

# Package ‘bpcp’

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**Type** Package

**Title** Beta Product Confidence Procedure for Right Censored Data

**Version** 1.5.1

**Date** 2026-02-17

**Depends** stats, survival, ggplot2, methods

**Description** Calculates nonparametric pointwise confidence intervals for the survival distribution for right censored data, and for medians [Fay and Brittain <DOI:10.1002/sim.6905>]. Has two-sample tests for dissimilarity (e.g., difference, ratio or odds ratio) in survival at a fixed time, and differences in medians [Fay, Proschan, and Brittain <DOI:10.1111/biom.12231>]. Basically, the package gives exact inference methods for one- and two-sample exact inferences for Kaplan-Meier curves (e.g., generalizing Fisher's exact test to allow for right censoring), which are especially important for latter parts of the survival curve, small sample sizes or heavily censored data. Includes mid-p options.

**License** GPL (>= 2)

**LazyLoad** yes

**NeedsCompilation** no

**Repository** CRAN

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**Suggests** testthat (>= 3.0.0), exact2x2, exactci, scales, survminer, tidyverse, purrr, abind, data.table, dplyr, tidyr

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bpcp-package	<i>Pointwise Confidence Intervals Associated with the Survival Distribution for Right Censored Data</i>
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### Description

The package has functions to give several different methods for calculating pointwise confidence intervals for a single survival distribution for right censored data. There is also a two-sample test for dissimilarity (measured by difference, ratio, or odds ratio) between two survival distributions at a fixed point in time.

The recommended confidence interval for a single sample is the beta product confidence procedure (using [bpcp](#)), and the recommended test for the two-sample test is the melded BPCP test (using [bpcp2samp](#)).

Other confidence intervals and two sample tests are included in the package primarily to compare them to the recommended ones. (And justify the recommendations).

Also included is a difference in medians test that applies only to non-censored data and is designed to guarantee coverage for all sample sizes (see [mdiffmedian.test](#)). The test makes no assumptions about the distributions, so that, unlike the Hodges-Lehmann method, tied data are allowed and a shift assumption is not needed.

### Details

Package: bpcp  
Type: Package  
Version: 1.4.2  
Date: 2022-03-11  
License: GPL2  
LazyLoad: yes

The most important function for the single sample case is the `bpcp` which gives confidence intervals for the survival distribution for right censored data with nice small sample properties. That function creates an `kmcILR` object which has 6 methods: `summary` (create a data frame with estimates and confidence intervals), `plot` (plot Kaplan-Meier with confidence intervals), `lines` (add confidence intervals to a plot), `StCI` (pick out survival and confidence interval at specific times), `median` (pick out median and confidence interval on median), and `quantile` (pick out any quantile and its confidence interval). A mid-p option for `bpcp` is now available. It gives closer to nominal coverage than the standard (`midp=FALSE`) BPCP. For details see Fay et al (2013) on the standard BPCP and Fay and Brittain (2016) on the mid-p option.

For the two-sample test see `bpcp2samp`. This test for equality reduces to Fisher's exact test when there is no censoring. When there is censoring, the test is expected to maintain at least nominal coverage. For details see Fay et al (2015).

### Author(s)

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### References

Fay, MP, Brittain, E, and Proschan, MA. (2013). Pointwise Confidence Intervals for a Survival Distribution with Small Samples or Heavy Censoring. *Biostatistics* 14(4): 723-736 doi: 10.1093/biostatistics/kxt016. (copy available at <http://www.niaid.nih.gov/about/organization/dcr/brb/staff/Pages/michael.aspx>).

Fay, MP, Proschan, MA, and Brittain, E (2015). Combining One Sample Confidence Procedures for Inference in the Two Sample Case. *Biometrics* 71:146-156.

Fay, MP, and Brittain, E (2016). Finite Sample Pointwise Confidence Intervals for a Survival Distribution with Right-Censored Data. *Statistics in Medicine*. doi: 10.1002/sim.6905.

### See Also

[bpcp](#)

### Examples

```
data(leuk)
## since there are ties at time=6
## and the data are truncated to the nearest integer, use Delta=1
bfit<-bpcp(leuk$time,leuk$status,Delta=1)
## plot Kaplan-Meier and 95 pct Beta Product Confidence Intervals
plot(bfit,xlab="time (weeks)")
```

```
## details
summary(bfit)
quantile(bfit)
StCI(bfit,2)
```

---

betaMeldTest

*Melded Beta Test*


---

## Description

This function gives a two sample melded beta test together with the associated melded confidence intervals. It can be used when the confidence distributions (or upper and lower confidence distributions) for the one sample parameters are beta, and one is interested in either the difference, odds ratio, or ratio of those two one sample parameters. The betaMeldTest is usually called by [bpcp2samp](#), and not called directly by the user.

## Usage

```
betaMeldTest(betaParms1, betaParms2,
             nullparm = NULL,
             parmtype = c("difference", "oddsratio", "ratio","cdfratio","logsratio"),
             conf.level = 0.95, conf.int = TRUE,
             alternative = c("two.sided", "less", "greater"),
             eps = 10^-8, dname = "", estimate1 = NA, estimate2 = NA)
```

## Arguments

betaParms1	a list of the beta parameters for group 1
betaParms2	a list of the beta parameters for group 2
nullparm	null value of the parameter of interest, default of NULL gives 0 if parmtype='difference' and 1 otherwise
parmtype	parameter type for comparing the survival function of the two groups, either 'difference' 'ratio' 'oddsratio' or 'cdfratio'
conf.level	confidence level, e.g., 0.95
conf.int	logical, calculate confidence interval?
alternative	character, either 'two.sided', 'less', or 'greater'
eps	small value to make integration tractable
dname	name describing data
estimate1	estimate of mean for beta parameter of group 1 (statistic of htest object)
estimate2	estimate of mean for beta parameter for group 2 (parameter of htest object)

**Details**

If the upper and lower confidence distributions for both samples are described by beta distributions, then you can create a CD test using this function. For example, if you have sample 1 is binomial with  $x$  (with  $0 < x < n$ ) out of  $n$  positive responses, then the  $100(1-\alpha)$  confidence interval is  $qbeta(\alpha/2, x, n-x+1)$  and  $qbeta(1-\alpha/2, x+1, n-x)$ . So the lower confidence distribution is beta with parameters  $a=x$  and  $b=n-x+1$ , and the upper CD is beta with parameters  $a=x+1$  and  $b=n-x$ .

See [bpcp2samp](#) for a full description of the parmtypes.

**Value**

an object of class 'htest'

**Examples**

```
fisher.test(matrix(c(4,5,2,22),2,2),alternative="greater")
```

```
betaMeldTest(
  betaParms1=list(alower=2,blower=22+1,upper=2+1,bupper=22),
  betaParms2=list(alower=4,blower=5+1,upper=4+1,bupper=5),
  alternative="greater",parmtype="oddsratio",
  estimate1=2/24,estimate2=4/9)
```

---

bpcp2samp

*Melded BPCP test*


---

**Description**

Tests for dissimilarity between two groups in their survival distributions at a fixed point in time. Can operationalize that dissimilarity as 'difference', 'ratio' or 'oddsratio'.

