Package ‘BASS’

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Author Devin Francom [aut, cre], Bruno Sanso [ths], Kellin Rumsey [aut]
Maintainer Devin Francom <devinfrancom@gmail.com>
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Bayesian Adaptive Spline Surfaces (BASS)

Description

Fits a BASS model using RJMCMC. Optionally uses parallel tempering to improve mixing. Can be used with scalar or functional response. Also can use categorical inputs.

Usage

bass(
  xx,
  y,
  maxInt = 3,
  maxInt.func = 3,
  maxInt.cat = 3,
  xx.func = NULL,
  degree = 1,
  maxBasis = 1000,
  npart = NULL,
  npart.func = NULL,
  nmcmc = 10000,
  nburn = 9000,
  thin = 1,
  g1 = 0,
  g2 = 0,
  s2.lower = 0,
  h1 = 10,
  h2 = 10,
  a.tau = 0.5,
  b.tau = NULL,
  w1 = 5,
  w2 = 5,
  beta.prior = "g",
  temp.ladder = NULL,
  start.temper = NULL,
  curr.list = NULL,
save.yhat = TRUE,
small = FALSE,
verbose = TRUE,
ret.str = F
)

Arguments

**xx**
a data frame or matrix of predictors. Categorical predictors should be included as factors.

**y**
a response vector (scalar response) or matrix (functional response). Note: If \(\sum(y^2)\) is large (i.e. \(1\times10^8\)), please center/rescale (and rescale \(g_1\) and \(g_2\) if necessary).

**maxInt**
integer for maximum degree of interaction in spline basis functions. Defaults to the number of predictors, which could result in overfitting.

**maxInt.func**
(functional response only) integer for maximum degree of interaction in spline basis functions describing the functional response.

**maxInt.cat**
(categorical input only) integer for maximum degree of interaction of categorical inputs.

**xx.func**
a vector, matrix or data frame of functional variables.

**degree**
degree of splines. Stability should be examined for anything other than 1.

**maxBasis**
maximum number of basis functions. This should probably only be altered if you run out of memory.

**npart**
minimum number of non-zero points in a basis function. If the response is functional, this refers only to the portion of the basis function coming from the non-functional predictors. Defaults to 20 or 0.1 times the number of observations, whichever is smaller.

**npart.func**
same as npart, but for functional portion of basis function.

**nmcmc**
number of RJMCMC iterations.

**nburn**
number of the nmcmc iterations to disregard.

**thin**
keep every thin samples

**g1**
shape for IG prior on \(\sigma^2\).

**g2**
shape for IG prior on \(\sigma^2\).

**s2.lower**
lower bound for \(s_2\). Turns IG prior for \(s_2\) into a truncated IG.

**h1**
shape for gamma prior on \(\lambda\).

**h2**
rate for gamma prior on \(\lambda\). This is the primary way to control overfitting. A large value of h2 favors fewer basis functions.

**a.tau**
shape for gamma prior on \(\tau\).

**b.tau**
rate for gamma prior on \(\tau\). Defaults to one over the number of observations, which centers the prior for the basis function weights on the unit information prior.

**w1**
nominal weight for degree of interaction, used in generating candidate basis functions. Should be greater than 0.
w2  nominal weight for variables, used in generating candidate basis functions. Should be greater than 0.

beta.prior  what type of prior to use for basis coefficients, "g" or "jeffreys"

temp.ladder  temperature ladder used for parallel tempering. The first value should be 1 and the values should increase.

start.temper  when to start tempering (after how many MCMC iterations). Defaults to 1000 or half of burn-in, whichever is smaller.

curr.list  list of starting models (one element for each temperature), could be output from a previous run under the same model setup.

save.yhat  logical; should predictions of training data be saved?

small  logical; if true, returns a smaller object by leaving out curr.list and other unnecessary objects. Use in combination with save.yhat to get smaller memory footprint for very large models.

verbose  logical; should progress be displayed?

ret.str  logical; return data and prior structures

Details

Explores BASS model space by RJMCMC. The BASS model has

\[ y = f(x) + \epsilon, \quad \epsilon \sim N(0, \sigma^2) \]

\[ f(x) = a_0 + \sum_{m=1}^{M} a_m B_m(x) \]

and \( B_m(x) \) is a BASS basis function (tensor product of spline basis functions). We use priors

\[ a \sim N(0, \sigma^2 / \tau (B'B)^{-1}) \]

\[ M \sim Poisson(\lambda) \]

as well as the priors mentioned in the arguments above.

