

Package: PEcAn.emulator (via r-universe)

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Type Package
Title Gaussian Process Emulator
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Description Implementation of a Gaussian Process model (both likelihood and bayesian approaches) for kriging and model emulation. Includes functions for sampling design and prediction.
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arate	<i>arate</i>
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Description

Acceptance rate

Usage

arate(x)

Arguments

x vector of MCMC samples

Author(s)

Michael Dietze

calcSpatialCov	<i>calcSpatialCov</i>
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Description

calcSpatialCov

Usage

calcSpatialCov(x, ...)

Arguments

<code>x</code>	either a spatial distance matrix or a list of component spatial distance matrices
<code>...</code>	Additional arguments

Author(s)

Michael Dietze

<code>calcSpatialCov.list</code>	<i>calcSpatialCov.list</i>
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Description

Currently assumes an exponential spatial dependency

Usage

```
## S3 method for class 'list'
calcSpatialCov(d, psi, tau)
```

Arguments

<code>d</code>	list of component spatial distance matrices
<code>psi</code>	spatial corr
<code>tau</code>	spatial var

Details

can make gaussian by passing squared distance matrix

Author(s)

Michael Dietze

<code>calcSpatialCov.matrix</code>	<code>calcSpatialCov.matrix</code>
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Description

Currently assumes an exponential spatial dependency

Usage

```
## S3 method for class 'matrix'
calcSpatialCov(d, psi, tau)
```

Arguments

<code>d</code>	spatial distance matrix
<code>psi</code>	spatial corr
<code>tau</code>	spatial var

Details

can make gaussian by passing squared distance matrix

Author(s)

Michael Dietze

<code>distance</code>	<code>distance</code>
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Description

distance

Usage

```
distance(x, power = 1)
```

Arguments

<code>x</code>	matrix of locations in physical or parameter space
<code>power</code>	exponent used for calculating distance, default value of 2 = Pythagorean distance

Value

dst

Author(s)

Michael Dietze

distance.martix	<i>distance.matrix</i>
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Description

distance.matrix

Usage

```
distance.matrix(x, power = 1, dim = 2)
```

Arguments

x	matrix of locations in physical or parameter space
power	exponent used for calculating distance, default value of 2 = Pythagorean distance
dim	dimension

Value

d

Author(s)

Michael Dietze

distance12.martix	<i>distance12.matrix</i>
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Description

distance12.matrix

Usage

```
distance12.matrix(x, n1, power = 1)
```

Arguments

x	matrix of locations in parameter space
n1	number of rows in the original dataset
power	exponent used for calculating distance, default value of 2 = Pythagorean distance

Value

d

Author(s)

Michael Dietze

GaussProcess	<i>GaussProcess</i>
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Description

GaussProcess

Usage

```
GaussProcess(  
  x,  
  y,  
  isotropic = TRUE,  
  nugget = TRUE,  
  method = "bayes",  
  ngibbs = 5000,  
  burnin = 1000,  
  thin = 1,  
  jump.ic = c(1.1, 0.2),  
  prior = "IG",  
  mix = "joint",  
  psi = NULL,  
  zeroMean = FALSE,  
  exclude = NULL,  
  ...  
)
```

Arguments

x	set of independent variables
y	dependent variable
isotropic	Boolean indicating whether the GP is fit isotropically. If FALSE, distances are calculated deparately for each direction
nugget	allows additional error in Y rather than fix interpolation to go through points
method	method for calculating correlations
ngibbs	number of MCMC iterations (per chain) to run
burnin	Number of samples to discard as burnin (auto must be FALSE)
thin	thinning of the matrix to make things faster. Default is to thin to 1

jump.ic	initial condition for jump standard deviation.
prior	'unif', 'IG'
mix	joint=mix over psi simultaneously, each=mix over psi individually
psi	spatial corr
zeroMean	True if mean is 0, else false
exclude	<- isn't used anywhere, should be dropped
...	Additional arguments

Author(s)

Michael Dietze

gp_mle

*gp_mle***Description**

gp_mle

Usage

gp_mle(theta, d, nugget, myY, maxval = Inf)

Arguments

theta	proposed parameter vector: [mu, tauw, tauv, phi1...phiK]
d	spatial distance matrix
nugget	allows additional error in Y rather than fix interpolation to go through points
myY	vector of observed data
maxval	maximum value

Value

val

Author(s)

Michael Dietze

gp_mle2	<i>gp_mle2</i>
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Description

zero mean version

Usage

gp_mle2(theta, d, nugget, myY, maxval = Inf)