**Usage**

```
bpcp2samp(time, status, group, testtime = NULL, parmtype =
  c("difference", "oddsratio", "ratio", "efflogs",
    "effcdf", "cdfratio", "logsratio", "one.minus.ratio",
    "one.minus.cdfratio"), nullparm = NULL, alternative =
  c("two.sided", "less", "greater"), conf.level = 0.95,
  midp = FALSE, changeGroupOrder = FALSE, control =
  bpcp2sampControl(), add.eps = 1e-10)

delta2samp(time,status,group, testtime=NULL,conf.level=0.95,
  zero.one.adjustment=FALSE,
  method=c("standard","reg_hybrid","adj_hybrid","sh_adj_hybrid"),
  parmtype=c("difference","oddsratio","ratio","efflogs","effcdf"),
  nullparm=NULL,
  alternative=c("two.sided","less","greater"),
  changeGroupOrder=FALSE)
```

**Arguments**

time	time to event for each observation
status	status of event time, 1 is observed, 0 is right censored
group	group for test, should have two levels, to change order use as factor and change order of levels
testtime	vector of fixed times to test between the two survival distributions, default of NULL will return results for all distinct times in the data
parmtime	parameter type for comparing the survival function of the two groups, either 'difference' 'ratio' 'oddsratio' 'cdfratio' 'effcdf' 'efflogs' 'one.minus.ratio' or 'one.minus.cdfratio' (see details)
nullparm	null value of the parameter of interest, default of NULL gives 0 if parmtime='difference' and 1 otherwise
alternative	character, either 'two.sided', 'less', or 'greater'
conf.level	confidence level, e.g., 0.95
midp	logical, do mid-p tests and confidence intervals?
changeGroupOrder	logical, change the order of the groups?
control	list of control parameters, see <a href="#">bpcp2sampControl</a>
add.eps	numeric value to add onto censored observations, default is 1e-10
zero.one.adjustment	default=FALSE, if true performs ad hoc modifications to the delta method when Kaplan-Meier estimators are 0 or 1.
method	the delta method for constructing estimates and confidence intervals. 'standard' uses the KM estimate and greenwood variance; 'reg_hybrid' uses the KM estimate and Borkowf's regular hybrid variance; 'adj_hybrid' uses the KM estimate and Borkowf's adjusted hybrid variance; and 'sh_adj_hybrid' uses a shrunken KM estimate and Borkowf's adjusted hybrid variance

**Details**

There are two main functions for two-sample testing, `bpcp2samp`, which gives melded confidence intervals, and `delta2samp`, which gives confidence intervals based on the delta method and Borkowf's modifications to it.

The melded confidence interval method is a very general procedure to create confidence intervals for the two sample tests by combining one sample confidence intervals. If  $S_1$  and  $S_2$  are the survival value at `testtime` from sample 1 (first value of group) and sample 2 (second value of group) respectively, then we can get confidence intervals on the  $S_2/S_1$  (`parmtime='difference'`),  $S_2/S_1$  (`parmtime='ratio'`),  $(S_2*(1-S_1))/(S_1*(1-S_2))$  (`parmtime='oddsratio'`),  $(1-S_1)/(1-S_2)=F_1/F_2$  (`parmtime='cdfratio'`),  $1-S_2/S_1$  (`parmtime='one.minus.ratio'`), or  $1-(1-S_1)/(1-S_2)=1-F_1/F_2$  (`parmtime='one.minus.cdfratio'`). Some `parmtime`s may return estimates that are NA (see note).

The resulting melded CIs appear to guarantee coverage as long as the one sample confidence intervals from which the melded CIs are derived have guaranteed coverage themselves. So since we use the BPCP for the one sample intervals and they appear to guarantee coverage (see Fay, Brittain, and Proschan, 2013), we expect the melded BPCP intervals to have at least nominal coverage. Note

that when there is no censoring the melded CIs derived from the one-sample BPCPs, give matching inferences to Fisher's exact test (i.e., give theoretically identical p-values) when testing the null hypothesis of equality ( $S1=S2$ ). For details see Fay, Proschan and Brittain (2015).

The original melded CIs focused on combining one sample CIs that that guarantee coverage. We can apply the melding to other CIs as well, such as the mid-p style CIs. The mid-p CIs are not designed to guarantee coverage, but are designed to have close to the nominal coverage 'on average' over all the possible values of the parameters. The usual p-value is derived from  $\Pr[\text{see observed data or more extreme under null}]$ , while the mid p-value version comes from  $(1/2) \Pr[\text{see obs data}] + \Pr[\text{see more extreme data}]$ . Mid-p CIs come from inverting the test that uses the mid p-value instead of the usual p-value.

The delta methods create confidence intervals for two sample tests by combining one-sample estimates for survival and variance, either using the Greenwood variance (`method="standard"`), or by substituting the Greenwood variance for ones developed by Borkowf (2005) which have been shown by simulation to be less biased than Greenwood. The zero.one modifications give more reasonable intervals when the Kaplan-Meier estimate of either of the groups is 0 or 1. Unlike the melded BPCP method, we have shown the delta methods to have coverage less than nominal in some situations.

For backwards compatibility we continue to allow the `parmtime="one.minus.cdfratio"`, but it is the same as `parmtime="effcdf"`. Additionally, `parmtime="one.minus.ratio"` is not an option for `delta2samp`.

Due to the assumption that censoring occurs after events in cases where there are ties, we have an `add.eps` option that will add a pseudo-increase to all censored observations for accurate p-values and confidence intervals at a given testtime.

## Value

The functions return an object of class either "htest" if testtime is NULL, otherwise they will return an object of class "twosamp"

A list with class "htest" contains the following components:

<code>statistic</code>	estimate of S1, survival at testtime for group 1
<code>parameter</code>	estimate of S2, survival at testtime for group 2
<code>p.value</code>	p-value for the test
<code>conf.int</code>	a confidence interval for the parameter determined by <code>parmtime</code>
<code>estimate</code>	estimate of parameter determined by <code>parmtime</code> (see note)
<code>null.value</code>	the specified null hypothesized value of the parameter determined by <code>parmtime</code>
<code>alternative</code>	type of alternative with respect to the <code>null.value</code> , either 'two.sided', 'greater' or 'less'
<code>method</code>	a character string describing the test
<code>data.name</code>	a character string describing the parameter determined by <code>parmtime</code>

A list with class "twosamp" contains the following components:

<code>L</code>	left endpoint of interval
<code>Lin</code>	logical vector, include left endpoint?
<code>R</code>	right endpoint of interval

Rin	logical vector, include right endpoint?
interval	interval of survival and confidence interval as determined by L, Lin, R, Rin
g1	name of group 1 as determined by group
est_group1	one-sample survival estimate for group 1 in interval/at time point
lower_group1	one-sample lower pointwise confidence limit for group 1 in interval/at time point
upper_group1	one-sample upper pointwise confidence limit for group 1 in interval/at time point
g2	name of group 2 as determined by group
est_group2	one-sample survival estimate for group 2 in interval/at time point
lower_group2	one-sample lower pointwise confidence limit for group 2 in interval/at time point
upper_group2	one-sample upper pointwise confidence limit for group 2 in interval/at time point
beta	estimate of parameter determined by parmtime (see note)
lower	the lower limit of the confidence interval for the parameter determined by parmtime
upper	the upper limit of the confidence interval for the parameter determined by parmtime
conf.level	confidence level
p.value	p-value for the test
null.value	the specified null hypothesized value of the parameter determined by parmtime
alternative	type of alternative with respect to the null.value, either 'two.sided', 'greater' or 'less'
method	a character string describing the test

### Note

When `parmtime='ratio'` and both  $S_1=S_2=0$ , then since  $0/0$  is undefined, the estimate is set to NA. This makes sense because if the true value of  $S_1$  and  $S_2$  are extremely small, then it is very likely we will observe  $S_1=0$  and  $S_2=0$ ; however, extremely different ratios can both give a high probability of observing  $S_1=S_2=0$ . For example,  $0.001/0.00001=100$  and  $0.00001/0.001 = 1/100$  give very extreme and opposite estimates. For similar reasons, `parmtime='oddsratio'` gives NA for  $S_1=S_2=0$  or  $S_1=S_2=1$ , `parmtime='cdfratio'` gives NA for  $S_1=S_2=1$ , `parmtime='one.minus.ratio'` gives NA for  $S_1=S_2=0$ , and `parmtime='one.minus.cdfratio'` gives NA for  $S_1=S_2=1$ .

