Package: survAH (via r-universe)

November 22, 2026

Type Package

Title Survival Data Analysis using Average Hazard

Version 1.2.1

Date 2026-11-21

Description Performs two-sample comparisons based on average hazard with survival weight (AHSW) or general censoring-free incidence rate (CFIR) proposed by Uno and Horiguchi (2023) <doi:10.1002/sim.9651>.

License GPL-2

Depends survival, R (>= 2.10)

Encoding UTF-8

LazyData true

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Config/roxygen2/version 8.1.1

NeedsCompilation no

Author Hajime Uno [aut] (ORCID: <https://orcid.org/0000-0003-0622-8471>), Miki Horiguchi [aut, cre] (ORCID: <https://orcid.org/0000-0002-9800-1954>), Zihan Qian [aut] (ORCID: <https://orcid.org/0009-0006-1050-1847>)

Maintainer Miki Horiguchi <horiguchimiki@gmail.com>

Repository https://cran.r-universe.dev

Date/Publication 2026-11-22 09:30:02 UTC

RemoteUrl https://github.com/cran/survAH

RemoteRef HEAD

RemoteSha 027b619a2e6a042656a41a1853d7615903513325

Contents

survAH-package 2
ah1 3
ah2 4
ahreg 6
ahreg.sample.data 8
cm214_pfs 9
print.ah2 10
print.ahreg 11

Index **12**

`survAH-package` *Survival Data Analysis using Average Hazard*

Description

The survAH package performs two-sample comparisons based on average hazard with survival weight (AHSW) or general censoring-free incidence rate (CFIR) proposed by Uno and Horiguchi (2023) <doi:10.1002/sim.9651>.

Author(s)

Maintainer: Miki Horiguchi <horiguchimiki@gmail.com> (ORCID)

Authors:

- Miki Horiguchi <horiguchimiki@gmail.com> (ORCID)
- Hajime Uno (ORCID)
- Zihan Qian (ORCID)

References

Uno H and Horiguchi M. Ratio and difference of average hazard with survival weight: new measures to quantify survival benefit of new therapy. Statistics in Medicine. 2023; 42(7):936-952. <doi:10.1002/sim.9651>

Uno H, Tian L, Horiguchi M, Hattori S, Kehl KL. Regression models for average hazard. Biometrics. 2024; 80(2):ujae037. <doi:10.1093/biomtc/ujae037>

Horiguchi M, Tian L, Kehl KL, Uno H. Assessing delayed treatment benefits of immunotherapy using long-term average hazard: a novel test/estimation approach. Lifetime Data Anal. 2025; 31(4):784-809. <doi:10.1007/s10985-025-09671-0>

Qian Z, Tian L, Horiguchi M, Uno H. A novel stratified analysis method for testing and estimating overall treatment effects on time-to-event outcomes using average hazard with survival weight. Stat Med. 2025; 44(7):e70056. <doi:10.1002/sim.70056>

See Also

survival survRM2 surv2sampleComp

ah1 *Average Hazard (one sample)*

Description

Calculates the average hazard with survival weight and the corresponding asymptotic confidence interval for a single sample.

Usage

```
ah1(time, status, tau, conf.int=0.95)
```

Arguments

time	A numeric vector of follow-up times for right-censored data.
status	A numeric vector indicating the event status; 1 = event occurred, 0 = right censored.
tau	A scalar specifying the end time point (tau) for calculating the average hazard. If tau = NULL, the default is the maximum time point at which the risk set size in both groups is at least 10.
conf.int	A numeric value specifying the confidence level for confidence intervals. The default is 0.95.

Details

It also provides the log-transformed t-year event rate and restricted mean survival time (RMST) along with their variances as intermediate products. Note that the confidence intervals for the t-year event rate and RMST are based on log-scale values. As a result, the confidence intervals may differ slightly from those generated by the **surv2sampleComp** or **survRM2** packages.

