

# Package ‘emplik2’

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**Title** Empirical Likelihood Ratio Test for Two Samples with Censored Data

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**Depends** R (>= 2.15.0)

**Imports** stats

**Description** Calculates the p-value for a mean-type hypothesis (or multiple mean-type hypotheses) based on two samples with censored data.

**License** GPL (>= 2)

**NeedsCompilation** no

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e12.cen.EMm

*Computes p-value for multiple mean-type hypotheses, based on two independent samples that may contain censored data.*


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### Description

This function uses the EM algorithm to calculate a maximized empirical likelihood ratio for a set of  $p$  hypotheses as follows:

$$H_o : E(g(x, y) - mean) = 0$$

where  $E$  indicates expected value;  $g(x, y)$  is a vector of user-defined functions  $g_1(x, y), \dots, g_p(x, y)$ ; and  $mean$  is a vector of  $p$  hypothesized values of  $E(g(x, y))$ . The two samples  $x$  and  $y$  are assumed independent. They may be uncensored, right-censored, left-censored, or left-and-right (“doubly”) censored. A p-value for  $H_o$  is also calculated, based on the assumption that  $-2 \cdot \log(\text{empirical likelihood ratio})$  is asymptotically distributed as  $\text{chisq}(p)$ .

### Usage

```
e12.cen.EMm(x, dx, y, dy, p, H, xc=1:length(x), yc=1:length(y),
  mean, maxit=10)
```

### Arguments

x	a vector of the data for the first sample
dx	a vector of the censoring indicators for x: 0=right-censored, 1=uncensored, 2=left-censored
y	a vector of the data for the second sample
dy	a vector of the censoring indicators for y: 0=right-censored, 1=uncensored, 2=left-censored
p	the number of hypotheses
H	a matrix defined as $H = [H_1, H_2, \dots, H_p]$ , where $H_k = [g_k(x_i, y_j) - mu_k], k = 1, \dots, p$
xc	a vector containing the indices of the x datapoints
yc	a vector containing the indices of the y datapoints
mean	the hypothesized value of $E(g(x, y))$
maxit	a positive integer used to control the maximum number of iterations of the EM algorithm; default is 10

### Details

The value of  $mean_k$  should be chosen between the maximum and minimum values of  $g_k(x_i, y_j)$ ; otherwise there may be no distributions for  $x$  and  $y$  that will satisfy  $H_o$ . If  $mean_k$  is inside this interval, but the convergence is still not satisfactory, then the value of  $mean_k$  should be moved closer to the NPMLE for  $E(g_k(x, y))$ . (The NPMLE itself should always be a feasible value for  $mean_k$ .)

**Value**

e12.cen.EMm returns a list of values as follows:

xd1	a vector of unique, uncensored $x$ -values in ascending order
yd1	a vector of unique, uncensored $y$ -values in ascending order
temp3	a list of values returned by the e12.test.wtm function (which is called by e12.cen.EMm)
mean	the hypothesized value of $E(g(x, y))$
NPMLE	a non-parametric-maximum-likelihood-estimator vector of $E(g(x, y))$
logel00	the log of the unconstrained empirical likelihood
logel	the log of the constrained empirical likelihood
"-2LLR"	-2*(log-likelihood-ratio) for the $p$ simultaneous hypotheses
Pval	the $p$ -value for the $p$ simultaneous hypotheses, equal to $1 - \text{pchisq}(-2LLR, \text{df} = p)$
logvec	the vector of successive values of logel computed by the EM algorithm (should converge toward a fixed value)
sum_muvec	sum of the probability jumps for the uncensored $x$ -values, should be 1
sum_nuvec	sum of the probability jumps for the uncensored $y$ -values, should be 1

**Author(s)**

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**References**

- Barton, W. (2009). PhD dissertation at University of Kentucky, estimated completion Dec. 2009.
- Chang, M. and Yang, G. (1987). "Strong Consistency of a Nonparametric Estimator of the Survival Function with Doubly Censored Data." *Ann. Stat.*, 15, pp. 1536-1547.
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- Zhou, M. (2005). "Empirical likelihood ratio with arbitrarily censored/truncated data by EM algorithm." *J. Comput. Graph. Stat.*, 14, pp. 643-656.
- Zhou, M. (2009) emplik package on CRAN website. Dr. Zhou is my PhD advisor at the University of Kentucky. My e12.cen.EMm function extends Dr. Zhou's e1.cen.EM2 function from one-sample to two-samples.

