

# Package ‘csci’

May 8, 2026

**Type** Package

**Title** Current Status Confidence Intervals

**Version** 0.9.3

**Date** 2020-12-02

**Author** Sungwook Kim

**Maintainer** Michael P. Fay <mfay@niaid.nih.gov>

**Description** Calculates pointwise confidence intervals for the cumulative distribution function of the event time for current status data, data where each individual is assessed at one time to see if they had the event or not by the assessment time.

**License** GPL-3

**Depends** R (>= 3.5.0), exactci

**NeedsCompilation** no

**Repository** CRAN

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csci-package	<i>Current Status Confidence Intervals</i>
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## Description

Calculates pointwise confidence intervals for the cumulative distribution function of the event time for current status data, data where each individual is assessed at one time to see if they had the event or not by the assessment time.

**Details**

The DESCRIPTION file:

```
Package:      csci
Type:        Package
Title:       Current Status Confidence Intervals
Version:     0.9.3
Date:       2020-12-02
Author:      Sungwook Kim
Maintainer:  Michael P. Fay <mfay@niaid.nih.gov>
Description: Calculates pointwise confidence intervals for the cumulative distribution function of the event time for current
License:     GPL-3
Depends:    R (>= 3.5.0), exactci
```

Index of help topics:

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controlCSCI	Function for control parameters for algorithms used in CSCI.
csci-package	Current Status Confidence Intervals
hepABulg	Hepatitis A Data from Bulgaria

The package only has one main function [CSCI](#) and one data set [hepABulg](#).

**Author(s)**

Sungwook Kim  
 Maintainer: Michael P. Fay <mfay@niaid.nih.gov>

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controlCSCI	<i>Function for control parameters for algorithms used in CSCI.</i>
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**Description**

Allows chainging of default parameters.

**Usage**

```
controlCSCI(power = 2/3,
  quan_p = c(0.25, 0.5, 0.75, 0.8, 0.85, 0.9, 0.95, 0.99),
  xp_hat = c(0.06402, 0.28506, 0.80694, 0.98729, 1.22756, 1.60246, 2.26916, 3.8363),
  intF = 1000)
```

**Arguments**

power	for defining $m$ in the algorithm when <code>type='VALID'</code> : $m=\text{ceiling}(n^{\text{power}})$ , where $n=\text{length}(C)$
quan_p	quantile associated with <code>xp_hat</code> , used when <code>type='LIKELIHOOD'</code>
xp_hat	estimated quantile of the distribution of the log likelihood ratio (see e.g., Table 2 of Banerjee and Wellner, 2001), used when <code>type='LIKELIHOOD'</code>
intF	number of intervals to partition the $F$ space ( $F=c(1:(\text{intF}-1)/\text{intF})$ ), used when <code>type='LIKELIHOOD'</code>

**Details**

For `power`, see Kim, et al 2020. For details on the other values, see the code for the `type='LIKELIHOOD'` algorithm and Banerjee and Wellner, 2001.

**Value**

A list of the argument values.

**References**

Banerjee, M. and J. A. Wellner (2001). Likelihood ratio tests for monotone functions. *Ann. Statist.* 29 (6), 1699-1731.

Kim, S, Fay, MP, Proschan, MA (2020). Valid and Approximately Valid Confidence Intervals for Current Status Data. (see <https://arxiv.org/abs/1805.06488>).

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CSCI

*Pointwise Confidence Intervals for Current Status Data*


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**Description**

Calculates several different methods for getting pointwise confidence intervals for current st

**Usage**

```
CSCI(C, D, times=NULL, type = c("VALID", "ABA", "LIKELIHOOD"),
      conf.level = 0.95, control=controlCSCI())
```

**Arguments**

C	a vector of assesment times
D	a vector of indicators of event at or before the assessment time
times	a vector of times, $t$ , to give the confidence interval for the event time distribution, $F(t)$ . If NULL then set to <code>sort(unique(C))</code> .
type	type of confidence interval, either "VALID", "ABA", or "LIKELIHOOD" (see details)

<code>conf.level</code>	confidence level for intervals (for <code>type="LIKELIHOOD"</code> only specific values are allowed, see note)
<code>control</code>	list with parameters for algorithms, see <code>controlCSCI</code>

### Details

The function does three types of pointwise confidence intervals for the cumulative distribution function for the event time at the times specified by `times`. When `type="VALID"` the function gives a method that guarantees that the coverage will be at least nominal, but the confidence intervals are not ensured to be monotonic over the times of interest. When `type="ABA"` the function gives an approximate method that does not guarantee coverage, but has been shown by simulation to have good coverage for smoothly changing distributions, and it does ensure monotonicity (see Kim, et al, 2020). When `type="LIKELIHOOD"` the function gives an asymptotic likelihood ratio test-based confidence interval that does not guarantee coverage (Banerjee and Wellner, 2001).

### Value

A list with 2 objects:

<code>ciTable_all</code>	data.frame with NPML and associated confidence intervals for all possible time values (not output for <code>type='LIKELIHOOD'</code> )
<code>ciTable_times</code>	data.frame with NPML and associated confidence intervals for the values of <code>'times'</code> argument

### Note

Because the likelihood ratio test goes to a non-standard asymptotic distribution, we do not calculate quantiles from that distribution, but take them from Table 2 of Banerjee and Wellner (2001). Because of this, when `type="LIKELIHOOD"` then `conf.level` must be one of 0.25,0.50,0.75,0.80,0.85,0.90,0.95, or 0.99.

### Author(s)

Sungwook Kim

### References

- Banerjee, M. and J. A. Wellner (2001). Likelihood ratio tests for monotone functions. *Ann. Statist.* 29 (6), 1699-1731.
- Kim, S, Fay, MP, Proschan, MA (2020). Valid and Approximately Valid Confidence Intervals for Current Status Data. (see <https://arxiv.org/abs/1805.06488>).

### Examples

```
data(hepABulg)
CSCI(C=hepABulg$age,D=hepABulg$testPos,type="VALID")
```

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`hepABulg`*Hepatitis A Data from Bulgaria*

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**Description**

Hepatitis A data from Bulgaria, collected from school-children and blood donors by Prof. G. Frosner, Munich (from Keiding, 1991, Table 1).

**Usage**

```
data("hepABulg")
```

**Format**

A data frame with 850 observations on the following 2 variables.

`age` a numeric vector

`testPos` a numeric vector, Hepatitis A positive=1, or not=0

**Details**

Each row in the data frame represents an individual and the age tested in years and the results of the hepatitis A test (1=positive, 0=negative). Ages of the individuals range from 1 to 86 years old.

**Source**

Keiding, N (1991). Age-specific Incidence and Prevalence: a Statistical Perspective. JRSS A 154(3): 371-412 (Table 2).

**Examples**

```
data(hepABulg)
head(hepABulg)
```

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