Package 'MRHawkes'

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Type Package

Title Multivariate Renewal Hawkes Process

Version 1.0

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Maintainer Tom Stindl <t.stindl@unsw.edu.au>

Description Simulate a (bivariate) multivariate renewal Hawkes (MRHawkes)
self-exciting process, with given immigrant hazard rate functions and
offspring density function. Calculate the likelihood of a MRHawkes process
with given hazard rate functions and offspring density function for an
(increasing) sequence of event times. Calculate the Rosenblatt residuals of the
event times. Predict future event times based on observed event times up to a
given time. For details see Stindl and Chen (2018) <doi:10.1016/j.csda.2018.01.021>.

License GPL (>= 2)

Depends IHSEP, stats

NeedsCompilation no

Repository CRAN

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MRHawkes-package   *Multivariate Renewal Hawkes Process*

Description

Simulate the (bivariate) multivariate renewal Hawkes (MRHawkes) process with a given distribution for the two waiting times between immigrants, given offspring density functions, and also the branching ratios. Calculation of the likelihood of a MRHawkes process model with a given sequence of (distinct) event times and labels up to a censoring time. Calculate the Rosenblatt residuals of fitting an MRHawkes process model to a sequence of event times and labels. Calculate the (filtering) distribution of the index of the most recent immigrant. Predict the time of the next event since the censoring time. Predict event times from the censoring time to a future time point.

Details

The DESCRIPTION file:

Package:	MRHawkes
Type:	Package
Title:	Multivariate Renewal Hawkes Process
Version:	1.0
Date:	2018-08-15
Author:	Tom Stindl and Feng Chen
Maintainer:	Tom Stindl <t.stindl@unsw.edu.au>
Description:	Simulate a (bivariate) multivariate renewal Hawkes (MRHawkes) self-exciting process, with given immi
License:	GPL (>=2)
Depends:	IHSEP, stats
NeedsCompilation:	no
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                  function
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Author(s)

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References

Chen, F. and Stindl, T. (2017). Direct Likelihood Evaluation for the Renewal Hawkes Process. Journal of Computational and Graphical Statistics.

Stindl, T. & Chen, F. (2018). Likelihood based inference for the multivariate renewal Hawkes process. Computational Statistics and Data Analysis.

Wheatley, S., Filimonov, V., and Sornette, D. (2016) The Hawkes process with renewal immigration & its estimation with an EM algorithm. Computational Statistics and Data Analysis. 94: 120-135.

---

fivaqks	*Fiji and Vanuatu Earthquake Data*

Description

Times and magnitudes (Richter scale) of earthquakes in the regions of Fiji and Vanuatu, for the period 1990-2015.

Usage

```
data(fivaqks)
```

Format

A data set containing 22 variables for earthquakes around Fiji and Vanuatu from 1991 to 2015.

time Time of quake

latitude Latitude of the quake

longitude Longitude of the quake

mag Magnitude of the quake

Source

United States Geological Survey (USGS)

Examples

```
data(fivaqks)
```

---

mllMRH *Minus loglikelihood of an (bivariate) MRHawkes model*

Description

Calculates the minus loglikelihood of an (bivariate) MRHawkes model with given immigration hazard functions μ, offspring density functions h and bracnhing ratios η for the event times and types data on the interval $[0, cens]$.

Usage

```
mllMRH(data, cens, par,
       h1.fn = function(x, p) 1 / p * exp( - x / p),
       h2.fn = function(x, p) 1 / p * exp( - x / p),
       mu1.fn = function(x, p){
              exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                   pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                   log.p = TRUE))
       },
       mu2.fn = function(x, p){
              exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                   pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                   log.p = TRUE))
       },
       H1.fn = function(x, p) pexp(x, rate = 1 / p),
       H2.fn = function(x, p) pexp(x, rate = 1 / p),
       Mu1.fn = function(x, p){
         - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                   log.p = TRUE)
       },
       Mu2.fn = function(x, p){
         - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                   log.p = TRUE)
       })
```

Arguments

data	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
cens	A scalar. The censoring time.
par	A numeric vector. Contains the ten parameters of the model, in order of the immigration parameters $\mu(.)$ for the two renewal distributions, the two offspring parameters $h(.)$ and lastly the four branching ratios η.

h1.fn	A (vectorized) function. The offspring density function for type one events.
h2.fn	A (vectorized) function. The offspring density function for type two events.
mu1.fn	A (vectorized) function. The immigration hazard function for events of type one.
mu2.fn	A (vectorized) function. The immigration hazard function for events of type two.
H1.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type one events.
H2.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type two events.
Mu1.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type one events.
Mu2.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type two events.