Value

An object of class 'bass'. The other output will only be useful to the advanced user. Rather, users may be interested in prediction and sensitivity analysis, which are obtained by passing the entire object to the predict.bass or sobol functions.

See Also

predict.bass for prediction and sobol for sensitivity analysis.
Examples

## Not run:

### univariate example

## simulate data (Friedman function)

```r
f <- function(x) {
  10*sin(pi*x[,1]*x[,2])+20*(x[,3]-.5)^2+10*x[,4]+5*x[,5]
}
sigma <- 1 # noise sd
n <- 500 # number of observations
x <- matrix(runif(n*10), n, 10) # 10 variables, only first 5 matter
y <- rnorm(n, f(x), sigma)

## fit BASS, no tempering
mod <- bass(x, y)
plot(mod)

## fit BASS, tempering
mod <- bass(x, y, temp.ladder = 1.3^(0:8), start.temper = 1000)
plot(mod)

## prediction
npred <- 1000
xpred <- matrix(runif(npred*10), npred, 10)
pred <- predict(mod, xpred, verbose = TRUE) # posterior predictive samples
true.y <- f(xpred)
plot(true.y, colMeans(pred), xlab = "true values", ylab = "posterior predictive means")
abline(a = 0, b = 1, col = 2)

## sensitivity
sens <- sobol(mod)
plot(sens, cex.axis = .5)
```

### functional example

## simulate data (Friedman function with first variable as functional)

```r
sigma <- 1 # noise sd
n <- 500 # number of observations
nfunc <- 50 # size of functional variable grid
xfunc <- seq(0, 1, length.out = nfunc) # functional grid
x <- matrix(runif(n*9), n, 9) # 9 non-functional variables, only first 4 matter
X <- cbind(rep(xfunc, each = n), kronecker(rep(1, nfunc), x)) # to get y
y <- matrix(f(X), nrow = n) + rnorm(n*nfunc, 0, sigma)

## fit BASS
mod <- bass(x, y, xx.func = xfunc)
plot(mod)

## prediction
npred <- 100
xpred <- matrix(runif(npred*9), npred, 9)
```

bassBasis

Bayesian Adaptive Spline Surfaces (BASS) with basis decomposition of response

Description

Fits a BASS model to basis coefficients under the specified basis.

Usage

bassBasis(dat, n.cores = 1, parType = "fork", ...)

Arguments

dat  
list that includes elements xx, n.pc (number of basis functions), basis (dimension m x n.pc), newy (dimension n.pc x n), trunc.error (optional truncation error with dimension n x m), y.m (vector mean removed before basis decomposition with dimension m), y.s (vector sd scaled before basis decomposition with dimension m). See the documentation of bassPCA for more details.

n.cores  
integer number of cores (threads) to use

parType  
either "fork" or "socket". Forking is typically faster, but not compatible with Windows. If n.cores==1, parType is ignored.

...  
arguments to be passed to bass function calls.

Details

Under a user defined basis decomposition, fits a bass model to each PCA basis coefficient independently, bass(dat$xx, dat$newy[i,], ...) for i in 1 to n.pc, possibly in parallel. The basis does not need to be orthogonal, but independent modeling of basis coefficients should be sensible.
Value

An object of class 'bassBasis' with two elements:

- **mod.list**: list (of length \( n \cdot \text{pc} \)) of individual bass models
- **dat**: same as dat above

See Also

- *predict.bassBasis* for prediction and *sobolBasis* for sensitivity analysis.

