Package 'gcemod'

September 24, 2026

Type Package

Title Generalized Competing Event Models with Lunn-McNeil Testing

Version 0.3.0

Date 2026-09-02

Description Fits generalized competing event (GCE) models and estimates covariate effects on omega-plus, the ratio of the hazard for an event of interest to the hazard for a competing event, on both the cause-specific (Cox) and subdistribution (Fine-Gray) hazard scales. Confidence intervals and p-values are obtained from the Lunn-McNeil (1995) stacked (augmented) data approach. The package builds GCE risk scores from the model linear predictor, identifies risk-score cutpoints that maximize the separation in omega-plus between groups, and produces cumulative incidence (``alligator'') plots by risk group and calibration plots of predicted versus observed omega-plus. It also compares covariate effects across the primary, competing, and total (composite) events, and estimates covariate effects on the ratio of cumulative incidence functions (a cumulative-incidence-scale GCE model). Methods follow Carmona et al. (2014) <doi:10.1016/j.ijrobp.2014.03.047>, Mell et al. (2024) <doi:10.1016/j.eururo.2023.01.020>, and Lunn and McNeil (1995) <doi:10.2307/2532940>.

License GPL (>= 2)

Encoding UTF-8

Language en-US

LazyData true

Depends R (>= 3.5.0)

Imports survival, cmprsk, ggplot2 (>= 3.5.2), patchwork, stats

Suggests testthat (>= 3.0.0), knitr, rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

Config/roxygen2/version 8.0.0

NeedsCompilation no

Author Loren Mell [aut, cre]

Maintainer Loren Mell <lmell@ucsd.edu>

Repository CRAN

Date/Publication 2026-09-24 04:20:07 UTC

Contents

`gcecif` *Generalized competing event model on the cumulative-incidence-ratio scale*

Description

Fits a generalized competing event (GCE) model on the *cumulative incidence* scale, estimating covariate effects on the ratio of cumulative incidences $\rho(t) = F_1(t)/F_2(t)$ at a landmark time `t`, where F_1 and F_2 are the cumulative incidence functions of the event of interest and the competing event. $\rho(t)$ is the odds that a subject's *realized* event by time `t` is the event of interest rather than the competing event, so `gcecif()` is a cumulative-incidence-scale companion to the cause-specific (`gcecox`) and subdistribution (`gcefg`) omega+ models and returns a compatible `"gcemod"` object.

Effects are estimated by jackknife pseudo-observation regression. Two equivalent parameterizations are provided (both estimate the effect on $\log \rho(t)$): `method = "logit"` (default) regresses pseudo-values of the bounded share $\pi_1 = F_1/(F_1 + F_2)$ by a logit-link GEE, and `method = "logratio"` regresses pseudo-values of $\log \rho$ directly by an identity-link GEE (ordinary least squares). Both use a robust (sandwich) variance. A GCE risk score is formed from the model linear predictor, so `exp(riskscore)` is a subject's ρ relative to the average subject (see `gce_riskscore`, `gce_scaling`).

Usage

```
gcecif(
  Time,
  Ind,
  Cov,
  M = 5,
  t,
  method = c("logit", "logratio"),
  ridge = 0,
  conf.level = 0.95
)
```

Arguments

`Time`	numeric vector of follow-up times.
`Ind`	a data frame of event indicators: column 1 = event of interest, column 2 = competing event (`0`/`1`).
`Cov`	a data frame of covariates (factors are expanded automatically).
`M`	number of bins for the ρ risk plot (default `5`).
`t`	landmark time at which ρ is evaluated.
`method`	estimation scale: `"logit"` (default; logit-link GEE on the share) or `"logratio"` (identity-link GEE on $\log \rho$).
`ridge`	non-negative ridge penalty on the covariate coefficients (not the intercept), used only with `method = "logit"` to stabilize weakly identified fits. Default `0`.
`conf.level`	confidence level (default `0.95`).