Value

Value of the negative log-liklihood.

Author(s)

Tom Stindl <t.stindl@unsw.edu.au> Feng Chen <feng.chen@unsw.edu.au>

Examples

```
## Magnitude 5.5 or greater earthquakes over the 25 year period from
## 01/01/1991 to 31/12/2015.
data(fivaqks);
near.fiji <- grep("Fiji", fivaqks$place)
near.vanuatu <- grep("Vanuatu", fivaqks$place)
t.beg <- strptime("1991-01-01 00:00:00", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t.end <- strptime("2015-12-31 23:59:59", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t0 <- 0
t1 <- as.numeric(t.end - t.beg)
tms <- strptime(fivaqks$time, "%Y-%m-%dT%H:%M:%OSZ", tz = "UTC")
ts <- as.numeric(tms[-1] - t.beg)
ts <- c(as.numeric(tms[1] - t.beg)/24, ts)
ts.fi <- ts[near.fiji]; ts.fi <- ts.fi[ts.fi >= 0 & ts.fi <= t1]
ts.va <- ts[near.vanuatu]; ts.va <- ts.va[ts.va >=0 & ts.va <= t1]
ts.c <- c(ts.fi, ts.va)
z.c <- c(rep(1, times = length(ts.fi)), rep(2, times = length(ts.va)))
o <- order(ts.c)
data <- cbind(ts.c[o], z.c[o])

## calculate the minus loglikelihood of an (bivariate) MRHawkes with some
## parameters the default hazard functions and density functions are Weibull
## and exponential respectivley
mllMRH(data, cens = t1, par = c(0.488, 20.10, 0.347, 9.53, 461, 720,
                               0.472, 0.293, 0.399, -0.0774))
```

```
## calculate the MLE for the parameter assuming known parametric forms
## of the immigrant hazard function and offspring density functions.

system.time(est <- optim(c(0.488, 20.10, 0.347, 9.53, 461, 720,
                           0.472, 0.293, 0.399, -0.0774),
                         mllMRH, data = data, cens = t1,
                         control = list(maxit = 5000, trace = TRUE),
                         hessian = TRUE)
)
## point estimate by MLE
est$par
## standard error estimates:
diag(solve(est$hessian))^0.5
```

---

mllMRH1   *Minus loglikelihood of an (bivariate) MRHawkes model with most re-*
                                 cent immigrant probabilities

---

Description

Calculates the minus loglikelihood of an (bivariate) RHawkes model with given immigration hazard
functions μ, common offspring density functions h and bracnhing ratios η for event times and event
types data on interval $[0, cens]$. The same as mllMRH although this version also returns the most
recent immigrant probabilities at the censoring.

Usage

```
mllMRH1(data, cens, par,
     h1.fn = function(x, p) 1 / p * exp( - x / p),
     h2.fn = function(x, p) 1 / p * exp( - x / p),
     mu1.fn = function(x, p){
             exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                 pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                 log.p = TRUE))
     },
     mu2.fn = function(x, p){
             exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                 pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                 log.p = TRUE))
     },
     H1.fn = function(x, p) pexp(x, rate = 1 / p),
     H2.fn = function(x, p) pexp(x, rate = 1 / p),
     Mu1.fn = function(x, p){
       - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                 log.p = TRUE)
     },
```

```
        Mu2.fn = function(x, p){
          - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                     log.p = TRUE)
        })
```

Arguments

data	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
cens	A scalar. The censoring time.
par	A numeric vector. Contains the ten parameters of the model, in order of the immigration parameters $\mu(.)$ for the two renewal distributions, the two offspring parameters $h(.)$ and lastly the four branching ratios η.
h1.fn	A (vectorized) function. The offspring density function for type one events.
h2.fn	A (vectorized) function. The offspring density function for type two events.
mu1.fn	A (vectorized) function. The immigration hazard function for events of type one.
mu2.fn	A (vectorized) function. The immigration hazard function for events of type two.
H1.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type one events.
H2.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type two events.
Mu1.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type one events.
Mu2.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type two events.