**Examples**

```

x<-c(10, 80, 209, 273, 279, 324, 391, 415, 566, 85, 852, 881, 895, 954, 1101, 1133,
1337, 1393, 1408, 1444, 1513, 1585, 1669, 1823, 1941)
dx<-c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0)
y<-c(21, 38, 39, 51, 77, 185, 240, 289, 524, 610, 612, 677, 798, 881, 899, 946, 1010,
1074, 1147, 1154, 1199, 1269, 1329, 1484, 1493, 1559, 1602, 1684, 1900, 1952)
dy<-c(1, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0)
nx<-length(x)
ny<-length(y)
xc<-1:nx
yc<-1:ny
wx<-rep(1,nx)
wy<-rep(1,ny)
maxit<-10
mean=c(0.5,0.5)
p<-2
H1<-matrix(NA,nrow=nx,ncol=ny)
H2<-matrix(NA,nrow=nx,ncol=ny)
for (i in 1:nx) {
  for (j in 1:ny) {
    H1[i,j]<-(x[i]>y[j])
    H2[i,j]<-(x[i]>1060) } }
H=matrix(c(H1,H2),nrow=nx,ncol=p*ny)

# Ho1: X is stochastically equal to Y
# Ho2: mean of X equals mean of Y

eI2.cen.EMm(x, dx, y, dy, p, H, xc=1:length(x), yc=1:length(y),
  mean, maxit=10)

# Result: Pval is 0.6310234, so we cannot with 95 percent confidence reject the two
# simultaneous hypotheses Ho1 and Ho2

```

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eI2.cen.EMs

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*Computes p-value for a single mean-type hypothesis, based on two independent samples that may contain censored data.*


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**Description**

This function uses the EM algorithm to calculate a maximized empirical likelihood ratio for the hypothesis

$$H_o : E(g(x, y) - mean) = 0$$

where  $E$  indicates expected value;  $g(x, y)$  is a user-defined function of  $x$  and  $y$ ; and  $mean$  is the hypothesized value of  $E(g(x, y))$ . The samples  $x$  and  $y$  are assumed independent. They may be uncensored, right-censored, left-censored, or left-and-right (“doubly”) censored. A p-value for  $H_o$  is also calculated, based on the assumption that  $-2*\log(\text{empirical likelihood ratio})$  is approximately distributed as  $\text{chisq}(1)$ .

**Usage**

```
e12.cen.EMs(x,dx,y,dy,fun=function(x,y){x>=y}, mean=0.5, maxit=25)
```

**Arguments**

x	a vector of the data for the first sample
dx	a vector of the censoring indicators for x: 0=right-censored, 1=uncensored, 2=left-censored
y	a vector of the data for the second sample
dy	a vector of the censoring indicators for y: 0=right-censored, 1=uncensored, 2=left-censored
fun	a user-defined, continuous-weight-function $g(x, y)$ used to define the mean in the hypothesis $H_o$ . The default is <code>fun=function(x,y){x&gt;=y}</code> .
mean	the hypothesized value of $E(g(x, y))$ ; default is 0.5
maxit	a positive integer used to set the number of iterations of the EM algorithm; default is 25

**Details**

The value of *mean* should be chosen between the maximum and minimum values of  $g(x_i, y_j)$ ; otherwise there may be no distributions for  $x$  and  $y$  that will satisfy  $H_o$ . If *mean* is inside this interval, but the convergence is still not satisfactory, then the value of *mean* should be moved closer to the NPMLLE for  $E(g(x, y))$ . (The NPMLLE itself should always be a feasible value for *mean*.)