Details

Because $F_k(t) = \int_0^t S(u^-)\, h_k(u)\, du$ with S the all-cause survivor, $\rho(t)$ is a survival-weighted time-average of the instantaneous cause-specific hazard ratio $\omega^+(u)$; under a time-constant ω^+ it equals ω^+ exactly. The ratio of cumulative incidences is a non-collapsible, marginal-over-time measure, so `exp(coef)` is interpreted as a conditional association with the realized event mix, not a mechanism-level per-cause effect.

The estimand is defined for a genuine competing-risks setting, in which both $F_1(t)$ and $F_2(t)$ are appreciable at the landmark `t`. If the competing event is effectively absent, or `t` precedes appreciable competing-event incidence, $\log \rho$ is weakly identified; the optional `ridge` penalty stabilizes such fits.

Value

An object of class `"gcemod"` (subclass `"gcecif"`) with: `coef` (log ρ ratios), `result` (ratio table with CIs and p-values), `omnibus` (Wald test that all ρ ratios equal 1), `riskscore` (linear predictor), `scaling` (covariate means/SDs and per-SD effects), `F1`, `F2`, `rho0` (baseline ρ at the mean covariate profile), `rho` (per-subject fitted ρ), `pseudo` (per-subject pseudo-values), and the design matrix, time, and cause coding used by `gce_tidy`.

References

Andersen PK, Klein JP, Rosthoj S (2003). Generalized linear models for correlated pseudo-observations, with applications to multi-state models. *Biometrika* 90:15-27.

See Also

gcecox, gcefg, gce_tidy, gce_riskscore

Examples

```
data(prostate)
Ind <- data.frame(event = as.integer(prostate$status == 1),
                  competing = as.integer(prostate$status == 2))
Cov <- prostate[, c("age", "psa", "gleason", "t2b", "comorbidity")]
fit <- gcecif(prostate$time, Ind, Cov, t = 10)
summary(fit)
gce_tidy(fit)
```

---

gcecox *Generalized competing event model via cause-specific Cox regression*

Description

Fits a generalized competing event (GCE) model on the cause-specific hazard scale and estimates covariate effects on ω^+ (event of interest vs. competing event) using the Lunn-McNeil stacked model (see lunnmcneil), with 95% confidence intervals, Wald p-values, and an omnibus test. A GCE risk score is formed from the model linear predictor, and per-subject $\omega = \omega^+/(1+\omega^+)$ is returned for comparison with observed values.

Usage

```
gcecox(
  Time,
  Ind,
  Cov,
  M = 5,
  t,
  conf.level = 0.95,
  cluster.se = TRUE,
  standardize = FALSE
)
```

Arguments

Time	numeric vector of follow-up times.
Ind	a data frame of event indicators. Column 1 = event of interest, column 2 = competing event (0/1). A third column, if present, is ignored.

Cov	a data frame of covariates.
M	number of bins for the ω^+ risk plot (default 5).
t	time point at which per-subject ω / ω^+ are evaluated.
conf.level	confidence level (default 0.95).
cluster.se	logical; cluster-robust SEs in the Lunn-McNeil model (default TRUE).
standardize	logical; controls only the *reported* omega+ ratio scale (default FALSE = per natural covariate unit; TRUE = per 1 SD). The risk score is *always* the normalized (mean-centered) linear predictor regardless of this setting, so cutpoints, plots, and the predicted-vs-observed omega calibration are unaffected. Covariate means/SDs are available in $scaling (see gce_scaling).

Value

An object of class "gcemod" (subclass "gcecox") with: coef (log ω^+ ratios), result (ratio table with CIs and p-values), omnibus (Lunn-McNeil global test), riskscore (linear predictor), omega / omegaplus (per-subject values at t), omegaplot and omegatimeplot (ggplot objects), and the fitted Lunn-McNeil model.

