Package: NHPoisson (via r-universe)

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Type Package

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Description Tools for modelling, ML estimation, validation analysis and simulation of non homogeneous Poisson processes in time.

License GPL (>= 2)

NeedsCompilation no

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Contents

`NHPoisson-package` *Statistical modelling of non homogeneous Poisson processes*

Description

NHPoisson provides tools for the modelling and maximum likelihood estimation of non homogeneous Poisson processes (NHPP) in time, where the intensity is formulated as a function of (time-dependent) covariates. A comprehensive toolkit for model selection, residual analysis and diagnostic of the fitted model is also provided. Finally, it permits random generation of NHPP.

Details

Package:	NHPoisson
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Version:	3.0
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Author(s)

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See Also

evir, **extRemes**, **POT**, **ppstat**, **spatstat**, **yuima**

addAIC.fun *Calculate the AIC for all one-covariate additions to the current model*

Description

This function fits all models that differ from the current model by adding a single covariate from those supplied, and calculates their AIC value. It selects the best covariate to be added to the model, according to the AIC.

Usage

```
addAIC.fun(mlePP, covariatesAdd, startAdd = NULL, modSim = FALSE,...)
```

Arguments

mlePP	A "mlePP"-class object; usually the output from fitPP.fun. It defines the current model. The fitted model cannot include fixed parameters.
covariatesAdd	Matrix of the potential covariates to be added to the model; each column must contain a covariate.
startAdd	Optional. The vector of initial values for the estimation algorithm of the coefficients of each potential covariate. If it is NULL, initial values equal to 0 are used. Remark that in contrast to argument start of fitPP.fun, startAdd is a numeric vector not a list.
modSim	Logical flag. If it is FALSE, information about the process is shown on the screen. For automatic selection processes, the option TRUE should be preferred.
...	Further arguments to pass to AIC, for example the constant k for the AIC calculation.

Details

The definition of AIC uses constant k=2, but a different value k can be passed as an additional argument. The best covariate to be added is the one which leads to the model with the lowest AIC value and it improves the current model if the new AIC is lower than the current one.

Value

A list with the following components

AICadd	Vector of the AIC values obtained from adding to the current model each covariate in covariatesAdd.
posminAIC	An integer indicating the number of the column of covariatesAdd with the covariate leading to the minimum AIC.
namecov	Name of the covariate leading to the minimum AIC.
AICcurrent	AIC value of the current (initial) model.
newCoef	A (named) list with the initial value for the coefficient of the best covariate to be added. It is used in stepAICmle.fun.

See Also

dropAIC.fun, stepAICmle.fun, LRTpv.fun

Examples

```
data(BarTxTn)

BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))

#The initial model contains only the intercept
 mod1Bind<-fitPP.fun(covariates=NULL, posE=BarEv$Px, inddat=BarEv$inddat,
 tit='BAR  Intercept ',  start=list(b0=1))
#the potential covariates
covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)
dimnames(covB)<-list(NULL,c('cos','sin','TTx','Txm31', 'Txm31**2'))

aux<-addAIC.fun(mod1Bind, covariatesAdd=covB)
```

BarTxTn *Barcelona temperature data*

Description

Barcelona daily temperature series during the summer months (May, June, July, August and September) from 1951 to 2004.

Usage

```
data(BarTxTn)
```

Details

Variables

dia: Postion of the day in the year, from 121 (1st of May) to 253 (30th of September).

mes: Month of the year, from 5 to 9.

ano: Year, from 1951 to 2004.

diames: Position of the day in the month, from 1 to 30 or 31.

Tx: Daily maximum temperature.

Tn: Daily minimum temperature.

Txm31: Local maximum temperature signal. Lowess of Tx with a centered window of 31 days.

Txm15: Local maximum temperature signal. Lowess of Tx with a centered window of 15 days.

Tnm31: Local minimum temperature signal. Lowess of Tn with a centered window of 31 days.

Tnm15: Local minimum temperature signal. Lowess of Tn with a centered window of 15 days.

TTx: Long term maximum temperature signal. Lowess of Tx with a centered 40% window.

TTn: Long term minimum temperature signal. Lowess of Tn with a centered 40% window.

References

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Examples

```
data(BarTxTn)
```

`CalcRes.fun` *Calculate NHPP residuals on overlapping intervals*

Description

This function calculates raw and scaled residuals of a NHPP based on overlapping intervals. The scaled residuals can be Pearson or any other type of scaled residuals defined by the function $h(t)$.

Usage

```
CalcRes.fun(mlePP, lint, h = NULL, typeRes = NULL)
```

Arguments

`mlePP`	An object of class `mlePP-class`; usually, the output from `fitPP.fun`.
`lint`	Length of the intervals to calculate the residuals.
`h`	Optional. Weight function to calculate the scaled residuals. By default, Pearson residuals with $h(t) = 1/\sqrt{\hat{\lambda}(t)}$ are calculated.
`typeRes`	Optional. Label indicating the type of scaled residuals. By default, Pearson residuals are calculated and label is 'Pearson'.

Details

The raw residuals are based on the increments of the raw process $R(t) = N_t - \int_0^t \hat{\lambda}(u)du$ in overlapping intervals (l_1, l_2) centered on t:

$$r'(l_1, l_2) = R(l_2) - R(l_1) = \sum_{t_i \in (l_1, l_2)} I_{t_i} - \int_{l_1}^{l_2} \hat{\lambda}(u)du.$$

Residuals $r'(l_1, l_2)$ are made 'instantaneous' dividing by the length of the intervals (specified by the argument lint), $r(l_1, l_2) = r'(l_1, l_2)/(l_2 - l_1)$. A residual is calculated for each time in the observation period.

The function also calculates the residuals scaled with the function $h(t)$

$$r_{sca}(l_1, l_2) = \sum_{t_i \in (l_1, l_2)} h(t_i) - \int_{l_1}^{l_2} h(u)\hat{\lambda}(u)du.$$

By default, Pearson residuals with $h(t) = 1/\sqrt{\hat{\lambda}(t)}$ are calculated.

Value

A list with elements

`RawRes`	Numeric vector of the raw residuals.
`ScaRes`	A list with elements ScaRes (vector of the scaled residuals) and typeRes (name of the type of scaled residuals).
`emplambda`	Numeric vector of the empirical estimator of the PP intensity on the considered intervals.
`fittedlambda`	Numeric vector of the sum of the intensities $\hat{\lambda}(t)$ on the considered intervals, divided by the length of the interval.
`lintV`	Numeric vector of the exact length of each interval. The exact length is defined as the number of observations in each interval used in the estimation (observations with inddat=1).
`lint`	Input argument.
`typeI`	Label indicating the type of intervals used to calculate the residuals, 'Overlapping'.
`h`	Input argument.
`mlePP`	Input argument.

References

Abaurrea, J., Asin, J., Cebrian, A.C. and Centelles, A. (2007). Modeling and forecasting extreme heat events in the central Ebro valley, a continental-Mediterranean area. *Global and Planetary Change*, 57(1-2), 43-58.

Baddeley, A., Turner, R., Moller, J. and Hazelton, M. (2005). Residual analysis for spatial point processes. *Journal of the Royal Statistical Society*, Series B 67,617-666.

Brillinger, D. (1994). Time series, point processes and hybrids. *Can. J. Statist.*, 22, 177-206.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Lewis, P. (1972). Recent results in the statistical analysis of univariate point processes. In *Stochastic point processes* (Ed. P. Lewis), 1-54. Wiley.

See Also

`unifres.fun`, `graphres.fun`

Examples

```
X1<-rnorm(1000)
X2<-rnorm(1000)

modE<-fitPP.fun(tind=TRUE,covariates=cbind(X1,X2),
 posE=round(runif(40,1,1000)), inddat=rep(1,1000),
 tim=c(1:1000), tit="Simulated example",start=list(b0=1,b1=0,b2=0),
 dplot=FALSE,modCI=FALSE,modSim=TRUE)


#Residuals, based on overlapping intervals of length 50, from the fitted NHPP modE

ResE<-CalcRes.fun(mlePP=modE, lint=50)
```

`CalcResD.fun` *Calculate NHPP residuals on disjoint intervals*

Description

This function calculates raw and scaled residuals of a NHPP based on disjoint intervals. The scaled residuals can be Pearson or any other type of scaled residuals defined by the function $h(t)$.

Usage

```
CalcResD.fun(mlePP, h = NULL, nint = NULL, lint = NULL, typeRes = NULL,
 modSim = "FALSE")
```

Arguments

`mlePP`	An object of class `mlePP-class`; usually, the output from `fitPP.fun`.
`lint`	Optional. Length of the intervals to calculate the residuals.
`h`	Optional. Weight function to calculate the scaled residuals. By default, Pearson residuals with $h(t) = 1/\sqrt{\hat{\lambda}(t)}$ are calculated.
`typeRes`	Optional. Label indicating the type of scaled residuals. By default, Pearson residuals are calculated and label is 'Pearson'.
`modSim`	Logical flag. If it is FALSE, some information on the intervals is shown on the screen.
`nint`	Number of intervals used to calculate the residuals. Intervals with the same length are considered. Only one of lint or nint must be specified.

Details

The intervals used to calculate the residuals can be specified either by nint or lint; only one of the arguments must be provided. If nint is specified, intervals of equal length are calculated.