### Author(s)

Michael P. Fay

### References

- Borkowf, C. B. (2005). A simple hybrid variance estimator for the Kaplan-Meier survival function. *Statistics in Medicine* 24, 827-851.
- Fay, MP, Brittain, E, and Proschan, MA. (2013). Pointwise Confidence Intervals for a Survival Distribution with Small Samples or Heavy Censoring. *Biostatistics* 14(4): 723-736 doi: 10.1093/biostatistics/kxt016. (copy available at <http://www.niaid.nih.gov/about/organization/dcr/brb/staff/Pages/michael.aspx>).
- Fay, MP, Proschan, MA, and Brittain, E (2015) Combining One Sample Confidence Procedures for Inferences in the Two Sample Case. *Biometrics* 71:146-156.

**Examples**

```

data(leuk2)
# test difference of S(20) values
# S(20)=survival function at 20 weeks
bpcp2samp(leuk2$time,leuk2$status,leuk2$treatment,
  20,parmtpe="difference")
# test ratio of S(20) in two treatment groups,
bpcp2samp(leuk2$time,leuk2$status,leuk2$treatment,
  20,parmtpe="ratio")
# change the order of the group variable to get the other ratio
bpcp2samp(leuk2$time,leuk2$status,leuk2$treatment,20,
  parmtpe="ratio",changeGroupOrder=TRUE)
# estimate treatment effect= 1 - F(20,trt)/F(20,plac),
# where F(20)=1-S(20) = Pr(T <=20) is the
# cumulative distribution function
# Test whether treatment effect is greater than 30 pct
bpcp2samp(leuk2$time,leuk2$status,leuk2$treatment,20,
  parmtpe="one.minus.cdfratio",nullparm=0.30,
  alternative="greater",
  changeGroupOrder=FALSE)

# Output estimates and CIs for all intervals within the data
bpcp2samp(leuk2$time,leuk2$status,leuk2$treatment,testtime=NULL)

# Test delta method using Greenwood variance estimator and zero-one adjustment
delta2samp(leuk2$time,leuk2$status,leuk2$treatment,20,method="standard", zero.one.adjustment=TRUE)

```

---

bpcp2sampControl

*Control function for [bpcp2samp](#)*


---

**Description**

Call function to change any one of options, and outputs a list with all defaults except argument that you changed.

**Usage**

```

bpcp2sampControl(Delta = 0, stype = "km", eps = 10^-8,
  nmc=10^6, method="mm.mc", seed=391291)

```

**Arguments**

Delta	width of grouped confidence intervals, defaults to 0
stype	type of survival estimate, either "km" for Kaplan-Meier or "mue" for median unbiased estimator
eps	small value to make integration tractable
nmc	number of Monte Carlo replications

method	either 'mm.mc' (method of moments for one sample, meld with Monte Carlo) or 'mc.mc' (Monte Carlo for one sample and melding), see details.
seed	random number seed, if NULL do not set random number seed

### Details

We set the seed by default, so that the same data set will always give the same results. If you are doing simulations, this setting of the seed will give problems. So use seed=NULL.

For method='mm.mc' this is shorthand for calculate the method of moments for one sample, and meld together the two sampling using Monte Carlo methods; however, technically, that is only done when midp=TRUE, if midp=FALSE then the melding uses numeric integration.

### Value

A list containing the 6 arguments.

### See Also

[bpcp2samp](#)

### Examples

```
bpcp2sampControl(Delta=1)
```

---

bpcpControl	<i>Inputs for adjusting numerical calculations in bpcp</i>
-------------	--

---

### Description

Function that returns a list of arguments.

### Usage

```
bpcpControl(midpMMtol = .Machine$double.eps^0.25,
            seed=49911,
            tolerance=.Machine$double.eps^0.5)
```

### Arguments

midpMMtol	value used for tol argument in uniroot call for calculating the midp method of moments method.
seed	seed for set.seed() when using Monte Carlo method. If is.null(seed) then do not set the seed.
tolerance	lowest positive value, such that $\text{abs}(x-y) < \text{tolerance}$ treats $x$ as equal to $y$ . Used in bpcp for seeing if difference between times are equal to Delta or not.

**Details**

When doing simulations on the Monte Carlo method, set `seed=NULL`. Then the seed will not be set at each replication. The default is to set the seed to 49911, so two analyses of the same data on the same version of R will give identical results.

**Value**

A list with components named as the arguments.

---

<code>fixtdiff</code>	<i>Two sample test for Difference in Survival at Fixed Time</i>
-----------------------	---

---

**Description**

Asymptotic two sample tests for difference in survival at a fixed time, using normal approximations and transformations. See Klien, et al (2007) for details.

**Usage**

```
fixtdiff(time,status,group, testtime,
         trans=c("identity","cloglog","log"),
         varpooled=TRUE, correct=FALSE, doall=FALSE)
```

**Arguments**

<code>time</code>	time to event for each observation
<code>status</code>	status of event time, 1 is observed, 0 is right censored
<code>group</code>	group for test, should have two levels, to change order use as factor and change order of levels
<code>testtime</code>	fixed time when you want to test for a difference
<code>trans</code>	type of transformation, one of 'identity', 'cloglog' or 'log'
<code>varpooled</code>	logical, pool the variance?
<code>correct</code>	logical, do continuity correction? Continuity correction for when <code>trans='identity'</code> and <code>varpooled</code> (see Warning)
<code>doall</code>	logical, do all transformations and corrections

**Details**

This function provides p-values for the two sample tests that the survival distributions are equal at time `testtime`. The tests are asymptotically normal tests and are described in Klein, et al (2007). These functions are mostly for simulations to evaluate the melded BPCP tests, see [bpcp2samp](#) and Fay et al (2015).

**Value**

A list with the following components:

plo	one-sided p-value, alternative: $S1(\text{testtime}) > S2(\text{testtime})$
phi	one-sided p-value, alternative: $S1(\text{testtime}) < S2(\text{testtime})$
p2	two-sided p-value, $\min(1, 2 * \text{plo}, 2 * \text{phi})$

**Warning**

Continuity correction derived from the case with no censoring (see Fleiss et al 3rd edition, pp. 50-55). May not make sense when there is censoring. Use at own risk.

**Author(s)**

Michael P. Fay

**References**

Fay, MP, Proschan, MA, and Brittain, E (2015) Combining One Sample Confidence Procedures for Inferences in the Two Sample Case. *Biometrics* 71:146-156.

Fleiss, Levin, Paik (2003) *Statistical Methods for Rates and Proportions*, 3rd edition.

Klein, Logan, Harhoff, and Andersen (2007). Analyzing survival curves at a fixed point in time. *Statistics in Medicine* 26(24): 4505-4519.

**Examples**

```
data(leuk2)
# Note that since the Kaplan-Meier survival at time=35 goes to
# zero for one group, the results for the log and cloglog
# transformations are undefined
fixtdiff(leuk2$time, leuk2$status, leuk2$treatment, 35, doall=TRUE)
```

---

kmci.object

*Kaplan-Meier (Survival Curve) Confidence Interval Object*

---

**Description**

The kmci class is returned by the functions [kmciTG](#) or [kmciSW](#). The class represents a fitted survival curve with pointwise confidence intervals.

Unlike the [kmciLR](#) class, which allows for confidence intervals to change at any time point, the kmci class only has the confidence intervals change at observed failures.

Objects of this class has methods for the functions `summary`, `plot`, `lines`.

**Arguments**

time	the time points of observed failures (assumed surv and lower and upper steps that these times)
cens	time points where there is censoring but no observed failure
surv	the estimate of survival at time t+0. This is a vector.
upper	upper confidence limit for the survival curve.
lower	lower confidence limit for the survival curve.
conf.level	the level of the confidence limits, e.g., 0.95.

**Structure**

The following components must be included in a legitimate kmci object.