Value

mll	minus log-likelihood
p	most recent immigrant probabilities at the censoring time
n	number of events

Author(s)

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See Also

mllMRH

Examples

```
data <- cbind(sort(runif(1000,0,1000)),
              sample(1:2, size = 1000, replace = TRUE))
tmp <- mllMRH1(data = data, cens = 1001,
               par = c(3,1.2,1/3,0.2,1,1,0.5,0.2,0.2,0.3))
## last immigrant probabilities
lip <- tmp$p
## sample last immigrant at censoring time for component one and
## component two respectively
c(sample(0:1000, 1, replace = TRUE, prob = rowSums(lip)),
sample(0:1000, 1, replace = TRUE, prob = colSums(lip)))
```

---

mllMRH2   *Minus loglikelihood of an (bivariate) MRHawkes model with Rosen-*
                           blatt residuals

Description

Calculates the minus loglikelihood of an (bivariate) RHawkes model with given immigration hazard functions μ, common offspring density functions h and bracnhing ratios η for event times and event types data on interval $[0, cens]$. The same as mllMRH although this version also returns the Rosenblatt residuals for goodness-of-fit assessment of the event times.

Usage

```
mllMRH2(data, cens, par,
       h1.fn = function(x, p) 1 / p * exp( - x / p),
       h2.fn = function(x, p) 1 / p * exp( - x / p),
       mu1.fn = function(x, p){
               exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                   pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                   log.p = TRUE))
       },
       mu2.fn = function(x, p){
             exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                 pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                 log.p = TRUE))
       },
       H1.fn = function(x, p) pexp(x, rate = 1 / p),
       H2.fn = function(x, p) pexp(x, rate = 1 / p),
       Mu1.fn = function(x, p){
         - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                    log.p = TRUE)
       },
       Mu2.fn = function(x, p){
         - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                    log.p = TRUE)
       })
```

Arguments

`data`	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
`cens`	A scalar. The censoring time.
`par`	A numeric vector. Contains the ten parameters of the model, in order of the immigration parameters $\mu(.)$ for the two renewal distributions, the two offspring parameters $h(.)$ and lastly the four branching ratios η.
`h1.fn`	A (vectorized) function. The offspring density function for type one events.
`h2.fn`	A (vectorized) function. The offspring density function for type two events.
`mu1.fn`	A (vectorized) function. The immigration hazard function for events of type one.
`mu2.fn`	A (vectorized) function. The immigration hazard function for events of type two.
`H1.fn`	A (vectorized) function. Its value at `t` gives the integral of the offspring density function from 0 to `t` for type one events.
`H2.fn`	A (vectorized) function. Its value at `t` gives the integral of the offspring density function from 0 to `t` for type two events.
`Mu1.fn`	A (vectorized) function. Its value at `t` gives the integral of the immigrant hazard function from 0 to `t` for type one events.
`Mu2.fn`	A (vectorized) function. Its value at `t` gives the integral of the immigrant hazard function from 0 to `t` for type two events.

Details

Calculate the MRHawkes point process Rosenblatt residuals

Value

`mll`	minus log-likelihood
`W`	Rosenblatt residuals of observed event times

Author(s)

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See Also

`mllMRH`

Examples

```
n <- 1000
data <- cbind(sort(runif(n,0,1000)),
              sample(1:2, size = n, replace = TRUE))
tmp <- mllMRH2(data = data, cens = 1001,
```

```
                      par = c(1,1,1,1,1,1,0.5,0.2,0.2,0.3))
pp <- ppoints(n)
par(mfrow=c(1,2))
plot(quantile(tmp$W,prob=pp),pp,type="l",
     main="Uniform QQ plot",
     xlab="Sample quantiles",ylab="Theoretical quantiles")
abline(a = 0, b = 1, col = 2)
a <- acf(tmp$W, main = "ACF Plot")
ks.test(tmp$W,"punif")
Box.test(tmp$W,lag=tail(a$lag,1))
```

---

predDen   *MRHawkes (bivariate) predictive density function*

Description

Calculates the predictive density of the next event time after the censoring time cens based on the observations over the interval [0,cens].