Value

An object of class ah1, which contains the following components:

need_stop	Logical indicator. TRUE when nonparametric inference is not supported at the specified tau, which happens when the Kaplan-Meier estimate of the survival probability at tau is zero or when no subject remains at risk at tau (the largest observed time is smaller than tau). In that case, the returned estimates and standard errors should not be reported; specify a smaller tau.
stop_reason	Character string giving the reason when need_stop = TRUE ("no subject at risk at tau" or "Kaplan-Meier estimate of S(tau) is zero"); NA otherwise.
max_time	The largest observed time in the data.
tau	The truncation time point used in the analysis.
result1	Estimated average hazard.

Author(s)

Hajime Uno, Miki Horiguchi

References

Uno H and Horiguchi M. Ratio and difference of average hazard with survival weight: new measures to quantify survival benefit of new therapy. Statistics in Medicine. 2023;1-17. <doi:10.1002/sim.9651>

Examples

```
#=====================================================================
# cm214_pfs: The sample reconstructed data of the CheckMate214 study.
# The code below reproduces the results reported by
# Uno and Horiguchi (StatMed; 2023) in Table 6.
#=====================================================================
D      = cm214_pfs
time   = D$time
status = D$status
tau    = 21

b = ah1(time=time, status=status, tau=tau, conf.int=0.95)
print(b)
```

---

ah2 *Two-Sample Comparison of Average Hazard*

Description

The ah2 function performs two-sample comparisons using the average hazard (AH) as a summary measure of the survival time distribution. Two kinds of between-group contrast metrics, the ratio of AH (RAH) and the difference in AH (DAH), are calculated.

Usage

```
ah2(time, status, arm, tau=NULL, conf.int=0.95, eta=0, strata=NULL)
```

Arguments

time	A numeric vector of follow-up times for right-censored data.
status	A numeric vector indicating the event status; 1 = event occurred, 0 = right censored.
arm	A binary vector indicating group assignment; elements should be either 0 or 1. Typically, 0 = control group and 1 = treatment group.
tau	A scalar specifying the end time point (tau) for calculating the average hazard. If tau = NULL, the default is the maximum time point at which the risk set size in both groups is at least 10.

conf.int	A numeric value specifying the confidence level for confidence intervals. The default is 0.95.
eta	A scalar specifying the start time point (eta) for calculating the average hazard over the time window [eta, tau]. The default is 0.
strata	An optional numeric vector specifying a stratification factor for stratified analysis. If strata = NULL (default), an unstratified analysis is performed.

Details

The function provides the AH for each of the two groups, the absolute difference and the absolute ratio of AH (DAH and RAH) between the two groups, and the corresponding confidence intervals. It also calculates p-values for the two-sided tests based on the RAH and DAH.

Value

An object of class ah2, which contains the following components:

note	A note indicating the time window used in the analysis, specified as [eta, tau].
n.obs	A summary of the number of observations, including the total number, number of events by tau, number of censored observations by tau, and the size of the risk set at tau.
ah	Estimated average hazard in each arm.
rah	Ratio of average hazards (RAH), calculated as treatment over control.
dah	Difference of average hazards (DAH), calculated as treatment minus control.
conventional_rah	Ratio of average hazards based on the conventional stratified analysis method.
conventional_dah	Difference of average hazards based on the conventional stratified analysis method.
stratified_ah	Estimated average hazard by arm based on the proposed stratified analysis method.
stratified_rah	Ratio of average hazards based on the proposed stratified analysis method.
stratified_dah	Difference of average hazards based on the proposed stratified analysis method.

Author(s)

Hajime Uno, Miki Horiguchi, Zihan Qian

References

Uno H and Horiguchi M. Ratio and difference of average hazard with survival weight: new measures to quantify survival benefit of new therapy. Statistics in Medicine. 2023; 42(7):936-952. <doi:10.1002/sim.9651> Horiguchi M, Tian L, Kehl KL, Uno H. Assessing delayed treatment benefits of immunotherapy using long-term average hazard: a novel test/estimation approach. Lifetime Data Anal. 2025; 31(4):784-809. <doi:10.1007/s10985-025-09671-0> Qian Z, Tian L, Horiguchi M, Uno H. A novel stratified analysis method for testing and estimating overall treatment effects on time-to-event outcomes using average hazard with survival weight. Stat Med. 2025; 44(7):e70056. <doi:10.1002/sim.70056>