The raw residuals are based on the increments of the raw process $R(t) = N_t - \int_0^t \hat{\lambda}(u)du$ in disjoint intervals (l_1, l_2) centered on t:

$$r'(l_1, l_2) = R(l_2) - R(l_1) = \sum_{t_i \in (l_1, l_2)} I_{t_i} - \int_{l_1}^{l_2} \hat{\lambda}(u)du.$$

Residuals $r'(l_1, l_2)$ are made 'instantaneous' dividing by the length of the intervals (specified by the argument lint), $r(l_1, l_2) = r'(l_1, l_2)/(l_2 - l_1)$.

The function also calculates the residuals scaled with the function $h(t)$

$$r_{sca}(l_1, l_2) = \sum_{t_i \in (l_1, l_2)} h_{t_i} - \int_{l_1}^{l_2} h(u)\hat{\lambda}(u)du.$$

By default, Pearson residuals with $h(t) = 1/\sqrt{\hat{\lambda}(t)}$ are calculated.

Value

A list with elements

`RawRes`	Numeric vector of the raw residuals.
`ScaRes`	A list with elements ScaRes (vector of the scaled residuals) and typeRes (name of the type of scaled residuals).
`emplambda`	Numeric vector of the empirical estimator of the PP intensity on the considered intervals.
`fittedlambda`	Numeric vector of the sum of the intensities $\hat{\lambda}(t)$ on the considered intervals, divided by the length of the interval.
`lintV`	Numeric vector of the exact length of each interval. The exact length is defined as the number of observations in each interval used in the estimation (observations with inddat=1).
`lint`	Input argument.
`nint`	Input argument.
`pm`	Numeric vector of the mean point of the intervals.
`typeI`	Label indicating the type of intervals used to calculate the residuals, 'Disjoint' .
`h`	Input argument.
`mlePP`	Input argument.

References

Abaurrea, J., Asin, J., Cebrian, A.C. and Centelles, A. (2007). Modeling and forecasting extreme heat events in the central Ebro valley, a continental-Mediterranean area. *Global and Planetary Change*, 57(1-2), 43-58.

Baddeley, A., Turner, R., Moller, J. and Hazelton, M. (2005). Residual analysis for spatial point processes. *Journal of the Royal Statistical Society*, Series B 67,617-666.

Brillinger, D. (1994). Time series, point processes and hybrids. *Can. J. Statist.*, 22, 177-206.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Lewis, P. (1972). Recent results in the statistical analysis of univariate point processes. In *Stochastic point processes* (Ed. P. Lewis), 1-54. Wiley.

See Also

CalcRes.fun, unifres.fun, graphres.fun

Examples

```
X1<-rnorm(1000)
X2<-rnorm(1000)


modE<-fitPP.fun(tind=TRUE,covariates=cbind(X1,X2),
 posE=round(runif(40,1,1000)), inddat=rep(1,1000),
 tim=c(1:1000), tit="Simulated example",start=list(b0=1,b1=0,b2=0),
 dplot=FALSE,modCI=FALSE,modSim=TRUE)

#Residuals, based on 20 disjoint intervals of length 50, from the fitted NHPP modE

ResDE<-CalcResD.fun(mlePP=modE,lint=50)
```

CIdelta.fun *Confidence intervals for $\lambda(t)$ using delta method*

Description

Given the $\hat{\beta}$ covariance matrix (or its estimation), an approximate confidence interval for each $\lambda(t)$ is calculated using the delta method.

Usage

```
CIdelta.fun(VARbeta, lambdafit, covariates, clevel = 0.95)
```

Arguments

VARbeta	(Estimated) Covariance matrix of the $\hat{\beta}$ parameter vector.
lambdafit	Numeric vector of fitted values of the PP intensity $\hat{\lambda}(t)$.
covariates	Matrix of covariates to estimate the PP intensity.
clevel	Confidence level of the confidence intervals. A value in the interval (0,1).

Value

A list with elements

LIlambda	Numeric vector of the lower values of the intervals.
UIlambda	Numeric vector of the upper values of the intervals.
lambdafit	Input argument.

Note

fitPP.fun calls CIdelta.fun when the argument is *CIty='Delta'*.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

CItran.fun, fitPP.fun, VARbeta.fun

Examples

```
aux<-CIdelta.fun(VARbeta=0.01, lambdafit=exp(rnorm(100)), covariates=matrix(rep(1,100)),
  clevel=0.95)
```

CItran.fun *Confidence intervals for $\lambda(t)$ based on transformation*

Description

Given the $\hat{\beta}$ covariance matrix (or its estimation), an approximate confidence interval for each $\lambda(t) = \exp(\nu(t))$ is calculated using a transformation of the confidence interval for the linear predictor $\nu(t) = \mathbf{X(t)}\beta$. The transformation is $\exp(I_i)$, where I_i are the confidence limits of $\nu(t)$.

Usage

```
CItran.fun(VARbeta, lambdafit, covariates, clevel = 0.95)
```

Arguments

VARbeta	(Estimated) Coariance matrix of the $\hat{\beta}$ parameter vector.
lambdafit	Numeric vector of fitted values of the PP intensity $\hat{\lambda}(t)$.
covariates	Matrix of covariates to estimate the PP intensity.
clevel	Confidence level of the confidence intervals. A value in the interval (0,1).

Value

A list with elements

LIlambda	Numeric vector of the lower values of the intervals.
UIlambda	Numeric vector of the upper values of the intervals.
lambdafit	Input argument.

Note

`fitPP.fun` calls `CItran.fun` when the argument is *CIty='Transf'*.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

`CIdelta.fun`, `fitPP.fun`, `VARbeta.fun`

Examples

```
aux<-CItran.fun(VARbeta=0.01, lambdafit=exp(rnorm(100)), covariates=matrix(rep(1,100)),
  clevel=0.95)
```

---

confintAsin.fun *Compute confidence intervals for the β parameters*

Description

This function computes confidence intervals for the β parameters.

Usage

```
confintAsin.fun(mlePP, level = 0.95)
```

Arguments

mlePP	A "mlePP"-class object; usually the output from fitPP.fun.
level	The confidence level required for the intervals.

Details

The confidence intervals calculated by this function are based on the asymptotic normal approximation of th MLE of the β parameters, that is $(\hat{\beta} - z_{(1-\alpha/2)}s.e.(\hat{\beta}), \hat{\beta} + z_{(1-\alpha/2)}s.e.(\hat{\beta}))$ with $\alpha = 1 - level$

Value

A matrix with two columns, the first contains the lower limits of the confidence intervals of all the parameters and the second the upper limits.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

confint, VARbeta.fun

Examples

```
data(BarTxTn)

covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)

BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))

mod1B<-fitPP.fun(covariates=covB,
 posE=BarEv$Px, inddat=BarEv$inddat,
 tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=-1,b3=0,b4=0,b5=0))

confintAsin.fun(mod1B)
```

`dropAIC.fun` *Calculate the AIC for all one-covariate deletions from the current model*

Description

This function fits all models obtained from the current model by deleting one covariate (except the intercept), and calculates their AIC value. It selects the best covariate to be deleted, according to the AIC value.

Usage

```
dropAIC.fun(mlePP, modSim = FALSE,...)
```

Arguments

`mlePP`	A "`mlePP`"-class object; usually the output from `fitPP.fun`. It defines the current model. The fitted model cannot include fixed parameters.
`modSim`	Logical flag. If it is FALSE, information about the process is shown on the screen. For automatic selection processes, the option TRUE should be preferred.
`...`	Further arguments to pass to `AIC`, for example the constant k for the AIC calculation.

Details

The definition of AIC uses constant k=2, but a different value k can be passed as an additional argument. The best covariate to be deleted is the one whose deletion leads to the model with the lowest AIC value and it improves the current model if the new AIC is lower than the current one.

Value

A list with the following components

`AICadd`	Vector of the AIC values obtained from deleting each covariate of the current model.
`posminAIC`	An integer indicating the number of the column of the covariates matrix with the covariate leading to the minimum AIC.
`namecov`	Name of the covariate leading to the minimum AIC.
`AICcurrent`	AIC value of the current (initial) model.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Venables, W. N. and Ripley, B. D. (2002). *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

addAIC.fun, stepAICmle.fun, LRTpv.fun

Examples

```
data(BarTxTn)

BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))

covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)

dimnames(covB)<-list(NULL,c('cos','sin','TTx','Txm31', 'Txm31**2'))

mod1B<-fitPP.fun(covariates=covB, posE=BarEv$Px, inddat=BarEv$inddat,
 tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=10,b3=0,b4=0,b5=0))


aux<-dropAIC.fun(mod1B)
```

---

emplambda.fun *Empirical occurrence rates of a NHPP on overlapping intervals*

Description

This function calculates the empirical occurrence rates of a point process on overlapping intervals. The empirical rate centered in each time of the observation period is calculated using intervals of a given length. A plot of the empirical rate over time can be performed optionally.