Usage

```
predDen(x, data, cens, par,
        h1.fn = function(x, p) 1 / p * exp( - x / p),
        h2.fn = function(x, p) 1 / p * exp( - x / p),
        mu1.fn = function(x, p){
          exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                           log.p = TRUE))
        },
        mu2.fn = function(x, p){
         exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                           log.p = TRUE))
        },
        H1.fn = function(x, p) pexp(x, rate = 1 / p),
        H2.fn = function(x, p) pexp(x, rate = 1 / p),
        Mu1.fn = function(x, p){
         - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                      log.p = TRUE)
        },
        Mu2.fn = function(x, p){
         - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                      log.p = TRUE)
        })
```

Arguments

x	A scalar. The amount of time after the censoring tine cens.
data	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
cens	A scalar. The censoring time.
par	A numeric vector containing the twelve parameters of the model, in order of the immigration parameters $\mu(.)$ for the two component distributions, the four offspring parameters $h(.)$ and lastly the four branching ratios η.
h1.fn	A (vectorized) function. The offspring density function for type one events.
h2.fn	A (vectorized) function. The offspring density function for type two events.
mu1.fn	A (vectorized) function. The immigration hazard function for events of type one.
mu2.fn	A (vectorized) function. The immigration hazard function for events of type two.
H1.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type one events.
H2.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type two events.
Mu1.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type one events.
Mu2.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type two events.

Value

The predictive density of the next event time evaluated at x.

Author(s)

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Examples

```
## Magnitude 5.5 or greater earthquakes over the 25 year period from
## 01/01/1991 to 31/12/2015.
data(fivaqks);
near.fiji <- grep("Fiji", fivaqks$place)
near.vanuatu <- grep("Vanuatu", fivaqks$place)
t.beg <- strptime("1991-01-01 00:00:00", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t.end <- strptime("2015-12-31 23:59:59", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t0 <- 0
t1 <- as.numeric(t.end - t.beg)
tms <- strptime(fivaqks$time, "%Y-%m-%dT%H:%M:%OSZ", tz = "UTC")
ts <- as.numeric(tms[-1] - t.beg)
ts <- c(as.numeric(tms[1] - t.beg)/24, ts)
```

```
ts.fi <- ts[near.fiji]; ts.fi <- ts.fi[ts.fi >= 0 & ts.fi <= t1]
ts.va <- ts[near.vanuatu]; ts.va <- ts.va[ts.va >=0 & ts.va <= t1]
ts.c <- c(ts.fi, ts.va)
z.c <- c(rep(1, times = length(ts.fi)), rep(2, times = length(ts.va)))
o <- order(ts.c)
data <- cbind(ts.c[o], z.c[o])
curve(predDen(x, data = data, cens = t1,
              par = c(0.488, 20.10, 0.347, 9.53, 461, 720,
                      0.472, 0.293, 0.399, -0.0774))
      ,0 ,200, col = "red", lwd = 2, ylab = "Density")
```

---

simMRHawkes   *Simulate an (bivariate) renewal Hawkes (MRHawkes) process*

Description

Simulate an (bivairate) renewal Hawkes (MRHawkes) process with given renewal immigration distribution functions μ, offspring density functions h and branching ratios η using the cascading structure of the process.

Usage

```
simMRHawkes(re.dist1 = rweibull, par.redist1 = list(shape = 3, scale = 1.2),
            re.dist2 = rweibull, par.redist2 = list(shape = 1/3, scale = 0.2),
            h1.fn = function(x, p.h1) 1/p.h1 * exp(-x/p.h1),
            h2.fn = function(x, p.h2) 1/p.h2 * exp(-x/p.h2),
            p.h1 = 1, p.h2 = 1,
            eta11 = 0.3, eta12 = 0.1, eta21 = 0.1, eta22 = 0.3, cens = 100,
            B = 10, B0 = 50,
        max.h1 = max(optimize(h1.fn, c(0, cens), maximum = TRUE, p = p.h1)$obj,
                     h1.fn(0, p.h1), h1.fn(cens, p.h1)) * 1.1,
        max.h2 = max(optimize(h2.fn, c(0, cens), maximum = TRUE, p = p.h2)$obj,
                     h2.fn(0, p.h2), h2.fn(cens, p.h2)) * 1.1)
```