**See Also**

[kmciLR.object](#), [plot.kmci](#), [summary.kmci](#), [StCI.kmci](#), [median.kmci](#), [quantile.kmci](#).

---

kmciLR.object

*Kaplan-Meier (Survival Curve) Confidence Interval LR Tidy Object*

---

**Description**

The kmciLR class allows for confidence intervals to change at any time point, while the kmci class only has the confidence intervals change at observed failures.

Objects of this class has methods for the functions `summary`, `plot`.

`formula`, `data`, `nmc=0`, `alpha=.05`, `Delta=0`, `stype="km"`, `midp=FALSE`, `monotonic=NULL`, `control=bpepControl()`

**Arguments**

cens	time points where there is censoring but no observed failure
surv	the estimate of survival in the interval described by L and R. This is a vector.
upper	upper confidence limit for the survival curve in the interval described by L and R.
lower	lower confidence limit for the survival curve in the interval described by L and R.
L	vector of left ends of interval associated with lower and upper
Lin	vector of logicals, should left end of interval be included?
R	vector of right ends of interval associated with lower and upper
Rin	vector of logicals, should right end of interval be included?
Interval	character vector describing intervals
stype	character vector giving type of survival estimate, either 'km' or 'mue'
conf.level	the level of the confidence limits, e.g., 0.95.

**Structure**

The following components must be included in a legitimate kmciLR object.

**See Also**

[plot.kmciLR](#), [summary.kmciLR](#), [bpcp](#).

---

kmciLRgroup.object      *Kaplan-Meier (Survival Curve) Confidence Interval LR Group Object*

---

**Description**

The kmciLRgroup class is returned by the function [bpcpfit](#) when the plotstyle = "standard", and represents a fitted survival curve with pointwise confidence intervals. This object will contain more than one fitted survival curve with the corresponding pointwise confidence intervals based on a treatment/grouping variable.

The kmciLRgroup class allows for confidence intervals to change at any time point (similar to the [kmciLR](#) class), while the [kmci](#) class only has the confidence intervals change at observed failures.

Objects of this class has methods for the functions [summary](#), [plot](#), [print](#), [quantile](#), and [median](#).

When printed, objects of this class will display the total number of subjects, total number of events, median survival time, and the confidence limits(for the pre-specified confidence level), by treatment group if applicable.

**Arguments**

cens	time points where there is censoring but no observed failure
surv	the estimate of survival in the interval described by L and R. This is a vector.
upper	upper confidence limit for the survival curve in the interval described by L and R.
lower	lower confidence limit for the survival curve in the interval described by L and R.
L	vector of left ends of interval associated with lower and upper
Lin	vector of logicals, should left end of interval be included?
R	vector of right ends of interval associated with lower and upper
Rin	vector of logicals, should right end of interval be included?
Interval	character vector describing intervals
stype	character vector giving type of survival estimate, either 'km' or 'mue'
conf.level	the level of the confidence limits, e.g., 0.95.
num	total number of subjects at the start of that survival curve.
events	total number of events (observed failures) for that survival curve.

**Structure**

A `kmcilRgroup` object is a list of `kmcilR` objects (also lists). The length of the `kmcilRgroup` object corresponds to the number of treatment/grouping variables; each item in the list is a `kmcilR` object for the given treatment (the name of each item in the list is the name of each group). If no grouping variable is given, the output is a `kmcilR` object.

The following components must be included in each element of a legitimate `kmcilRgroup` object.

**See Also**

[plot.kmcilRgroup](#), [summary.kmcilRgroup](#), [print.kmcilRgroup](#), [quantile.kmcilRgroup](#), [median.kmcilRgroup](#), [bpcpfit](#).

---

`kmcilRtidy.object`      *Kaplan-Meier (Survival Curve) Confidence Interval LR Tidy Object*

---

**Description**

The `kmcilRtidy` class is returned by the function `bpcpfit` when the `plotstyle = "ggplot"`, and represents a fitted survival curve with pointwise confidence intervals. This object may contain more than one fitted survival curve with the corresponding pointwise confidence intervals based on a treatment/grouping variable, if one is specified in the formula of `bpcpfit`.

The `kmcilRtidy` class allows for confidence intervals to change at any time point (similar to the `kmcilR` class), while the `kmcilR` class only has the confidence intervals change at observed failures.

Objects of this class has methods for the functions `summary`, `plot`, `print`, `quantile`, and `median`.

When printed, objects of this class will display the total number of subjects, total number of events, median survival time, and the confidence limits(for the pre-specified confidence level), by treatment group if applicable.

**Arguments**

<code>cens</code>	time points where there is censoring but no observed failure
<code>surv</code>	the estimate of survival in the interval described by L and R. This is a vector.
<code>upper</code>	upper confidence limit for the survival curve in the interval described by L and R.
<code>lower</code>	lower confidence limit for the survival curve in the interval described by L and R.
<code>L</code>	vector of left ends of interval associated with lower and upper
<code>Lin</code>	vector of logicals, should left end of interval be included?
<code>R</code>	vector of right ends of interval associated with lower and upper
<code>Rin</code>	vector of logicals, should right end of interval be included?
<code>Interval</code>	character vector describing intervals
<code>stype</code>	character vector giving type of survival estimate, either 'km' or 'mue'
<code>conf.level</code>	the level of the confidence limits, e.g., 0.95.
<code>num</code>	total number of subjects at the start of that survival curve.
<code>events</code>	total number of events (observed failures) for that survival curve.

**Structure**

A `kmciLRtidy` object is a list of `kmciLR` objects (also lists). The length of the `kmciLRtidy` object corresponds to the number of treatment/grouping variables; each item in the list is a `kmciLR` object for the given treatment (the name of each item in the list is the name of each group). If no grouping variable is given, the output is a list of 1 `kmciLR` object.

The following components must be included in each element of a legitimate `kmciLRtidy` object.

**See Also**

[plot.kmciLRtidy](#), [summary.kmciLRtidy](#), [print.kmciLRtidy](#), [quantile.kmciLRtidy](#), [median.kmciLRtidy](#), [bpcpfit](#).

---

kmtestALL

*Pointwise confidence intervals for survival for right censored data.*

---

**Description**

These functions give several different methods for calculating pointwise confidence intervals for the survival distribution for right censored data. The recommended confidence intervals are the beta product ones given by `bpcp` or `bpcpfit`.

The other confidence intervals are included primarily to show that the beta product confidence procedure (using `bpcp`) has better coverage than the best alternatives. See details for a description of all the methods.

**Usage**

```
bpcp(time, status, nmc=0, alpha=.05, Delta=0, stype="km", midp=FALSE,
      monotonic=NULL, control=bpcpControl())
```

```
bpcpfit(time, ...)
```

```
## Default S3 method:
```

```
bpcpfit(time, status = NULL, group = NULL, formula=NULL, nmc=0, alpha=NULL,
        conf.level=0.95, Delta=0, stype="km", midp=FALSE,
        monotonic=NULL, control=bpcpControl(), plotstyle = "ggplot",
        data=NULL, subset=NULL, na.action=NULL, ...)
```

```
## S3 method for class 'formula'
```

```
bpcpfit(formula, data, subset, na.action, ...)
```

```
kmciBorkowf(time, status, type="log", alpha = 0.05)
```

```
kmtestBoot(time, status, tstar, pstar, M = 1000, alpha = 0.05)
```

```
kmtestConstrainBoot(time, status, tstar, pstar, M = 1000, alpha = 0.05)
```

```
kmtestConstrainBeta(time, status, tstar, pstar, alpha=.05)
```

```
kmciSW(time, status, alpha = 0.05)
```

```
kmciTG(time, status, alpha = 0.05)
```

```
kmci1TG(time, status, tstar, alpha = 0.05)
```

```
kmtestALL(time, status, t0, S0, cens=NULL, M=1000, NMC=10^5, alpha=0.05)
```