**Value**

e12.cen.EMs returns a list of values as follows:

xd1	a vector of the unique, uncensored $x$ -values in ascending order
yd1	a vector of the unique, uncensored $y$ -values in ascending order
temp3	a list of values returned by the <code>e12.test.wts</code> function (which is called by <code>e12.cen.EMs</code> )
mean	the hypothesized value of $E(g(x, y))$
funNPMLLE	the non-parametric-maximum-likelihood-estimator of $E(g(x, y))$
logel00	the log of the unconstrained empirical likelihood
logel	the log of the constrained empirical likelihood
"-2LLR"	$-2*(\logel - \logel00)$
Pval	the estimated p-value for $H_o$ , computed as $1 - \text{pchisq}(-2LLR, \text{df} = 1)$
logvec	the vector of successive values of <code>logel</code> computed by the EM algorithm (should converge toward a fixed value)
sum_muvec	sum of the probability jumps for the uncensored $x$ -values, should be 1
sum_nuvec	sum of the probability jumps for the uncensored $y$ -values, should be 1
constraint	the realized value of $\sum_{i=1}^n \sum_{j=1}^m (g(x_i, y_j) - \text{mean}) \mu_i \nu_j$ , where $\mu_i$ and $\nu_j$ are the probability jumps at $x_i$ and $y_j$ , respectively, that maximize the empirical likelihood ratio. The value of <code>constraint</code> should be close to 0.

**Author(s)**

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**References**

- Barton, W. (2009). PhD dissertation at University of Kentucky, estimated completion Dec. 2009.
- Chang, M. and Yang, G. (1987). "Strong Consistency of a Nonparametric Estimator of the Survival Function with Doubly Censored Data." *Ann. Stat.*, 15, pp. 1536-1547.
- Dempster, A., Laird, N., and Rubin, D. (1977). "Maximum Likelihood from Incomplete Data via the EM Algorithm." *J. Roy. Statist. Soc., Series B*, 39, pp.1-38.
- Gomez, G., Julia, O., and Utzet, F. (1992). "Survival Analysis for Left-Censored Data." In Klein, J. and Goel, P. (ed.), *Survival Analysis: State of the Art*. Kluwer Academic Publishers, Boston, pp. 269-288.
- Li, G. (1995). "Nonparametric Likelihood Ratio Estimation of Probabilities for Truncated Data." *J. Amer. Statist. Assoc.*, 90, pp. 997-1003.
- Owen, A.B. (2001). *Empirical Likelihood*. Chapman and Hall/CRC, Boca Raton, pp.223-227.
- Turnbull, B. (1976). "The Empirical Distribution Function with Arbitrarily Grouped, Censored and Truncated Data." *J. Roy. Statist. Soc., Series B*, 38, pp. 290-295.
- Zhou, M. (2005). "Empirical likelihood ratio with arbitrarily censored/truncated data by EM algorithm." *J. Comput. Graph. Stat.*, 14, pp. 643-656.
- Zhou, M. (2009) emplik package on CRAN website. Dr. Zhou is my PhD advisor at the University of Kentucky. My e12.cen.EMs function extends Dr. Zhou's e1.cen.EM function from one-sample to two-samples.

**Examples**

```
x<-c(10,80,209,273,279,324,391,415,566,785,852,881,895,954,1101,
1133,1337,1393,1408,1444,1513,1585,1669,1823,1941)
dx<-c(1,2,1,1,1,1,1,2,1,1,1,1,1,1,0,0,1,0,0,0,0,1,1,0)
y<-c(21,38,39,51,77,185,240,289,524,610,612,677,798,881,899,946,
1010,1074,1147,1154,1199,1269,1329,1484,1493,1559,1602,1684,1900,1952)
dy<-c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,1,1,1,0,0,0,0,0,1,0,0,0)

# Ho1: X is stochastically equal to Y
e12.cen.EMs(x, dx, y, dy, fun=function(x,y){x>=y}, mean=0.5, maxit=25)
# Result: Pval = 0.7090658, so we cannot with 95 percent confidence reject Ho1

# Ho2: mean of X equals mean of Y
e12.cen.EMs(x, dx, y, dy, fun=function(x,y){x-y}, mean=0.5, maxit=25)
# Result: Pval = 0.9695593, so we cannot with 95 percent confidence reject Ho2
```

e12.test.wtm

Computes maximum-likelihood probability jumps for multiple mean-type hypotheses, based on two independent uncensored samples