Usage

```
emplambda.fun(posE, t, lint, plotEmp = TRUE, inddat = NULL, tit ="",
scax = NULL, scay = NULL)
```

Arguments

posE	Numeric vector of the position of the occurrence points of the NHPP (or any point process in time).
t	Time index of the observation period. The simplest option is 1,...,n with n the length of the period.
lint	Length of the intervals used to calculate the rates.
plotEmp	Logical flag. If it is TRUE, a plot of the empirical rate is carried out.
inddat	Optional. Index vector equal to 1 for the observations used in the estimation process By default, all the observations are considered, see POTevents.fun.
tit	Character string. A title for the plot.

scax	Optional. A two element vector indicating the x-scale for the plot.
scay	Optional. A two element vector indicating the y-scale for the plot.

Value

A list with elements

emplambda	Vector of the empirical rates.
lint	Input argument.

See Also

emplambdaD.fun, fitPP.fun, POTevents.fun

Examples

```
data(BarTxTn)

BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))

# empirical rate based on overlapping intervals
emplambdaB<-emplambda.fun(posE=BarEv$Px,inddat=BarEv$inddat, t=c(1:8415),
 lint=153,  tit="Barcelona")
```

---

emplambdaD.fun *Empirical occurrence rates of a NHPP on disjoint intervals*

Description

This function calculates the empirical occurrence rates of a point process using disjoint intervals. The rate is assigned to the mean point of the interval. A plot of the empirical rate over time can be performed optionally.

Usage

```
emplambdaD.fun(posE, t, lint=NULL, nint = NULL, plotEmp = TRUE, inddat = NULL,
tit = "", scax = NULL, scay = NULL)
```

Arguments

posE	Numeric vector of the position of the occurrence points of the NHPP (or any point process in time).
t	Time index of the observation period. The simplest option is 1,...,n with n the length of the period.

lint	Optional (alternative argument to nint). Length of the intervals used to calculate the rates.
nint	Optional (alternative argument to lint). Number of intervals (of equal length) used to to calculate the rates. It is an alternative way to lint for identifying the intervals.
plotEmp	Logical flag. If it is TRUE, a plot of the empirical rate is carried out.
inddat	Optional. Index vector equal to 1 for the observations used in the estimation process. By default, all the observations are considered, see POTevents.fun.
tit	Character string. A title for the plot.
scax	Optional. A two element vector indicating the x-scale for the plot.
scay	Optional. A two element vector indicating the y-scale for the plot.

Details

The intervals can be specified either by nint or lint; only one of the arguments must be provided.

Value

A list with elements

emplambda	Vector of the empirical rates.
lint	Input argument.
nint	Input argument.

See Also

emplambda.fun, fitPP.fun, POTevents.fun

Examples

```
data(BarTxTn)

BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))


# empirical rate based on disjoint intervals using nint to specify the intervals
emplambdaDB<-emplambdaD.fun(posE=BarEv$Px,inddat=BarEv$inddat, t=c(1:8415),
 nint=55)

# empirical rate based on disjoint intervals using lint to specify the intervals
emplambdaDB<-emplambdaD.fun(posE=BarEv$Px,inddat=BarEv$inddat, t=c(1:8415),
 lint=153)
```

extractAIC-methods *Method* mle *for Function* extractAIC

Description

Method for generic function extractAIC for objects of the S4-class mle or mlePP. It is the same method as in **stats4** (that method is not available outside that package).

Methods

signature(fit = "ANY")

signature(fit = "mle")

fitPP.fun *Fit a non homogeneous Poisson Process*

Description

This function fits by maximum likelihood a NHPP where the intensity $\lambda(t)$ is formulated as a function of covariates. It also calculates and plots approximate confidence intervals for $\lambda(t)$.

Usage

```
fitPP.fun(covariates = NULL, start, fixed=list(), posE = NULL, inddat = NULL,
POTob = NULL,  nobs = NULL, tind = TRUE, tim = NULL, minfun="nlminb",
 modCI = "TRUE", CIty = "Transf", clevel = 0.95,
 tit = "", modSim = "FALSE", dplot = TRUE, xlegend = "topleft",
lambdaxlim=NULL,lambdaylim=NULL,...)
```

Arguments

covariates	Matrix of the covariates to be included in the linear predictor of the PP intensity (each column is a covariate). It is advisable to give names to the columns of this matrix (using dimnames), since they will be used in the output. Otherwise the default names 'Covariate i' are used. The offset covariates must be included in this matrix. A maximum of 50 covariates are allowed.
start	Named list of the initial values for the estimation of the β parameters (including fixed parameters). The names of the list must be (compulsory): b0 (for the intercept), b1 (for the first column in covariates), b2 (for the second column), b3 (for the third column), etc.
fixed	Named list of the fixed β parameters. The elements of this list must be elements of the list start.
posE	Optional (see Details section). Numeric vector of the position of the PP occurrence points.

inddat	Optional (see Details section). Index vector equal to 1 for the observations used in the estimation process By default, all the observations are considered.
POTob	Optional (see Details section). List with elements T and thres that defines the PP resulting from a POT approach; see POTevents.fun for more details.
nobs	Optional. Number of observations in the observation period; it is only neccessary if POTob, inddat and covariates are NULL.
tind	Logical flag. If it is TRUE, an independent term is fitted in the linear predictor. It cannot be a character string, so TRUE and not'TRUE' should be used.
tim	Optional. Time vector of the observation period. By default, a vector 1,...n is considered.
minfun	Label indicating the function to minimize the negative of the loglikelihood function. There are two possible values: "nlminb" (the default option) and "optim". In the last case, the method of optimization can be chosen with an additional method argument.
modCI	Logical flag. If it is TRUE, confidence intervals for $\lambda(t)$ values are calculated.
CIty	Label indicating the method to calculate the approximate confidence intervals for $\lambda(t)$. It can be "Transf" for transformed asymptotic intervals (default) or "Delta" for the delta method; see CItran.fun and CIdelta.fun for details.
clevel	Confidence level of the confidence intervals.
tit	Character string. A title for the plot.
modSim	Logical flag. If it is FALSE, information on the estimation process is shown on the screen. For simulation process, the option TRUE should be preferred.
dplot	Logical flag. If it is TRUE, the fitted intensity is plotted.
xlegend	Label indicating the position where the legend on the graph will be located.
lambdaxlim	Optional. Numeric vector of length 2, giving the lowest and highest values which determine the x range.
lambdaylim	Optional. Numeric vector of length 2, giving the lowest and highest values which determine the y range.
...	Further arguments to pass to optim or to nlminb (depending on the value of the minfun argument).

Details

A Poisson process (PP) is usually specified by a vector containing the occurrence points of the process $(t_i)_{i=1}^k$, (argument posE). Since PP are often used in the framework of POT models, fitPP.fun also provides the possibility of using as input the series of the observed values in a POT model $(x_i)_{i=1}^n$ and the threshold used to define the extreme events (argument POTob).

In the case of PP defined by a POT approach, the observations of the extreme events which are not defined as the occurrence point are not considered in the estimation. This is done through the argument inddat, see POTevents.fun. If the input is provided via argument POTob, index inddat is calculated automatically. See *Coles (2001)* for more details on the POT approach.

The maximization of the loglikelihood function can be done using two different optimization routines, optim or nlminb, selected in the argument minfun. Depending on the covariates included in the function, one routine can succeed to converge when the other fails.

This function allows us to keep fixed some β parameters (offset terms). This can be used to specify an a priori known component to be included in the linear predictor during fitting. The fixed parameters must be specified in the `fixed` argument (and also in `start`); the fixed covariates must be included as columns of `covariates`.

The estimation of the $\hat{\beta}$ covariance matrix is based on the asymptotic distribution of the MLE $\hat{\beta}$, and calculated as the inverse of the negative of the hessian matrix. Confidence intervals for $\lambda(t)$ can be calculated using two approaches specified in the argument `CIty`. See *Casella (2002)* for more details on ML theory and delta method.

Value

An object of class `mlePP`, which is a subclass of `mle`. Consequently, many of the generic functions with `mle` methods, such as `logLik` or `summary`, can be applied to the output of this function. Some other generic functions related to fitted models, such as `AIC` or `BIC`, can also be applied to `mlePP` objects.

Note

A homogeneous Poisson process (HPP) can be fitted as a particular case, using an intensity defined by only an intercept and no covariate.

References

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Coles, S. (2001). *An introduction to statistical modelling of extreme values.* Springer.

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Kutoyants Y.A. (1998).*Statistical inference for spatial Poisson processes.* Lecture notes in Statistics 134. Springer.

See Also

`POTevents.fun`, `globalval.fun`, `VARbeta.fun`, `CItran.fun`, `CIdelta.fun`

Examples

```
#model fitted  using as input posE and inddat and  no confidence intervals

data(BarTxTn)
covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)
BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))


mod1B<-fitPP.fun(covariates=covB,
 posE=BarEv$Px, inddat=BarEv$inddat,
 tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=-1,b3=0,b4=0,b5=0))
```

```
#model fitted  using as input  a list from POTevents.fun and with  confidence intervals

tiempoB<-BarTxTn$ano+rep(c(0:152)/153,55)

mod2B<-fitPP.fun(covariates=covB,
 POTob=list(T=BarTxTn$Tx, thres=318),
 tim=tiempoB, tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=-1,b3=0,b4=0,b5=0),CIty="Delta",modCI=TRUE,
 modSim=TRUE)

#model  with a fixed parameter (b0)

mod1BF<-fitPP.fun(covariates=covB,
 posE=BarEv$Px, inddat=BarEv$inddat,
 tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-89,b1=1,b2=10,b3=0,b4=0,b5=0),
 fixed=list(b0=-100))
```

`GenEnv.fun` *Calculation of simulated envelopes*

Description

This function calculates a point estimation and an envelope for a given statistic using a Monte Carlo approach. The statistic must be a function of the occurrence points of a NHPP.