Examples

```r
## Not run:

## simulate data (Friedman function)

f <- function(x){
  10*sin(pi*x[,1]*x[,2])+20*(x[,3]-.5)^2+10*x[,4]+5*x[,5]
}

## simulate data (Friedman function with first variable as functional)

sigma <- .1 # noise sd
n <- 500 # number of observations
nfunc <- 50 # size of functional variable grid
xfunc <- seq(0,1,length.out=nfunc) # functional grid
x <- matrix(runif(n*9),n,9) # 9 non-functional variables, only first 4 matter
X <- cbind(rep(xfunc,each=n),kronecker(rep(1,nfunc),x)) # to get y
y <- matrix(f(X),nrow=n)+rnorm(n*nfunc,0,sigma)

## fit BASS

library(parallel)

mod <- bassPCA(x,y,n.pc=5,n.cores=min(5,parallel::detectCores()))

plot(mod$mod.list[[1]])
plot(mod$mod.list[[2]])
plot(mod$mod.list[[3]])
plot(mod$mod.list[[4]])
plot(mod$mod.list[[5]])

hist(mod$dat$trunc.error)

## prediction

n.pred <- 100
x.pred <- matrix(runif(n.pred*9),n.pred,9)
X.pred <- cbind(rep(xfunc,each=n.pred),kronecker(rep(1,nfunc),x.pred))
y.pred <- matrix(f(X.pred),nrow=n.pred)

pred <- predict(mod,x.pred,mcmc.use=1:1000) # posterior predictive samples (each is a curve)

matplot(apply(pred,2:3,mean),type='l',xlab='observed',ylab='mean prediction')

abline(a=0,b=1,col=2)

matplot(t(y.pred),type='l') # actual

matplot(t(apply(pred,2:3,mean)),type='l') # mean prediction

## sensitivity

sens <- sobolBasis(mod,int.order = 2,ncores = max(parallel::detectCores()-2,1),
                     mcmc.use=1000) # for speed, only use a few samples

plot(sens)
```
## calibration

\[
x_{\text{true}} \leftarrow \text{runif}(0,0,1) \quad \# \text{what we are trying to learn}
\]

\[
y_{\text{obs}} \leftarrow f(\text{cbind}(x_{\text{func}}, \text{kroncker}(\text{rep}(1,n_{\text{func}}, t(x_{\text{true}})))) + \text{rnorm}(n_{\text{func}}, 0, 1)) \quad \# \text{calibration data (with measurement error)}
\]

\[
\text{plot}(y_{\text{obs}})
\]

\[
cal \leftarrow \text{calibrate.bassBasis}(y = y_{\text{obs}}, \text{mod} = \text{mod},
\text{discrep.mean} = \text{rep}(0,n_{\text{func}}),
\text{discrep.mat} = \text{diag}(n_{\text{func}})[,1:2] \times 0.0000001,
\text{sd.est} = 1,
\text{s2.df} = 50,
\text{s2.ind} = \text{rep}(1,n_{\text{func}}),
\text{meas.error.cor} = \text{diag}(n_{\text{func}}),
\text{bounds} = \text{rbind}(\text{rep}(0,9), \text{rep}(1,9)),
\text{n.mcmc} = \text{10000},
\text{temperature.ladder} = 1.05^{(0:30)} , \text{type} = 1)
\]

\[
n_{\text{burn}} = 5000
\]

\[
uu = \text{seq}(n_{\text{burn}}, 10000, 5)
\]

\[
\text{pairs}(\text{rbind}(\text{cal}$\text{theta}[uu,1,], x_{\text{true}}), \text{col} = \text{c(rep}(1, \text{length}(uu)), 2), \text{ylim} = \text{c}(0,1), \text{xlim} = \text{c}(0,1))
\]

\[
\text{pred} \leftarrow \text{apply}(\text{predict}(\text{mod, cal$theta[uu,1,]}, \text{nugget} = \text{T}, \text{trunc.error} = \text{T},
\text{mcmc.use} = \text{cal$ii[uu]}), 3, \text{function}(x) \text{diag}(x) + \text{rnorm}(\text{length}(uu), 0, \text{sqrt}(\text{cal$s2[uu,1,1]})))
\]

\[
\text{qq} \leftarrow \text{apply}(\text{pred}, 2, \text{quantile}, \text{probs} = \text{c}(0.025, 0.975))
\]

\[
\text{matplot}(t(\text{qq}), \text{col} = \text{'lightgrey'}, \text{type} = 'l')
\]

\[
\text{lines}(y_{\text{obs}}, \text{lwd} = 3)
\]

## minimal example for CRAN testing

\[
\text{mod} \leftarrow \text{bassPCA}(1:10, \text{matrix}(1:20, 10), n_{\text{pc}} = 2, \text{n.mcmc} = 2, n_{\text{burn}} = 1)
\]

---

**bassPCA**

*Bayesian Adaptive Spline Surfaces (BASS) with PCA decomposition of response*

**Description**

Decomposes a multivariate or functional response onto a principal component basis and fits a BASS model to each basis coefficient.

