hat
```



```

# print the cumulative baseline hazard estimate
estimation.cohort$Lambda0.Tau1Tau2.hat

# print the pure risk estimate
estimation.cohort$Pi.x.Tau1Tau2.hat

# Estimation using the stratified case-cohort with known design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
             weight = weights.true, id = id, robust = TRUE)
estimation.casecohort <- estimation(mod = mod, Tau1 = Tau1, Tau2 = Tau2, x = x,
                                   missing.data = TRUE,
                                   riskmat.phase2 = riskmat.phase2,
                                   dNt.phase2 = dNt.phase2)

# print the vector with log-relative hazard estimates
estimation.casecohort$beta.hat

# print the cumulative baseline hazard estimate
estimation.casecohort$Lambda0.Tau1Tau2.hat

# print the pure risk estimate
estimation.casecohort$Pi.x.Tau1Tau2.hat

```

```
estimation.CumBH      estimation.CumBH
```

Description

Estimates the log-relative hazard, baseline hazards at each unique event time and cumulative baseline hazard in a given time interval [Tau1, Tau2].

Usage

```
estimation.CumBH(mod, Tau1 = NULL, Tau2 = NULL, missing.data = FALSE,
                riskmat.phase2 = NULL, dNt.phase2 = NULL, status.phase2 = NULL)
```

Arguments

mod	a Cox model object, result of function coxph.
Tau1	left bound of the time interval considered for the cumulative baseline hazard. Default is the first event time.
Tau2	right bound of the time interval considered for the cumulative baseline hazard. Default is the last event time.
missing.data	was data on the p covariates missing for certain individuals in the phase-two data (i.e., was a third phase of sampling performed)? If <code>missing.data = TRUE</code> , the arguments below need to be provided. Default is <code>FALSE</code> .

`riskmat.phase2` at risk matrix for the phase-two data at all of the case event times, even those with missing covariate data. Needs to be provided if `missing.data = TRUE`.

`dNt.phase2` counting process matrix for failures in the phase-two data. Needs to be provided if `missing.data = TRUE` and `status.phase2 = NULL`.

`status.phase2` vector indicating the case status in the phase-two data. Needs to be provided if `missing.data = TRUE` and `dNt.phase2 = NULL`.

Details

`estimation.CumBH` returns the log-relative hazard estimates provided by `mod`, and estimates the baseline hazard point mass at any event time non-parametrically.

`estimation.CumBH` works for estimation from a case-cohort with design weights or calibrated weights, when the case-cohort consists of the subcohort and cases not in the subcohort (i.e., case-cohort obtained from two phases of sampling), as well as with design weights when covariate data was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling).

Value

`beta.hat`: vector of length p with log-relative hazard estimates.

`lambda0.t.hat`: vector with baseline hazards estimates at each unique event time.

`Lambda0.Tau1Tau2.hat`: cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

References

Breslow, N. (1974). Covariance Analysis of Censored Survival Data. *Biometrics*, 30, 89-99.

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.PR](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), and [influences.PR.missingdata](#)

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

cohort      <- dataexample.missingdata$cohort # a simulated cohort
casecohort  <- dataexample.missingdata$casecohort # a simulated stratified case-cohort
riskmat.phase2 <- dataexample.missingdata$riskmat.phase2
dNt.phase2  <- dataexample.missingdata$dNt.phase2

# Estimation using the whole cohort

mod.cohort <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = cohort,
                  robust = TRUE)
estimation.cohort <- estimation.CumBH(mod = mod.cohort, Tau1 = 0, Tau2 = 8)
```

```

# print the vector with log-relative hazard estimates
estimation.cohort$beta.hat

# print the cumulative baseline hazard estimate
estimation.cohort$Lambda0.Tau1Tau2.hat

# Estimation using the stratified case-cohort with known design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
             weight = weights.true, id = id, robust = TRUE)
estimation.casecohort <- estimation.CumBH(mod = mod, Tau1 = 0, Tau2 = 8,
                                         missing.data = TRUE,
                                         riskmat.phase2 = riskmat.phase2,
                                         dNt.phase2 = dNt.phase2)

# print the vector with log-relative hazard estimates
estimation.casecohort$beta.hat

# print the cumulative baseline hazard estimate
estimation.casecohort$Lambda0.Tau1Tau2.hat

```

estimation.PR

estimation.PR

Description

Estimates the pure risk in the time interval $[\text{Tau1}, \text{Tau2}]$ and for a covariate profile x , from the log-relative hazard and cumulative baseline hazard values.

Usage

```
estimation.PR(beta, Lambda0.Tau1Tau2, x = NULL)
```

Arguments

beta	vector of length p with log-relative hazard values.
Lambda0.Tau1Tau2	cumulative baseline hazard in $[\text{Tau1}, \text{Tau2}]$.
x	vector of length p , specifying the covariate profile considered for the pure risk. Default is $(0, \dots, 0)$.

Value

Pi.x.Tau1Tau2.hat : pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), and [influences.PR.missingdata](#).

Examples

```
estimation.PR(beta = c(-0.2, 0.25, -0.3), Lambda0.Tau1Tau2 = 0.03,
              x = c(-1, 1, -0.6))
```

```
estimation.weights.phase3
      estimation.weights.phase3
```

Description

Estimates the weights for the third phase of sampling (due to missingness).

Usage

```
estimation.weights.phase3(B.phase3, total.phase2, gamma0 = NULL, niter.max = NULL,
                          epsilon.stop = NULL)
```

Arguments

B.phase3	matrix for the case-cohort (phase-three data), with phase-three sampling strata indicators. It should have as many columns as phase-three strata ($J^{(3)}$), with one 1 per row, to indicate the phase-three stratum position.
total.phase2	vector of length $J^{(3)}$ with un-weighted column totals for B in the phase-two data (i.e., using all the individuals, even the ones with missing covariate data).
gamma0	vector of length $J^{(3)}$ with initial values for γ (Lagrangian multipliers), to be used as seed in the iterative procedure. Default is $(0, \dots, 0)$.
niter.max	maximum number of iterations for the iterative optimization algorithm. Default is 10^4 iterations.
epsilon.stop	threshold for the difference between the estimated weighted total and the total in the whole cohort. If this difference is less than the value of epsilon.stop, no more iterations will be performed. Default is 10^{-10} .


```
# print estimated phase-three weights
#estimation.weights.p3$estimated.weights
```

influences	<i>influences</i>
------------	-------------------

Description

Computes the influences on the log-relative hazard, baseline hazards at each unique event time, cumulative baseline hazard in a given time interval [Tau1, Tau2] and on the pure risk in [Tau1, Tau2] and for a given covariate profile x . Can take calibration of the design weights into account.

Usage

```
influences(mod, Tau1 = NULL, Tau2 = NULL, x = NULL, calibrated = NULL,
A = NULL)
```

Arguments

mod	a cox model object, result of function <code>coxph</code> .
Tau1	left bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the first event time.
Tau2	right bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the last event time.
x	vector of length p , specifying the covariate profile considered for the pure risk. Default is $(0, \dots, 0)$.
calibrated	are calibrated weights used for the estimation of the parameters? If <code>calibrated = TRUE</code> , the argument below needs to be provided. Default is <code>FALSE</code> .
A	$n \times q$ matrix with the values of the auxiliary variables used for the calibration of the weights in the whole cohort. Needs to be provided if <code>calibrated = TRUE</code> .

Details

`influences` works for estimation from a case-cohort with design weights or calibrated weights (case-cohort consisting of the subcohort and cases not in the subcohort, i.e., case-cohort obtained from two phases of sampling).

If covariate information is missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling), use `influences.missingdata`.