It calls the auxiliary function `funSim.fun` (not intended for the users), see Details section.

Usage

```
GenEnv.fun(nsim, lambda, fun.name, fun.args = NULL, clevel = 0.95,
cores = 1, fixed.seed=NULL)
```

Arguments

`nsim`	Number of simulations for the calculations.
`lambda`	Numeric vector of the intensity $\lambda(t)$ (or $\hat{\lambda}(t)$) of the NHPP.
`fun.name`	Name of the function defining the statistic to be estimated.
`fun.args`	Additional arguments for the function fun.name.
`clevel`	Confidence level of the envelope.
`cores`	Optional. Number of cores of the computer to be used in the calculations. Default: one core is used.
`fixed.seed`	An integer or NULL. If it is an integer, that is the value used to set the seed in random generation processes. It it is NULL, a random seed is used.

Details

The auxiliary function `funSim.fun` generates a simulated sample of the occurrence points in a NHPP and calculates the corresponding statistic using the simulated points.

Value

A list with elements

`valmed`	Point estimation (mean value) of the statistic to be calculated.
`valinf`	Lower value of the simulated CI.
`valsup`	Upper value of the simulated CI.
`lambda`	Input argument.
`nsim`	Input argument.
`nsimval`	Number of valid simulations (used in the calculation of the CI and the point estimation).
`fixed.seed`	Input argument.

See Also

`simNHP.fun`, `resQQplot.fun`

Examples

```
# Calculation of the point estimation and a 95% CI based on 100 simulations
#for the second occurrence time of a NHPP with intensity lambdat.
#posk.fun(x, k) is a function that returns the value in the row k of vector x.

lambdat<-runif(1000,0.01,0.02)
aux<-GenEnv.fun(lambda=lambdat,fun.name="posk.fun",fun.args=2,nsim=100)

#if we want reproducible results, we can fixed the seed in the generation process
#(the number of cores used in the calculations must also be the same to reproduce
#the result)

aux<-GenEnv.fun(lambda=lambdat,fun.name="posk.fun",fun.args=2,nsim=100,fixed.seed=123)

#the result (with 1 core): Lower interval:  25.55; Mean value:  136.06; Upper interval:  288
```

`globalval.fun` *Perform a global validation analysis for a NHPP*

Description

This function performs a thorough validation analysis for a fitted NHPP. It calculates the (generalized) uniform and the raw (or scaled) residuals, performs residual plots for the uniform residuals, and time residual and lurking variable plots for the raw or scaled residuals. It also plots the fitted and empirical estimations of the NHPP intensity. Optionally, it also performs a residual QQplot.

Usage

```
globalval.fun(mlePP, lint = NULL, nint = NULL, Xvar = NULL,
namXvar = NULL, Xvart = NULL, namXvart = NULL,  h = NULL, typeRes = NULL,
typeResLV="Pearson",typeI = "Disjoint", nsim = 100, clevel = 0.95,
resqqplot = FALSE, nintLP = 100, tit = "", flow = 0.5, addlow = FALSE,
histWgraph=TRUE,plotDisp=c(2,2), indgraph = FALSE, scax = NULL, scay = NULL,
legcex = 0.5, cores = 1, xlegend = "topleft", fixed.seed=NULL)
```

Arguments

mlePP	An object of class mlePP-class; usually, the output from fitPP.fun.
lint	Length of the intervals used to calculate the residuals.
nint	Number of intervals used to calculate the residuals. Intervals of equal length are considered. Only used if typeI="Disjoint". In that case, only one of the arguments lint or nint must be specified.
Xvar	Optional. Matrix of the lurking variables (each column is a variable).
namXvar	Optional. Vector of names of the variables in Xvar.
Xvart	Optional. Matrix of the variables for the residual plots (each column is a variable). A time plot is performed in all the cases.
namXvart	Optional. Vector of names of the variables in Xvart.
h	Optional. Weight function to calculate the scaled residuals. By default, Pearson residuals with $$h(t) = 1/\sqrt{\hat{\lambda}(t)}$$ are calculated. This function is used to calculate both the scaled residuals and the residuals for the lurking variables (except if typeResLV="Raw").
typeRes	Optional. Label indicating the type of scaled residuals. By default, Pearson residuals are calculated and label is "Pearson".
typeResLV	Label indicating the type of residuals ("Raw" or any type of scaled residuals such as "Pearson") to calculate the residuals for the lurking variable plots.
typeI	Label indicating the type ("Overlapping" or "Disjoint") of intervals used to calculate the residuals.
clevel	Confidence level of the residual envelopes.
resqqplot	Logical flag. It is is TRUE, a residual qqplot is carried out.
nsim	Number of simulations for the residual qqplot.
nintLP	Number of levels considered in the lurking variables. It is used as argument nint in the call of the function graphResCov.fun.
tit	Character string. A title for the plot.
flow	Argument f for the lowess smoother of the raw (or scaled) residual plots, see lowess.
addlow	Logical flag. If it is TRUE, a lowess is added in the residual plots.

histWgraph	Logical flag. If it is TRUE, a new graphical device is opened with the option record=TRUE, so that the history of all plots is recorded in the new device. This option may not work on some platforms; for example, RStudio does not allow the user to open new graphical devices.
plotDisp	A vector of the form c(nr, nc). The residual plots in graphresU.fun, graphres.fun and graphResCov.fun will be drawn in a nr×nc layout. It is used as argument mfrow in par. By default, a 2 × 2 layout is used.
indgraph	Logical flag. If it is TRUE, the validation plots (except the residual versus variables plots) in graphresU.fun are carried out in four 1 × 1 layouts. By default, a 2 × 2 layout is used.
scax	Optional. Vector of two values indicating the range of values for the x-axis in the fitted and empirical rate plot. An adequate range is selected by default.
scay	Optional. Vector of two values indicating the range of values for the x-axis in the fitted and empirical rate plot. An adequate range is selected by default.
legcex	cex argument for the legend in the residual time plots (see par for details).
cores	Optional. Number of cores of the computer to be used in the calculations. Default: one core is used.
xlegend	Argument xlegend used in the call of the function graphrate.fun; see that function for details.
fixed.seed	An integer or NULL. It is the argument for resQQplot.fun.

Details

If typeI="Overlapping", argument lint is compulsory. If typeI="Disjoint", only one of the arguments lint or nlint must be specified.

Value

A list with the same elements that CalcRes.fun or CalcResD.fun (depending on the value of the argument typeI).

References

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

graphres.fun, graphrate.fun, resQQplot.fun, graphResCov.fun, graphresU.fun

Examples

```
data(BarTxTn)

covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)
```

```
modB<-fitPP.fun(tind=TRUE,covariates=covB,
 POTob=list(T=BarTxTn$Tx, thres=318),
 tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=10,b3=0,b4=0,b5=0),CIty="Transf",modCI=TRUE,
 modSim=TRUE,dplot=FALSE)

#Since  only one graphical device is opened  and  the argument histWgraph is TRUE
#by default, the different plots can be scrolled up and down with the "Page Up"
#and "Page Down" keys.

aux<-globalval.fun(mlePP=modB,lint=153, typeI="Disjoint",
 typeRes="Raw",typeResLV="Raw", resqqplot=FALSE)

#If typeRes and typeResLV are not specified, Pearson residuals are calculated
#by default.

aux<-globalval.fun(mlePP=modB,lint=153, typeI="Disjoint",
 resqqplot=FALSE)
```

`graphrate.fun` *Plot fitted and empirical PP occurrence rates*

Description

This function calculates the empirical and the cumulative fitted occurrence rate of a PP on overlapping or disjoint intervals and plot them versus time.

Usage

```
graphrate.fun(objres = NULL, fittedlambda = NULL, emplambda = NULL, t = NULL,
lint = NULL, typeI = "Disjoint", tit = "", scax = NULL, scay = NULL,
xlegend = "topleft",histWgraph=TRUE)
```

Arguments

`objres`	Optional. A list with (at least) elements fittedlambda, emplambda, t, and typeI. For example, the output from `CalcRes.fun` or `CalcResD.fun`; see those functions for details.
`fittedlambda`	Optional. Numeric vector of the cumulative fitted intensities $\hat{\lambda}(t)$ over the considered intervals (and usually divided by the length of the interval).
`emplambda`	Optional. Numeric vector of the empirical PP occurrence rates estimated over the considered intervals (usually divided by the length of the interval).
`t`	Optional. Time vector of the PP observation period.
`lint`	Optional. Length of the intervals used to calculate the empirical and the (cumulative) fitted occurrence intensities.

typeI	Label indicating the type ('Overlapping' or 'Disjoint') of the intervals.
tit	Character string. A title for the plot.
scax	Optional. Vector of two values giving the range of values for the x-axis. An adequate range is selected by default.
scay	Optional. Vector of two values giving the range of values for the y-axis. An adequate range is selected by default.
xlegend	Label indicating the position where the legend on the graph will be located.
histWgraph	Logical flag. If it is TRUE, a new graphical device is opened with the option record=TRUE. This option may not work on some platforms; for example, RStudio does not allow the user to open new graphical devices.