See Also

gcefg, lunnmcneil, gce_cutpoints

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
Cov <- hn[, c("age", "smoker", "t_cat", "n_cat", "p16")]
fit <- gcecox(hn$time, Ind, Cov, M = 5, t = 5)
summary(fit)
```

---

gcefg *Generalized competing event model via Fine-Gray regression*

Description

Fits a generalized competing event (GCE) model on the subdistribution hazard scale and estimates covariate effects on ω^+ using a Lunn-McNeil-style stacked Fine-Gray model (see lunnmcneil with type = "finegray"), giving 95% confidence intervals, Wald p-values, and an omnibus test from one joint model. A GCE risk score is formed from the model linear predictor, and per-subject ω^+ / ω at time t are returned for comparison with observed values.

Usage

```
gcefg(Time, Ind, Cov, M = 5, t, conf.level = 0.95, standardize = FALSE)
```

Arguments

`Time`	numeric vector of follow-up times.
`Ind`	a data frame of event indicators. Column 1 = event of interest, column 2 = competing event (`0`/`1`).
`Cov`	a data frame of covariates (factors are expanded to indicators).
`M`	number of bins for the ω^+ risk plot (default `5`).
`t`	time point at which per-subject ω^+ / ω are evaluated.
`conf.level`	confidence level (default `0.95`).
`standardize`	logical; controls only the *reported* omega+ ratio scale (default `FALSE` = per natural covariate unit; `TRUE` = per 1 SD). The risk score is always the normalized (mean-centered) linear predictor. Covariate means/SDs are in `$scaling` (see `gce_scaling`).

Value

An object of class `"gcemod"` (subclass `"gcefg"`) with the same components as `gcecox` on the sub-distribution scale.

See Also

`gcecox`, `lunnmcneil`

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
Cov <- hn[, c("age", "smoker", "t_cat", "n_cat", "p16")]
fit <- gcefg(hn$time, Ind, Cov, M = 5, t = 5)
summary(fit)
```

`gce_alligator` *Alligator plot: cumulative incidence by risk group and event type*

Description

Plots the cause-specific cumulative incidence functions (CIFs) of the event of interest and the competing event over time on a single panel, with risk groups distinguished by color and event types by line type (event of interest solid, competing event dashed). In higher-risk groups the event-of-interest CIF rises above the competing-event CIF and the curves separate like an alligator's open jaws.

The x-axis is truncated at the model's readout time `t`, with tick marks at 1-unit (e.g. 1-year) intervals. The y-axis auto-scales its cap to the smallest of 25/50/75/100% that covers the peak cumulative incidence (so low-incidence settings are not compressed), with ticks at 10% (or 5% when capped at 25%). Numbers at risk for each group are shown in an aligned panel below the plot. Gray's test across groups is attached.

Usage

```
gce_alligator(
  object,
  groups = 2,
  method = c("optimal", "quantile"),
  criterion = c("omegaplus", "cif"),
  xlab = "Time (years)",
  ylab = "Cumulative incidence",
  group.lab = "Risk group",
  risk.table = TRUE,
  ymax = NULL
)
```

Arguments

object	a "gcemod" object from gcecox, gcefg, or gcecif.
groups	a gce_cutpoints result, a grouping factor of length n, or a single integer giving the number of risk groups (default 2). When an integer is given, the groups are derived with gce_cutpoints using method.
method	grouping rule used when groups is an integer: "optimal" (default) or "quantile" (equal-sized groups). Ignored when groups is a cutpoints object or a factor.
criterion	optimal-search criterion when groups is an integer and method = "optimal": "omegaplus" (default, log-ω^+ separation; not tail-sensitive) or "cif" (joint Gray statistic on the observed cumulative incidence of both events). See gce_cutpoints.
xlab, ylab	axis labels.
group.lab	legend title for the risk groups (default "Risk group").
risk.table	logical; show numbers at risk in an aligned panel below the plot (default TRUE).
ymax	optional numeric upper cap for the y-axis (0-1). If NULL (default) the cap auto-scales to 25/50/75/100% based on the peak incidence.

