Package 'survAH'

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Type Package

Title Survival Data Analysis using Average Hazard

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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)

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RoxygenNote 7.2.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

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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)

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>

See Also

survival survRM2 surv2sampleComp

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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)
```

Arguments

time	The follow-up time for right censored data.
status	The event indicator, 1=event, and 0=right censored.
arm	The group indicator for comparison. The elements of this vector take either 1 or 0. Normally, 0=control group, 1=active treatment group.
tau	A scalar value to specify a time point for calculating the average hazard. When tau=NULL, the default value (i.e., the maximum time point where the size of risk set for both groups remains at least 10) is used.
conf.int	A confidence coefficient for calculating confidence intervals. The default is conf.int=0.95.

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.

note	the truncation time point used in the analysis
n.obs	the number of observations (total number, number of events by tau, number of censoring by tau, and size of risk set at tau)
ah	the estimated average hazard by arm
rah	the ratio of average hazards (RAH; treatment over control)
dah	the difference of average hazard (DAH; treatment minus control)

Author(s)

Hajime Uno, Miki Horiguchi

References

Horiguchi M and Uno H. 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
arm    = D$arm
tau    = 21

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

---

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>

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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'

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