Details

Either the argument objres or the set of arguments (fittedlambda, emplambda, t) must be specified. If objres is provided, fittedlambda, emplambda, t,lint and typeI are ignored.

In order to make comparable the empirical and the fitted occurrence rates, a cumulative fitted rate must be used. That means that argument fittedlambda must be the sum of the intensities fitted by the model over the same interval where the empirical rates have been calculated.

See Also

CalcRes.fun, CalcResD.fun

Examples

```
##plot of rates based on overlapping intervals
graphrate.fun(emplambda=runif(500,0,1), fittedlambda=runif(500,0,1),
 t=c(1:500), lint=100, tit="Example", typeI="Overlapping")

#plot of rates based on disjoint intervals
graphrate.fun(emplambda=runif(50,0,1), fittedlambda=runif(50,0,1),
 t=c(1:50), lint=10, tit="Example", typeI="Disjoint")

#Example using objres as input. In this example X1 has no influence on the rate;
#consequently the fitted rate is almost a constant.

X1<-rnorm(1000)

modE<-fitPP.fun(tind=TRUE,covariates=cbind(X1),
 posE=round(runif(40,1,1000)), inddat=rep(1,1000),
 tim=c(1:1000), tit="Simulated example", start=list(b0=1,b1=0),
 modCI=FALSE,modSim=TRUE,dplot=FALSE)

ResDE<-CalcResD.fun(mlePP=modE,lint=50)

graphrate.fun(ResDE, tit="Example")
```

graphres.fun *Plot NHPP residuals versus time or monotonous variables*

Description

This function plots residuals of a NHPP (raw or scaled, overlapping or disjoint) versus time or other variables which are monotonous functions.

Usage

```
graphres.fun(objres = NULL, typeRes = "Raw", t = NULL, res = NULL, lint = NULL,
posE = NULL, fittedlambda = NULL, typeI = "Disjoint", Xvariables = NULL,
namXv = NULL, histWgraph=TRUE, plotDisp=c(2,2), addlow = FALSE, lwd = 2,
tit = "", flow = 0.5, xlegend = "topleft", legcex = 0.5)
```

Arguments

objres	Optional. A list with (at least) elements t, typeI and Rawres and/or ScaRes, depending on the value of typeRes. For example, the output list from the functions CalcRes.fun or CalcResD.fun; see those functions for details.
typeRes	Label indicating the type of residuals ("Raw" or any type of scaled residuals such as "Pearson").
t	Optional. Time vector of the PP observation period.
res	Optional. Vector of residuals.
lint	Optional. Length of the intervals used to calculate the residuals.
posE	Optional. Numeric vector of the PP occurrence times. Only used when typeI = "Overlapping".
fittedlambda	Optional. Vector of the cumulative fitted PP intensity over the intervals. Used to calculate the envelopes when typeRes="Raw".
typeI	Label indicating the type ("Overlapping" or "Disjoint") of intervals.
Xvariables	Optional. Matrix of the variables for the residual plots (each column is a variable).
namXv	Optional. Vector of the names of the variables in Xvariables.
histWgraph	Logical flag. If it is TRUE, a new graphical device is opened with the option record=TRUE, so that the history of all plots is recorded in the new device. This option may not work on some platforms; for example, RStudio does not allow the user to open new graphical devices.
plotDisp	A vector of the form c(nr, nc). The residual plots will be drawn in a nr$\times$nc array. It is used as argument mfrow in par. By default, a 2×2 window is used.
tit	Character string. A title for the plots.
addlow	Logical flag. If it is TRUE, a lowess is added to the residual plots.
lwd	Argument lwd for plotting the lowess lines, see par for details.
flow	Argument f for the lowess, see lowess for details.
xlegend	Label giving the position of the graph where the legend will be located.
legcex	Argument cex for the legend, see par for details.

Details

Either argument objres or pair of arguments (t,res) must be specified. If objres is provided, arguments t,res, typeRes, typeI, posE and fittedlambda are ignored.

A residual plot versus time is always performed. These plots are intended for time or variables which are monotonous functions, since residuals are calculated over a given time interval and plotted versus the value of the variables in the mean point of the interval.

A smoother (lowess) of the residuals can be optionally added to the plots. In the case of overlapping intervals, the residuals of the occurrence points are marked differently from the rest. In the case typeRes="Raw" (if argument fittedlambda is available) or typeRes="Pearson", envelopes for the residuals are also plotted. The envelopes are based on an approach analogous to the one shown in Baddeley et al. (2005) for spatial Poisson processes. The envelopes for raw residuals are,

$$\pm \frac{2}{l_2 - l_1} \sqrt{\sum_{i \in (l_1, l_2)} \hat{\lambda}(i)}$$

where index i runs over the integers in the interval (l_1, l_2). The envelopes for the Pearson residuals are,

$$\pm 2/\sqrt{l_2 - l_1}.$$

These plots allow us to analyze the effect on the intensity, of the covariates included in the model or other potentially influent variables. They show if the mean or the dispersion of the residuals vary sistematically, see for example residual analysis in Atkinson (1985) or Collett (1994).

References

Atkinson, A. (1985). *Plots, transformations and regression.* Oxford University Press.

Baddeley, A., Turner, R., Moller, J. and Hazelton, M. (2005). Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B*, 67, 617-666.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Collett, D. (1994). Modelling survival data in medical research. Chapman & Hall.

See Also

graphrate.fun

Examples

```
#Example using objres as input

X1<-c(1:1000)**0.5

modE<-fitPP.fun(tind=TRUE,covariates=cbind(X1),
 posE=round(runif(40,1,1000)), inddat=rep(1,1000),
 tim=c(1:1000), tit="Simulated example", start=list(b0=1,b1=0),
 modSim = TRUE, dplot = FALSE)

ResDE<-CalcResD.fun(mlePP=modE,lint=50)
```

```
graphres.fun(objres=ResDE, typeRes="Raw", Xvariables=cbind(X1),
 namXv=c("X1"), plotDisp=c(2,1), addlow=TRUE,tit="Example")


#Example using the set of arguments res, t and fittedlambda as input
#In this case, with typeI="Disjoint", only values of t, fittedlambda and Xvariables
#in the midpoint of the intervals must be provided.

#Since   a 1X1 layout is  specified in plotDisp and only one
#graphical device is opened by default, the two  resulting plots can be scrolled
#up and down  with the "Page Up" and "Page Down" keys.

X1<-c(1:500)**0.5
graphres.fun(res=rnorm(50),posE=round(runif(50,1,500)),
 fittedlambda=runif(500,0,1)[seq(5,495,10)],
 t=seq(5,495,10), typeRes="Raw", typeI="Disjoint",Xvariables=X1[seq(5,495,10)],
 namXv=c("X1"), plotDisp=c(1,1), tit="Example 2",lint=10)
```

`graphResCov.fun` *Perform lurking variable plots for a set of variables*

Description

This function performs lurking variable plots for a set of variables. The function `graphResX.fun` performs the lurking variable plot for one variable and `graphResCov.fun` calls this function for a set of variables; see `graphResX.fun` for details.

Usage

```
graphResCov.fun(Xvar, nint, mlePP, h = NULL, typeRes = "Pearson", namX = NULL,
 histWgraph=TRUE, plotDisp=c(2,2), tit = "")
```

Arguments

`Xvar`	Matrix of variables (each column is a variable).
`nint`	Number of intervals each covariate is divided into to perform the lurking variable plot.
`mlePP`	An object of class `mlePP-class`; usually, the output from `fitPP.fun`.
`typeRes`	Label indicating the type of residuals ("Raw" or any type of scaled residuals such as "Pearson") used in the plots.
`h`	Optional. Weight function used to calculate the scaled residuals (if typeRes is not equal to "Raw"). By default, Pearson residuals with $h(t) = 1/\sqrt{\hat{\lambda}(t)}$ are calculated. $\hat{\lambda}(t)$ is provided by element lambdafit in mlePP.
`namX`	Optional. Vector of the names of the variables in Xvar.

histWgraph	Logical flag. If it is TRUE, a new graphical device is opened with the option record=TRUE, so that the history of all plots is recorded in the new device. This option may not work on some platforms; for example, RStudio does not allow the user to open new graphical devices.
plotDisp	A vector of the form c(nr, nc). The lurking variable plots will be drawn in a nr×nc array. It is used as argument mfrow in par. By default, a 2×2 window is used.
tit	Character string. A title for the plot.

Value

A list with elements

mXres	Matrix of residuals (each column contains the residuals of a variable).
mXm	Matrix of mean values (each column contains the mean values of a variable in each interval).
mXpc	Matrix of the quantiles that define the intervals of each variable (each column contains the quantiles of one variable).
nint	Input argument.
mlePP	Input argument.

References

Atkinson, A. (1985). *Plots, transformations and regression.* Oxford University Press.

