Package: PEcAn.emulator (via r-universe)

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Type Package

Title Gausian Process Emulator

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Imports methods, mvtnorm, coda (>= 0.18), MCMCpack

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` *arate*

Description

Acceptance rate

Usage

```
arate(x)
```

Arguments

x	vector of MCMC samples

Author(s)

Michael Dietze

`calcSpatialCov` *calcSpatialCov*

Description

calcSpatialCov

Usage

```
calcSpatialCov(x, ...)
```

Arguments

x	either a spatial distance matrix or a list of component spatial distance matrices
...	Additional arguments

Author(s)

Michael Dietze

`calcSpatialCov.list` *calcSpatialCov.list*

Description

Currently assumes an exponential spatial dependency

Usage

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

Arguments

d	list of component spatial distance matrices
psi	spatial corr
tau	spatial var

Details

can make gaussian by passing squared distance matrix

Author(s)

Michael Dietze

calcSpatialCov.matrix *calcSpatialCov.matrix*

Description

Currently assumes an exponential spatial dependency

Usage

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

Arguments

d	spatial distance matrix
psi	spatial corr
tau	spatial var

Details

can make gaussian by passing squared distance matrix

Author(s)

Michael Dietze

distance *distance*

Description

distance

Usage

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

Arguments

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

Value

dst

Author(s)

Michael Dietze

`distance.martix` *distance.matrix*

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`	dimenstion

Value

d

Author(s)

Michael Dietze

`distance12.martix` *distance12.matrix*

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` *GaussProcess*

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 simultanously, 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

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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 *gp_mle2*

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 *groupid*

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

`ic`	optional data vector
`rate`	target acceptance rate
`...`	Addtional 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 *mvjump*

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 *multivariate version of jump class*

Description

multivariate version of jump class

nderiv *nderiv*

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` *p*

Description

p

Usage

```
p(x, ...)
```

Arguments

`x`	jump distribution
`...`	Additional arguments

`p.jump` *p.jump*

Description

p.jump

Usage

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

Arguments

`jmp`	jump parameter

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

jmp	jump parameter

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

den	density object
xnew	new x coordinate

Value

ynew

Author(s)

Michael Dietze

predict.GP *predict.GP*

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

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summarize.GP *summarize.GP*

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

jmp	jump parameter
chain	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

jmp	jump parameter
chain	mcmc chain

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