Examples

```
#=====================================================================
# cm214_pfs: The sample reconstructed data of the CheckMate214 study.
#=====================================================================
# The code below reproduces the results reported by
# Uno H and Horiguchi M (StatMed; 2023) in Table 6.
D      = cm214_pfs
time   = D$time
status = D$status
arm    = D$arm
tau    = 21

a = ah2(time=time, status=status, arm=arm, tau=tau, conf.int=0.95, eta=0)
print(a, digits=3)


# The code below reproduces the results reported by
# Horiguchi M, Tian L, Kehl K.L, Uno H (arXiv; 2024) in Table 3.
b = ah2(time=time, status=status, arm=arm, tau=21, conf.int=0.95, eta=7)
print(b, digits=3)


#=====================================================================
# Stratified analysis example
#=====================================================================
D      = myeloid
time   = D$futime/365.25
status = D$death
arm    = as.numeric(D$trt=="A")
tau    = 3
strata = as.numeric(D$flt3)

b = ah2(time=time, status=status, arm=arm, strata=strata, tau=tau)
print(b, digits=3)
```

---

ahreg *Regression Analysis with Average Hazard*

Description

The ahreg function performs a regression analysis for the average hazard (AH).

Usage

```
ahreg(formula, tau, data, link="log", conf.int=0.95,
             cens_strata=NULL, cens_covs=NULL, maxiter=20, tol=1e-15)
```

Arguments

formula	A formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object of the form Surv(time, status) as returned by the Surv function.
tau	A scalar value to specify a time point for calculating the average hazard.
data	A data.frame in which to interpret the variables named in the formula.
link	A link function to be used, either "log" (default) or "identity".
conf.int	A confidence coefficient for calculating confidence intervals. The default is conf.int=0.95.
cens_strata	A variable name for specifying group-specific censoring. Only one of cens_strata or cens_cov can be specified. The default is NULL.
cens_covs	A set of variable names used for modeling censoring time distribution. Only one of cens_strata or cens_covs can be specified. The default is NULL.
maxiter	The maximum number of Newton-Raphson iterations. The default is 20.
tol	The convergence criterion for the Newton-Raphson iterations; the iterations stop when the squared norm of the update is at most tol. The default is 1e-15.

Details

The function implements the average hazard regression of Uno et al. (2024).

The data must have one record per subject with entry at time zero, right censoring, and baseline covariates; delayed entry and multiple records per subject are not supported.

Endpoint convention: an event recorded exactly at tau is counted as an event in [0, tau], following the usual convention that events precede censorings at tied times; it contributes person-time tau with weight 1/G(tau), where G is the estimated censoring survival function, the same weight as an observation censored at tau, which is taken to have survived beyond tau and contributes person-time tau only. This is the convention used by ah1 and ah2. The sample estimating equation in Uno et al. (2024) is written with I(X < tau) under the continuous-time assumption, where ties at tau have probability zero; the population quantity, pr(T <= tau | Z), is the same under either convention.

Censoring model: with cens_covs, the censoring time distribution is modeled by a Cox model fitted with coxph() using Efron tie handling (ties = "efron"). The Stata implementation stahreg uses stcox, efron for the same reason.

Input checks: the function stops when tau exceeds the largest observed time (overall or within a censoring stratum), when the estimated censoring survival probability is zero for a subject whose weight is needed, when the covariates are collinear, or when no event is observed before tau under the log link. It warns when fewer than 10 subjects are at risk at tau (overall or within a censoring stratum), when the largest inverse probability of censoring weight exceeds 20, and when the Newton-Raphson iterations do not converge.

Value

an object of class ahreg.

result	A table containing the coefficient estimates, standard errors, confidence intervals, z-values, and two-sided p-values for each predictor.

The object also carries attributes, including `beta` (the coefficient estimates), `beta.var` (their variance-covariance matrix), `ipcw` (the inverse probability of censoring weights), `ipcw_max` (the largest weight), `n_risk_tau` (the number of subjects at risk at `tau`), and `convergence_information` (a list with `convergence`, 0 if converged and 9 otherwise, `iterations`, and the iteration history).