### Arguments

time	time to event or censoring
status	status vector, 1 is event, 0 is censoring (if NULL assumes all are events)
group	vector of treatments or groups, if applicable
formula	a formula object, which must have a Surv object as the response on the left of the ~ operator and, if desired, a grouping/treatment variable on the right. For a single survival curve the right hand side should be ~ 1.
data	a data frame in which to interpret the variables named in the formula.
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs.
alpha	1- conf.level
conf.level	confidence level. To be used in place of alpha starting in version 1.4
nmc	number of Monte Carlo replications from each beta distribution, nmc=0 means use method of moments for beta parameters instead
NMC	same as nmc
Delta	width of grouped confidence intervals, defaults to 0 (rarely need to change this, even with ties, see details)
stype	type of survival estimate, either "km" for Kaplan-Meier or "mue" for median unbiased estimator
midp	logical, calculate the mid-p type of interval?
monotonic	logical, force lower and upper confidence limits to be monotonic over time? If NULL: nmc=0 gives TRUE, nmc>0 gives FALSE
control	list with arguments for adjusting numeric calculation. Generally does not need to be changed. See <a href="#">bpcpControl</a>
plotstyle	which type of plot to use, "ggplot" will produce a kmciLRtidy object that will be plotted with ggplot. "standard" will produce a kmciLRgroup object (if there are groups) which will be plotted with base R. If there are no groups, "standard" will produce a kmciLR object.
tstar	time to test survival distribution
pstar	null survival distribution
M	number of bootstrap replications
t0	null hypothesis time for survival test
S0	null hypothesis value of survival at t0
cens	vector of censoring times (even those with failures before it), used for Binomial test. If NULL gives NA for binom test
type	see details
...	Extra parameters to be passed.

## Details

The recommended functions to calculate beta product confidence intervals are either `bpcp` or `bpcpfit`. The function `bpcp` has the original function arguments, while the `bpcpfit` function allows formulas similar to those used in the `survival` package, allowing separate analyses by group, and allowing easier use of `ggplot2` methods. The numerical output for the `bpcpfit` function is the same as multiple calls of `bpcp` for each group level.

The standard beta product confidence procedure (i.e., with `midp=FALSE`) will give pointwise confidence intervals for the survival function,  $S$ , with right censored data. This means that for any given  $t$ , we get confidence intervals for  $S(t)$  with the following properties. When there is no censoring or Progressive Type II censoring the BPCP guarantees central coverage (e.g., the error rate on either side of the 95 percent confidence interval is guaranteed to be less than 2.5 percent). For general independent censoring the BPCP is asymptotically equivalent to standard methods such as the normal approximation with Greenwood variance, and hence the BPCP (as with the other confidence intervals given here) has asymptotically accurate coverage of  $S(t)$  for any  $t > 0$ .

The `bpcpfit` function will produce multiple survival curves with the pointwise confidence intervals for right censored data for different treatment/grouping variables. Only a treatment/grouping variable can be specified in this function. No other covariates should be included. Data can be input as either a formula or as a default method. If the `plotstyle` argument is "ggplot" (the default), then `bpcpfit` will return a `kmciLRtidy` object that can be passed into "plot", and it will return a generic `ggplot`. If there is no group variable, a `kmciLRtidy` object will still be created. The `kmciLRtidy` object can also be passed to `tidykmciLR`, which returns a dataframe that can be passed into `ggplot` for custom plotting. If the `plotstyle` argument is "standard", then `bpcpfit` will return a `kmciLRgroup` object that can be passed into "plot", which will return a base R plot. If there is no treatment variable, a `kmciLR` object will be created.

There is also a mid-p version of the BPCP. The BPCP is derived from using the known distribution of the failure times, and acting conservatively between the failure times (see Fay, Brittain, and Proschan, 2013 for details). Instead of acting conservatively between the failure times, the `midp=TRUE` version combines the distributions for the previous failure and the future failure time (see Fay and Brittain, 2016).

For description of how `bpcp` with different values of  $\Delta$  works, see "Beta Product Confidence Intervals for Discrete Failure Times" vignette (especially Section 2.2). Note especially that confidence intervals exactly at the failure times when  $\Delta=0$  are handled differently before Version 1.3.0 than from Version  $\geq 1.3.0$ . For users not interested in details who only want to know the recommended confidence intervals on right censored data when ties are allowed, we recommend the `bpcp` function version 1.3.0 or greater using the default  $\Delta=0$  argument. That recommendation will give pointwise confidence intervals that treats ties similarly to the way that the Kaplan-Meier estimator treats ties, and hence will give confidence intervals that enclose the Kaplan-Meier estimate.

Now we describe the other methods.

In general the functions are of three naming types: `kmtestXX`, `kmci1XX` and `kmciXX`, where `XX` changes for different methods. Functions `kmtestXX` only test whether  $S(t_{\text{star}}) = p_{\text{star}}$  and return a vector of 1s for reject and 0s for fail to rejecting either of the one-sided or the two-sided hypotheses. Functions `kmci1XX` only give confidence intervals at  $S(t_{\text{star}})$ , while `kmciXX` give confidence intervals for all values of  $t$ . The standard methods calculate the confidence intervals at the observed failure times and carry them forward (e.g., `kmciTG`, `kmciSW`) and the results are objects of class `kmci`. More involved methods allow confidence intervals to change after censored objects (e.g., `kmciBorkowf`, `bpcp`) and the results are objects of class `kmciLR`.

The function `kmtestBoot` tests  $S(t^*)=p^*$  using the nonparametric bootstrap (sampling vectors of (time,status) with replacement) with the percentile method as described in Efron (1981). The function `kmtestConstrainBoot` and `kmtestConstrainBeta` tests  $S(t^*)=p^*$  using the constrained Bootstrap or constrained Beta method described in Barber and Jennison (1999).

The function `kmciITG` does a confidence interval only at  $t^*$ , while `kmciTG` does a confidence interval at all the observed event times. The method can be derived as a likelihood ratio test and is described in Thomas and Grunkemeier (1975). It has asymptotically correct coverage, which is rigorously proved in Murphy (1995). You can also think of the method as the empirical likelihood applied to the survival distribution for right censored data (see Owen, 2001, p. 144-145).

The function `kmciSW` calculates confidence intervals using Edgeworth expansions as described in Strawderman and Wells (1997). Note, Strawderman, Parzen and Wells (1997) is easier to understand than Strawderman and Wells (1997).

Borkowf (2005) creates confidence intervals for the Kaplan-Meier survival estimate for right censored data. He allows the confidence interval to change at censoring times as well as at failure times.

Four types of confidence intervals may be selected. The asymptotic normal approximation (`type="norm"`), the shifted K-M estimate with normal approximation (`type="norms"`), the log transformed normal approximation using the delta method (`type="log"`), and the log transformed normal approximation using the delta method with the shifted K-M (`type="logs"`).

The function `kmtestALL` performs hypothesis tests on all the methods except the unconstrained bootstrap method (unless  $M=0$  then it does not test the constrained bootstrap method either). The output is a matrix with three columns with a value of 1 representing either (1) rejection for two-sided test implying the estimate is greater than the null, (2) rejection for two-sided test implying the estimate less than the null, or (3) any rejection of the two-sided test. Each row represents a different test.

The `kmci`, `kmciLR`, `kmciLRtidy`, or `kmciLRgroup` classes have the following methods: `"plot"`, `"lines"`, `"summary"`, `"quantile"`, and `"median"`. Additionally, you can pull out survival and confidence intervals from these objects at specific times using `"StCI"`.

## Value

The functions return an object of class either `kmci`, `kmciLR`, `kmciLRtidy` or `kmciLRgroup` (see details).