Baddeley, A., Turner, R., Moller, J. and Hazelton, M. (2005). Residual analysis for spatial point processes. *Journal of the Royal Statistical Society*, Series B 67,617-666.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

graphResX.fun, graphres.fun

Examples

```
#Simulated process without any relationship with variables Y1 and Y2
#The plots are performed dividing the  variables into  50 intervals
#Raw residuals.

X1<-rnorm(500)
X2<-rnorm(500)
auxmlePP<-fitPP.fun(posE=round(runif(50,1,500)), inddat=rep(1,500),
 covariates=cbind(X1,X2),start=list(b0=1,b1=0,b2=0))

Y1<-rnorm(500)
Y2<-rnorm(500)
```

```
res<-graphResCov.fun(mlePP=auxmlePP, Xvar=cbind(Y1,Y2), nint=50,
 typeRes="Raw",namX=c("Y1","Y2"),plotDisp=c(2,1))

#If more variables were specified in the argument Xvar, with
#the same 2X1 layout specified in plotDisp, the resulting plots could be
#scrolled up and down with the "Page Up" and "Page Down" keys.
```

---

graphresU.fun *Validation analysis of PP uniform (generalized) residuals*

Description

This function checks the properties that must be fulfilled by the uniform (generalized) residuals of a PP: uniform character and uncorrelation. Optionally, the existence of patterns versus covariates or potentially influent variables can be graphically analyzed.

Usage

```
graphresU.fun(unires, posE,  Xvariables = NULL, namXv = NULL, flow = 0.5,
 tit = "", addlow = TRUE, histWgraph=TRUE, plotDisp=c(2,2), indgraph = FALSE)
```

Arguments

unires	Numeric vector of the uniform residuals.
posE	Numeric vector of the occurrence times of the PP.
Xvariables	Matrix of variables to perform the residual plots (each column is a variable).
namXv	Optional. Vector of names of the variables in Xvariables.
tit	Character string. A title for the plot.
addlow	Logical flag. If it is TRUE, a lowess is added to the plots.
flow	Argument f for the lowess smoother; see lowess for details.
histWgraph	Logical flag. If it is TRUE, a new graphical device is opened with the option record=TRUE, so that the history of all plots is recorded in the new device. This option may not work on some platforms; for example, RStudio does not allow the user to open new graphical devices.
plotDisp	A vector of the form c(nr, nc). The residual versus variables plots will be drawn in a nr×nc array. It is used as argument mfrow in par. By default, a 2 × 2 layout is used.
indgraph	Logical flag. If it is TRUE, the validation plots (except the residuals versus variables plots) are carried out in four1 × 1 layouts. By default, a 2 × 2 layout is used.

Details

The validation analysis of the uniform character consists in a uniform Kolmogorov-Smirnov test and a qqplot with a 95% confidence band based on a beta distribution. The analysis of the serial correlation is based on the Pearson correlation coefficient, Ljung-Box tests and a lagged serial correlation plot. An index plot of the residuals and residual plots versus the variables in argument Xvariables are performed to analyze the effect of covariates or other potentially influent variables. These plots will show if the mean or dispersion of the residuals vary sistematically, see model diagnostic of Cox-Snell residuals in Collett (1994) for more details.

References

Abaurrea, J., Asin, J., Cebrian, A.C. and Centelles, A. (2007). Modeling and forecasting extreme heat events in the central Ebro valley, a continental-Mediterranean area. *Global and Planetary Change*, 57(1-2), 43-58.

Baddeley, A., Turner, R., Moller, J. and Hazelton, M. (2005). Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B*, 67, 617-666.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Collett, D. (1994). Modelling survival data in medical research. Chapman \& Hall.

Ogata, Y. (1988). Statistical models for earthquake occurrences and residual analysis for point processes. *Journal of the American Statistical Association*, 83(401), 9-27.

See Also

unifres.fun, transfH.fun

Examples

```
#Since  only one graphical device is opened  and the argument histWgraph
#is TRUE by default, the resulting residual plots  (three pages with the
#considered 1X2 layout for the residual versus variables plot)
#can be scrolled up and down with the "Page Up" and "Page Down" keys.

X1<-rnorm(500)
X2<-rnorm(500)

graphresU.fun(unires=runif(30,0,1),posE=round(runif(30,0,500)),
  Xvariables=cbind(X1,X2), namXv=c("X1","X2"),tit="Example",flow=0.7,plotDisp=c(1,2))
```

---

graphResX.fun *Perform a lurking variable plot*

Description

This function performs a lurking variable plot to analyze the residuals in terms of different levels of the variable.

Usage

```
graphResX.fun(X, nint, mlePP, typeRes = "Pearson", h = NULL, namX = NULL)
```

Arguments

X	Numeric vector, the variable for the lurking variable plot.
nint	Number of intervals or levels the variable is divided into.
mlePP	An object of class mlePP-class; usually, the output from fitPP.fun.
typeRes	Label indicating the type of residuals ('Raw' or any type of scaled residuals such as 'Pearson').
h	Optional. Weight function used to calculate the scaled residuals (if typeRes is not equal to 'Raw'). By default, Pearson residuals with $h(t) = 1/\sqrt{\hat{\lambda}(t)}$ are calculated. $\hat{\lambda}(t)$ is provided by the lambdafit slot in mlePP.
namX	Optional. Name of variable X.

Details

The residuals for different levels of the variable are analyzed. For a variable $X(t)$, the considered levels are

$$W(P_{X,j}, P_{X,j+1}) = \{t : P_{X,j} \leq X(t) < P_{X,j+1}\}$$

where $P_{X,i}$ is the sample j-percentile of X. This type of plot is specially useful for variables which are not a monotonous function of time.

In the case typeRes='Raw' or typeRes='Pearson', envelopes for the residuals are also plotted. The envelopes are based on an approach analogous to the one in Baddeley et al. (2005) for spatial Poisson processes. The envelopes for raw residuals are

$$\pm \frac{2}{l_W} \sqrt{\sum_i \hat{\lambda}(i)}$$

where index i runs over the integers in the level $W(P_{X,j}, P_{X,j+1})$, and l_W is its length (number of observations in W). The envelopes for the Pearson residuals are,

$$\pm 2/\sqrt{l_W}.$$

Value

A list with elements

Xres	Vector of residuals.
xm	Vector of the mean value of the variable in each interval.
pc	Vector of the quantiles that define the levels of the variable.
typeRes	Input argument.
namX	Input argument.
lambdafit	Input argument.
posE	Input argument.

References

Atkinson, A. (1985). *Plots, transformations and regression.* Oxford University Press.

Baddeley, A., Turner, R., Moller, J. and Hazelton, M. (2005). Residual analysis for spatial point processes. *Journal of the Royal Statistical Society*, Series B 67, 617-666.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

graphResCov.fun, graphres.fun

Examples

```
##Simulated process not related to variable X
##Plots dividing the  variable into  50 levels

X1<-rnorm(500)
X2<-rnorm(500)
auxmlePP<-fitPP.fun(posE=round(runif(50,1,500)), inddat=rep(1,500),
 covariates=cbind(X1,X2),start=list(b0=1,b1=0,b2=0))



##Raw residuals
res<-graphResX.fun(X=rnorm(500),nint=50,mlePP=auxmlePP,typeRes="Raw")

##Pearson residuals
res<-graphResX.fun(X=rnorm(500),nint=50,mlePP=auxmlePP,typeRes="Pearson")
```

LRTpv.fun — *Calculate the p-value of a likelihood ratio test for each covariate in the model*

Description

This function calculates, for each covariate in the model (except the intercept), the p-value of a likelihood ratio test comparing the original fitted NHPP with the model excluding that covariate from the linear predictor.

Usage

```
LRTpv.fun(mlePP)
```

Arguments

mlePP	An object of class mlePP-class; usually, the output from fitPP.fun. The fitted model cannot include fixed parameters.

Details

A LRT is carried for all the covariates in the linear predictor except the intercept. If the model has not an intercept and there is only one covariate, no test can be carried out.

Value

A matrix with one column, which contains the LRT p-values for all the covariates in the model (except the intercept)

See Also

fitPP.fun, testlik.fun, dropAIC.fun, addAIC.fun

Examples

```
data(BarTxTn)
covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)
BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))

mod1B<-fitPP.fun(tind=TRUE,covariates=covB,
 posE=BarEv$Px, inddat=BarEv$inddat,
 tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=10,b3=0,b4=0,b5=0),dplot=FALSE, modCI=FALSE)

LRTpv.fun(mod1B)
```

---

mlePP-class *Class "mlePP" for results of maximum likelihood estimation of Poisson processes with covariates*

Description

This class encapsulates the output from the maximum likelihood estimation of a Poisson process where the intensity is modeled as a linear function of covariates.

Objects from the Class

Objects can be created by calls of the form `new("mlePP", ...)`, but most often as the result of a call to fitPP.fun.

Slots

call: Object of class "language". The call to fitPP.fun.

coef: Object of class "numeric". The estimated coefficientes of the model.

`fullcoef`: Object of class `"numeric"`. The full coefficient vector, including the fixed parameters of the model. It has an attribute, called 'TypeCoeff' which shows the names of the fixed parameters.

`vcov`: Object of class `"matrix"`. Approximate variance-covariance matrix of the estimated coefficients. It has an attribute, called 'CalMethod' which shows the method used to calcualte the inverse of the information matrix: 'Solve function', 'Cholesky', 'Not possible' or 'Not required' if `modCI=FALSE`.

`min`: Object of class `"numeric"`. Minimum value of objective function, that is the negative of the loglikelihood function.

`details`: Object of class `"list"`. The output returned from `optim`. If `nlminb` is used to minimize the function, it is NULL.