Value

A ggplot/patchwork object. The Gray's-test result, the plotted CIF data, the numbers-at-risk table, and the cutpoints are attached as attributes "grays_test", "data", "n.risk", and "cutpoints".

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
fit <- gcecox(hn$time, Ind, hn[, c("age", "t_cat", "p16")], M = 5, t = 5)
gce_alligator(fit, groups = 2)
```

gce_calibration *Calibration of predicted vs. observed omega+ by risk rank*

Description

Groups subjects into equal-sized rank groups on the GCE risk score and compares the model-predicted quantity with an observed estimate in each group. For omega+ models (gcecox, gcefg) the predicted ω^+ (or ω) is compared with observed cause-specific Nelson-Aalen cumulative hazards at time `t`: $\omega^+_{obs} = H_1(t)/H_2(t)$ and $\omega_{obs} = H_1(t)/(H_1(t) + H_2(t))$. For a gcecif fit the predicted cumulative-incidence ratio ρ (or share π_1) is compared with the observed Aalen-Johansen cumulative incidence within the group: $\rho_{obs} = F_1(t)/F_2(t)$ and $\pi_{1,obs} = F_1(t)/(F_1(t)+F_2(t))$. A calibration plot (predicted vs. observed with the identity line) and the underlying table are returned.

Usage

```
gce_calibration(object, which = NULL, groups = 5)
```

Arguments

`object`	a `"gcemod"` object from gcecox, gcefg, or gcecif.
`which`	quantity to calibrate. For omega+ models `"omegaplus"` (default) or `"omega"`; for a gcecif fit `"rho"` (default) or `"share"`. If `NULL` the model-appropriate default is used.
`groups`	number of rank groups (default 5).

Value

A `ggplot` object (predicted vs. observed). The calibration table is attached as attribute `"data"`.

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
fit <- gcecox(hn$time, Ind, hn[, c("age", "t_cat", "p16")], M = 5, t = 5)
gce_calibration(fit, which = "omegaplus", groups = 5)
```

`gce_cutpoints` *Risk-score cutpoints for GCE risk stratification*

Description

Splits subjects into ordered risk groups on the GCE risk score. With `method = "optimal"` the cutpoint(s) maximize a separation criterion by a greedy forward search; with `method = "quantile"` equal-sized groups are used.

The default criterion, `"omegaplus"`, maximizes the between-group separation in **log** ω^+ (equivalently, the risk score / linear predictor). This is the additive scale on which the joint event-of-interest-vs-competing ω^+ contrast is defined, and – unlike separation measured on the exponential ω^+ scale – it is **not** sensitive to a few extreme high-risk subjects, so the search does not chase high-risk tails and tends to return balanced, well-separated groups. The alternative `"cif"` maximizes a joint Gray's test statistic (summed across both competing events) on the observed cumulative incidence.

Usage

```
gce_cutpoints(
  object,
  groups = 2,
  method = c("optimal", "quantile"),
  criterion = c("omegaplus", "cif"),
  min.prop = 0.1,
  nperm = 0,
  labels = NULL
)
```

Arguments

`object`	a `"gcemod"` object from `gcecox`, `gcefg`, or `gcecif`. For a `gcecif` fit the per-group summary reports mean ρ and share instead of ω^+ / ω; the `"omegaplus"` criterion still means separation on the risk-score (linear-predictor) scale.
`groups`	number of groups (default 2).
`method`	`"optimal"` (default) or `"quantile"`.
`criterion`	optimal-search criterion: `"omegaplus"` (default, log-ω^+ separation) or `"cif"` (joint Gray statistic on observed cumulative incidence of both events).
`min.prop`	minimum proportion of subjects per group (default `0.1`).
`nperm`	number of permutations for the selection-adjusted p-value (default `0` = not computed). When `nperm > 0`, the maximally-selected joint Gray statistic is permuted (risk score vs. outcome) to give a p-value accounting for the data-driven choice of cutpoint.
`labels`	optional character labels for the groups (low to high risk).