`influences` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 3.2 if `calibrated = FALSE`, and as in Section 4.3 if `calibrated = TRUE`.

If `calibrated = FALSE`, the influences are only provided for the individuals in the case-cohort. If `calibrated = TRUE`, the influences are provided for all the individuals in the cohort.

Value

`infl1.beta`: matrix with the overall influences on the log-relative hazard estimates.

`infl1.lambda0.t`: matrix with the overall influences on the baseline hazards estimates at each unique event time.

`infl1.Lambda0.Tau1Tau2.hat`: vector with the overall influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`infl1.Pi.x.Tau1Tau2.hat`: vector with the overall influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`infl12.beta`: matrix with the phase-two influences on the log-relative hazard estimates. Returned if `calibrated = TRUE`.

`infl12.lambda0.t`: matrix with the phase-two influences on the baseline hazards estimates at each unique event time. Returned if `calibrated = TRUE`.

`infl12.Lambda0.Tau1Tau2.hat`: vector with the phase-two influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$. Returned if `calibrated = TRUE`.

`infl12.Pi.x.Tau1Tau2.hat`: vector with the phase-two influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x . Returned if `calibrated = TRUE`.

`beta.hat`: vector of length p with log-relative hazard estimates.

`lambda0.t.hat`: vector with baseline hazards estimates at each unique event time.

`Lambda0.Tau1Tau2.hat`: cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`Pi.x.Tau1Tau2.hat`: pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample, package="CaseCohortCoxSurvival")

cohort      <- dataexample$cohort # a simulated cohort
casecohort  <- dataexample$casecohort # a simulated stratified case-cohort
A           <- dataexample$A # matrix with auxiliary variables values in the cohort

Tau1        <- 0 # given time interval for the pure risk
Tau2        <- 8
x           <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the whole cohort
```

```

mod.cohort <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = cohort,
                    robust = TRUE)
estimation.cohort <- influences(mod.cohort, Tau1 = Tau1, Tau2 = Tau2, x = x)

# print the vector with log-relative hazard estimates
#estimation.cohort$beta.hat

# print the cumulative baseline hazard estimate
#estimation.cohort$Lambda0.Tau1Tau2.hat

# print the pure risk estimate
#estimation.cohort$Pi.x.Tau1Tau2.hat

# print the influences on the log-relative hazard estimates
#estimation.cohort$infl.beta

# print the influences on the cumulative baseline hazard estimate
#estimation.cohort$infl.Lambda0.Tau1Tau2

# print the influences on the pure risk estimate
#estimation.cohort$infl.Pi.x.Tau1Tau2

# Estimation using the stratified case-cohort with weights calibrated on A
mod.calib <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                  weight = weights.calib, id = id, robust = TRUE)
estimation.calib <- influences(mod.calib, A = A, calibrated = TRUE,
                              Tau1 = Tau1, Tau2 = Tau2, x = x)

# print the influences on the log-relative hazard estimates
#estimation.calib$infl.beta

# print the influences on the cumulative baseline hazard estimate
#estimation.calib$infl.Lambda0.Tau1Tau2

# print the influences on the pure risk estimate
#estimation.calib$infl.Pi.x.Tau1Tau2

# print the phase-two influences on the log-relative hazard estimates
#estimation.calib$infl2.beta

# print the phase-two influences on the cumulative baseline hazard estimate
#estimation.calib$infl2.Lambda0.Tau1Tau2

# print the phase-two influences on the pure risk estimate
#estimation.calib$infl2.Pi.x.Tau1Tau2

```


Description

Computes the influences on the log-relative hazard, baseline hazards at each unique event time, and on the cumulative baseline hazard in a given time interval [Tau1, Tau2]. Can take calibration of the design weights into account.

Usage

```
influences.CumBH(mod, Tau1 = NULL, Tau2 = NULL, A=NULL, calibrated = NULL)
```

Arguments

mod	a cox model object, result of function coxph.
Tau1	left bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the first event time.
Tau2	right bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the last event time.
A	$n \times q$ matrix with the values of the auxiliary variables used for the calibration of the weights in the whole cohort. Needs to be provided if calibrated = TRUE.
calibrated	are calibrated weights used for the estimation of the parameters? If calibrated = TRUE, the argument below needs to be provided. Default is FALSE.

Details

influences.CumBH works for estimation from a case-cohort with design weights or calibrated weights (case-cohort consisting of the subcohort and cases not in the subcohort, i.e., case-cohort obtained from two phases of sampling).

If covariate information is missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling), use [influences.CumBH.missingdata](#).

influences.CumBH uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 3.2 if calibrated = FALSE, and as in Section 4.3 if calibrated = TRUE.

If calibrated = FALSE, the influences are only provided for the individuals in the case-cohort. If calibrated = TRUE, the influences are provided for all the individuals in the cohort.

Value

infl1.beta: matrix with the overall influences on the log-relative hazard estimates.

infl1.lambda0.t: matrix with the overall influences on the baseline hazards estimates at each unique event time.

infl1.Lambda0.Tau1Tau2.hat: vector with the overall influences on the cumulative baseline hazard estimate in [Tau1, Tau2].

infl2.beta: matrix with the phase-two influences on the log-relative hazard estimates. Returned if calibrated = TRUE.

infl2.lambda0.t: matrix with the phase-two influences on the baseline hazards estimates at each unique event time. Returned if calibrated = TRUE.

`infl2.Lambda0.Tau1Tau2.hat`: vector with the phase-two influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$. Returned if `calibrated = TRUE`.

`beta.hat`: vector of length p with log-relative hazard estimates.

`lambda0.t.hat`: vector with baseline hazards estimates at each unique event time.

`Lambda0.Tau1Tau2.hat`: cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences](#), [influences.RH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample, package="CaseCohortCoxSurvival")
cohort      <- dataexample$cohort # a simulated cohort
casecohort  <- dataexample$casecohort # a simulated stratified case-cohort
A           <- dataexample$A # matrix with auxiliary variables values in the cohort

Tau1       <- 0 # given time interval for the pure risk
Tau2       <- 8
x          <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the whole cohort

mod.cohort <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = cohort,
                   robust = TRUE)
estimation.cohort <- influences.CumBH(mod.cohort, Tau1 = Tau1, Tau2 = Tau2)

# print the vector with log-relative hazard estimates
#estimation.cohort$beta.hat

# print the cumulative baseline hazard estimate
#estimation.cohort$Lambda0.Tau1Tau2.hat

# print the influences on the log-relative hazard estimates
#estimation.cohort$infl.beta

# print the influences on the cumulative baseline hazard estimate
#estimation.cohort$infl.Lambda0.Tau1Tau2

# Estimation using the stratified case-cohort with weights calibrated on A

mod.calib <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                  weight = weights.calib, id = id, robust = TRUE)
estimation.calib <- influences.CumBH(mod.calib, A = A, calibrated = TRUE,
```

```

                                Tau1 = Tau1, Tau2 = Tau2)

# print the influences on the log-relative hazard estimates
#estimation.calib$infl.beta

# print the influences on the cumulative baseline hazard estimate
#estimation.calib$infl.Lambda0.Tau1Tau2

# print the phase-two influences on the log-relative hazard estimates
#estimation.calib$infl2.beta

# print the phase-two influences on the cumulative baseline hazard estimate
#estimation.calib$infl2.Lambda0.Tau1Tau2

```

```

influences.CumBH.missingdata
                                influences.CumBH.missingdata

```

Description

Computes the influences on the log-relative hazard, baseline hazards at each unique event time, and on the cumulative baseline hazard in a given time interval [Tau1, Tau2], when covariate data is missing for certain individuals in the phase-two data.