Arguments

re.dist1	The renewal distribution for type one events.
re.dist2	The renewal distribution for type two events.
par.redist1	A numeric list. The parameters of the renewal distribution for type one events.
par.redist2	A numeric list. The parameters of the renewal distribution for type two events.
h1.fn	A (vectorized) function. The offspring density function for type one events.
h2.fn	A (vectorized) function. The offspring density function for type two events.
p.h1	A numeric vector. The paramters of the offspring density for type one events.
p.h2	A numeric vector. The paramters of the offspring density for type two events.

eta11	A numeric scalar. The self-exciting branching ratio for type one events.
eta12	A numeric scalar. The cross-exciting branching ratio for type one events due to the effects of a type two event.
eta21	A numeric scalar. The cross-exciting branching ratio for type two events due to the effects of a type one event.
eta22	A numeric scalar. The self-exciting branching ratio for type two events.
cens	A scalar. The censoring time.
B	A numeric scalar. Tuning parameter
B0	A numeric scalar. Tuning parameter
max.h1	A numeric scalar. The maximum value of the offspring density for type one events.
max.h2	A numeric scalar. The maximum value of the offspring density for type two events.

Details

The function works by simulating the arrival times of immigrants accoridng to the respective renewal immigration distribution for each event type. The birth times ofoffspring from each immigrant are then simulated according to an non-stationary multivariate Hawkes Process (NSMHP) with appropriate baseline and excitation functions.

Value

A numeric matrix. The row coloumn contains the event times in ascending order while the second coloumn contains the corresponding event type.

Author(s)

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Examples

```
B <- 10; i <- 0;
data <- replicate(B,
                  {cat(i<<-i+1,'\n');
                  simMRHawkes(re.dist1 = rweibull,
                              par.redist1 = list(shape = 3, scale = 1.2),
                              re.dist2 = rweibull,
                              par.redist2 = list(shape = 1 / 3, scale = 0.2),
                              p.h1 = 1, p.h2 = 1,
                              eta11 = 0.3, eta12 = 0.1,
                              eta21 = 0.1, eta22 = 0.3,
                              cens = 100)
                  })
```

---

simNSMHP   *Simulate a (bivariate) non-stationary multivariate Hawkes process*
                                  (NSMHP)

Description

Simulate a bivariate non-stationary multivariate Hawkes process (NSMHP) with given given baseline intensity functions and self-excitation functions using the cascading structure of the process.

Usage

```
simNSMHP(TT = 100,
         nu1 = function(t) 0.6*exp(-t),
         nu2 = function(t) 0.2*exp(-t),
         g11 = function(t) 0.6*exp(-t),
         g12 = function(t) 0.2*exp(-t),
         g21 = function(t) 0.1*exp(-t),
         g22 = function(t) 0.5*exp(-t))
```

Arguments

TT	A scalar. The censoring time.
nu1	Basline intensity function for type one events.
nu2	Basline intensity function for type two events.
g11	Self-exciting function for type one events given the parent is a type two event.
g12	Cross-exciting function for type one events given the parent is a type two event.
g21	Cross-exciting function for type two events given the parent is a type one event.
g22	Self-exciting function for type two events given the parent is a type two event.

Details

The function works by simulating generation 0 events according to independent Poisson processes with the baseline intensity functions; then keep simulating future generation events as long as the number of the previous generation events of any type is non-zero. For each event type, we simulate these events according to M independent Poisson processes with the appropriate excitation intensity. When this recursive process stops, return events of all generations with their respective type labels as the events of the NSMHP on the interval (0,T].

Value

offspr1	All offspring events of type one
offspr2	All offspring events of type two

Author(s)

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Examples

```
B <- 10; i <- 0;
data <- replicate(B,
                  {cat(i<<-i+1,'\n');
                  simNSMHP(TT = 100)
                  })
```

---

simpred   *Simulate a fitted (bivariate) MRHawkes process model*

Description

Simulate a fitted bivariate MRHawkes process model after the censoring time cens to a future time point cens.tilde using the cascading structure of the process.