**Usage**

bassPCA(
    xx = NULL,
    y = NULL,
)
bassPCA

dat = NULL,
n.pc = NULL,
perc.var = 99,
n.cores = 1,
parType = "fork",
center = T,
scale = F,
...
)

Arguments

xx a data frame or matrix of predictors with dimension n x p. Categorical predictors should be included as factors.
y a response matrix (functional response) with dimension n x m.
dat optional (for more control) list with elements xx (same as above), y (same as above), n.pc (number of principal components used), basis (principal components with dimension m x n.pc), newy (reduced dimension y with dimension n.pc x n), trunc.error (optional truncation error with dimension n x m), y.m (vector mean removed before PCA with dimension m), y.s (vector sd scaled before PCA with dimension m). If dat is specified, xx, y and n.pc do not need to be specified.
n.pc number of principal components to use
perc.var optionally specify percent of variance to explain instead of n.pc
n.cores integer number of cores (threads) to use
parType either "fork" or "socket". Forking is typically faster, but not compatible with Windows. If n.cores==1, parType is ignored.
center logical whether to subtract the mean before getting the principal components, or else a numeric vector of dimension m for the center to be used
scale logical whether to divide by the standard deviation before getting the principal components, or else a numeric vector of dimension m for the scale to be used...

Details

Gets the PCA decomposition of the response y, and fits a bass model to each PCA basis coefficient,
bass(dat$xx,dat$newy[i,],...) for i in 1 to n.pc, possibly in parallel.

Value

An object of class 'bassBasis' with two elements:

mod.list list (of length n.pc) of individual bass models
dat same as dat above

See Also

predict.bassBasis for prediction and sobolBasis for sensitivity analysis.
Examples

## Not run:
## simulate data (Friedman function)
f<-function(x){
  10*sin(pi*x[,1]*x[,2])+20*(x[,3]-.5)^2+10*x[,4]+5*x[,5]
}
## simulate data (Friedman function with first variable as functional)
sigma<-.1 # noise sd
n<-500 # number of observations
nfunc<-50 # size of functional variable grid
xfunc<-seq(0,1,length.out=nfunc) # functional grid
x<-matrix(runif(n*9),n,9) # 9 non-functional variables, only first 4 matter
X<-cbind(rep(xfunc,each=n),kronecker(rep(1,nfunc),x)) # to get y
y<-matrix(f(X),nrow=n)+rnorm(n*nfunc,0,sigma)

## fit BASS
library(parallel)
mod<-bassPCA(x,y,n.pc=5,n.cores=min(5,parallel::detectCores()))
plot(mod$mod.list[[1]])
plot(mod$mod.list[[2]])
plot(mod$mod.list[[3]])
plot(mod$mod.list[[4]])
plot(mod$mod.list[[5]])
hist(mod$dat$trunc.error)

## prediction
npred<-100
xpred<-matrix(runif(npred*9),npred,9)
Xpred<-cbind(rep(xfunc,each=npred),kronecker(rep(1,nfunc),xpred))
ypred<-matrix(f(Xpred),nrow=npred)
pred<-predict(mod,xpred,mcmc.use=1:1000) # posterior predictive samples (each is a curve)
matplot(ypred,apply(pred,2:3,mean),type="l",xlab="observed",ylab="mean prediction")
abline(a=0,b=1,col=2)
matplot(t(ypred),type='l') # actual
matplot(t(apply(pred,2:3,mean)),type='l') # mean prediction

## sensitivity
sens<-sobolBasis(mod,int.order = 2,ncores = max(parallel::detectCores()-2,1),
mcmc.use=1000) # for speed, only use a few samples
plot(sens)

## calibration
x.true<-runif(9,0,1) # what we are trying to learn
yobs<-f(xfunc,kronecker(rep(1,nfunc),t(x.true)))+
rnorm(nfunc,0,1) # calibration data (with measurement error)
plot(yobs)

cal<-calibrate.bassBasis(y=yobs,mod=mod,
discrep.mean=rep(0,nfunc),
discrep.mat=diag(nfunc)[1:2]*.0000001,
calibrate.bassBasis

Calibrate a bassPCA or bassBasis Model to Data

Description

Robust modular calibration of a bassPCA or bassBasis emulator using adaptive Metropolis, tempering, and decorrelation steps in an effort to be free of any user-required tuning.