`kmci`, `kmciLR`, `kmciLRtidy`, and `kmciLRgroup` objects are lists. `kmciLRtidy` and `kmciLRgroup` are lists of `kmciLR` objects, one element for each treatment/group. They contain elements

<code>surv</code>	survival distribution in interval/at time point
<code>lower</code>	lower pointwise confidence limit in interval/at time point
<code>upper</code>	upper pointwise confidence limit in interval/at time point
<code>time</code>	time of survival or confidence interval

while the `kmciLR` have intervals represented by the four elements

<code>L</code>	left endpoint of interval
<code>Lin</code>	logical vector, include left endpoint?
<code>R</code>	right endpoint of interval

Rin                    logical vector, include right endpoint?  
 and results from bpcp additionally have an element

betaParms            list with 4 elements of beta parameters associated with the CIs: alower, blower, aupper, bupper

kmciLR objects contained in the kmciLRgroup and kmciLRgroup have the elements

num                    total number of subjects

events                total number of events (observed failures)

### Author(s)

Michael Fay

### References

Fay, MP, Brittain, E, and Proschan, MA. (2013). Pointwise Confidence Intervals for a Survival Distribution with Small Samples or Heavy Censoring. *Biostatistics* 14 (4): 723-736. (copy available at <http://www.niaid.nih.gov/about/organization/dcr/brb/staff/Pages/michael.aspx>).

Fay, MP, and Brittain, E (2016). Finite Sample Pointwise Confidence Intervals for a Survival Distribution with Right-Censored Data. *Statistics in Medicine*.35: 2726-2740.

Barber and Jennison (1999) *Biometrics*, 55: 430-436.

Borkowf (2005) *Statistics in Medicine*, 24: 827-851.

Efron (1981) *JASA* 76:312-319.

Murphy (1995) *JASA* 90: 1399-1405.

Owen (2001) *Empirical Likelihood*. Chapman and Hall: New York.

Strawderman and Wells (1997) *JASA* 92:1356-1374.

Strawderman, Parzen and Wells (1997) *Biometrics* 53: 1399-1415.

Thomas and Grunkemeier (1975) *JASA* 70: 865-871.

### See Also

The `kmci`, `kmciLR`, `kmciLRtidy`, or `kmciLRgroup` objects have methods: "`plot`", "`lines`", "`summary`", "`quantile`", and "`median`", "`StCI`".

### Examples

```
library(bpcp)
data(leuk)
data(leuk2)

### Recommended method is bpcp
### since the data are truncated to the nearest integer
### use Delta=1 option
out<-bpcp(leuk$time,leuk$status,Delta=1)
summary(out)
```

```

median(out)
plot(out)

### bpcpfit for multiple survival curves
a <- bpcpfit(Surv(time, status)~treatment, data=leuk2)
b <- bpcpfit(Surv(time, status)~1, data=leuk2)
fitBPsurv <- bpcpfit(Surv(time, status)~treatment, data=leuk2)
fitBPsurv

bpcpfit(leuk2$time, leuk2$status, leuk2$treatment)
bpcpfit(leuk2$time, leuk2$status, plotstyle = "standard")

### Borkowf 2005 method
norm<-kmciBorkowf(leuk$time,leuk$status,type="norm")
norms<-kmciBorkowf(leuk$time,leuk$status,type="norms")
## check Table VII of Borkowf
I<-c(1,2,3,5,7,8,9,11,13,15,17,19,21,23,25,27,29,31,33)
round(data.frame(lowerNorm=norm$lower[I],
  upperNorm=norm$upper[I],lowerNormS=norms$lower[I],
  upperNorms=norms$upper[I],row.names=norm$Interval[I]),3)

### Strawderman and Wells (1997) method
swci<-kmciSW(leuk$time,leuk$status)
summary(swci)

### Thomas and Grunkemeier 1975 method
x<-kmciTG(leuk$time,leuk$status)
summary(x)
## compare to Table 1, Sample 2, of Thomas and Grunkemeier (1975)
StCI(x,c(10,20))

```

---

leuk

*Acute Leukemia data (treatment only) from Freireich et al (1963).*


---

## Description

This is only the 21 patients who received 6-mercaptopurine (6-MP). There were 21 patients who got placebo (see [leuk2](#) for complete data).

See also Borkowf (2005)

## Usage

```
data(leuk)
```

**Format**

A data frame with 21 observations on the following 2 variables.

time time in remission (in weeks)  
status event status, 1 is relapse, 0 is censored

**References**

Borkowf (2005) *Statistics in Medicine*, 24: 827-851.  
Freireich et al (1963) *Blood* 21(6):699-716.

**See Also**

[leuk2](#) for complete data.

**Examples**

```
data(leuk)
```

---

leuk2

*Acute Leukemia data from Freireich et al (1963).*

---

**Description**

In this study there were 21 pairs of subjects, and within each pair one subject received 6-mercaptopurine (6-MP) and one got placebo. The data are right censored.

See also Gehan (1965) who used the data ignoring the pairing so that he could illustrate his famous two-sample (non-paired) rank test.

**Usage**

```
data(leuk2)
```

**Format**

A data frame with 42 observations on the following variables.

time time in remission (in weeks)  
status event status, 1 is relapse, 0 is censored  
treatment treatment group: either 'placebo' or '6-MP'  
pair pair id number

**References**

Gehan (1965) *Biometrika* 52:203-223.  
Freireich et al (1963) *Blood* 21(6):699-716.

**See Also**

[leuk](#) is only the treated group

**Examples**

```
data(leuk2)
```

---

mdiffmedian.test	<i>Melded Difference in Medians Test</i>
------------------	--

---

**Description**

Tests for a difference in two medians. No assumptions about the two distributions are needed (may be discrete with ties allowed, no shift assumption is required). Uses the melded confidence interval derived from the one sample confidence intervals associated with the sign test (a version that allows for ties). Derivation of the test does not require large samples, and confidence intervals are intended to guarantee coverage regardless of sample size.

**Usage**

```
mdiffmedian.test(x1, x2, nulldiff = 0,  
                 alternative = c("two.sided", "less", "greater"),  
                 conf.level = 0.95)
```

**Arguments**

x1	vector of numeric responses from group 1
x2	vector of numeric responses from group 2
nulldiff	difference in medians under the null, median(x2)-median(x1)
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
conf.level	confidence level of the interval.

**Details**

The melded confidence interval method is a general method for combining two one-sample confidence intervals (CIs). In this function, we use the melded CI method on the two one-sample CIs from the sign test that allows for ties. This creates CIs for the difference in medians that requires very few assumptions. In particular, ties are allowed and no shift assumption is needed. For details see Fay, Proschan and Brittain (2015).

**Value**

a list of class 'htest' with elements:

statistic	median of x1
parameter	median of x2
p.value	p-value of the test
conf.int	confidence interval for the difference in medians
estimate	median(x2)-median(x1)
null.value	null hypothesis value for difference in medians
alternative	type of alternative hypothesis
method	description of test
data.name	description of input

**Note**

This function does not allow censoring. Also, there is a price for not needing large samples nor assumptions about the distributions: if you do not have enough data, your confidence intervals may be the entire real line. For example, if you have continuous data with equal sample sizes in both groups, then if you have 6 or fewer observations in each group, then the 95 percent confidence interval on the difference in medians will be  $(-\text{Inf}, \text{Inf})$ .

**Author(s)**

Michael P. Fay

**References**

Fay, MP, Proschan, MA, Brittain, E (2015). Combining One-sample confidence procedures for inference in the two-sample case. *Biometrics*. 71: 146-156.

**Examples**

```
set.seed(1)
trtA<-rpois(20,1.5)
trtB<-rpois(23,5.5)
mdiffmedian.test(trtA,trtB)
```

---

plot.kmciLR                    *Plot and lines methods for kmci, kmciLR, kmciLRtidy, and kmciLRgroup objects.*

---

## Description

Plots survival curves and/or confidence intervals. kmciLR objects from the bpcp function will plot using base R plot. If a kmciLRtidy object is created using bpcpfit (plotstyle = "ggplot"), the plot will display using ggplot. If a kmciLRgroup object is created using bpcpfit (plotstyle = "standard"), the plot will display using base R.