Usage

```

influences.CumBH.missingdata(mod, riskmat.phase2, dNt.phase2 = NULL,
status.phase2 = NULL, Tau1 = NULL, Tau2 = NULL, estimated.weights = FALSE,
B.phase2 = NULL)

```

Arguments

<code>mod</code>	a cox model object, result of function <code>coxph</code> .
<code>riskmat.phase2</code>	at risk matrix for the phase-two data at all of the cases event times, even those with missing covariate data.
<code>dNt.phase2</code>	counting process matrix for failures in the phase-two data. Needs to be provided if <code>status.phase2 = NULL</code> .
<code>status.phase2</code>	vector indicating the case status in the phase-two data. Needs to be provided if <code>dNt.phase2 = NULL</code> .
<code>Tau1</code>	left bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the first event time.
<code>Tau2</code>	right bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the last event time.
<code>estimated.weights</code>	are the weights for the third phase of sampling (due to missingness) estimated? If <code>estimated.weights = TRUE</code> , the argument below needs to be provided. Default is <code>FALSE</code> .

B.phase2 matrix for the phase-two data, with phase-three sampling strata indicators. It should have as many columns as phase-three strata ($J^{(3)}$), with one 1 per row, to indicate the phase-three stratum position. Needs to be provided if `estimated.weights = TRUE`.

Details

`influences.CumBH.missingdata` works for estimation from a case-cohort with design weights and when covariate data was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling).

If there are no missing covariates in the phase-two sample, use `influences.CumBH` with either design weights or calibrated weights.

`influences.CumBH.missingdata` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 5.4 if `estimated.weights = TRUE`, and as in Web Appendix H if `estimated.weights = FALSE`.

Value

`inf1.beta`: matrix with the overall influences on the log-relative hazard estimates.

`inf1.lambda0.t`: matrix with the overall influences on the baseline hazards estimates at each unique event time.

`inf1.Lambda0.Tau1Tau2.hat`: vector with the overall influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`inf12.beta`: matrix with the phase-two influences on the log-relative hazard estimates.

`inf12.lambda0.t`: matrix with the phase-two influences on the baseline hazards estimates at each unique event time.

`inf12.Lambda0.Tau1Tau2.hat`: vector with the phase-two influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`inf13.beta`: matrix with the phase-three influences on the log-relative hazard estimates.

`inf13.lambda0.t`: matrix with the phase-three influences on the baseline hazards estimates at each unique event time.

`inf13.Lambda0.Tau1Tau2.hat`: vector with the phase-three influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`beta.hat`: vector of length p with log-relative hazard estimates.

`lambda0.t.hat`: vector with baseline hazards estimates at each unique event time.

`Lambda0.Tau1Tau2.hat`: cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.


```
dNt.phase2 = dNt.phase2,
estimated.weights = TRUE,
B.phase2 = B.phase2,
Tau1 = 0, Tau2 = 8)
```

influences.missingdata

influences.missingdata

Description

Computes the influences on the log-relative hazard, baseline hazards at each unique event time, cumulative baseline hazard in a given time interval [Tau1, Tau2] and on the pure risk in [Tau1, Tau2] and for a given covariate profile x, when covariate data is missing for certain individuals in the phase-two data.

Usage

```
influences.missingdata(mod, riskmat.phase2, dNt.phase2 = NULL,
status.phase2 = NULL, Tau1 = NULL, Tau2 = NULL, x = NULL,
estimated.weights = FALSE, B.phase2 = NULL)
```

Arguments

mod	a cox model object, result of function coxph.
riskmat.phase2	at risk matrix for the phase-two data at all of the cases event times, even those with missing covariate data.
dNt.phase2	counting process matrix for failures in the phase-two data. Needs to be provided if status.phase2 = NULL.
status.phase2	vector indicating the case status in the phase-two data. Needs to be provided if dNt.phase2 = NULL.
Tau1	left bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the first event time.
Tau2	right bound of the time interval considered for the cumulative baseline hazard and pure risk. Default is the last event time.
x	vector of length p , specifying the covariate profile considered for the pure risk. Default is (0,...,0).
estimated.weights	are the weights for the third phase of sampling (due to missingness) estimated? If estimated.weights = TRUE, the argument below needs to be provided. Default is FALSE.
B.phase2	matrix for the phase-two data, with phase-three sampling strata indicators. It should have as many columns as phase-three strata ($J^{(3)}$), with one 1 per row, to indicate the phase-three stratum position. Needs to be provided if estimated.weights = TRUE.

Details

`influences.missingdata` works for estimation from a case-cohort with design weights and when covariate data was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling).

If there are no missing covariates in the phase- two sample, use `influences` with either design weights or calibrated weights.

When covariate information was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling), use `influences.missingdata`.

`influences.missingdata` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 5.4 if `estimated.weights = TRUE`, and as in Web Appendix H if `estimated.weights = FALSE`.

Value

`inf11.beta`: matrix with the overall influences on the log-relative hazard estimates.

`inf11.lambda0.t`: matrix with the overall influences on the baseline hazards estimates at each unique event time.

`inf11.Lambda0.Tau1Tau2.hat`: vector with the overall influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`inf11.Pi.x.Tau1Tau2.hat`: vector with the overall influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`inf12.beta`: matrix with the phase-two influences on the log-relative hazard estimates.

`inf12.lambda0.t`: matrix with the phase-two influences on the baseline hazards estimates at each unique event time.

`inf12.Lambda0.Tau1Tau2.hat`: vector with the phase-two influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`inf12.Pi.x.Tau1Tau2.hat`: vector with the phase-two influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`inf13.beta`: matrix with the phase-three influences on the log-relative hazard estimates.

`inf13.lambda0.t`: matrix with the phase-three influences on the baseline hazards estimates at each unique event time.

`inf13.Lambda0.Tau1Tau2.hat`: vector with the phase-three influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`inf13.Pi.x.Tau1Tau2.hat`: vector with the phase-three influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`beta.hat`: vector of length p with log-relative hazard estimates.

`lambda0.t.hat`: vector with baseline hazards estimates at each unique event time.

`Lambda0.Tau1Tau2.hat`: cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

`Pi.x.Tau1Tau2.hat`: pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

cohort      <- dataexample.missingdata$cohort # a simulated cohort
casecohort  <- dataexample.missingdata$casecohort # a simulated stratified case-cohort
# phase-two data: dataexample.missingdata$casecohort.phase2
riskmat.phase2 <- dataexample.missingdata$riskmat.phase2
dNt.phase2   <- dataexample.missingdata$dNt.phase2
B.phase2    <- dataexample.missingdata$B.phase2

Tau1 <- 0 # given time interval for the pure risk
Tau2 <- 8
x    <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the stratified case-cohort with true known design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
             weight = weights.true, id = id, robust = TRUE)

estimation <- influences.missingdata(mod = mod, riskmat.phase2 = riskmat.phase2,
                                   dNt.phase2 = dNt.phase2, Tau1 = Tau1,
                                   Tau2 = Tau2, x = x)