Usage

calibrate.bassBasis(
  y,  
  mod,  
  type,  
  sd.est,  
  s2.df,  
  s2.ind,  
  meas.error.cor,  
  bounds,  
  discrep.mean,  
  discrep.mat,  
  nmcmc = 10000,  
  temperature.ladder = 1.05^(0:30),  
  decor.step.every = 100,  
  nburn = 5000,  
  uu <- seq(nburn, 10000, 5)  
)

## End(Not run)
## minimal example for CRAN testing
mod <- bassPCA(1:10, matrix(1:20, 10), n.pc = 2, nmcmc = 2, nburn = 1)
Arguments

- `y`: vector of calibration data
- `mod`: a emulator of class `bassBasis`, whose predictions should match `y` (i.e., predictions from `mod` should be the same length as `y`)
- `type`: one of c(1, 2). 1 indicates a model that uses independent truncation error variance, no measurement error correlation, and discrepancy on a basis while type 2 indicates a model that uses a full truncation error covariance matrix, a full measurement error correlation matrix, a fixed full discrepancy covariance matrix, and a fixed discrepancy mean. 1 is for situations where computational efficiency is important (because `y` is dense), while 2 is only for cases where `y` is a short vector.
- `sd.est`: vector of prior estimates of measurement error standard deviation
- `s2.df`: vector of degrees of freedom for measurement error sd prior estimates
- `s2.ind`: index vector, same length as `y`, indicating which `sd.est` goes with which `y`
- `meas.error.cor`: a fixed correlation matrix for the measurement errors
- `bounds`: a 2xp matrix of bounds for each input parameter, where p is the number of input parameters.
- `discrep.mean`: discrepancy mean (fixed), only used if `type`=2
- `discrep.mat`: discrepancy covariance (fixed, for type 2) or basis (if not square, for type 1)
- `nmcmc`: number of MCMC iterations.
- `temperature.ladder`: an increasing vector, all greater than 1, for tempering. Geometric spacing is recommended, so that you have (1+delta)^n(0:ntemps), where delta is small (typically between 0.05 and 0.2) and ntemps is the number of elements in the vector.
- `decor.step.every`: integer number of MCMC iterations between decorrelation steps.
- `verbose`: logical, whether to print progress.

Details

Fits a modular Bayesian calibration model, with

\[ y = Kw(\theta) + Dv + \epsilon, \quad \epsilon \sim N(0, \sigma^2 R) \]

\[ f(x) = a_0 + \sum_{m=1}^{M} a_mB_m(x) \]

and \( B_m(x) \) is a BASS basis function (tensor product of spline basis functions). We use priors

\[ a \sim N(0, \sigma^2 / \tau(B'B)^{-1}) \]

\[ M \sim Poisson(\lambda) \]

as well as the priors mentioned in the arguments above.
Value

An object

See Also

predict.bassBasis for prediction and sobolBasis for sensitivity analysis.