### Description

This function computes the maximum-likelihood probability jumps for multiple mean-type hypotheses, based on two samples that are independent, uncensored, and weighted. The target function for the maximization is the constrained log(empirical likelihood) which can be expressed as,

$$\sum_{dx_i=1} wx_i \log \mu_i + \sum_{dy_j=1} wy_j \log \nu_j - \eta(1 - \sum_{dx_i=1} \mu_i) - \delta(1 - \sum_{dy_j=1} \nu_j) - \lambda(\mu^T H_1 \nu, \dots, \mu^T H_p \nu)^T$$

where the variables are defined as follows:

$x$  is a vector of uncensored data for the first sample

$y$  is a vector of uncensored data for the second sample

$wx$  is a vector of estimated weights for the first sample

$wy$  is a vector of estimated weights for the second sample

$\mu$  is a vector of estimated probability jumps for the first sample

$\nu$  is a vector of estimated probability jumps for the second sample

$H_k = [g_k(x_i, y_j) - mean_k]$ ,  $k = 1, \dots, p$ , where  $g_k(x, y)$  is a user-chosen function

$H = [H_1, \dots, H_p]$  (used as argument in e1.cen.EMM function, which calls e12.test.wtm)

$mean$  is a vector of length  $p$  of hypothesized means, such that  $mean_k$  is the hypothesized value of  $E(g_k(x, y))$

$E$  indicates "expected value"

### Usage

```
e12.test.wtm(xd1,yd1,wxd1new, wyd1new, muvec, nuvec, Hu, Hmu, Hnu, p, mean, maxit=10)
```

### Arguments

xd1	a vector of uncensored data for the first sample
yd1	a vector of uncensored data for the second sample
wxd1new	a vector of estimated weights for xd1
wyd1new	a vector of estimated weights for yd1
muvec	a vector of estimated probability jumps for xd1
nuvec	a vector of estimated probability jumps for yd1
Hu	$H_u = [H_1 - [mean_1], \dots, H_p - [mean_p]]$ , $dx_i = 1, dy_j = 1$
Hmu	a matrix, whose calculation is shown in the example below
Hnu	a matrix, whose calculation is shown in the example below

p	the number of hypotheses
mean	a vector of hypothesized values of $E(g_k(u, v)), k = 1, \dots, p$
maxit	a positive integer used to control the maximum number of iterations in the Newton-Raphson algorithm; default is 10

### Details

This function is called by `e12.cen.EMm`. It is listed here because the user may find it useful elsewhere.

The value of  $mean_k$  should be chosen between the maximum and minimum values of  $g_k(xd1_i, yd1_j)$ ; otherwise there may be no distributions for  $xd1$  and  $yd1$  that will satisfy the mean-type hypothesis. If  $mean_k$  is inside this interval, but the convergence is still not satisfactory, then the value of  $mean_k$  should be moved closer to the NPMLE for  $E(g(xd1, yd1))$ . (The NPMLE itself should always be a feasible value for  $mean_k$ .) The calculations for this function are derived in Owen (2001).

### Value

`e12.test.wtm` returns a list of values as follows:

constmat	a matrix of row vectors, where the $k$ th row vector holds successive values of $\mu^T H_k \nu, k = 1, \dots, p$ , generated by the Newton-Raphson algorithm
lam	the vector of Lagrangian multipliers used in the calculations
muvec1	the vector of probability jumps for the first sample that maximize the weighted empirical likelihood
nuvec1	the vector of probability jumps for the second sample that maximize the weighted empirical likelihood
mean	the vector of hypothesized means

### Author(s)

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### References

Owen, A.B. (2001). Empirical Likelihood. Chapman and Hall/CRC, Boca Raton, pp.223-227.

