Package 'bnpmr'

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Type Package

Title Bayesian Monotonic Nonparametric Regression

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Description Implements the Bayesian nonparametric monotonic regression method described in Bornkamp & Ickstadt (2009), Biometrics, 65, 198-205.

License GPL

LazyLoad yes

NeedsCompilation yes

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`bnpmr-package` *Monotonic Regression*

Description

Implements the Bayesian monotonic regression method described in Bornkamp and Ickstadt (2009)

Details

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Date:	2018-04-07
License:	GPL
LazyLoad:	yes

Author(s)

Bjoern Bornkamp

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References

Bornkamp, B., Ickstadt, K. (2009). Bayesian nonparametric estimation of continuous monotone functions with applications to dose-response analysis. Biometrics, 65, 198-205.

See Also

pred.bnpmr, bnpmr

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bnpmr *Monotonic regression*

Description

Bayesian monotonic regression as described in Bornkamp and Ickstadt (2009).

Usage

```
bnpmr(y, x, prior = NULL, start = NULL, niter = 10000, pMoves = NULL,
      thin = 1, burnIn = 0, prop = NULL, seed = 1, size = 50)
```

Arguments

y	vector of dependent values
x	vector of independent values (the code internally standardizes x to [0,1])
prior	A list specifying prior parameters V, m, d, a - as defined in Biometrics paper p. 201 by default the noninformative choice of eqn (6) is chosen. vL, vU - lower and upper bound for uniform distribution of nu la, lb - alpha, beta parameter of beta prior for m (the TSP distribution mode) alpha - prior parameter for Dirichlet distribution (called gamma in the Biometrics paper)

lambda - prior parameter for truncated Poisson distr

`start` starting values for
nJ: number of components
jl: modes of TSP distributions (called m in the Biometrics paper see eqn (5))
jv: called nu in the Biometrics paper (eqn (5))
jh: weights of the components (sum to 1) called w_i in the Biometrics paper

`niter,burnIn,thin` number of iterations, thinning and burn-in

`pMoves` probabilities for the different move types

`prop`

`seed`

`size` size of the vectors in C++ code (all vectors only have finite size determined by `size`)

Value

A list with entries (among others)
dimcount - posterior simulations of number of components
jl - posterior sims of m
jv - posterior sims of nu
jh - posterior sims of w
beta - posterior sims of beta vector
s2 - posterior sims of s**2

Author(s)

Bjoern Bornkamp

References

Bornkamp, B. and Ickstadt, K. (2009). Bayesian Nonparametric Estimation of Continuous Monotone Functions with Applications to DoseResponse Analysis. Biometrics, 65, 198-205

See Also

`pred.bnpmr`

Examples

```
#############################################################################
## example 1
## generate some example data
x <- seq(0,1,length=100)
y <- 2+3*x/(0.05+x)+rnorm(100, 0, 1)
## run bnpmr function (with "default" parameters and priors)
res <- bnpmr(y, x)
```

```
sq <- seq(0,1,length=101)
aa <- pred.bnpmr(sq, res)
out005 <- apply(aa, 2, quantile, prob = 0.05)
out050 <- apply(aa, 2, median)
out095 <- apply(aa, 2, quantile, prob = 0.95)
## plot result
plot(x,y)
lines(sq, out005)
lines(sq, out050)
lines(sq, out095)
curve(2+3*x/(x+0.05), add=TRUE, col=2)

#########################################################################
## example 2 with a sparse dose-design
## closer to what we actually see in pharmaceutical dose-finding trials
x <- rep(c(0,0.05,0.2,0.6,1), each = 10)
y <- 2+3*x^5/(0.05^5+x^5)+rnorm(length(x), 0, 1)

res <- bnpmr(y, x)
sq <- seq(0,1,length=101)
aa <- pred.bnpmr(sq, res)
out005 <- apply(aa, 2, quantile, prob = 0.05)
out050 <- apply(aa, 2, median)
out095 <- apply(aa, 2, quantile, prob = 0.95)

plot(x,y, ylim = c(0,8))
lines(sq, out005)
lines(sq, out050)
lines(sq, out095)
curve(2+3*x^5/(x^5+0.05^5), add=TRUE, col=2)

#### now reanalyse using different prior
## use prior that says placebo response = 0 with small uncertainty
## (just to check code)
V <- matrix(c(0.01,0,0,10), nrow=2)
prior <- list(alpha = 1, lambda = 0.5, m = c(0, 1), V=V, a=3.6, d=4, la=1,lb=2)
res2 <- bnpmr(y, x, prior = prior)
aa <- pred.bnpmr(sq, res2)
out005 <- apply(aa, 2, quantile, prob = 0.05)
out050 <- apply(aa, 2, median)
out095 <- apply(aa, 2, quantile, prob = 0.95)
lines(sq, out005, col = "green")
lines(sq, out050, col = "green")
lines(sq, out095, col = "green")
```

`pred.bnpmr` *Predict Bayesian monotonic regression object*

Description

Predict Bayesian monotonic regression object

Usage

```
pred.bnpmr(x, res)
```

Arguments

x	where to predict the function (should be a vector with entries in [0,1])
res	the output of the bnpmr function

Value

A matrix containing the function simulations in the rows.

Author(s)

Bjoern Bornkamp

See Also

bnpmr

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ptsp *Distribution function of the two-sided power distribution*

Description

Distribution function of the two-sided power distribution

Usage

```
ptsp(x, m, n)
```

Arguments

x	Vector of numeric values in [0,1]
m,n	Distribution parameters, m is the mode of the distribution

Author(s)

Bjoern Bornkamp

References

van Dorp, R. and Kotz, S. (2002) The standard two-sided power distribution and its properties. The American Statistician, 56, 90-99

Examples

```
curve(ptsp(x, 0.5, 1), 0, 1)
curve(ptsp(x, 0.5, 2), 0, 1, add = TRUE)
curve(ptsp(x, 0.5, 5), 0, 1, add = TRUE)
curve(ptsp(x, 0.5, 10), 0, 1, add = TRUE)
```

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