## Usage

```
## S3 method for class 'kmci'
plot(x, ...)

## S3 method for class 'kmciLR'
plot(x, XLAB = "time", YLAB = "Survival", YLIM = c(0, 1),
      ciLTY = 2, ciCOL = gray(0.8), mark.time = NULL,
      linetype = "both", ...)

## S3 method for class 'kmciLR'
lines(x, lty = c(2, 1), col = c(gray(0.8), gray(0)),
      linetype = "both", mark.time = NULL, ...)

## S3 method for class 'kmci'
lines(x, ...)

## S3 method for class 'kmciLRtidy'
plot(x, ...)

## S3 method for class 'kmciLRgroup'
plot(x, XLAB="Time", YLAB="Survival",
      YLIM=c(0,1), ciLTY=2, ciCOL=gray(.8), linetype="both", ...)
```

## Arguments

x	kmci, kmciLR, kmciLRtidy, or kmciLRgroup object (created by functions described in <a href="#">kmttestALL</a> )
XLAB	label for x axis
YLAB	label for y axis
YLIM	limits for y axis
ciLTY	lty (line type) for confidence intervals
ciCOL	col (color) for confidence intervals
col	vector of colors, first element used for ci second for survival curve

lty	vector of line types, first element used for ci second for survival curve
mark.time	put hash marks for censored objects (default puts marks of stype="km" but not if stype="mue")
linetype	character, which lines to draw: either 'both', 'surv' or 'ci'
...	Extra parameters to be passed. Any argument in plot.kmciLR can be passed from plot.kmci, similarly for line. Other parameters are usually graphical parameters passed to plot and segment calls within function.

### Examples

```

data(leuk)
## kmciTG creates kmci object
fitTG<-kmciTG(leuk$time,leuk$status)
plot(fitTG)
## bpcp creates kmciLR object
fitBP<-bpcp(leuk$time,leuk$status)
lines(fitBP,lwd=3,lty=1,col=gray(.5),linetype="ci")
legend(0,.2,legend=c("Kaplan-Meier","Thomas-Grunkemeier 95 pct C
I","Beta Product 95 pct CI"),
      lwd=c(1,1,3),lty=c(1,2,1),col=c(gray(0),gray(.8),gray(.5)))
data(leuk2)
## bpcpfit creates kmciLR object which is plotted with ggplot
fitBPsurv <- bpcpfit(Surv(time, status)~treatment, data=leuk2)
plot(fitBPsurv)
## this works even if no treatment variable is specified
plot(bpcpfit(Surv(time, status)~1, data=leuk2))

## if plotstyle "standard" is specified, a base R plot is produced
a <- bpcpfit(leuk2$time, leuk2$status, leuk2$treatment, plotstyle = "standard")
plot(a)

#can also create a tidy object to customize ggplot further
tidy <- tidykmciLR(fitBPsurv)
ggplot(tidy, aes(x = time, y = surv, ymin = lower, ymax = upper, col = group)) +
  geom_line(show.legend=FALSE) + geom_ribbon(alpha = .2, aes(fill=group)) +
  xlab("Time") + ylab("Survival") +
  ggtitle("K-M curves with bpcp CIs")

```

---

plot.twosamp

*Plot methods for twosamp objects.*

---

### Description

Plots one-sample survival curves and confidence intervals, paneled by group. plot.twosamp uses base R, whereas plot.twosamptidy use ggplot.

### Usage

```

## S3 method for class 'twosamp'
plot(x, ...)

```

**Arguments**

x                    twosamp object (created by function `bpcp2samp` or `delta2samp`)  
 ...                  Extra parameters to be passed. Other parameters are usually graphical parameters passed to `plot` and `segment` calls within function.

**Examples**

```
data(leuk2)
## bpcp2samp creates twosamp object
compare_leuk2<-bpcp2samp(leuk2$time,leuk2$status, leuk2$treatment)
# creates base R plot
plot(compare_leuk2)
```

---

print.kmciLRtidy            *Print A Short Summary of a kmciLRtidy, kmciLRgroup, or kmciLR Object*

---

**Description**

Print number of observations, number of events, and the median survival with confidence limits for the median of a `kmciLRtidy`, `kmciLRgroup`, or `kmciLR` object with pointwise confidence intervals. The confidence limits will match those specified in the `bpcp` or `bpcpfit` function.

**Usage**

```
## S3 method for class 'kmciLR'
print(x, ...)
## S3 method for class 'kmciLRtidy'
print(x, ...)
## S3 method for class 'kmciLRgroup'
print(x, ...)
```

**Arguments**

x                    a `kmciLRtidy`, `kmciLRgroup`, or `kmciLR` object  
 ...                  extra arguments

**Examples**

```
library(bpcp)
data(leuk2)
practice <- bpcpfit(Surv(time, status)~treatment, data=leuk2)
practice

bpcpfit(Surv(time, status)~1, data=leuk2)

bpcpfit(Surv(time, status)~1, data=leuk2, plotstyle = "standard")
bpcpfit(leuk2$time, leuk2$status, leuk2$treatment, plotstyle = "standard")
```

---

quantile.kmciLR	<i>Quantiles or Medians from kmci, kmciLR, kmciLRtidy, or kmciLRgroup objects.</i>
-----------------	--

---

### Description

Get quantiles or median with the associated confidence intervals from a kmci, kmciLR, kmciLRtidy, or kmciLRgroup object.

### Usage

```
## S3 method for class 'kmciLR'
quantile(x, probs = c(0.25, 0.5, 0.75), ...)
## S3 method for class 'kmci'
quantile(x, probs = c(0.25, 0.5, 0.75), ...)
## S3 method for class 'kmciLRtidy'
quantile(x, probs = c(0.25, 0.5, 0.75), ...)
## S3 method for class 'kmciLRgroup'
quantile(x, probs = c(0.25, 0.5, 0.75), ...)
## S3 method for class 'kmciLR'
median(x, ...)
## S3 method for class 'kmci'
median(x, ...)
## S3 method for class 'kmciLRtidy'
median(x, ...)
## S3 method for class 'kmciLRgroup'
median(x, ...)
```

### Arguments

x	a kmci, kmciLR, kmciLRtidy, or kmciLRgroup object
probs	vector of probability to calculate quantiles
...	parameters passed

### Value

A kmciLRtidy or kmciLRgroup object will produce a list of matrices.

The matrix has same number of rows as probs and 4 columns

S(q)	probs, survival estimate at quantile
q	quantile
lower	lower confidence limit of q
upper	upper confidence limit of q

**Examples**

```

data(leuk)
data(leuk2)
## kmciTG creates kmci object
fitTG<-kmciTG(leuk$time,leuk$status)
quantile(fitTG)
## bpcp creates kmciLR object
fitBP<-bpcp(leuk$time,leuk$status)
median(fitBP)

## kmciLRtidy and kmciLRgroups from bpcpfit
practice <- bpcpfit(Surv(time, status)~treatment, data=leuk2)
quantile(practice)
median(practice)

quantile(bpcpfit(leuk2$time, leuk2$status, leuk2$treatment, plotstyle = "standard"))

```

---

sclerosis

*Pilot study of treatment of severe systemic sclerosis (Nash, et al, 2007).*


---

**Description**

Severe systemic sclerosis is a serious autoimmune disease affecting multiple organs including the heart, lungs, kidney, and skin. Between 1997 and 2005, a cohort of 34 patients was enrolled in a single arm pilot study of high-dose immunosuppressive therapy and autologous hetapoietic cell transplantation

**Usage**

```
data(sclerosis)
```

**Format**

A data frame with 34 observations on the following 3 variables.

```

day  time to death or censoring, in days
year  time to death or censoring, in years (day/365.25)
status  0 is censored, 1 is event

```

**References**

Nash, R.A., McSweeney, P.A., Crofford, L.J., Abidi, M., Chen, C.S., Godwin, J.D., Gooley, T.A., Holmberg, L., Henstorf, G., LeMaistre, C.F., others (2007). "High-dose immunosuppressive therapy and autologous hematopoietic cell transplantation for severe systemic sclerosis: long-term follow-up of the US multicenter pilot study" *Blood* 110 (4): 1388-.

