Package ‘smlePH’

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Type Package

Title Sieve Maximum Full Likelihood Estimation for the Right-Censored Proportional Hazards Model

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Description Fitting the full likelihood proportional hazards model and extracting the residuals.

URL `https://github.com/taehwa015/smlePH/`

BugReports `https://github.com/taehwa015/smlePH/issues/`

Encoding UTF-8

RoxygenNote 7.2.3

Suggests knitr, rmarkdown

Imports MASS, splines2, stats

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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Contents

`smle_ph` *Fit the full likelihood proportional hazards model*

Description

Fit the proportional hazards model with maximum full likelihood estimation. Sieve estimation is used for estimating the baseline hazard function.

Usage

```
smle_ph(y, d, x)
```

Arguments

`y`	n-vector of survival time (> 0).
`d`	n-vector of right-censoring indicator, `1`: observed; `0`: right-censored.
`x`	p-dimensional matrix of covariates.

Details

see Choi et al., (2026+) for detailed method explanation.

Value

`smle_ph` returns a list containing the following components:

- `Coef`: regression estimator and its inferential results.
- `Cum.hazard`: baseline cumulative hazard function estimates.

References

Choi et al., (2026+) Residual-Based Sieve Maximum Full Likelihood Estimation for the Proportional Hazards Model

Examples

```
library(smlePH)
set.seed(111)
n = 200
beta = c(1, -1, 0.5, -0.5, 1)
p = length(beta)
beta = matrix(beta, ncol = 1)
R = matrix(c(rep(0, p^2)), ncol = p)
diag(R) = 1
mu = rep(0, p)
SD = rep(1, p)
S = R * (SD %*% t(SD))
x = MASS::mvrnorm(n, mu, S)
```

```
T = (-log(runif(n)) / (2 * exp(x %*% beta)))^(1/2)
C = runif(n, min = 0, max = 2.9)
y = apply(cbind(T,C), 1, min)
d = (T <= C)+0
ord = order(y)
y = y[ord]; x = x[ord,]; d = d[ord]
smle_ph(y = y, d = d, x = x)
```

`smle_resid` *Extract residuals of the full likelihood proportional hazards model*

Description

This function extracts residuals of the full likelihood proportional hazards model estimated by the sieve estimation. Deviance-type and score-type residuals are available.

Usage

```
smle_resid(y, d, x, fit, type = c("score", "deviance"))
```

Arguments

`y`	survival time (> 0).
`d`	right-censoring indicator, `1`: observed; `0`: right-censored.
`x`	p-dimensional covariates matrix.
`fit`	an object comes from the function `smle_ph`.
`type`	type of residual, either `deviance` or `score`.

Details

see Choi et al., (2026+) for detailed method explanation.

Value

`smle_resid` returns a numeric vector (if `type = "deviance"`) or a matrix (if `type = "score"`) of residuals extracted from the `object`.

References

Choi et al., (2026+) Residual-Based Sieve Maximum Full Likelihood Estimation for the Proportional Hazards Model

Examples

```
library(smlePH)
# The 'fit' comes from an example description of smle_ph()
smle_resid(y = y, d = d, x = x, fit = fit, type = "deviance")
smle_resid(y = y, d = d, x = x, fit = fit, type = "score")
```

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