Examples

```r
## Not run:
## simulate data (Friedman function)
f<-function(x){
  10*sin(pi*x[,1]*x[,2])+20*(x[,3]-.5)^2+10*x[,4]+5*x[,5]
}
## simulate data (Friedman function with first variable as functional)
sigma<-.1 # noise sd
n<-500 # number of observations
nfunc<-50 # size of functional variable grid
xfunc<-(0:1,length.out=nfunc) # functional grid
x<-matrix(runif(n*9),n,9) # 9 non-functional variables, only first 4 matter
X<-cbind(rep(xfunc,each=n),kronecker(rep(1,nfunc),x)) # to get y
y<-matrix(f(X),nrow=n)+rnorm(n*nfunc,0,sigma)

## fit BASS
library(parallel)
mod<-bassPCA(x,y,n.pc=5,n.cores=min(5,parallel::detectCores()))
plot(mod$mod.list[[1]])
plot(mod$mod.list[[2]])
plot(mod$mod.list[[3]])
plot(mod$mod.list[[4]])
plot(mod$mod.list[[5]])

hist(mod$dat$trunc.error)

## prediction
npred<-100
xpred<-matrix(runif(npred*9),npred,9)
Xpred<-cbind(rep(xfunc,each=npred),kronecker(rep(1,nfunc),xpred))
ypred<-matrix(f(Xpred),nrow=npred)
pred<-predict(mod,xpred,mcmc.use=1:1000) # posterior predictive samples (each is a curve)
matplot(ypred,apply(pred,2:3,mean),type='l',ylab='mean prediction')
abline(a=0,b=1,col=2)
matplot(t(ypred),type='l') # actual
matplot(t(apply(pred,2:3,mean)),type='l') # mean prediction

## sensitivity
sens<-sobolBasis(mod,int.order = 2,ncores = max(parallel::detectCores()+2,1),
mcmc.use=1000) # for speed, only use a few samples
plot(sens)

## calibration
```
```
x.true<-runif(9,0,1) # what we are trying to learn
yobs<-f(cbind(xfunc,kronecker(rep(1,nfunc),t(x.true)))) +
    rnorm(nfunc,0,1) # calibration data (with measurement error)
plot(yobs)

cal<-calibrate.bassBasis(y=yobs,mod=mod,
    discrep.mean=rep(0,nfunc),
    discrep.mat=diag(nfunc)[1:2]*.0000001,
    sd.est=.1,
    s2.df=50,
    s2.ind=rep(1,nfunc),
    meas.error.cor=diag(nfunc),
    bounds=rbind(rep(0,9),rep(1,9)),
    nmcmc=10000,
    temperature.ladder=1.05^(0:30),type=1)

nburn<-5000
uu<-seq(nburn,10000,5)
pairs(rbind(cal$theta[uu,1,,],x.true),col=c(rep(1,length(uu)),2),ylim=c(0,1),xlim=c(0,1))
pred<-apply(predict(mod,cal$theta[uu,1,,],nugget = T, trunc.error = T,
    mcmc.use = cal$ii[uu],3,function(x) diag(x)+rnorm(length(uu),0,sqrt(cal$s2[uu,1,1])))
    qq<-apply(pred,2,quantile,probs=c(.025,.975))
    matplot(t(qq),col='lightgrey',type='l')
    lines(yobs,lwd=3)

## End(Not run)
## minimal example for CRAN testing
mod<-bassPCA(1:10,matrix(1:20,10),n.pc=2,nmcmc=2,nburn=1)
```

---

**plot.bass**  

**BASS Plot Diagnostics**

**Description**

Generate diagnostic plots for BASS model fit.

**Usage**

```r
## S3 method for class 'bass'
plot(x, quants = c(0.025, 0.975), ...)
```

**Arguments**

- `x`  
  a bass object.

- `quants`  
  quantiles for intervals, if desired. NULL if not desired.

- `...`  
  graphical parameters.
Details

The first two plots are trace plots for diagnosing convergence. The third plot is posterior predicted vs observed, with intervals for predictions. The fourth plot is a histogram of the residuals (of the posterior mean model), with a red curve showing the assumed Normal density (using posterior mean variance). If `bass` was run with `save.yhat = FALSE`, the third and fourth plots are omitted.

See Also

`bass`, `predict.bass`, `sobol`

Examples

```r
# See examples in bass documentation.
```

---

**plot.bassBasis**  

**BASS Plot Diagnostics**

**Description**

Generate diagnostic plots for BASS model fit.

**Usage**

```r
## S3 method for class 'bassBasis'
plot(x, quants = c(0.025, 0.975), pred = T, ...)
```

**Arguments**

- `x`: a `bassBasis` object.
- `quants`: quantiles for intervals, if desired. NULL if not desired.
- `pred`: logical, should predictive performance be plotted?
- `...`: graphical parameters.

**Details**

The first two plots are trace plots for diagnosing convergence. The third plot is posterior predicted vs observed, with intervals for predictions. The fourth plot is a histogram of the residuals (of the posterior mean model). If `pred = FALSE`, the third and fourth plots are omitted.

