

# Package ‘LogrankA’

July 2, 2014

**Type** Package

**Title** Logrank Test for Aggregated Survival Data

**Version** 1.0

**Date** 2013-07-15

**Author** Jonas Richter-Dumke and Roland Rau

**Maintainer** Jonas Richter-Dumke <jrd.r.project@gmail.com>

**Description** LogrankA provides a logrank test across unlimited groups with the possibility to input aggregated survival data.

**Suggests** MASS, survival

**License** GPL-2

**NeedsCompilation** no

**Repository** CRAN

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LogrankA-package

*Logrank Test for Aggregated Survival Data*

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**Description**

LogrankA provides a logrank test across unlimited groups with the possibility to input aggregated survival data.

**Details**

Package: LogrankA  
 Type: Package  
 Version: 1.0  
 Date: 2013-07-15  
 License: GPL-2

The package contains the function LogrankA.

### Author(s)

Jonas Richter-Dumke and Roland Rau

Maintainer: Jonas Richter-Dumke <jrd.r.project@gmail.com>

### References

Peto, R. et al. (1977). "Design and analysis of randomized clinical trials requiring prolonged observation of each patient". II. analysis and examples. In: British journal of cancer 35.1, pp. 1-39.

Ziegler, A., S. Lange, and R. Bender (2007). "Ueberlebenszeitanalyse: Der Log-Rang-Test". In: Deutsche Medizinische Wochenschrift 132, pp. 39-41.

### See Also

[Surv](#), [survdiff](#)

### Examples

```
library(survival)
library(MASS)

## data: survival of australian aids patients (individual and aggregated)

aids2.ind <- Aids2 # import australian aids data
aids2.ind$status <- as.numeric(aids2.ind$status) - 1 # recode status to 0/1
stime.days <- aids2.ind$death - aids2.ind$diag # generate survival time in weeks
aids2.ind$stime <- round(stime.days / 7, 0)
aids2.ind$agegr <- cut(aids2.ind$age, # generate age groups
                     c(0, 20, 40, 60, 100), right = FALSE)
aids2.ind <- aids2.ind[, c(5, 8, 9)] # keep only important columns
aids2.aggr <- aggregate(aids2.ind$stime, # transform to aggregated data
                      by = list(aids2.ind$status, aids2.ind$stime,
                                aids2.ind$agegr),
                      FUN = length)
colnames(aids2.aggr) <- c("status", "stime", "agegr", "n")
# generate survival objects for individual and aggregated data
surv.ind <- Surv(aids2.ind$stime, aids2.ind$status)
surv.aggr <- Surv(aids2.aggr$stime, aids2.aggr$status)

## logrank test on individual and aggregated data
```

```
# logrank on individual data
LogrankA(surv = surv.ind,
         group = aids2.ind$agegr)
# logrank on aggregated data
LogrankA(surv = surv.aggr,
         group = aids2.aggr$agegr,
         weight = aids2.aggr$n)
```

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LogrankA

*Logrank Test for Aggregated Survival Data*


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### Description

LogrankA provides a logrank test across unlimited groups with the possibility to input aggregated survival data.

### Usage

```
LogrankA(surv, group, weight)
```

### Arguments

surv	An object of type <code>survival</code> is expected as input argument <code>surv</code> . This object is generated with the function <code>Surv</code> of the package <code>survival</code> and holds information about the survival time and censoring status of each observation.
group	Argument <code>group</code> provides the group affiliation of each observation in the survival argument.
weight	The argument <code>weight</code> is optional. It specifies the number of occurrences for each value combination in an aggregated dataset. Expected is a non-negative numeric vector.

### Details

The `group` and `weight` arguments must correspond to the entries in the `surv` argument. Therefore the `group` and `weight` vectors must be equal in length to the time and status columns in the survival object of `surv`.

If the `weight` argument is not specified it is assumed that the input data is not aggregated.

More than a single group must be specified.

### Value

<code>p.chi2</code>	P-value of chi-squared test of logrank test statistic.
<code>df</code>	Degrees of freedom used for chi-squared test.
<code>LR</code>	Value of logrank test statistic.
<code>lr.parameter</code>	Number of observations, observed events, expected events, $(O-E)^2/E$ for each group.

In addition a short text summary of the logrank test is printed to the console.

**Note**

For an in-depth explanation of LogrankA please see the package vignette.

**Author(s)**

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**References**

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**See Also**

[Surv](#), [survdiff](#)

**Examples**

```
library(survival)
library(MASS)

## data: survival of australian aids patients (individual and aggregated)

aids2.ind <- Aids2 # import australian aids data
aids2.ind$status <- as.numeric(aids2.ind$status) - 1 # recode status to 0/1
stime.days <- aids2.ind$death - aids2.ind$diag # generate survival time in weeks
aids2.ind$stime <- round(stime.days / 7, 0)
aids2.ind$agegr <- cut(aids2.ind$age, # generate age groups
                     c(0, 20, 40, 60, 100), right = FALSE)
aids2.ind <- aids2.ind[, c(5, 8, 9)] # keep only important columns
aids2.aggr <- aggregate(aids2.ind$stime, # transform to aggregated data
                      by = list(aids2.ind$status, aids2.ind$stime,
                                aids2.ind$agegr),
                      FUN = length)
colnames(aids2.aggr) <- c("status", "stime", "agegr", "n")
# generate survival objects for individual and aggregated data
surv.ind <- Surv(aids2.ind$stime, aids2.ind$status)
surv.aggr <- Surv(aids2.aggr$stime, aids2.aggr$status)

## logrank test on individual and aggregated data

# logrank on individual data
LogrankA(surv = surv.ind,
         group = aids2.ind$agegr)
# logrank on aggregated data
LogrankA(surv = surv.aggr,
         group = aids2.aggr$agegr,
         weight = aids2.aggr$n)
```

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