`minuslogl`: Object of class `"function"`. The negative of the loglikelihood function.

`nobs`: Object of class `"integer"`. The number of observations.

`method`: Object of class `"character"`. It is a bit different from the slot in the extended class `mle`: here, it is the input argument `minfun` of `fitPP.fun` instead of the method used in `optim` (this information already appears in `details`).

`detailsb`: Object of class `"list"`.The output returned from `nlminb`. If `optim` is used to minimize the function, it is NULL.

`npar`: Object of class `"integer"`. Number of estimated parameters.

`inddat`: Object of class `"numeric"`. Input argument of `fitPP.fun`.

`lambdafit`: Object of class `"numeric"`. Vector of the fitted intensity $\hat{\lambda}(t)$.

`LIlambda`: Object of class `"numeric"`. Vector of lower limits of the CI.

`UIlambda`: Object of class `"numeric"`. Vector of upper limits of the CI.

`convergence`: Object of class `"integer"`. A code of convergence. 0 indicates successful convergence.

`posE`: Object of class `"numeric"`. Input argument of `fitPP.fun`.

`covariates`: Object of class `"matrix"`. Input argument of `fitPP.fun`.

`tit`: Object of class `"character"`. Input argument of `fitPP.fun`.

`tind`: Object of class `"logical"`. Input argument of `fitPP.fun`.

`t`: Object of class `"numeric"`. Input argument of `fitPP.fun`.

Extends

Class `"mle"`, directly.

Methods

Most of the S4 methods in **stats4** for the S4-class `mle` can be used. Also a `mle` method for the generic function `extractAIC` and a version of the `profile mle` method adapted to the `mlePP` objects are available:

coef `signature(object = "mle")`

logLik `signature(object = "mle")`

nobs `signature(object = "mle")`

show `signature(object = "mle")`

summary `signature(object = "mle")`

update `signature(object = "mle")`

vcov `signature(object = "mle")`

confint `signature(object = "mle")`

extractAIC `signature(object = "mle")`

profile `signature(fitted = "mlePP")`

Some other generic functions related to fitted models, such as `AIC` or `BIC`, can also be applied to `mlePP` objects.

Note

Let us remind that, as in all the S4-classes, the symbol @ must be used instead of $ to name the slots: mlePP@covariates, mlepp@lambdafit, etc.

See Also

`fitPP.fun`, `mle`

Examples

```
showClass("mlePP")
```

`POTevents.fun` *Calculate extreme events using a POT approach*

Description

This function calculates the characteristics of the extreme events of a series (x_i) defined using a peak over threshold (POT) method with an extreme threshold. The initial and the maximum intensity positions, the mean excess, the maximum excess and the length of each event are calculated.

Usage

```
POTevents.fun(T, thres, date = NULL)
```

Arguments

`T`	Numeric vector, the series (x_i) to calculate the extreme events.
`thres`	Threshold value used to define the extreme events.
`date`	Optional. A vector or matrix indicating the date of each observation.

Details

One of the elements of the output from this function is a vector (inddat) which marks the observations that should be used in the estimation of a point process, resulting from a POT approach. The observations to be considered in the estimation are marked with 1 and correspond to the non occurrence observations and to a single occurrence point per event. The occurence point is defined as the point where maximum intensity of the event occurs.The observations in an extreme event which are not the occurrence point are marked with 0 and treated as non observed.

Value

A list with components

`Pi`	Vector of the initial points of the extreme events.
`datePi`	Date of the initial points Pi.
`Px`	Vector of the points of maximum excess of the extreme events.
`datePx`	Vector of the date of the maximum excess points Px.
`Im`	Vector of the mean excesses (over the threshold) of the extreme events.
`Ix`	Vector of the maximum excesses (over the threshold) of the extreme events.
`L`	Vector of the lengths of the extreme events.
`inddat`	Index equal to 1 in the observations used in the estimation process and to 0 in the others.

See Also

`fitPP.fun`

Examples

```
data(BarTxTn)
dateB<-cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$diames)
BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318, date=dateB)
```

`profile-methods` *Method* `mlePP` *for Function* `profile`

Description

Method for generic function `profile` for objects of the S4-class `mlePP`. It is almost identical to the method `mle` for this function in **stats4**, but small changes have to be done due to the differences in the arguments of the functions `mle` and `fitPP.fun`. In order to profile an `mlePP` object, its `vcov` slot cannot be missing. That means that if the function `fitPP.fun` is used to create the object, the argument `modCI=TRUE` must be used.

Methods

`signature(fitted = "mlePP")`

`resQQplot.fun` *Perform a qqplot for the residuals of a NHPP*

Description

This function performs a qqplot comparing the empirical quantiles of the residuals with the expected quantiles under the fitted NHPP, calculated by a Monte Carlo approach.

It calls the auxiliary function `resSim.fun` (not intended for the users), see Details section.

Usage

```
resQQplot.fun(nsim, objres, covariates, clevel = 0.95, cores = 1,
tit ="", fixed.seed=NULL, histWgraph=TRUE)
```

Arguments

`nsim`	Number of simulations for the calculations.
`objres`	A list with the same elements of the output list from the function `CalcRes.fun` or `CalcResD.fun`.
`covariates`	Matrix of covariates to fit the NHPP (each column is a covariate).
`clevel`	Confidence level of the residual envelope.
`cores`	Optional. Number of cores of the computer to be used in the calculations. Default: one core is used.
`tit`	Character string. A title for the plot.
`fixed.seed`	An integer or NULL. If it is an integer, that is the value used to set the seed in random generation processes. It it is NULL, a random seed is used.
`histWgraph`	Logical flag. Only used in Windows platforms. If it is TRUE, a new graphical device is opened with the option `record=TRUE`.

Details

The expected quantiles are calculated as the median values of the simulated samples. Confidence intervals for each quantile $r_{(i)}$ with pointwise significance level `clevel` are calculated as quantiles of probability 1-clevel /2 and clevel/2 of the simulated sample for each residual.

All type of residuals (disjoint or overlapping and Pearson or raw residuals) are supported by this function. However, the qqplot for overlapping residuals can be a high time consuming process. So, disjoint residuals should be prefered in this function.

The auxiliary function `resSim.fun` generates a NHPP with intensity $\lambda(t)$, fits the model using the covariate matrix and calculates the residuals.

Value

A list with elements

resmed	Numeric vector containing the mean of the simulated residuals in each point.
ressup	Numeric vector of the upper values of the simulated envelopes.
resinf	Numeric vector of the lower values of the simulated envelopes.
objres	Input argument.
nsim	Input argument.
fixed.seed	Input argument.

References

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

simNHP.fun, GenEnv.fun

Examples

```
X1<-rnorm(500)
X2<-rnorm(500)

aux<-fitPP.fun(tind=TRUE,covariates=cbind(X1,X2),
 posE=round(runif(40,1,500)), inddat=rep(1,500),
 tim=c(1:500), tit="Simulated example", start=list(b0=1,b1=0,b2=0),dplot=FALSE)

auxRes<-CalcResD.fun(mlePP=aux,lint=50)


#if we want reproducible results, we can fixed the seed in the generation process
#(the number of cores used in the calculations must also be the same to reproduce
# the result)

auxqq<-resQQplot.fun(nsim=50,objres=auxRes, covariates=cbind(X1,X2), fixed.seed=123)
```

---

simNHP.fun *Generate the occurrence points of a NHPP*

Description

This function generates the occurrence times of the points of a NHPP with a given time-varying intensity $\lambda(t)$, in a period (0, T). The length of argument lambda determines T, the length of the observation period.

It calls the auxiliary function buscar (not intended for the users), see Details section.

Usage

```
simNHP.fun(lambda, fixed.seed=NULL)
```

Arguments

lambda	Numeric vector, the time varying intensity $\lambda(t)$ to generate the NHPP.
fixed.seed	An integer or NULL. If it is an integer, that is the value used to set the seed in random generation processes. It it is NULL, a random seed is used.

Details

The generation of the NHPP points consists in two steps. First, the points of a homogeneous PP of intensity 1 are generated using independent exponentials. Then, the homogeneous occurrence times are transformed into the points of a non homogeneous process with intensity $\lambda(t)$. This transformation is performed by the auxiliary function buscar (not intended for the user).

Value

A list with elements

posNH	Numeric vector of the occurrences times of the NHPP generated in the observation period (0,T).
lambda	Input argument.
fixed.seed	Input argument.

References

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Ross, S.M. (2006). *Simulation.* Academic Press.

See Also

GenEnv.fun, resQQplot.fun

Examples

```
#Generation of the occurrence times of a homogeneours PP with  constant intensity
#0.01 in a period  of time of length 1000

aux<-simNHP.fun(lambda=rep(0.01,1000))
aux$posNH

#if we want reproducible results, we can fixed the seed in the generation process
aux<-simNHP.fun(lambda=rep(0.01,1000),fixed.seed=123)
aux$posNH

#and the result is:
#  [1]  85 143 275 279 284 316 347 362 634 637 738 786 814 852 870 955
```

```
#Generation of  the occurrence times of a NHPP with  time-varying intensity t in
#a period  of time of length 500

t<-runif(500, 0.01,0.1)
aux<-simNHP.fun(lambda=t)
aux$posNH
```

---

stepAICmle.fun *Choose the best PP model by AIC in a stepwise algorithm*

Description

Performs stepwise model selection by AIC for Poisson proces models estimated by maximum likelihood.