# print the influences on the log-relative hazard estimates
# estimation$infl1.beta

# print the influences on the cumulative baseline hazard estimate
#estimation$infl.Lambda0.Tau1Tau2

# print the influences on the pure risk estimate
#estimation$infl.Pi.x.Tau1Tau2

# print the phase-two influences on the log-relative hazard estimates
#estimation$infl2.beta

# print the phase-two influences on the cumulative baseline hazard estimate
#estimation$infl2.Lambda0.Tau1Tau2

# print the phase-two influences on the pure risk estimate
#estimation$infl2.Pi.x.Tau1Tau2

# print the phase-three influences on the log-relative hazard estimates
#estimation$infl3.beta

# print the phase-three influences on the cumulative baseline hazard estimate
#estimation$infl3.Lambda0.Tau1Tau2
```



```

# print the phase-three influences on the pure risk estimate
#estimation$infl3.Pi.x.Tau1Tau2

# Estimation using the stratified case-cohort with estimated weights, and
# accounting for the estimation through the influences

mod.est <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                 weight = weights.est, id = id, robust = TRUE)

estimation.est <- influences.missingdata(mod.est,
                                         riskmat.phase2 = riskmat.phase2,
                                         dNt.phase2 = dNt.phase2,
                                         estimated.weights = TRUE,
                                         B.phase2 = B.phase2, Tau1 = Tau1,
                                         Tau2 = Tau2, x = x)

```

influences.PR

influences.PR

Description

Computes the influences on the pure risk in the time interval [Tau1, Tau2] and for a given covariate profile x , from that on the log-relative hazard and cumulative baseline hazard. Can take calibration of the design weights into account.

Usage

```

influences.PR(beta, Lambda0.Tau1Tau2, x = NULL, infl.beta,
              infl.Lambda0.Tau1Tau2, calibrated = NULL, infl2.beta = NULL,
              infl2.Lambda0.Tau1Tau2 = NULL)

```

Arguments

<code>beta</code>	vector of length p with log-relative hazard values.
<code>Lambda0.Tau1Tau2</code>	cumulative baseline hazard in [Tau1, Tau2].
<code>x</code>	vector of length p , specifying the covariate profile considered for the pure risk. Default is (0,...,0).
<code>infl.beta</code>	matrix with the overall influences on the log-relative hazard estimates.
<code>infl.Lambda0.Tau1Tau2</code>	vector with the overall influences on the cumulative baseline hazard estimate in [Tau1, Tau2].
<code>calibrated</code>	are calibrated weights used for the estimation of the parameters? If <code>calibrated = TRUE</code> , the arguments below need to be provided. Default is <code>FALSE</code> .
<code>infl2.beta</code>	matrix with the phase-two influences on the log-relative hazard estimates. Needs to be provided if <code>missing.data = TRUE</code> .

`infl12.Lambda0.Tau1Tau2`

vector with the phase-two influences on the cumulative baseline hazard estimate in `[Tau1, Tau2]`. Needs to be provided if `missing.data = TRUE`.

Details

`influences.PR` works for estimation from a case-cohort with design weights or calibrated weights (case-cohort consisting of the subcohort and cases not in the subcohort, i.e., case-cohort obtained from two phases of sampling).

If covariate information is missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling), use `influences.PR.missingdata`.

`influences` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 3.2 if `calibrated = FALSE`, and as in Section 4.3 if `calibrated = TRUE`.

If `calibrated = FALSE`, the influences are only provided for the individuals in the case-cohort. If `calibrated = TRUE`, the influences are provided for all the individuals in the cohort.

Value

`infl1.Pi.x.Tau1Tau2.hat`: vector with the overall influences on the pure risk estimate in `[Tau1, Tau2]` and for covariate profile `x`.

`infl12.Pi.x.Tau1Tau2.hat`: vector with the phase-two influences on the pure risk estimate in `[Tau1, Tau2]` and for covariate profile `x`. Returned if `calibrated = TRUE`.

`Pi.x.Tau1Tau2.hat`: pure risk estimate in `[Tau1, Tau2]` and for covariate profile `x`.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample, package="CaseCohortCoxSurvival")
cohort      <- dataexample$cohort # a simulated cohort
casecohort  <- dataexample$casecohort # a simulated stratified case-cohort
A           <- dataexample$A # matrix with auxiliary variables values in the cohort

Tau1        <- 0 # given time interval for the pure risk
Tau2        <- 8
x           <- c(-1, 1, -0.6) # given covariate profile for the pure risk
v           <- c(1, 1, 0.6) # over covariate profile

# Estimation using the whole cohort
```

```

mod.cohort <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = cohort,
                    robust = TRUE)
estimation.cohort <- influences(mod.cohort, Tau1 = Tau1, Tau2 = Tau2, x = x)
beta.hat.cohort <- estimation.cohort$beta.hat
Lambda0.hat.cohort <- estimation.cohort$Lambda0.Tau1Tau2.hat
infl.beta.cohort <- estimation.cohort$infl.beta
infl.Lambda0.cohort <- estimation.cohort$infl.Lambda0.Tau1Tau2

estimation.cohort2 <- influences.PR(beta = beta.hat.cohort,
                                   Lambda0.Tau1Tau2 = Lambda0.hat.cohort,
                                   x = v, infl.beta = infl.beta.cohort,
                                   infl.Lambda0.Tau1Tau2 = infl.Lambda0.cohort)

# print the influences on the pure risk estimate for profile v
#estimation.cohort2$infl.Pi.x.Tau1Tau2

# Estimation using the stratified case-cohort with weights calibrated on A

mod.calib <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                  weight = weights.calib, id = id, robust = TRUE)
estimation.calib <- influences(mod.calib, A = A, calibrated = TRUE,
                              Tau1 = Tau1, Tau2 = Tau2, x = x)
beta.hat.calib <- estimation.calib$beta.hat
Lambda0.hat.calib <- estimation.calib$Lambda0.Tau1Tau2.hat
infl.beta.calib <- estimation.calib$infl.beta
infl.Lambda0.calib <- estimation.calib$infl.Lambda0.Tau1Tau2
infl2.beta.calib <- estimation.calib$infl2.beta
infl2.Lambda0.calib <- estimation.calib$infl2.Lambda0.Tau1Tau2

estimation.calib2 <- influences.PR(beta = beta.hat.calib,
                                   Lambda0.Tau1Tau2 = Lambda0.hat.calib,
                                   x = v, infl.beta = infl.beta.calib,
                                   infl.Lambda0.Tau1Tau2 = infl.Lambda0.calib,
                                   calibrated = TRUE,
                                   infl2.beta = infl2.beta.calib,
                                   infl2.Lambda0.Tau1Tau2 = infl2.Lambda0.calib)

# print the influences on the pure risk estimate for profile v
#estimation.calib2$infl.Pi.x.Tau1Tau2

# print the phase-two influences on the pure risk estimate for profile v
#estimation.calib2$infl2.Pi.x.Tau1Tau2

```

influences.PR.missingdata

influences.PR.missingdata

Description

Computes the influences on the pure risk in the time interval [Tau1, Tau2] and for a given covariate profile x, from that on the log-relative hazard and cumulative baseline hazard, when covariate data

is missing for certain individuals in the phase-two data.

Usage

```
influences.PR.missingdata(beta, Lambda0.Tau1Tau2, x = NULL, inf12.beta,
  inf12.Lambda0.Tau1Tau2, inf13.beta, inf13.Lambda0.Tau1Tau2)
```

Arguments

<code>beta</code>	vector of length p with log-relative hazard values.
<code>Lambda0.Tau1Tau2</code>	cumulative baseline hazard in $[\text{Tau1}, \text{Tau2}]$.
<code>x</code>	vector of length p , specifying the covariate profile considered for the pure risk. Default is $(0, \dots, 0)$.
<code>inf12.beta</code>	matrix with the overall influences on the log-relative hazard estimates.
<code>inf12.Lambda0.Tau1Tau2</code>	vector with the overall influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.
<code>inf13.beta</code>	matrix with the phase-three influences on the log-relative hazard estimates.
<code>inf13.Lambda0.Tau1Tau2</code>	vector with the phase-three influences on the cumulative baseline hazard estimate in $[\text{Tau1}, \text{Tau2}]$.