**Examples**

```

data(sclerosis)
plot(bpcp(sclerosis$year, sclerosis$status))

```

---

StCI	<i>Get survival and confidence interval at t from kmci, kmciLR, or survfit object</i>
------	---

---

### Description

Just picks out the survival function and confidence interval in a different way depending on the type of object.

### Usage

```
## Default S3 method:
StCI(x, tstar, afterMax = "continue", ...)
```

```
## S3 method for class 'kmciLR'
StCI(x, tstar, ...)
```

### Arguments

x	a kmci or kmciLR object
tstar	a vector of times that you want survival and CI values
afterMax	character, what to do after tmax (see details)
...	further arguments to be passed to or from methods.

### Details

Since the Kaplan-Meier estimator is undefined after the last observation if it is censored and many confidence interval methods are not defined there either, we need to explicitly define what to do. (For objects of the kmciLR class, the confidence intervals are defined over the positive real line and the afterMax is ignored.) The afterMax has four options for this: 'continue' (keep surv and ci values the same as the last calculated one), 'zero' (surv and lower go to zero, upper stays same), 'zeroNoNA' (surv and lower go to zero, upper stays same unless it is NA, then it takes on the last non-missing upper value), 'half' (surv goes to half value, lower goes to zero, upper stays same).

### Value

The function StCI returns a data frame with the following variables. (It also has an attribute: 'conf.level').

time	this is tstar
survival	survival at tstar
lower	lower confidence limit at tstar
upper	upper confidence limit at tstar

**Author(s)**

Michael Fay

**See Also**[kmci](#), [kmciLR](#)**Examples**

```
data(leuk)
## compare to table 1 of Thomas and Grunkmeier (1975)
StCI(kmciTG(leuk$time,leuk$status),c(10,20))
```

---

summary.kmciLR	<i>Summary method for kmci, kmciLR, kmciLRtidy, or kmciLRgroup object.</i>
----------------	--

---

**Description**

Creates a data frame with time (for kmci) or time interval (for kmciLR, kmciLRtidy, and kmciLRgroup), survival, lower and upper pointwise confidence intervals. For kmciLRtidy and kmciLRgroup objects, the group (treatment) variable is also included.

**Usage**

```
## S3 method for class 'kmciLR'
summary(object, ...)
## S3 method for class 'kmci'
summary(object, ...)
## S3 method for class 'kmciLRtidy'
summary(object, ...)
## S3 method for class 'kmciLRgroup'
summary(object, ...)
```

**Arguments**

object	kmci, kmciLR, kmciLRtidy, or kmciLRgroup object
...	extra arguments

**Value**

creates a data frame. See description.

**Examples**

```

data(leuk)
## kmciTG creates kmci object
fitTG<-kmciTG(leuk$time,leuk$status)
summary(fitTG)
## bpcp creates kmciLR object
fitBP<-bpcp(leuk$time,leuk$status)
summary(fitBP)
data(leuk2)
## bpcpfit creates kmciLRtidy or kmciLRgroup object
fitBPsurv <- bpcpfit(Surv(time, status)~treatment, data=leuk2)
summary(fitBPsurv)
summary(Surv(time, status)~treatment, data=leuk2, plotstyle = "standard")

```

---

summary.twosamp

*Summary method for twosamp object.*


---

**Description**

Creates a data frame with time intervals, survival estimate for each groups, beta estimates, lower and upper pointwise confidence intervals, and p-values

**Usage**

```

## S3 method for class 'twosamp'
summary(object, ...)

```

**Arguments**

object	twosamp object
...	extra arguments

**Value**

creates a data frame. See description.

**Examples**

```

data(leuk2)
## bpcp2samp creates twosamp object
compare_leuk2<-bpcp2samp(leuk2$time,leuk2$status, leuk2$treatment)
summary(compare_leuk2)

```

---

tidykmcilR	<i>Dataframe of kmcilRtidy, kmcilRgroup, or a kmcilR object.</i>
------------	--

---

**Description**

Takes a `kmcilRtidy`, `kmcilRgroup`, or a `kmcilR` object (a list) and converts it into a dataframe, which can further be used in plotting. Every two time points represents a time interval.

**Usage**

```
tidykmcilR(x)
```

**Arguments**

`x` a `kmcilRtidy`, `kmcilRgroup`, or `kmcilR` object

**Details**

creates a dataframe. See description.

**Value**

This function returns a dataframe with the following columns:

<code>time</code>	Time
<code>surv</code>	Value of survival curve at that time point
<code>lower</code>	Lower bound of the CI for the survival curve
<code>upper</code>	Upper bound of the CI for the survival curve
<code>group</code>	treatment or grouping variable (if applicable)

There are two rows per time point representing the change in either the survival function or confidence bands.

**Examples**

```
library(bpcp)
data(leuk2)
practice <- bpcpfit(Surv(time, status)~treatment, data=leuk2)

tidy <- tidykmcilR(practice)
ggplot(tidy, aes(x = time, y = surv, ymin = lower, ymax = upper, col = group)) +
  geom_line(show.legend=FALSE) + geom_ribbon(alpha = .2, aes(fill=group)) + xlab("Time") +
  ylab("Survival") + ggtitle("K-M curves with bpcp CIs")
```

twosamp.object

*Two-sample Confidence Interval Object***Description**

The twosamp class is returned by the functions `bpcp2samp` or `delta2samp`. The class represents the comparison of two survival curves at each observed event time.

Unlike the `htest` class, which compares curves at specified testtimes, the `twosamp` class compares curves at all observed event times.

Objects of this class has methods for the functions `summary` and `plot`.

**Arguments**

L	left endpoint of interval
Lin	logical vector, include left endpoint?
R	right endpoint of interval
Rin	logical vector, include right endpoint?
interval	interval of survival and confidence interval as determined by L, Lin, R, Rin
g1	name of group 1 as determined by group
est_group1	one-sample survival estimate for group 1 in interval/at time point
lower_group1	one-sample lower pointwise confidence limit for group 1 in interval/at time point
upper_group1	one-sample upper pointwise confidence limit for group 1 in interval/at time point
g2	name of group 2 as determined by group
est_group2	one-sample survival estimate for group 2 in interval/at time point
lower_group2	one-sample lower pointwise confidence limit for group 2 in interval/at time point
upper_group2	one-sample upper pointwise confidence limit for group 2 in interval/at time point
beta	estimate of parameter determined by parmtime (see note)
lower	the lower limit of the confidence interval for the parameter determined by parmtime
upper	the upper limit of the confidence interval for the parameter determined by parmtime
conf.level	confidence level
p.value	p-value for the test
null.value	the specified null hypothesized value of the parameter determined by parmtime
alternative	type of alternative with respect to the null.value, either 'two.sided', 'greater' or 'less'
method	a character string describing the test

**Structure**

The following components must be included in a legitimate twosamp object. `structure(list(L=L, Lin=Lin, R=R, Rin=Rin, interval=interval, g1=g1, est_group1 = est_g1, lower_group1=lower_g1, upper_group1=upper_g1, g2=g2, est_group2 = est_g2, lower_group2=lower_g2, upper_group2=upper_g2, beta = beta, lower = lower, upper = upper, conf.level = conf.level, p.value = p.value, null.value = nullparm, alternative = alt, method = full.method), class = c("twosamp", "list"))`

**See Also**

[plot.twosamp](#), [summary.twosamp](#) [create.twosamp](#)

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