It calls the auxiliary function checkdim (not intended for the users).

Usage

```
stepAICmle.fun(ImlePP, covariatesAdd = NULL, startAdd = NULL,
direction = "forward", ...)
```

Arguments

ImlePP	A mlePP-class object; usually the output from fitPP.fun. It defines the initial model of the stepwise algorithm. The fitted model cannot include fixed parameters.
covariatesAdd	Matrix of the potential covariates to be added to the model; each column must contain a covariate. In the 'forward' and the 'both' directions, it is compulsory to assign a matrix to this argument. It is advisable to give names to the columns of this matrix (using dimnames) since, they will be used in the output. Otherwise the default names 'New Covariate i' are used.
startAdd	Optional. The vector of initial values for the estimation of the coefficients of each potential covariate. If it is NULL, initial values equal to 0 are used.
direction	Label indicating the direction of the algortihm: 'forward' (the default), 'backward' or 'both'.
...	Further arguments to pass to addAIC.fun and dropAIC.fun, for example the constant k for the AIC calculation

Details

Three directions, forward, backward and both, are implemented. The initial model is given by ImlePP and the algorithm stops when none of the covariates eliminated from the model or added from the potential covariates set (argument covariatesAdd) improves the model fitted in the previous step, according to the AIC. For the 'both' and 'forward' directions, the argument covariatesADD is compulsary, and the default NULL leads to an error.

In the 'both' direction, 'forward' and 'backward' steps are carried out alternatively. In the 'forward' direction, the initial model usually contains only the intercept.

Value

A mlePP-class object, the fit of the final PP model selectecd by the algorithm.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Venables, W. N. and Ripley, B. D. (2002). *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

addAIC.fun, dropAIC.fun, testlik.fun

Examples

```
data(BarTxTn)

BarEv<-POTevents.fun(T=BarTxTn$Tx,thres=318,
 date=cbind(BarTxTn$ano,BarTxTn$mes,BarTxTn$dia))

#The initial model contains only the inercept
 mod1Bind<-fitPP.fun(covariates=NULL, posE=BarEv$Px, inddat=BarEv$inddat,
 tit='BAR  Intercept ',  start=list(b0=1))
#the potential covariates
covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)
dimnames(covB)<-list(NULL,c('cos','sin','TTx','Txm31', 'Txm31**2'))

bb<-stepAICmle.fun(ImlePP=mod1Bind, covariates=covB, startAdd=c(1,-1,0,0,0),
direction='both')
```

---

testlik.fun *Likelihood ratio test to compare two nested models*

Description

This function performs a likelihood ratio test, a test to compare the fit of two models, where the first one (the null model ModR) is a particular case of the other (the alternative model ModG).

Usage

```
testlik.fun(ModG, ModR)
```

Arguments

ModG	An object of class mlePP-class; usually, the output from fitPP.fun.
ModR	An object of class mlePP-class; usually, the output from fitPP.fun.

Details

The test statistic is twice the difference in the log-likelihoods of the models. Under the null, the statistic follows a χ^2 distribution with degrees of freedom df2-df1,the number of parameters of modG and modR respectively.

Value

A list with elements

pv	P-value of the likelihood ratio test.
ModG	Input argument.
ModR	Input argument.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

See Also

fitPP.fun,LRTpv.fun

Examples

```
##The alternative model modB is specified  by the output fitPP.fun
##The null model modBR is specified  by a list with elments llik and npar


data(BarTxTn)

covB<-cbind(cos(2*pi*BarTxTn$dia/365), sin(2*pi*BarTxTn$dia/365),
 BarTxTn$TTx,BarTxTn$Txm31,BarTxTn$Txm31**2)


modB<-fitPP.fun(tind=TRUE,covariates=covB,
 POTob=list(T=BarTxTn$Tx, thres=318),
 tim=c(1:8415), tit="BAR Tx; cos, sin, TTx, Txm31, Txm31**2",
 start=list(b0=-100,b1=1,b2=10,b3=0,b4=0,b5=0),dplot=FALSE,modCI=TRUE, modSim=TRUE)



modBR<-fitPP.fun(tind=TRUE,covariates=covB[,1:4],
```

```
POTob=list(T=BarTxTn$Tx, thres=318),
tim=c(1:8415), tit="BAR Tx; cos, sin, TTx, Txm31",
start=list(b0=-100,b1=1,b2=10,b3=0,b4=0),dplot=FALSE,modCI=TRUE, modSim=TRUE)


aux<-testlik.fun(ModG=modB,ModR=modBR)
```

`transfH.fun` *Transform a NHPP into a HPP*

Description

This function transforms the points t_i^{NH} of a NHPP into the occurrence points t_i^H of a HPP of rate 1.

Usage

```
transfH.fun(mlePP)
```

Arguments

`mlePP`	An object of class `mlePP-class`; usually, the output from `fitPP.fun`.

Details

Transformation of the NHPP points t_i^{NH} into the HPP points t_i^H is based on the time scale transformation,

$$t_i^H = \int_0^{t_i^{NH}} \lambda(t)dt.$$

(usually the estimated value $\hat{\lambda}(t)$ is used in the transformation.)

Value

A list with elements

`posEH`	Numeric vector of the transformed occurrence times of the HPP.
`posE`	Slot of the input argument mlePP.
`lambdafit`	Slot of the input argument mlePP.
`inddat`	Slot of the input argument mlePP.

References

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Cox, D.R., Isham, V., 1980. *Point Processes*. Chapman and Hall.

Daley, D. and D. Vere-Jones (2003). *An Introduction to the Theory of Point Processes*. Springer.

See Also

simNHP.fun

Examples

```
X1<-rnorm(500)
X2<-rnorm(500)
auxmlePP<-fitPP.fun(posE=round(runif(50,1,500)), inddat=rep(1,500),
 covariates=cbind(X1,X2),start=list(b0=1,b1=0,b2=0))


posEH<-transfH.fun(auxmlePP)
```

---

unifres.fun *Calculate exponential and uniform (generalized) residuals of a HPP*

Description

This function calculates the exponential d_i and the uniform (generalized) residuals u_i of a HPP, using the occurrence points t_i.

Usage

```
unifres.fun(posEH)
```

Arguments

posEH	Numeric vector, the occurrence points of a HPP.

Details

The exponential residuals of a HPP are defined as the inter-event distances $d_i = t_i - t_{i-1}$, that are an i.i.d. exponential sample. The series d_i is an example of the generalized residuals proposed by Cox and Snell (1968). The uniform residuals, defined as the function $\exp(-d_i)$ of the exponential residuals, are an i.i.d. uniform sample, see Ogata (1988).

Value

A list with elements

expres	Numeric vector of the exponential residuals.
unires	Numeric vector of the uniform residuals.
posEH	Input argument.

References

Abaurrea, J., Asin, J., Cebrian, A.C. and Centelles, A. (2007). Modeling and forecasting extreme heat events in the central Ebro valley, a continental-Mediterranean area. *Global and Planetary Change*, 57(1-2), 43-58.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

Cox, D. R. and Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society, series B*, 30(2), 248-275. 83(401), 9-27.

Ogata, Y. (1988). Statistical models for earthquake occurrences and residual analysis for point processes.*Journal of the American Statistical Association*, 83(401), 9-27.

See Also

`transfH.fun`, `graphresU.fun`

Examples

```
## generates the occurrence times of a homogeneours PP with  constant intensity 0.01
## and calculates de residuals

aux<-simNHP.fun(lambda=rep(0.01,1000))

res<-unifres.fun(aux$posNH)
```

`VARbeta.fun` *Calculate the covariance matrix of the $\hat{\beta}$ vector.*

Description

This function estimates the covariance matrix of the ML estimators of the β parameters, using the asymptotic distribution and properties of the ML estimators.

Usage

```
VARbeta.fun(covariates, lambdafit)
```

Arguments

`covariates`	Matrix of covariates (each column is a covariate).
`lambdafit`	Numeric vector, the fitted PP intensity $\hat{\lambda}(t)$.

Details

The covariance matrix is calculated as the inverse of the negative of the hessian matrix. The inverse of the matrix is calculated using the solve function. If this function leads to an error in the calculation, the inverse is calculated via its Cholesky decomposition. If this option also fails, the covariance matrix is not estimated and a matrix of dimension 0×0 is returned.

Value

VARbeta — Coariance matrix of the $\hat{\beta}$ vector. It has an attribute, called 'CalMethod' which shows the method used to calculate the inverse of the matrix: 'Solve function', 'Cholesky' or 'Not possible'.

Note

The function fitPP.fun calls this function.

References

Casella, G. and Berger, R.L., (2002). *Statistical inference.* Brooks/Cole.

Cebrian, A.C., Abaurrea, J. and Asin, J. (2015). NHPoisson: An R Package for Fitting and Validating Nonhomogeneous Poisson Processes. *Journal of Statistical Software*, 64(6), 1-24.

See Also

CItran.fun, CIdelta.fun

Examples

```
lambdafit<-runif(100,0,1)
X<-cbind(rep(1,100),rnorm(100),rnorm(100))

aux<-VARbeta.fun(covariates=X, lambdafit=lambdafit)
```

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