**See Also**

`bassBasis`, `bassPCA`, `predict.bassBasis`, `sobolBasis`

**Examples**

```r
# See examples in bassBasis documentation.
```
**plot.bassSob**  
*Plot BASS sensitivity indices*

**Description**

Generate plots for sensitivity analysis of BASS.

**Usage**

```r
## S3 method for class 'bassSob'
plot(x, ...)
```

**Arguments**

- `x`: A `bassSob` object, returned from `sobol`.
- `...`: Graphical parameters.

**Details**

If `func.var` in the call to `sobol` was `NULL`, this returns boxplots of sensitivity indices and total sensitivity indices. If there were functional variables, they are labeled with letters alphabetically. Thus, if I fit a model with 4 categorical/continuous inputs and 2 functional inputs, the functional inputs are labeled a and b. If `func.var` was not `NULL`, then posterior mean functional sensitivity indices are plotted, along with the functional partitioned variance. Variables and interactions that are excluded did not explain any variance.

**See Also**

- `bass`, `predict.bass`, `sobol`

**Examples**

```r
# See examples in bass documentation.
```

---

**predict.bass**  
*BASS Prediction*

**Description**

Predict function for BASS. Outputs the posterior predictive samples based on the specified MCMC iterations.
predict.bass

Usage

## S3 method for class 'bass'
predict(
  object,
  newdata,
  newdata.func = NULL,
  mcmc.use = NULL,
  verbose = FALSE,
  nugget = FALSE,
  ...
)

Arguments

neutral            a fitted model, output from the bass function.
neutral.data       a matrix of new input values at which to predict. The columns should correspond
to the same variables used in the bass function.
neutral.data.func  a matrix of new values of the functional variable. If none, the same values will
be used as in the training data.
mcmc.use           a vector indexing which MCMC iterations to use for prediction.
verbose            logical; should progress be displayed?
nugget             logical; should predictions include error? If FALSE, predictions will be for
mean.
...                 further arguments passed to or from other methods.

Details

Efficiently predicts when two MCMC iterations have the same basis functions (but different weights).

Value

If model output is a scalar, this returns a matrix with the same number of rows as newdata and
columns corresponding to the the MCMC iterations mcmc.use. These are samples from the poste-
rior predictive distribution. If model output is functional, this returns an array with first dimension
corresponding to MCMC iteration, second dimension corresponding to the rows of newdata, and
third dimension corresponding to the rows of newdata.func.

See Also

bass for model fitting and sobol for sensitivity analysis.

Examples

# See examples in bass documentation.
**predict.bassBasis**  

**BASS Prediction**

**Description**

Predict function for BASS. Outputs the posterior predictive samples based on the specified MCMC iterations.

**Usage**

```r
## S3 method for class 'bassBasis'
predict(
  object,
  newdata,
  mcmc.use = NULL,
  trunc.error = FALSE,
  nugget = T,
  n.cores = 1,
  parType = "fork",
  ...
)
```

**Arguments**

- `object`: a fitted model, output from the `bass` function.
- `newdata`: a matrix of new input values at which to predict. The columns should correspond to the same variables used in the `bassBasis` or `bassPCA` functions.
- `mcmc.use`: a vector indexing which MCMC iterations to use for prediction.
- `trunc.error`: logical, use basis truncation error when predicting?
- `nugget`: logical, use individual `bass` nugget variances when predicting?
- `n.cores`: number of cores, though 1 is often the fastest.
- `parType`: either "fork" or "socket". Forking is typically faster, but not compatible with Windows. If `n.cores==1`, `parType` is ignored.
- `...`: further arguments passed to or from other methods.

**Details**

Prediction combined across `bass` models.

**Value**

An array with first dimension corresponding to MCMC iteration, second dimension corresponding to the rows of `newdata`, and third dimension corresponding to the multivariate/functional response.
See Also

`bassPCA` and `bassBasis` for model fitting and `sobolBasis` for sensitivity analysis.

Examples

# See examples in bass documentation.
**Description**

Decomposes the variance of the BASS model into variance due to main effects, two way interactions, and so on, similar to the ANOVA decomposition for linear models. Uses the Sobol’ decomposition, which can be done analytically for MARS models.