Details

`influences.PR.missingdata` works for estimation from a case-cohort with design weights and when covariate data was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling).

If there are no missing covariates in the phase- two sample, use `influences.PR` with either design weights or calibrated weights.

`influences.PR.missingdata` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 5.4 if `estimated.weights = TRUE`, and as in Web Appendix H if `estimated.weights = FALSE`.

Value

`inf1.Pi.x.Tau1Tau2.hat`: vector with the overall influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`inf12.Pi.x.Tau1Tau2.hat`: vector with the phase-two influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`inf13.Pi.x.Tau1Tau2.hat`: vector with the phase-three influences on the pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

`Pi.x.Tau1Tau2.hat`: pure risk estimate in $[\text{Tau1}, \text{Tau2}]$ and for covariate profile x .

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

cohort          <- dataexample.missingdata$cohort # a simulated cohort
casecohort     <- dataexample.missingdata$casecohort # a simulated stratified case-cohort
# phase-two data: dataexample.missingdata$casecohort.phase2
riskmat.phase2 <- dataexample.missingdata$riskmat.phase2
dNt.phase2     <- dataexample.missingdata$dNt.phase2
B.phase2       <- dataexample.missingdata$B.phase2

Tau1 <- 0 # given time interval for the pure risk
Tau2 <- 8
x    <- c(-1, 1, -0.6) # given covariate profile for the pure risk
v    <- c(1, 1, 0.6) # over covariate profile

# Estimation using the stratified case-cohort with true known design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
             weight = weights.true, id = id, robust = TRUE)

estimation <- influences.missingdata(mod = mod, riskmat.phase2 = riskmat.phase2,
                                   dNt.phase2 = dNt.phase2, Tau1 = Tau1,
                                   Tau2 = Tau2, x = x)

beta.hat      <- estimation$beta.hat
Lambda0.hat   <- estimation$Lambda0.Tau1Tau2.hat
infl.beta     <- estimation$infl.beta
infl.Lambda0 <- estimation$infl.Lambda0.Tau1Tau2
infl2.beta    <- estimation$infl2.beta
infl2.Lambda0 <- estimation$infl2.Lambda0.Tau1Tau2
infl3.beta    <- estimation$infl3.beta
infl3.Lambda0 <- estimation$infl3.Lambda0.Tau1Tau2

estimation2 <- influences.PR.missingdata(beta = beta.hat,
                                       Lambda0.Tau1Tau2 = Lambda0.hat,
                                       x = v, infl2.beta = infl2.beta,
                                       infl2.Lambda0.Tau1Tau2 = infl2.Lambda0,
                                       infl3.beta = infl3.beta,
                                       infl3.Lambda0.Tau1Tau2 = infl3.Lambda0)

# print the overall influences on the pure risk estimate for profile v
#estimation2$infl.Pi.x.Tau1Tau2
```

```

# print the phase-two influences on the pure risk estimate for profile v
#estimation2$infl2.Pi.x.Tau1Tau2

# print the phase-three influences on the pure risk estimate for profile v
#estimation2$infl3.Pi.x.Tau1Tau2

# Estimation using the stratified case-cohort with estimated weights, and
# accounting for the estimation through the influences

mod.est <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                weight = weights.est, id = id, robust = TRUE)

estimation.est <- influences.missingdata(mod.est,
                                       riskmat.phase2 = riskmat.phase2,
                                       dNt.phase2 = dNt.phase2,
                                       estimated.weights = TRUE,
                                       B.phase2 = B.phase2, Tau1 = Tau1,
                                       Tau2 = Tau2, x = x)

beta.hat.est      <- estimation.est$beta.hat
Lambda0.hat.est   <- estimation.est$Lambda0.Tau1Tau2.hat
infl.beta.est     <- estimation.est$infl.beta
infl.Lambda0.est  <- estimation.est$infl.Lambda0.Tau1Tau2
infl2.beta.est    <- estimation.est$infl2.beta
infl2.Lambda0.est <- estimation.est$infl2.Lambda0.Tau1Tau2
infl3.beta.est    <- estimation.est$infl3.beta
infl3.Lambda0.est <- estimation.est$infl3.Lambda0.Tau1Tau2
estimation.est2   <- influences.PR.missingdata(beta = beta.hat.est,
                                             Lambda0.Tau1Tau2 = Lambda0.hat.est,
                                             x = v, infl2.beta = infl2.beta.est,
                                             infl2.Lambda0.Tau1Tau2 = infl2.Lambda0.est,
                                             infl3.beta = infl3.beta.est,
                                             infl3.Lambda0.Tau1Tau2 = infl3.Lambda0.est)

```

influences.RH

influences.RH

Description

Computes the influences on the log-relative hazard. Can take calibration of the design weights into account.

Usage

```
influences.RH(mod, calibrated = NULL, A = NULL)
```

Arguments

<code>mod</code>	a cox model object, result of function <code>coxph</code> .
<code>calibrated</code>	are calibrated weights used for the estimation of the parameters? If <code>calibrated = TRUE</code> , the argument below needs to be provided. Default is <code>FALSE</code> .
<code>A</code>	$n \times q$ matrix with the values of the auxiliary variables used for the calibration of the weights in the whole cohort. Needs to be provided if <code>calibrated = TRUE</code> .

Details

`influences.RH` works for estimation from a case-cohort with design weights or calibrated weights (case-cohort consisting of the subcohort and cases not in the subcohort, i.e., case-cohort obtained from two phases of sampling).

If covariate information is missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling), use `influences.RH.missingdata`.

`influence.RH` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 3.2 if `calibrated = FALSE`, and as in Section 4.3 if `calibrated = TRUE`.

If `calibrated = FALSE`, the influences are only provided for the individuals in the case-cohort. If `calibrated = TRUE`, the influences are provided for all the individuals in the cohort.

Value

`infl1.beta`: matrix with the overall influences on the log-relative hazard estimates.

`infl2.beta`: matrix with the phase-two influences on the log-relative hazard estimates. Returned if `calibrated = TRUE`.

`beta.hat`: vector of length p with log-relative hazard estimates.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences](#), [influences.CumBH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample, package="CaseCohortCoxSurvival")

cohort      <- dataexample$cohort # a simulated cohort
casecohort  <- dataexample$casecohort # a simulated stratified case-cohort
A           <- dataexample$A # matrix with auxiliary variables values in the cohort

# Estimation using the whole cohort
```

```

mod.cohort <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = cohort,
  robust = TRUE)
estimation.cohort <- influences.RH(mod.cohort)

# print the vector with log-relative hazard estimates
#estimation.cohort$beta.hat

# print the influences on the log-relative hazard estimates
#estimation.cohort$infl.beta

# Estimation using the stratified case-cohort with weights calibrated on A
mod.calib <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
  weight = weights.calib, id = id, robust = TRUE)
estimation.calib <- influences.RH(mod.calib, A = A, calibrated = TRUE)

# print the influences on the log-relative hazard estimates
#estimation.calib$infl.beta

# print the phase-two influences on the log-relative hazard estimates
#estimation.calib$infl2.beta

```

`influences.RH.missingdata`

influences.RH.missingdata

Description

Computes the influences on the log-relative hazard, when covariate data is missing for certain individuals in the phase-two data.

Usage

```

influences.RH.missingdata(mod, riskmat.phase2, dNt.phase2 = NULL,
  status.phase2 = NULL, estimated.weights = FALSE, B.phase2 = NULL)

```

Arguments

<code>mod</code>	a cox model object, result of function <code>coxph</code> .
<code>riskmat.phase2</code>	at risk matrix for the phase-two data at all of the cases event times, even those with missing covariate data.
<code>dNt.phase2</code>	counting process matrix for failures in the phase-two data. Needs to be provided if <code>status.phase2 = NULL</code> .
<code>status.phase2</code>	vector indicating the case status in the phase-two data. Needs to be provided if <code>dNt.phase2 = NULL</code> .