Value

A list with: `groups` (ordered factor), `cutpoints` (on the risk-score scale), `summary` (per-group n, events, mean ω^+ / ω), and `test`. The `test` element reports the Lunn-McNeil ω^+ contrast between groups – a test that the ratio of cause-specific (or subdistribution) hazards differs across groups – with the univariable ω^+ ratio estimate and CI (`$omegaplus`), the joint test (`$statistic`, `$df`, `$p.value`), the per-event Gray tests for comparison (`$individual_gray`), and a selection-adjusted `$p.perm` when `nperm > 0`.

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
fit <- gcecox(hn$time, Ind, hn[, c("age", "t_cat", "p16")], M = 5, t = 5)
gce_cutpoints(fit, groups = 2)

# with a selection-adjusted permutation p-value (slower)
gce_cutpoints(fit, groups = 2, nperm = 200)
```

---

gce_performance *Discrimination (C-index) for a GCE model*

Description

Computes the cause-specific concordance (C-index) of the GCE risk score for the event of interest. For calibration (predicted vs. observed ω^+), see `gce_calibration`.

Usage

```
gce_performance(object, conf.level = 0.95)
```

Arguments

`object`	a `"gcemod"` object.
`conf.level`	confidence level for the C-index interval (default `0.95`).

Details

The C-index is computed with `concordance` using the event of interest as the outcome and the GCE risk score as the predictor. Higher risk scores denote higher risk; the statistic is oriented so that values above 0.5 indicate discrimination in the expected direction, and the `"flipped"` attribute of the result records whether the orientation was reversed.

Value

An object of class `"gce_performance"`: a named numeric vector with elements `estimate`, `se`, `lower`, and `upper`, carrying attributes `conf.level` and `flipped`. Printing the object displays the C-index with its confidence interval.

See Also

gce_calibration

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
fit <- gcecox(hn$time, Ind, hn[, c("age", "t_cat", "p16")], M = 5, t = 5)
gce_performance(fit)
```

---

gce_riskscore *Normalized risk score and relative omega+ for new subjects*

Description

Computes the GCE risk score for new subjects using the covariate means/SDs and coefficients stored in a fitted model. The score is the normalized (mean-centered) linear predictor, so `exp(riskscore)` is the subject's omega+ relative to the *average* subject in the fitting data (a value of 1 = same as average, 2 = twice the average omega+). For cause-specific (gcecox) models the absolute predicted omega+ and omega at the model's time `t` are also returned.

Usage

```
gce_riskscore(object, newdata)
```

Arguments

`object`	a "gcemod" object from gcecox, gcefg, or gcecif.
`newdata`	a data frame containing the covariates used to fit `object` (same column names). Factor levels not seen in the fitting data are treated as the reference level.

Value

A data frame with `riskscore` and `exp(riskscore)` relative to the average subject: `omegaplus_rel` for omega+ models (with absolute `omegaplus` and `omega` at time `t` for cause-specific fits), or `rho_rel` for a gcecif fit.

See Also

gce_scaling

Examples

```
data(prostate)
Ind <- data.frame(as.integer(prostate$status == 1), as.integer(prostate$status == 2))
fit <- gcecox(prostate$time, Ind, prostate[, c("age", "psa", "gleason")], M = 5, t = 10)
gce_riskscore(fit, newdata = prostate[1:5, ])
```

gce_scaling *Covariate scaling (means and SDs) used by the GCE risk score*

Description

Returns each covariate's mean and standard deviation (from the data used to fit the model), together with the per-SD log-omega+ coefficient and omega+ ratio. These are the quantities needed to reproduce the normalized risk score for new subjects (see `gce_riskscore`) and to interpret how far a subject sits from the average patient.

Usage

```
gce_scaling(object)
```

Arguments

`object`	a "gcemod" object from `gcecox`, `gcefg`, or `gcecif`.