Author(s)

Hajime Uno, Miki Horiguchi

References

Uno H, Tian L, Horiguchi M, Hattori S, Kehl KL. Regression models for average hazard. Biometrics. 2024; 80(2):ujae037. <doi:10.1093/biomtc/ujae037>

Examples

```
#=============================================================================
# ahreg.sample.data: Sample data from the pbc data in the survival package
#=============================================================================
D = ahreg.sample.data()


#-- Independent censoring
a1 = ahreg(Surv(time,status) ~ arm + edema + bili, tau=7, data=D)
print(a1)

#-- Group specific censoring
a2 = ahreg(Surv(time,status) ~ arm + edema + bili, tau=7, data=D, cens_strata="arm")
print(a2)

#-- Covariate dependent censoring via Cox
a3 = ahreg(Surv(time,status) ~ arm + edema + bili, tau=7, data=D, cens_covs=c("arm","edema"))
print(a3)

#-- Covariate dependent censoring via Cox (identity link)
a4 = ahreg(Surv(time,status) ~ arm + edema + bili, tau=7, data=D, cens_covs=c("arm","edema"),
           link="identity")
print(a4)
```

`ahreg.sample.data` *Generate a sample data from the pbc data*

Description

This is a function to retrieve 312 randomized patients from the pbc data.

Usage

```
ahreg.sample.data(t.unit="year")
```

Arguments

t.unit	Specify the time unit. It supports "year" (default), "month", and "day".

Details

The function creates a sample dataset to illustrate the usage of the function ahreg() in this package. The original pbc data in survival package consists of 418 patients data. This function loads the pbc data, select the 312 patients who were randomized. The status variable is edited, so that 1 indicates death and 0 indicates alive.

Value

returns a data frame

See Also

pbc in survival package

Examples

```
D=ahreg.sample.data()
head(D)
```

---

cm214_pfs *Sample Reconstructed Data of CheckMate214 Study*

Description

The progression-free survival data reconstructed from the publication of the CheckMate214 study.

Usage

```
data(cm214_pfs)
```

Format

A dataset containing 3 columns:

time the time-to-event variable (the time unit is month)

status the event indicator (1=event, 0=censor)

arm the treatment indicator (1=treatment, 0=control)

Details

This is a reconstructed patient-level data from the results reported by Motzer et al.(2018) <doi:10.1056/NEJMoa1712126>. The data consists of 847 patients with previously untreated clear-cell advanced renal-cell carcinoma; 425 for the nivolumab plus ipilimumab group (treatment) and 422 for the sunitinib group (control).

Source

Motzer RJ, Tannir NM, McDermott DF, et al. Nivolumab plus ipilimumab versus sunitinib in advanced renal-cell carcinoma. New England Journal of Medicine. 2018;378(14):1277–1290. <doi:10.1056/NEJMoa1712126> Guyot P, Ades AE, Ouwens MJ, Welton NJ. Enhanced secondary analysis of survival data: reconstructing the data from published Kaplan-Meier survival curves. BMC Med Res Methodol. 2012;12(1):9. <doi:10.1186/1471-2288-12-9>

`print.ah2` *print.ah2*

Description

S3 method for class 'ah2'

Usage

```
## S3 method for class 'ah2'
print(x, digits=3, ...)
```

Arguments

`x`	Object to be printed.
`digits`	Integer indicating the number of decimal places.
`...`	Further arguments ignored in this function.

Value

returns summary output for class 'ah2'

print.ahreg *print.ahreg*

Description

S3 method for class 'ahreg'

Usage

```
## S3 method for class 'ahreg'
print(x, digits=5, ...)
```

Arguments

x	Object to be printed.
digits	Integer indicating the number of decimal places.
...	Further arguments ignored in this function.

Value

returns summary output for class 'ahreg'

Index

∗ **datasets**
cm214_pfs, 9

ah1, 3, *7*
ah2, 4, *7*
ahreg, 6
ahreg.sample.data, 8

cm214_pfs, 9

print.ah2, 10
print.ahreg, 11

survAH *(*survAH-package*)*, 2
survAH-package, 2