<pre>R&gt; library("interval") R&gt; data("bcos", package = "i R&gt; head(bcos)</pre>	Interval")  STAT 222 Wec	lc 8 ng (mash-up)
left right treatment 1 45 Inf Rad 2 6 10 Rad 3 0 7 Rad 4 46 Inf Rad 5 46 Inf Rad 6 7 16 Rad	We demonstrate the two main functions in interval, ich used interval-censored breast cosmesis data set of Finkels from a study of two groups of breast cancer patients, twith chemotherapy (treatment = "RadChem") and those (treatment = "Rad"). The response is time (in mon retraction, and the data are interval-censored between was observed (left) and the first visit when the event was was not observed). The following provides the first few	stein and Wolfe (1985). The data are those treated with radiation therapy e treated with radiation therapy alone (ths) until the appearance of breast the last clinic visit before the event sobserved (right) (or Inf if the event
	or each treatment group in the breast cosmesis data sepa-	From Fay + Shaw 555 2010 36(2)
	right, type = "interval2") ~ treatment,	(linked on page)
treatment=Rad:     Interval Probability 1    (4,5]	data. The default method is the permutation test, a large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test, and large we automatically get the version based on the permutation test. The permutation test of the permutation test, and large we are all test of the permutation test. The permutation test of the permutation test, and large we are all test of the permutation test. The permutation test of the permutation test of the permutation test. The permutation test of the permutation test of the permutation test. The permutation test of the permutat	permutational central limit theorem:  "interval2") ~ treatment,  permutation form),  by treatment  s not equal
Tansformed Distribution  Transformed Distribution  Transformed Distribution  Transformed Distribution	treatment=Rad treatment=RadChem  80  90  70  80  80  80  80  80  80  80  80  8	

0.2

0.0

treatment=Rad

treatment=RadChem

Figure 2: Complementary log-log transformation of distribution from breast cosmesis used. If parallel then proportional hazards is a good model.

time

```
> biocLite("Icens")
Installing package(s) 'Icens'
package 'Icens' successfully unpacked and MD5 sums checked
> library(Icens) > library(interval)
Loading required package: MLEcens
> data(bcos)
> head(bcos)
                             > tail(bcos)
                                left right treatment
  left right treatment
    45
         Inf
                   Rad
                             89
                                  18
                                        24
                                             RadChem
2
     6
          10
                   Rad
                             90
                                  16
                                        60
                                             RadChem
3
     Λ
          7
                   Rad
                             91
                                  35
                                        39
                                             RadChem
4
    46
         Inf
                             92
                                  21
                                       Inf
                                             RadChem
                   Rad
5
                             93
                                        20
                                              RadChem
    46
         Inf
                   Rad
                                  11
6
     7
          16
                   Rad
                             94
                                  48
                                       Inf
                                              RadChem
> fit<-icfit(Surv(left,right,type="interval2")~treatment, data=bcos)</pre>
   summary(fit)
treatment=Rad:
                                          treatment=RadChem:
  Interval Probability
                                              Interval Probability
1
     (4,5]
                0.0463
                                           1
                                                 (4,5]
                                                            0.0433
2
     (6,7]
                0.0334
                                          2
                                                 (5,8]
                                                            0.0433
3
     (7,8]
                0.0887
                                          3
                                               (11, 12]
                                                            0.0692
  (11, 12)
                0.0708
                                           4
                                                            0.1454
                                               (16,17)
5
  (24, 25]
                0.0926
                                          5
                                                            0.1411
                                               (18, 19]
6
  (33,34]
                0.0818
                                          6
                                                            0.1157
                                               (19,20]
7
   (38,40]
                0.1209
                                          7
                                                            0.0999
                                               (24, 25)
                0.4656
                                          8
                                                            0.0709
   (46,48]
                                               (30,31]
                                          9
                                               (35,36)
                                                            0.1608
                                          10
                                               (44,48]
                                                            0.0552
                                           11
                                               (48,60]
                                                            0.0552
> plot(fit) #shading or not (RadChem bad)
> plot(fit, dtype = "link") #does cloglog, Fig 2
> test<-ictest(Surv(left,right,type="interval2")~treatment,data=bcos)</pre>
> test
        Asymptotic Logrank two-sample test (permutation form), Sun's scores
data: Surv(left, right, type = "interval2") by treatment
Z = -2.6684, p-value = 0.007622
alternative hypothesis: survival distributions not equal
                   n Score Statistic*
                             -9.141846
treatment=Rad
                   46
                              9.141846
treatment=RadChem 48
* like Obs-Exp, positive implies earlier failures than expected
> ictest(Surv(left,right,type="interval2")~treatment,data=bcos, scores="wmw", exact=TRU
        Exact Wilcoxon two-sample test (permutation form)
data: Surv(left, right, type = "interval2") by treatment
p-value = 0.026
alternative hypothesis: survival distributions not equal
                   n Score Statistic*
treatment=Rad
                            -5.656724
treatment=RadChem 48
                              5.656724
* like Obs-Exp, positive implies earlier failures than expected
p-value estimated from 999 Monte Carlo replications
99 percent confidence interval on p-value:
 0.009926283 0.048044749
```

> source("http://bioconductor.org/biocLite.R")