`estimated.weights`
are the weights for the third phase of sampling (due to missingness) estimated? If `estimated.weights = TRUE`, the argument below needs to be provided. Default is `FALSE`.

`B.phase2`
matrix for the phase-two data, with phase-three sampling strata indicators. It should have as many columns as phase-three strata ($J^{(3)}$), with one 1 per row, to indicate the phase-three stratum position. Needs to be provided if `estimated.weights = TRUE`.

Details

`influences.RH.missingdata` works for estimation from a case-cohort with design weights and when covariate data was missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling and consisting of individuals in the phase-two data without missing covariate information).

If there are no missing covariates in the phase- two sample, use `influences.RH` with either design weights or calibrated weights.

`influences.RH.missingdata` uses the influence formulas provided in Etievant and Gail (2023). More precisely, as in Section 5.4 if `estimated.weights = TRUE`, and as in Web Appendix H if `estimated.weights = FALSE`.

Value

`infl1.beta`: matrix with the overall influences on the log-relative hazard estimates.
`infl2.beta`: matrix with the phase-two influences on the log-relative hazard estimates.
`infl3.beta`: matrix with the phase-three influences on the log-relative hazard estimates.
`beta.hat`: vector of length p with log-relative hazard estimates.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[estimation](#), [estimation.CumBH](#), [estimation.PR](#), [influences.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

cohort      <- dataexample.missingdata$cohort # a simulated cohort
casecohort  <- dataexample.missingdata$casecohort # a simulated stratified case-cohort
# phase-two data: dataexample.missingdata$casecohort.phase2
riskmat.phase2 <- dataexample.missingdata$riskmat.phase2
dNt.phase2  <- dataexample.missingdata$dNt.phase2
B.phase2    <- dataexample.missingdata$B.phase2
```

```

# Estimation using the stratified case-cohort with true known design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
            weight = weights.true, id = id, robust = TRUE)

estimation <- influences.RH.missingdata(mod = mod,
                                       riskmat.phase2 = riskmat.phase2,
                                       dNt.phase2 = dNt.phase2)

# print the influences on the log-relative hazard estimates
#estimation$infl.beta

# print the phase-two influences on the log-relative hazard estimates
#estimation$infl2.beta

# print the phase-three influences on the log-relative hazard estimates
#estimation$infl3.beta

# Estimation using the stratified case-cohort with estimated weights, and
# accounting for the estimation through the influences

mod.est <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                weight = weights.est, id = id, robust = TRUE)

estimation.est <- influences.RH.missingdata(mod.est,
                                           riskmat.phase2 = riskmat.phase2,
                                           dNt.phase2 = dNt.phase2,
                                           estimated.weights = TRUE,
                                           B.phase2 = B.phase2)

```

product.covar.weight *product.covar.weight*

Description

Computes the product of joint design weights and joint sampling indicators covariances, needed for the phase-two component of the variance (with design or calibrated weights).

Usage

```
product.covar.weight(casecohort, stratified = NULL)
```

Arguments

casecohort if `stratified = TRUE`, data frame with `status` (case status), `W` (the J strata), `strata.m` (vector of length J with the numbers of sampled individuals in the strata) and `strata.n` (vector of length J with the strata sizes), for each individual in the stratified case-cohort data. If `stratified = FALSE`, data frame with `status` (case status), `m` (number of sampled individuals) and `n` (cohort size), for each individual in the un-stratified case-cohort data.

stratified was the sampling of the case-cohort stratified on W? Default is FALSE.

Details

product.covar.weight creates the matrix with the products of joint design weights and joint sampling indicator covariances, for the non-cases in the case cohort. In other words, it has as many rows and columns as non-cases in the case cohort, and contains the $w_{i,k,j}\sigma_{i,k,j}$, with

$w_{i,k,j} = \frac{n^{(j)}(n^{(j)}-1)}{m^{(j)}(m^{(j)}-1)}$ if individuals i and k in stratum j are both non-cases, and $w_{i,k,j} = \left(\frac{n^{(j)}}{m^{(j)}}\right)^2$ otherwise, $i \neq k \in \{1, \dots, n^{(j)}\}$, $j \in \{1, \dots, J\}$.

$w_{i,i,j} = \frac{n^{(j)}}{m^{(j)}}$ if individuals i in stratum j is a non-case, $i \in \{1, \dots, n^{(j)}\}$, $j \in \{1, \dots, J\}$.

$\sigma_{i,k,j} = \frac{m^{(j)}(m^{(j)}-1)}{n^{(j)}(n^{(j)}-1)} - \left(\frac{m^{(j)}}{n^{(j)}}\right)^2$ if individuals i and k in stratum j are both non-cases, $i \neq k \in \{1, \dots, n^{(j)}\}$, $j \in \{1, \dots, J\}$.

$\sigma_{i,i,j} = \frac{m^{(j)}}{n^{(j)}} - \left(1 - \frac{m^{(j)}}{n^{(j)}}\right)$ if individuals i in stratum j is a non-case, $i \in \{1, \dots, n^{(j)}\}$, $j \in \{1, \dots, J\}$.

See Section 3.3 in Etievant and Gail (2023).

Value

product.covar.weight: matrix with the products of joint design weights and joint sampling indicator covariances, for the non-cases in the case-cohort.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[variance](#), that uses product.covar.weight to compute the variance estimate that follows the complete variance decomposition (superpopulation and phase-two variance components).

Examples

```
data(dataexample, package="CaseCohortCoxSurvival")

casecohort <- dataexample$casecohort # a simulated stratified case-cohort

prod.covar.weight <- product.covar.weight(casecohort, stratified = TRUE)

nrow(prod.covar.weight)
ncol(prod.covar.weight)
sum(casecohort$status == 0) # number of non-cases in the case-cohort
```

robustvariance	<i>robustvariance</i>
----------------	-----------------------

Description

Computes the robust variance estimate, i.e., the sum of the squared influence functions, for a parameter such as log-relative hazard, cumulative baseline hazard or covariate specific pure-risk.

Usage

```
robustvariance(infl)
```

Arguments

<code>infl</code>	overall influences on a parameter such as log-relative hazard, cumulative baseline hazard or covariate specific pure-risk.
-------------------	--

Details

`robustvariance` works for estimation with design or calibrated weights from a case cohort obtained from two phases of sampling (i.e., case cohort consisting of the subcohort and cases not in the subcohort), or when covariate information was missing for certain individuals in the phase-two data (i.e., case cohort obtained from three phases of sampling and consisting of individuals in the phase-two data without missing covariate information).

Value

`robust.var`: robust variance estimate.

References

Barlow W. (1994). Robust Variance Estimation for the Case-Cohort Design. *Biometrics*, 50, 1064-1072.

Langholz B., Jiao J. (2007). Computational methods for case-cohort studies. *Computational Statistics & Data Analysis*, 51, 3737-37.

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[influences.RH](#), [influences.CumBH](#), [influences.PR](#), [influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#) and [variance](#).

Examples

```

data(dataexample, package="CaseCohortCoxSurvival")

casecohort <- dataexample$casecohort # a simulated stratified case cohort
A          <- dataexample$A # matrix with auxiliary variables values in the cohort