Usage

```
simpred(data, par, cens, cens.tilde,
        re.dist1 = rweibull,
        par.redist1 = list(shape = par[1], scale = par[2]),
        re.dist2 = rweibull,
        par.redist2 = list(shape = par[3], scale = par[4]),
        h1.fn = function(x, p.h1) 1 / p.h1 * exp( - x / p.h1),
        h2.fn = function(x, p.h2) 1 / p.h2 * exp( - x / p.h2),
        p.h1 = par[5], p.h2 = par[6],
        eta11 = par[7], eta12 = par[8], eta21 = par[9], eta22 = par[10],
        B = 10, B0 = 50, pnp1 = NULL,
        max.h1 = max(optimize(h1.fn, c(0, cens.tilde - cens), maximum = TRUE,
                          p = p.h1)$obj, h1.fn(0, p.h1),
                    h1.fn(cens.tilde - cens, p.h1)) * 1.1,
        max.h2 = max(optimize(h2.fn, c(0, cens.tilde - cens), maximum = TRUE,
                          p = p.h2)$obj, h2.fn(0, p.h2),
                    h2.fn(cens.tilde - cens, p.h2)) * 1.1)
```

Arguments

data	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
par	A numeric vector. Contains the ten parameters of the model, in order of the immigration parameters $\mu(.)$ for the two renewal distributions, the two offspring parameters $h(.)$ and lastly the four branching ratios η.
cens	A scalar. The censoring time.
cens.tilde	A scalar. The time that the simulation run uptil.
re.dist1	The renewal distribution for type one events.
re.dist2	The renewal distribution for type two events.

par.redist1	A numeric list. The parameters of the renewal distribution for type one events.
par.redist2	A numeric list. The parameters of the renewal distribution for type two events.
h1.fn	A (vectorized) function. The offspring density function for type one events.
h2.fn	A (vectorized) function. The offspring density function for type two events.
p.h1	A numeric vector. The paramters of the offspring density for type one events.
p.h2	A numeric vector. The paramters of the offspring density for type two events.
eta11	A numeric scalar. The self-exciting branching ratio for type one events.
eta12	A numeric scalar. The cross-exciting branching ratio for type one events due to the effects of a type two event.
eta21	A numeric scalar. The cross-exciting branching ratio for type two events due to the effects of a type one event.
eta22	A numeric scalar. The self-exciting branching ratio for type two events.
B	A numeric scalar. Tuning parameter
B0	A numeric scalar. Tuning parameter
pnp1	A numeric square matrix. The joint last immigrant probabilities.
max.h1	A numeric scalar. The maximum value of the offspring density for type one events.
max.h2	A numeric scalar. The maximum value of the offspring density for for type two events.

Value

A numeric matrix that contains the simulated event times from censoring time cens up until cens.tilde and the corresponding event types.

Author(s)

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Examples

```
## Magnitude 5.5 or greater earthquakes over the 25 year period from
## 01/01/1991 to 31/12/2015.
data(fivaqks);
near.fiji <- grep("Fiji", fivaqks$place)
near.vanuatu <- grep("Vanuatu", fivaqks$place)
t.beg <- strptime("1991-01-01 00:00:00", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t.end <- strptime("2015-12-31 23:59:59", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t0 <- 0
t1 <- as.numeric(t.end - t.beg)
tms <- strptime(fivaqks$time, "%Y-%m-%dT%H:%M:%OSZ", tz = "UTC")
ts <- as.numeric(tms[-1] - t.beg)
ts <- c(as.numeric(tms[1] - t.beg)/24, ts)
ts.fi <- ts[near.fiji]; ts.fi <- ts.fi[ts.fi >= 0 & ts.fi <= t1]
ts.va <- ts[near.vanuatu]; ts.va <- ts.va[ts.va >=0 & ts.va <= t1]
ts.c <- c(ts.fi, ts.va)
```

```
z.c <- c(rep(1, times = length(ts.fi)), rep(2, times = length(ts.va)))
o <- order(ts.c)
data <- cbind(ts.c[o], z.c[o])
# simulate future event time based on MLE fitted Rhawkes model
N <- 100; i <- 0;
data.pred <- replicate(N,
                          {cat(i<<-i+1,'\n');
                          simpred(data = data,
                                     par = c(0.488, 20.10, 0.347, 9.53,
                                             461, 720,
                                             0.472, 0.293, 0.399, -0.0774),
                                     cens = t1, cens.tilde = t1 + 1000)
                                     })
```