Value

A data frame with columns `term`, `mean`, `sd`, `coef_perSD` (log ratio per 1 SD) and the per-SD ratio (`omegaplus_ratio_perSD` for omega+ models, `rho_ratio_perSD` for a `gcecif` fit).

See Also

`gce_riskscore`

Examples

```
data(prostate)
Ind <- data.frame(as.integer(prostate$status == 1), as.integer(prostate$status == 2))
fit <- gcecox(prostate$time, Ind, prostate[, c("age", "psa", "gleason")], M = 5, t = 10)
gce_scaling(fit)
```

gce_tidy *Tidy a GCE model into a data frame of estimates*

Description

With `effects = FALSE` (the default) the omega+ ratio estimates are returned. With `effects = TRUE` a covariate-effects comparison table is returned that juxtaposes, for each covariate, the hazard ratio for the primary (event-of-interest) hazard, the competing-event hazard, the total (composite, any-event) hazard, and the relative hazard ratio (the omega+ ratio) from the GCE model, each with a confidence interval. This lets the investigator see whether a covariate acts mainly on the event of interest, the competing event, both, or on their balance.

Usage

```
gce_tidy(object, effects = FALSE, ...)
```

Arguments

object	a "gcemod" object from gcecox, gcefg, or gcecif. For a gcecif fit the relative column is the cumulative-incidence ratio (rho ratio) and the primary/competing/total columns are cause-specific hazard ratios.
effects	logical; if TRUE, return the primary/competing/total/ relative effects comparison table instead of the omega+ ratio table. Requires an object fit with **gcemod** >= 0.3.0 (which stores the design matrix). Default FALSE.
...	unused.

Details

The individual- and total-event columns are estimated on the same hazard scale as the fitted model: cause-specific Cox models for a gcecox fit, and Fine-Gray subdistribution models for a gcefg fit. The total (composite) event has no competing event, so its subdistribution and cause-specific hazards coincide and a Cox model on the composite endpoint is used in both cases.

Value

If effects = FALSE, a data frame with columns term, log_ratio, ratio, conf.low, conf.high, p.value. If effects = TRUE, a data frame with columns term, primary, competing, total, and relative, each a formatted "HR (low, high)" string.

Examples

```
data(hn)
Ind <- data.frame(event = as.integer(hn$status == 1),
                  competing = as.integer(hn$status == 2))
fit <- gcecox(hn$time, Ind, hn[, c("age", "t_cat", "p16")], M = 5, t = 5)
gce_tidy(fit)
gce_tidy(fit, effects = TRUE)
```

---

hn *Head-and-neck cancer competing-risks example dataset*

Description

An example head-and-neck cancer competing-risks dataset used to illustrate the **gcemod** functions. The data are provided for illustration only and do not represent real patients. The event of interest is cancer recurrence and the competing event is death without recurrence; recurrence is the more frequent event (recurrence-dominant, $\omega^{+} > 1$). Contrast with prostate.

Usage

```
hn
```

Format

A data frame with 1000 rows and 11 variables:

id sequential subject identifier

time follow-up time in years

status competing-risks status: 0 = censored, 1 = cancer recurrence (event of interest), 2 = death without recurrence (competing event)

age age at diagnosis (years)

ps ECOG performance status (factor: 0, 1, 2)

female sex indicator (1 = female)

smoker smoking indicator (1 = more than 10 pack-years)

t_cat T category (factor: 1-4)

n_cat N category (factor: 0-3)

p16 p16 status (1 = positive)

site primary site (factor: oropharynx, larynx, hypopharynx, oralcavity)

---

lunnmcneil *Lunn-McNeil stacked-model estimation of omega+ ratios*

Description

Estimates covariate effects on ω^+ (the ratio of the hazard for the event of interest to the hazard for the competing event) from a single stacked ("augmented") model, following Lunn and McNeil (1995). Each subject contributes one record per event type; the model is stratified by event type and the covariate-by-event-type interaction estimates $\log(\omega^+ \text{ ratio})$ with model-based standard errors, per-covariate Wald tests, and an omnibus multivariate Wald test.