Arguments

- | | |
|--------|---|
| theta | proposed parameter vector: [mu, tauw, tauv, phi1...phiK] |
| d | spatial distance matrix |
| nugget | allows additional error in Y rather than fix interpolation to go through points |
| myY | vector of observed data |
| maxval | maximum value |

groupid	<i>groupid</i>
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Description

groupid

Usage

groupid(x)

Arguments

- | | |
|---|----------------------------|
| x | matrix of parameter values |
|---|----------------------------|

Author(s)

Michael Dietze

`jump`*jump*

Description`jump`**Usage**`jump(ic = 0, rate = 0.4, ...)`**Arguments**

<code>ic</code>	optional data vector
<code>rate</code>	target acceptance rate
<code>...</code>	Additional arguments

Author(s)

Michael Dietze

`jump-class`*define a class for automatically tuning jump distributions*

Description

define a class for automatically tuning jump distributions

Author(s)

Michael Dietze

ldinvgamma	ldinvgamma
Description Log-dinvgamma, based on MCMCpack	
Usage ldinvgamma(x, shape, scale = 1)	
Arguments x vector of quantiles shape, scale shape and scale parameters for the inverse Gamma distribution	
Value log.density	
Author(s) Michael Dietze	
lhc	lhc

Description Latin Hyper Cube	
Usage lhc(x, n.samp)	
Arguments x <- list (n.dim x 2) n.samp number of samples	
Details Simple uniform sampling with LHC permutation	
Author(s) Michael Dietze	

mvjump	<i>mvjump</i>
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Description

multivariate version

Usage

mvjump(ic = 0, rate = 0.4, nc = 2, ...)

Arguments

- | | |
|------|--|
| ic | optional data vector |
| rate | target acceptance rate |
| nc | NetCDF object containing target variable |
| ... | Additional arguments |

mvjump-class	<i>multivariate version of jump class</i>
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Description

multivariate version of jump class

nderiv	<i>nderiv</i>
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Description

nderiv

Usage

nderiv(x, y)

Arguments

- | | |
|---|------------------------------------|
| x | Name of variable to plot on X axis |
| y | Name of variable to plot on Y axis |

Value

der

Author(s)

Michael Dietze

p	<i>p</i>
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Description

p

Usage

p(x, ...)

Arguments

x	jump distribution
...	Additional arguments

p.jump	<i>p.jump</i>
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Description

p.jump

Usage

```
## S3 method for class 'jump'
p(jmp)
```

Arguments

jmp	jump parameter
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Author(s)

Michael Dietze

p.mvjump

p.mvjump

Description

p.mvjump

Usage

```
## S3 method for class 'mvjump'  
p(jmp)
```

Arguments

jmp jump parameter

plot.jump

plot.jump

Description

plot.jump

Usage

```
## S3 method for class 'jump'  
plot(jmp)
```

Arguments

jmp jump parameter

Author(s)

Michael Dietze

`plot.mvjump`*plot.mvjump*

Description`plot.mvjump`**Usage**

```
## S3 method for class 'mvjump'
plot(jmp)
```

Arguments

<code>jmp</code>	jump parameter
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Author(s)

Michael Dietze

`predict.density`*predict.density*

Description

Simple interpolation of a density object to new points

Usage

```
## S3 method for class 'density'
predict(den, xnew)
```

Arguments

<code>den</code>	density object
<code>xnew</code>	new x coordinate

Value

`ynew`

Author(s)

Michael Dietze

predict.GP	<i>predict.GP</i>
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Description

predict.GP

Usage

```
## S3 method for class 'GP'  
predict(gp, xpred, cI = NULL, pI = NULL, splinefcns = NULL)
```

Arguments

gp	Gaussian Process
xpred	value of x where prediction should be made
cI	credible interval
pI	prediction interval
splinefcns	spline functions

Author(s)

Michael Dietze

summarize.GP	<i>summarize.GP</i>
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Description

summarize.GP

Usage

```
summarize.GP(gp, pdf_file = NULL, txt_file = NULL)
```

Arguments

gp	Gaussian Process
pdf_file	filename you want figures written out to
txt_file	filename you want figures written out to

Author(s)

Michael Dietze

`update.jump`*update.jump*

Description`update.jump`**Usage**

```
## S3 method for class 'jump'
update(jmp, chain)
```

Arguments

<code>jmp</code>	jump parameter
<code>chain</code>	mcmc chain

Value`jmp` updated jump parameter**Author(s)**`Michael Dietze`

`update.mvjump`*update.mvjump*

Description`update.mvjump`**Usage**

```
## S3 method for class 'mvjump'
update(jmp, chain)
```

Arguments

<code>jmp</code>	jump parameter
<code>chain</code>	mcmc chain

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