Tau1 <- 0 # given time interval for the pure risk
Tau2 <- 8
x     <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the stratified case cohort with weights calibrated on A

mod.calib <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                  weight = weights.calib, id = id, robust = TRUE)
estimation.calib <- influences(mod.calib, A = A, calibrated = TRUE,
                              Tau1 = Tau1, Tau2 = Tau2, x = x)

# robust variance estimate for the log-relative hazard
robustvariance(estimation.calib$infl.beta)

# robust variance estimate for the cumulative baseline hazard estimate
robustvariance(estimation.calib$infl.Lambda0.Tau1Tau2)

# robust variance estimate for the pure risk estimate
robustvariance(estimation.calib$infl.Pi.x.Tau1Tau2)

```

variance

variance

Description

Computes the variance estimate that follows the complete variance decomposition, for a parameter such as log-relative hazard, cumulative baseline hazard or covariate specific pure-risk.

Usage

```

variance(n, casecohort, weights = NULL, infl, calibrated = NULL,
        infl2 = NULL, cohort = NULL, stratified = NULL,
        variance.phase2 = NULL)

```

Arguments

n number of individuals in the whole cohort.

casecohort If `stratified = TRUE`, data frame with `status` (case status), `weights` (design, if they are not provided in the argument below), `W` (the J strata), `strata.m` (vector of length J with the numbers of sampled individuals in the strata) and `strata.n` (vector of length J with the strata sizes in the cohort), for each individual in the stratified case-cohort data. If `stratified = FALSE`, data frame with

	weights (design, if they are not provided in the argument below), m (number of sampled individuals) and n (cohort size), for each individual in the unstratified case-cohort data.
weights	vector with design weights for the individuals in the case-cohort data.
infl	matrix with the overall influences on the parameter.
calibrated	are calibrated weights used for the estimation of the parameters? If calibrated = TRUE, the arguments below need to be provided. Default is FALSE.
infl2	matrix with the phase-two influences on the parameter. Needs to be provided if calibrated = TRUE.
cohort	If stratified = TRUE, data frame with status (case status) and subcohort (subcohort sampling indicators) for each individual in the stratified case-cohort data. If stratified = FALSE, data frame with status (case status) and unstrat.subcohort (subcohort unstratified sampling indicators) for each individual in the unstratified case-cohort data. Needs to be provided if calibrated = TRUE.
stratified	was the sampling of the case-cohort stratified on W? Default is FALSE.
variance.phase2	should the phase-two variance component also be returned? Default is FALSE.

Details

variance works for estimation from a case-cohort with design weights or calibrated weights (case-cohort consisting of the subcohort and cases not in the subcohort, i.e., case-cohort obtained from two phases of sampling).

If covariate information is missing for certain individuals in the phase-two data (i.e., case-cohort obtained from three phases of sampling), use [variance.missingdata](#).

variance uses the variance formulas provided in Etievant and Gail (2023). More precisely, as in Section 3.3 if calibrated = FALSE, and as in Section 4.3 if calibrated = TRUE.

Value

variance: variance estimate.

variance.phase2: phase-two variance component.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[influences](#), [influences.RH](#), [influences.CumBH](#), [influences.PR](#), [robustvariance](#) and [variance.missingdata](#).

Examples

```

data(dataexample, package="CaseCohortCoxSurvival")

cohort      <- dataexample$cohort # a simulated cohort
n           <- nrow(cohort)
casecohort  <- dataexample$casecohort # a simulated stratified case-cohort
A           <- dataexample$A # matrix with auxiliary variables values in the cohort

Tau1        <- 0 # given time interval for the pure risk
Tau2        <- 8
x           <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the stratified case-cohort with design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
             weight = weights, id = id, robust = TRUE)

# parameters and influences estimation
estimation  <- influences(mod, Tau1 = Tau1, Tau2 = Tau2, x = x)
beta.hat    <- estimation$beta.hat
Lambda0.hat <- estimation$Lambda0.Tau1Tau2.hat
Pi.x.hat    <- estimation$Pi.x.Tau1Tau2.hat
infl.beta   <- estimation$infl.beta
infl.Lambda0 <- estimation$infl.Lambda0.Tau1Tau2
infl.Pi.x   <- estimation$infl.Pi.x.Tau1Tau2

# variance estimate for the log-relative hazard
variance(n = n, casecohort = casecohort, infl = infl.beta, stratified = TRUE)

# variance estimate for the cumulative baseline hazard estimate
variance(n = n, casecohort = casecohort, infl = infl.Lambda0, stratified = TRUE)

# variance estimate for the pure risk estimate
variance(n = n, casecohort = casecohort, infl = infl.Pi.x, stratified = TRUE)

# Estimation using the stratified case-cohort with calibrated weights

mod.calib <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                  weight = weights.calib, id = id, robust = TRUE)

# Parameters and influences estimation
estimation.calib <- influences(mod.calib, A = A, calibrated = TRUE,
                              Tau1 = Tau1, Tau2 = Tau2, x = x)
beta.hat.calib   <- estimation.calib$beta.hat
Lambda0.hat.calib <- estimation.calib$Lambda0.Tau1Tau2.hat
Pi.x.hat.calib   <- estimation.calib$Pi.x.Tau1Tau2.hat
infl.beta.calib  <- estimation.calib$infl.beta
infl.Lambda0.calib <- estimation.calib$infl.Lambda0.Tau1Tau2
infl.Pi.x.calib  <- estimation.calib$infl.Pi.x.Tau1Tau2
infl2.beta.calib <- estimation.calib$infl2.beta
infl2.Lambda0.calib <- estimation.calib$infl2.Lambda0.Tau1Tau2
infl2.Pi.x.calib <- estimation.calib$infl2.Pi.x.Tau1Tau2

```

```

# variance estimate for the log-relative hazard
variance(n = n, casecohort = casecohort, cohort = cohort, calibrated = TRUE,
         stratified = TRUE, infl = infl.beta.calib, infl2 = infl2.beta.calib)

# variance estimate for the cumulative baseline hazard estimate
variance(n = n, casecohort = casecohort, cohort = cohort, calibrated = TRUE,
         stratified = TRUE, infl = infl.Lambda0.calib,
         infl2 = infl2.Lambda0.calib)

# variance estimate for the pure risk estimate
variance(n = n, casecohort = casecohort, cohort = cohort, calibrated = TRUE,
         stratified = TRUE, infl = infl.Pi.x.calib, infl2 = infl2.Pi.x.calib)

```

variance.missingdata *variance.missingdata*

Description

Computes the variance estimate that follows the complete variance decomposition, for a parameter such as log-relative hazard, cumulative baseline hazard or covariate specific pure-risk, when covariate information is missing for individuals in the phase-two sample.

Usage