### Examples

```
#Ho1: P(X>Y) = 0.5
#Ho2: P(X>1060) = 0.5
#g1(x) = I[x > y]
#g2(y) = I[x > 1060]

mean<-c(0.5,0.5)
p<-2
```



```

xd1<-c(10,85,209,273,279,324,391,566,852,881,895,954,1101,1393,1669,1823,1941)
nx1=length(xd1)
yd1<-c(21,38,39,51,77,185,524,610,612,677,798,899,946,1010,1074,1147,1154,1329,1484,1602,1952)
ny1=length(yd1)

wxd1new<-c(2.267983, 1.123600, 1.121683, 1.121683, 1.121683, 1.121683, 1.121683,
  1.000000, 1.000000, 1.000000, 1.000000, 1.000000, 1.000000, 1.261740, 2.912753,
  2.912753, 2.912753)
muvec<-c(0.08835785, 0.04075290, 0.04012084, 0.04012084, 0.04012084, 0.04012084,
  0.04012084, 0.03538020, 0.03389263, 0.03389263, 0.03389263, 0.03322693, 0.04901516,
  0.05902008, 0.13065491, 0.13065491, 0.13065491)

wyd1new<-c(1.431653, 1.431653, 1.431653, 1.431653, 1.431653, 1.438453, 1.079955, 1.080832,
  1.080832, 1.080832, 1.080832, 1.000000, 1.000000, 1.000000, 1.000000, 1.000000,
  1.222883, 1.227865, 1.739636, 5.809616)
nuvec<-c(0.04249966, 0.04249966, 0.04249966, 0.04249966, 0.04249966, 0.04316922, 0.03425722,
  0.03463312, 0.03463312, 0.03463312, 0.03463312, 0.03300598, 0.03300598, 0.03333333,
  0.03333333, 0.03382827, 0.03382827, 0.04136800, 0.04229270, 0.05992020, 0.22762676)

H1u<-matrix(NA,nrow=nx1,ncol=ny1)
H2u<-matrix(NA,nrow=nx1,ncol=ny1)
for (i in 1:nx1) {
  for (j in 1:ny1) {
    H1u[i,j]<-(xd1[i]>yd1[j])
    H2u[i,j]<-(xd1[i]>1060) } }
Hu=matrix(c(H1u,H2u),nrow=nx1,ncol=p*ny1)
for (k in 1:p) {
  M1 <- matrix(mean[k], nrow=nx1, ncol=ny1)
  Hu[,((k-1)*ny1+1):(k*ny1)] <- Hu[,((k-1)*ny1+1):(k*ny1)] - M1}
Hmu <- matrix(NA,nrow=p, ncol=ny1*nx1)
Hnu <- matrix(NA,nrow=p, ncol=ny1*nx1)
for (i in 1:p) {
  for (k in 1:nx1) {
    Hmu[i, ((k-1)*ny1+1):(k*ny1)] <- Hu[k,((i-1)*ny1+1):(i*ny1)] } }
for (i in 1:p) {
  for (k in 1:ny1) {
    Hnu[i,((k-1)*nx1+1):(k*nx1)] <- Hu[(1:nx1),(i-1)*ny1+k]} }

eI2.test.wtm(xd1,yd1,wxd1new, wyd1new, muvec, nuvec, Hu, Hmu,
  Hnu, p, mean, maxit=10)

#muvec1
# [1] 0.08835789 0.04075290 0.04012083 0.04012083 0.04012083 0.04012083 0.04012083
# [8] 0.03538021 0.03389264 0.03389264 0.03389264 0.03322693 0.04901513 0.05902002
# [15] 0.13065495 0.13065495 0.13065495

#nuvec1
# [1] 0.04249967 0.04249967 0.04249967 0.04249967 0.04249967 0.04316920 0.03425722
# [8] 0.03463310 0.03463310 0.03463310 0.03463310 0.03300597 0.03300597 0.03333333
# [15] 0.03333333 0.03382827 0.03382827 0.04136801 0.04229269 0.05992018 0.22762677

# $lam

```

```
#      [,1]      [,2]
# [1,] 8.9549 -10.29119
```

---

e12.test.wts

*Computes maximum-likelihood probability jumps for a single mean-type hypothesis, based on two independent uncensored samples*


---

### Description

This function computes the maximum-likelihood probability jumps for a single mean-type hypothesis, based on two samples that are independent, uncensored, and weighted. The target function for the maximization is the constrained log(empirical likelihood) which can be expressed as,

$$\sum_{dx_i=1} wx_i \log \mu_i + \sum_{dy_j=1} wy_j \log \nu_j - \eta \left(1 - \sum_{dx_i=1} \mu_i\right) - \delta \left(1 - \sum_{dy_j=1} \nu_j\right) - \lambda \sum_{dx_i=1} \sum_{dy_j=1} (g(x_i, y_j) - mean) \mu_i \nu_j$$

where the variables are defined as follows:

