

# Package: survAWKMT2 (via r-universe)

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**Type** Package

**Title** Two-Sample Tests Based on Differences of Kaplan-Meier Curves

**Version** 1.0.1

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**Description** Tests for equality of two survival functions based on integrated weighted differences of two Kaplan-Meier curves.

**Imports** survival

**License** GPL-2

**NeedsCompilation** no

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**Repository** <https://mikihoriguchi.r-universe.dev>

**RemoteUrl** <https://github.com/cran/survAWKMT2>

**RemoteRef** HEAD

**RemoteSha** 562e0961f039ab34d06291214d3bc46a4fa73be0

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survAWKMT2-package      *Two-Sample Tests Based on Weighted Differences of Kaplan-Meier Curves*

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### Description

Tests for equality of two survival functions based on integrated weighted differences of two Kaplan-Meier curves.

### Author(s)

Miki Horiguchi, Hajime Uno

### References

Uno H, Tian L, Claggett B, Wei LJ. A versatile test for equality of two survival functions based on weighted differences of Kaplan-Meier curves. *Statistics in Medicine* 2015, 34, 3680-3695.

### See Also

survival

### Examples

```
D          = survival::pbc[1:312, c(2,3,4)] #The pbc data from 'survival' package
D$status   = as.numeric(D$status==2)
D$trt     = as.numeric(D$trt==2)
names(D)  = c("time", "status", "arm")
tau       = max(D[D[,2]==1,1])
nmethod   = 10 #Recommended to specify at least 10000 (default) or larger.

a = AWKMT2(indata=D, tau=tau, c_first=0, c_last=4, c_by=0.1, method="permutation",
           nmethod=nmethod, seed=1, v1=TRUE, v2=TRUE, test="1_side")
print(a)
```

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AWKMT2                      *Adaptively Weighted Kaplan-Meier Tests*

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### Description

Performs the two-sample tests based on adaptively weighted differences between two Kaplan-Meier curves proposed by Uno, Tian, Claggett and Wei (2015).

### Usage

```
AWKMT2(indata, tau, c_first=0, c_last=4, c_by=0.1, method="permutation",
       nmethod=10000, seed=1, v1=TRUE, v2=TRUE, test="1_side")
```

**Arguments**

<code>indata</code>	A data matrix (data frame). The 1st column is time-to-event variable, the 2nd column is event indicator (1=event, 0=censor), and the 3rd column is the treatment indicator (1=treat, 0=control). No missing values are allowed in this data matrix.
<code>tau</code>	A numeric value to specify the time interval of interest. The end of study time will be a general choice.
<code>c_first</code>	A first number in range to specify the search area of "c" for the versatile tests by Uno et al. (2015). Default is 0.
<code>c_last</code>	A last number in range to specify the search area of "c" for the versatile tests by Uno et al. (2015). Default is 4.
<code>c_by</code>	A number to specify the search area of "c" for the versatile tests by Uno et al. (2015). Default is 0.1.
<code>method</code>	A name of the resampling method. It supports "permutation" (default) and "perturbation".
<code>nmethod</code>	A number of iterations for the resampling. Recommended to specify at least 10000 (default) or larger.
<code>seed</code>	An integer value, used for the random number generation in the resampling procedures. Default is 1.
<code>v1</code>	Choice of the test statistic. When TRUE (default), v1 proposed by Uno et al. (2015) is used as a test statistic.
<code>v2</code>	Choice of the test statistic. When TRUE (default), v2 proposed by Uno et al. (2015) is used as a test statistic.
<code>test</code>	Specify "1_side" for the one-sided test where the alternative hypothesis is that treatment group is superior to control group with respect to survival. Specify "2_side" for the two-sided test where the alternative hypothesis is that treatment group is not equal to control group with respect to survival. Default is "1_side".

**Value**

A list with components:

<code>resampling_method</code>	The resampling method.
<code>crude_pvalue_T1_1_side</code>	The one-sided crude p-value of the test based on v1 in Uno et al. (2015).
<code>crude_pvalue_T2_1_side</code>	The one-sided crude p-value of the test based on v2 in Uno et al. (2015).
<code>crude_pvalue_T1_2_side</code>	The two-sided crude p-value of the test based on v1 in Uno et al. (2015).
<code>crude_pvalue_T2_2_side</code>	The two-sided crude p-value of the test based on v2 in Uno et al. (2015).
<code>bona_fide_pvalue_T1_1_side</code>	The one-sided bona-fide p-value of the test based on v1 in Uno et al. (2015).

`bona_fide_pvalue_T2_1_side`  
 The one-sided bona-fide p-value of the test based on  $v_2$  in Uno et al. (2015).  
`bona_fide_pvalue_T1_2_side`  
 The two-sided bona-fide p-value of the test based on  $v_1$  in Uno et al. (2015).  
`bona_fide_pvalue_T2_2_side`  
 The two-sided bona-fide p-value of the test based on  $v_2$  in Uno et al. (2015).

## References

Uno H, Tian L, Claggett B, Wei LJ. A versatile test for equality of two survival functions based on weighted differences of Kaplan-Meier curves. *Statistics in Medicine* 2015, 34, 3680-3695.

## See Also

survival

## Examples

```

D          = survival::pbc[1:312, c(2,3,4)] #The pbc data from 'survival' package
D$status  = as.numeric(D$status==2)
D$strtr   = as.numeric(D$strtr==2)
names(D)  = c("time", "status", "arm")
tau       = max(D[D[,2]==1,1])
nmethod   = 10 #Recommended to specify at least 10000 (default) or larger.

a = AWKMT2(indata=D, tau=tau, c_first=0, c_last=4, c_by=0.1, method="permutation",
           nmethod=nmethod, seed=1, v1=TRUE, v2=TRUE, test="1_side")
print(a)

```

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