```

variance.missingdata(n, casecohort, casecohort.phase2, weights,
                    weights.phase2, weights.p2.phase2, infl2, infl3, stratified.p2 = NULL,
                    estimated.weights = NULL)

```

Arguments

<code>n</code>	number of individuals in the whole cohort.
<code>casecohort</code>	If <code>stratified = TRUE</code> , data frame with W (the J phase-two strata), <code>strata.m</code> (vector of length J with the numbers of sampled individuals in the strata in the second phase of sampling) and <code>strata.n</code> (vector of length J with the strata sizes in the cohort), for each individual in the stratified case cohort data. If <code>stratified = FALSE</code> , data frame with m (number of sampled individuals in the second phase of sampling) and n (cohort size), for each individual in the unstratified case cohort data.
<code>casecohort.phase2</code>	If <code>stratified = TRUE</code> , data frame with W (the J phase-two strata), <code>strata.m</code> (vector of length J with the numbers of sampled individuals in the strata in the second phase of sampling), <code>strata.n</code> (vector of length J with the strata sizes in the cohort) and <code>phase3</code> (phase-three sampling indicator), for each individual in the phase-two sample. If <code>stratified = FALSE</code> , data frame with m (number of sampled individuals in the second phase of sampling), n (cohort size) and <code>unstrat.phase3</code> (phase-three sampling indicator), for each individual in the phase-two sample.

<code>weights</code>	vector with design weights for the individuals in the case cohort data.
<code>weights.phase2</code>	vector with design weights for the individuals in the phase-two sample.
<code>weights.p2.phase2</code>	vector with phase-two design weights for the individuals in the phase-two sample.
<code>infl2</code>	matrix with the phase-two influences on the parameter.
<code>infl3</code>	matrix with the phase-three influences on the parameter.
<code>stratified.p2</code>	was the second phase of sampling stratified on W ? Default is FALSE.
<code>estimated.weights</code>	were the phase-three weights estimated? Default is FALSE.

Details

`variance.missingdata` works for estimation from a case cohort with design weights and when covariate information was missing for certain individuals in the phase-two data (i.e., case cohort obtained from three phases of sampling and consisting of individuals in the phase-two data without missing covariate information).

If there are no missing covariates in the phase- two sample, use [variance](#) with either design weights or calibrated weights.

`variance.missingdata` uses the variance formulas provided in Etievant and Gail (2023). More precisely, as in Section 5.4 if `estimated.weights = TRUE`, and as in Web Appendix H.2 if `estimated.weights = FALSE`.

Value

variance: variance estimate.

References

Etievant, L., Gail, M.H. (2023). Cox model inference for relative hazard and pure risk from stratified weight-calibrated case-cohort data. Submitted.

See Also

[influences.missingdata](#), [influences.RH.missingdata](#), [influences.CumBH.missingdata](#), [influences.PR.missingdata](#), [robustvariance](#) and [variance](#).

Examples

```
data(dataexample.missingdata, package="CaseCohortCoxSurvival")

cohort      <- dataexample.missingdata$cohort # a simulated cohort
n           <- nrow(cohort)
casecohort  <- dataexample.missingdata$casecohort # a simulated stratified case cohort
casecohort.phase2 <- dataexample.missingdata$casecohort.phase2
riskmat.phase2 <- dataexample.missingdata$riskmat.phase2
dNt.phase2  <- dataexample.missingdata$dNt.phase2
B.phase2    <- dataexample.missingdata$B.phase2
```

```

Tau1   <- 0 # given time interval for the pure risk
Tau2   <- 8
x       <- c(-1, 1, -0.6) # given covariate profile for the pure risk

# Estimation using the stratified case cohort with true known design weights

mod <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
             weight = weights.true, id = id, robust = TRUE)

estimation <- influences.missingdata(mod = mod, riskmat.phase2 = riskmat.phase2,
                                   dNt.phase2 = dNt.phase2, Tau1 = Tau1,
                                   Tau2 = Tau2, x = x)

infl1.beta   <- estimation$infl1.beta
infl1.Lambda0 <- estimation$infl1.Lambda0.Tau1Tau2
infl1.Pi.x   <- estimation$infl1.Pi.x.Tau1Tau2
infl2.beta   <- estimation$infl2.beta
infl2.Lambda0 <- estimation$infl2.Lambda0.Tau1Tau2
infl2.Pi.x   <- estimation$infl2.Pi.x.Tau1Tau2
infl3.beta   <- estimation$infl3.beta
infl3.Lambda0 <- estimation$infl3.Lambda0.Tau1Tau2
infl3.Pi.x   <- estimation$infl3.Pi.x.Tau1Tau2

# variance estimate for the log-relative hazard
variance.missingdata(n = n, casecohort = casecohort,
                    casecohort.phase2 = casecohort.phase2,
                    weights = casecohort$weights.true,
                    weights.phase2 = casecohort.phase2$weights.true,
                    weights.p2.phase2 = casecohort.phase2$weights.p2.true,
                    infl2 = infl2.beta, infl3 = infl3.beta,
                    stratified.p2 = TRUE)

# variance estimate for the cumulative baseline hazard estimate
variance.missingdata(n = n, casecohort = casecohort,
                    casecohort.phase2 = casecohort.phase2,
                    weights = casecohort$weights.true,
                    weights.phase2 = casecohort.phase2$weights.true,
                    weights.p2.phase2 = casecohort.phase2$weights.p2.true,
                    infl2 = infl2.Lambda0, infl3 = infl3.Lambda0,
                    stratified.p2 = TRUE)

# variance estimate for the pure risk estimate
variance.missingdata(n = n, casecohort = casecohort,
                    casecohort.phase2 = casecohort.phase2,
                    weights = casecohort$weights.true,
                    weights.phase2 = casecohort.phase2$weights.true,
                    weights.p2.phase2 = casecohort.phase2$weights.p2.true,
                    infl2 = infl2.Pi.x, infl3 = infl3.Pi.x,
                    stratified.p2 = TRUE)

# Estimation using the stratified case cohort with estimated weights, and
# accounting for the estimation through the influences

```

```

mod.est <- coxph(Surv(times, status) ~ X1 + X2 + X3, data = casecohort,
                weight = weights.est, id = id, robust = TRUE)

estimation.est <- influences.missingdata(mod.est,
                                       riskmat.phase2 = riskmat.phase2,
                                       dNt.phase2 = dNt.phase2,
                                       estimated.weights = TRUE,
                                       B.phase2 = B.phase2, Tau1 = Tau1,
                                       Tau2 = Tau2, x = x)

infl.beta.est <- estimation.est$infl.beta
infl.Lambda0.est <- estimation.est$infl.Lambda0.Tau1Tau2
infl.Pi.x.est <- estimation.est$infl.Pi.x.Tau1Tau2
infl2.beta.est <- estimation.est$infl2.beta
infl2.Lambda0.est <- estimation.est$infl2.Lambda0.Tau1Tau2
infl2.Pi.x.est <- estimation.est$infl2.Pi.x.Tau1Tau2
infl3.beta.est <- estimation.est$infl3.beta
infl3.Lambda0.est <- estimation.est$infl3.Lambda0.Tau1Tau2
infl3.Pi.x.est <- estimation.est$infl3.Pi.x.Tau1Tau2

# variance estimate for the log-relative hazard
variance.missingdata(n = n, casecohort = casecohort,
                    casecohort.phase2 = casecohort.phase2,
                    weights = casecohort$weights.est,
                    weights.phase2 = casecohort.phase2$weights.est,
                    weights.p2.phase2 = casecohort.phase2$weights.p2.true,
                    infl2 = infl2.beta.est, infl3 = infl3.beta.est,
                    stratified.p2 = TRUE, estimated.weights = TRUE)

# variance estimate for the cumulative baseline hazard estimate
variance.missingdata(n = n, casecohort = casecohort,
                    casecohort.phase2 = casecohort.phase2,
                    weights = casecohort$weights.est,
                    weights.phase2 = casecohort.phase2$weights.est,
                    weights.p2.phase2 = casecohort.phase2$weights.p2.true,
                    infl2 = infl2.Lambda0.est, infl3 = infl3.Lambda0.est,
                    stratified.p2 = TRUE, estimated.weights = TRUE)

# variance estimate for the pure risk estimate
variance.missingdata(n = n, casecohort = casecohort,
                    casecohort.phase2 = casecohort.phase2,
                    weights = casecohort$weights.est,
                    weights.phase2 = casecohort.phase2$weights.est,
                    weights.p2.phase2 = casecohort.phase2$weights.p2.true,
                    infl2 = infl2.Pi.x.est, infl3 = infl3.Pi.x.est,
                    stratified.p2 = TRUE, estimated.weights = TRUE)

```

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