TmllMRH   *Minus loglikelihood of an (bivariate) MRHawkes model with trun-*
                            cated most recent immigrant probabilities

---

Description

Calculates the minus loglikelihood of an (bivariate) MRHawkes model with given immigration
hazard functions μ, offspring density functions h and bracnhing ratios η for event times and event
types data on interval $[0, cens]$ with truncated most recent immigrant probabilities looking back at
only the previous B event times.

Usage

```
TmllMRH(data, cens, par, B = 25,
        h1.fn = function(x, p) 1 / p * exp( - x / p),
        h2.fn = function(x, p) 1 / p * exp( - x / p),
        mu1.fn = function(x, p){
                exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                    pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                    log.p = TRUE))
        },
        mu2.fn = function(x, p){
                exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                    pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                    log.p = TRUE))
        },
        H1.fn = function(x, p) pexp(x, rate = 1 / p),
        H2.fn = function(x, p) pexp(x, rate = 1 / p),
        Mu1.fn = function(x, p){
          - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                     log.p = TRUE)
        },
        Mu2.fn = function(x, p){
```

```
            - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                      log.p = TRUE)
        })
```

Arguments

`data`	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
`cens`	A scalar. The censoring time.
`par`	A numeric vector. Contains the ten parameters of the model, in order of the immigration parameters $\mu(.)$ for the two renewal distributions, the two offspring parameters $h(.)$ and lastly the four branching ratios η.
`B`	A scalar. The number of previous events that are considered to be possible last immigrant arrivals.
`h1.fn`	A (vectorized) function. The offspring density function for type one events.
`h2.fn`	A (vectorized) function. The offspring density function for type two events.
`mu1.fn`	A (vectorized) function. The immigration hazard function for events of type one.
`mu2.fn`	A (vectorized) function. The immigration hazard function for events of type two.
`H1.fn`	A (vectorized) function. Its value at `t` gives the integral of the offspring density function from 0 to `t` for type one events.
`H2.fn`	A (vectorized) function. Its value at `t` gives the integral of the offspring density function from 0 to `t` for type two events.
`Mu1.fn`	A (vectorized) function. Its value at `t` gives the integral of the immigrant hazard function from 0 to `t` for type one events.
`Mu2.fn`	A (vectorized) function. Its value at `t` gives the integral of the immigrant hazard function from 0 to `t` for type two events.

Value

Value of the negative log-liklihood.

Author(s)

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Examples

```
## Magnitude 5.5 or greater earthquakes over the 25 year period from
## 01/01/1991 to 31/12/2015.
data(fivaqks);
near.fiji <- grep("Fiji", fivaqks$place)
near.vanuatu <- grep("Vanuatu", fivaqks$place)
t.beg <- strptime("1991-01-01 00:00:00", "%Y-%m-%d %H:%M:%S", tz = "UTC")
t.end <- strptime("2015-12-31 23:59:59", "%Y-%m-%d %H:%M:%S", tz = "UTC")
```

```
t0 <- 0
t1 <- as.numeric(t.end - t.beg)
tms <- strptime(fivaqks$time, "%Y-%m-%dT%H:%M:%OSZ", tz = "UTC")
ts <- as.numeric(tms[-1] - t.beg)
ts <- c(as.numeric(tms[1] - t.beg)/24, ts)
ts.fi <- ts[near.fiji]; ts.fi <- ts.fi[ts.fi >= 0 & ts.fi <= t1]
ts.va <- ts[near.vanuatu]; ts.va <- ts.va[ts.va >=0 & ts.va <= t1]
ts.c <- c(ts.fi, ts.va)
z.c <- c(rep(1, times = length(ts.fi)), rep(2, times = length(ts.va)))
o <- order(ts.c)
data <- cbind(ts.c[o], z.c[o])

## calculate the minus loglikelihood of an (bivariate) MRHawkes with some
## parameters the default hazard functions and density functions are Weibull
## and exponential respectivley
TmllMRH(data, cens = t1, par = c(0.488, 20.10, 0.347, 9.53, 461, 720,
                                 0.472, 0.293, 0.399, -0.0774), B = 200)

## calculate the MLE for the parameter assuming known parametric forms
## of the immigrant hazard function and offspring density functions.

  system.time(est <- optim(c(0.488, 20.10, 0.347, 9.53, 461, 720,
                             0.472, 0.293, 0.399, -0.0774),
                      TmllMRH, data = data, cens = t1, B = 200,
                      control = list(maxit = 5000, trace = TRUE),
                      hessian = TRUE)
  )
  ## point estimate by MLE
  est$par
  ## standard error estimates:
  diag(solve(est$hessian))^0.5
```