Usage

```
lunnmcneil(
  Time,
  cause,
  Cov,
  event = 1,
  competing = 2,
  type = c("coxph", "finegray"),
  cluster.se = TRUE,
  conf.level = 0.95,
  standardize = FALSE,
  ...
)
```

Arguments

`Time`	numeric vector of follow-up times.
`cause`	event indicator per subject: `0` = censored, and the codes in `event` and `competing` for the two event types.
`Cov`	a data frame of covariates (factors are expanded to indicators).
`event`	code marking the event of interest (default `1`).
`competing`	code marking the competing event (default `2`).
`type`	`"coxph"` (cause-specific, default) or `"finegray"` (subdistribution).
`cluster.se`	logical; cluster-robust (subject) SEs (default `TRUE`).
`conf.level`	confidence level (default `0.95`).
`standardize`	logical; controls only the *reported* coefficient scale (default `FALSE`). `FALSE` reports omega+ ratios per natural covariate unit; `TRUE` reports them per 1 SD. This is a reparameterization, so Wald tests, p-values, and the omnibus test are identical either way. The covariate means/SDs (`$center`, `$scale`) are always returned.
`...`	passed to `coxph`.

Details

Two hazard scales are supported:

`type = "coxph"` Cause-specific hazards. The augmented data set duplicates each subject into an "event" stratum and a "competing" stratum; the interaction coefficient is exactly the difference in cause-specific log-hazards, i.e. $\log(\omega^+)$. This is the original Lunn-McNeil construction and the interaction MLE equals the difference of two separate cause-specific Cox fits.

`type = "finegray"` Subdistribution hazards. Risk-set-weighted data are generated for each event type with `finegray`, stacked, and fit with a single weighted, event-type-stratified `coxph`. The interaction estimates the difference in subdistribution log-hazards. Because subjects recur across the weighted risk sets, cluster-robust (subject) standard errors are used. This is an extension of Lunn-McNeil to the subdistribution scale.

Subject records are duplicated in both cases, so cluster-robust standard errors (clustered on subject) are the default.

Value

An object of class `"gce_lunnmcneil"`: a list with the fitted model (`$fit`), the omega+ coefficient table (`$omegaplus`), the reference (competing-event) coefficients (`$beta_competing`), the omnibus test (`$omnibus`), the design column names (`$terms`), and the hazard scale (`$type`).

References

Lunn M, McNeil D (1995) Applying Cox regression to competing risks. *Biometrics* 51:524-32.

Examples

```
data(hn)
Cov <- hn[, c("age", "smoker", "t_cat", "n_cat", "p16")]
lunnmcneil(hn$time, hn$status, Cov, type = "coxph")
lunnmcneil(hn$time, hn$status, Cov, type = "finegray")
```

`prostate` *Prostate cancer competing-risks example dataset*

Description

An example prostate cancer competing-risks dataset used to illustrate the **gcemod** functions. The data are provided for illustration only and do not represent real patients. The event of interest is distant metastasis or prostate-cancer death and the competing event is death from other causes; the competing event is the more frequent (competing-death-dominant, $\omega^{+} < 1$). Contrast with hn.

Usage

```
prostate
```

Format

A data frame with 1000 rows and 9 variables:

id sequential subject identifier

time follow-up time in years

status competing-risks status: 0 = censored, 1 = distant metastasis or prostate-cancer death (event of interest), 2 = death from other causes (competing event)

age age at diagnosis (years)

ps performance status (factor: 0, 1)

psa pre-treatment PSA (ng/mL, capped at 20)

gleason Gleason grade group (factor: "<=6", "3+4", "4+3", ">=8")

t2b stage indicator (1 = T2b or higher)

comorbidity significant comorbidity indicator (1 = yes)

Index