$x$  is a vector of data for the first sample

$y$  is a vector of data for the second sample

$wx$  is a vector of estimated weights for the first sample

$wy$  is a vector of estimated weights for the second sample

$\mu$  is a vector of estimated probability jumps for the first sample

$\nu$  is a vector of estimated probability jumps for the second sample

### Usage

```
e12.test.wts(u, v, wu, wv, mu0, nu0, indicmat, mean)
```

### Arguments

<code>u</code>	a vector of uncensored data for the first sample
<code>v</code>	a vector of uncensored data for the second sample
<code>wu</code>	a vector of estimated weights for <code>u</code>
<code>wv</code>	a vector of estimated weights for <code>v</code>
<code>mu0</code>	a vector of estimated probability jumps for <code>u</code>
<code>nu0</code>	a vector of estimated probability jumps for <code>v</code>
<code>indicmat</code>	a matrix $[g(u_i, v_j) - mean]$ where $g(u, v)$ is a user-chosen function
<code>mean</code>	a hypothesized value of $E(g(u, v))$ , where $E$ indicates “expected value.”

**Details**

This function is called by e12.cen.EMs. It is listed here because the user may find it useful elsewhere.

The value of *mean* should be chosen between the maximum and minimum values of  $(u_i, v_j)$ ; otherwise there may be no distributions for  $u$  and  $v$  that will satisfy the mean-type hypothesis. If *mean* is inside this interval, but the convergence is still not satisfactory, then the value of *mean* should be moved closer to the NPMLE for  $E(g(u, v))$ . (The NPMLE itself should always be a feasible value for *mean*.) The calculations for this function are derived in Owen (2001).

**Value**

e12.test.wts returns a list of values as follows:

u	the vector of uncensored data for the first sample
wu	the vector of weights for $u$
jumpu	the vector of probability jumps for $u$ that maximize the weighted empirical likelihood
v	the vector of uncensored data for the second sample
wv	the vector of weights for $v$
jumpv	the vector of probability jumps for $v$ that maximize the weighted empirical likelihood
lam	the value of the Lagrangian multiplier found by the calculations

**Author(s)**

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**References**

Owen, A.B. (2001). Empirical Likelihood. Chapman and Hall/CRC, Boca Raton, pp.223-227.

**Examples**

```
u<-c(10, 209, 273, 279, 324, 391, 566, 785)
v<-c(21, 38, 39, 51, 77, 185, 240, 289, 524)
wu<-c(2.442931, 1.122365, 1.113239, 1.113239, 1.104113, 1.104113, 1.000000, 1.000000)
wv<-c( 1, 1, 1, 1, 1, 1, 1, 1, 1)
mu0<-c(0.3774461, 0.1042739, 0.09649724, 0.09649724, 0.08872055, 0.08872055, 0.0739222, 0.0739222)
nu0<-c(0.1013718, 0.1013718, 0.1013718, 0.1013718, 0.1013718, 0.1013718, 0.1095413, 0.1287447,
  0.1534831)
mean<-0.5

#let fun=function(x,y){x>=y}
indicmat<-matrix(nrow=8,ncol=9,c(
-0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,
-0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,
-0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,
```

```
-0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,  
-0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,  
-0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,  
-0.5, -0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5,  
-0.5, -0.5, -0.5, -0.5, 0.5, 0.5, 0.5, 0.5,  
-0.5, -0.5, -0.5, -0.5, -0.5, -0.5, 0.5, 0.5))  
e12.test.wts(u,v,wu,wv,mu0,nu0,indicmat,mean)  
  
# jumpu  
# [1] 0.3774461, 0.1042739, 0.09649724, 0.09649724, 0.08872055, 0.08872055, 0.0739222, 0.0739222  
  
# jumpv  
# [1] 0.1013718, 0.1013718, 0.1013718, 0.1013718, 0.1013718, 0.1013718, 0.1095413, 0.1287447,  
# [9] 0.1534831  
  
# lam  
# [1] 7.055471
```

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