---

typeRes	*Minus loglikelihood of an (bivariate) MRHawkes model with Universal residuals*

Description

Calculates the minus loglikelihood of an (bivariate) RHawkes model with given immigration hazard functions μ, common offspring density functions h and bracnhing ratios η for event times and event types data on interval $[0, cens]$. The same as mllMRH although this version also returns the Universal residuals for goodness-of-fit assessment of the event types.

Usage

```
typeRes(data, cens, par, U = runif(length(data[,1])),
        h1.fn = function(x, p) 1 / p * exp( - x / p),
        h2.fn = function(x, p) 1 / p * exp( - x / p),
        mu1.fn = function(x, p){
```

```
                 exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                       pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                               log.p = TRUE))
             },
             mu2.fn = function(x, p){
               exp(dweibull(x, shape = p[1], scale = p[2], log = TRUE) -
                       pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                               log.p = TRUE))
             },
             H1.fn = function(x, p) pexp(x, rate = 1 / p),
             H2.fn = function(x, p) pexp(x, rate = 1 / p),
             Mu1.fn = function(x, p){
               - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                           log.p = TRUE)
             },
             Mu2.fn = function(x, p){
               - pweibull(x, shape = p[1], scale = p[2], lower.tail = FALSE,
                           log.p = TRUE)
             })
```

Arguments

data	A two column matrix. The first column contains the event times sorted in ascending order. The second column contains the corresponding event type with the label one or two.
cens	A scalar. The censoring time.
par	A numeric vector. Contains the ten parameters of the model, in order of the immigration parameters $\mu(.)$ for the two renewal distributions, the two offspring parameters $h(.)$ and lastly the four branching ratios η.
U	A numeric vector. Contains auxillary uniform random varables on the unit interval.
h1.fn	A (vectorized) function. The offspring density function for type one events.
h2.fn	A (vectorized) function. The offspring density function for type two events.
mu1.fn	A (vectorized) function. The immigration hazard function for events of type one.
mu2.fn	A (vectorized) function. The immigration hazard function for events of type two.
H1.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type one events.
H2.fn	A (vectorized) function. Its value at t gives the integral of the offspring density function from 0 to t for type two events.
Mu1.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type one events.
Mu2.fn	A (vectorized) function. Its value at t gives the integral of the immigrant hazard function from 0 to t for type two events.

Details

Calculate the MRHawkes point process Universal residuals

Value

mll	minus log-likelihood
V	Universal residuals of observed event types

Author(s)

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See Also

mllMRH

Examples

```
n <- 1000
data <- cbind(sort(runif(n,0,1000)),
              sample(1:2, size = n, replace = TRUE))
tmp <- typeRes(data = data, cens = 1001,
               par = c(1,1,1,1,1,1,0.5,0.2,0.2,0.3))
pp <- ppoints(n)
par(mfrow=c(1,2))
plot(quantile(tmp$V,prob=pp),pp,type="l",
     main="Uniform QQ plot",
     xlab="Sample quantiles",ylab="Theoretical quantiles")
abline(a = 0, b = 1, col = 2)
a <- acf(tmp$V, main = "ACF Plot")
ks.test(tmp$V,"punif")
Box.test(tmp$V,lag=tail(a$lag,1))
```

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