**Usage**

```r
sobol(
  bassMod, 
  prior = NULL, 
  prior.func = NULL, 
  mcmc.use = NULL, 
  func.var = NULL, 
  xx.func.var = NULL, 
  verbose = TRUE, 
  getEffects = FALSE 
)
```

**Arguments**

- `bassMod` a fitted model output from the `bass` function.
- `prior` a list of priors; uniform, truncated mixture of Normals or Ts for continuous; vector of category weights for categorical. Default is uniform over range of data.
- `prior.func` prior for functional variable. In almost all cases, keep this as the uniform default.
- `mcmc.use` an integer vector indexing which MCMC iterations to use for sensitivity analysis.
- `func.var` an integer indicating which functional variable to make sensitivity indices a function of. Disregard if `bassMod` is non-functional or if scalar sensitivity indices are desired.
- `xx.func.var` grid for functional variable specified by `func.var`. Disregard if `func.var` is not specified. If `func.var` is specified and `xx.func.var` not specified, the grid used to fit `bass` will be used.
- `verbose` logical; should progress be displayed?
- `getEffects` logical; should Sobols ANOVA decomposition be computed?

**Details**

Performs analytical Sobol’ decomposition for each MCMC iteration in `mcmc.use` (each corresponds to a MARS model), yielding a posterior distribution of sensitivity indices. Can obtain Sobol’ indices as a function of one functional variable.
sobolBasis

Value

If non-functional (func.var = NULL), a list with two elements:

S a data frame of sensitivity indices with number of rows matching the length of mcmc.use. The columns are named with a particular main effect or interaction. The values are the proportion of variance in the model that is due to each main effect or interaction.

T a data frame of total sensitivity indices with number of rows matching the length of mcmc.use. The columns are named with a particular variable.

Otherwise, a list with four elements:

S an array with first dimension corresponding to MCMC samples (same length as mcmc.use), second dimension corresponding to different main effects and interactions (labeled in names.ind), and third dimension corresponding to the grid used for the functional variable. The elements of the array are sensitivity indices.

S.var same as S, but scaled in terms of total variance rather than percent of variance.

names.ind a vector of names of the main effects and interactions used.

xx the grid used for the functional variable.

See Also

bass for model fitting and predict.bass for prediction.

Examples

# See examples in bass documentation.

sobolBasis

BASS Sensitivity Analysis

Description

Decomposes the variance of the BASS model into variance due to main effects, two way interactions, and so on, similar to the ANOVA decomposition for linear models. Uses the Sobol’ decomposition, which can be done analytically for MARS models.

Usage

sobolBasis(
  mod,
  int.order,
  prior = NULL,
  mcmc.use = NULL,
  nind = NULL,
n.cores = 1,
parType = "fork",
plot = F,
verbose = T)

Arguments

mod
output from the `bassBasis` or `bassPCA` function.

int.order
an integer indicating the highest order of interactions to include in the Sobol decomposition.

prior
a list with the same number of elements as there are inputs to mod. Each element specifies the prior for the particular input. Each prior is specified as a list with elements dist (one of c("normal", "student", "uniform")), trunc (a vector of dimension 2 indicating the lower and upper truncation bounds, taken to be the data bounds if omitted), and for "normal" or "student" priors, mean (scalar mean of the Normal/Student, or a vector of means for a mixture of Normals or Students), sd (scalar standard deviation of the Normal/Student, or a vector of standard deviations for a mixture of Normals or Students), df (scalar degrees of freedom of the Student, or a vector of degrees of freedom for a mixture of Students), and weights (a vector of weights that sum to one for the mixture components, or the scalar 1). If unspecified, a uniform is assumed with the same bounds as are represented in the input to mod.

mcmc.use
an integer indicating which MCMC iteration to use for sensitivity analysis. Defaults to the last iteration.

nind
number of Sobol indices to keep (will keep the largest nind).

n.cores
number of cores to use (nearly linear speedup for adding cores).

parType
either "fork" or "socket". Forking is typically faster, but not compatible with Windows. If n.cores==1, parType is ignored.

plot
logical; whether to plot results.

verbose
logical; print progress.

Details

Performs analytical Sobol’ decomposition for each MCMC iteration in mcmc.use (each corresponds to a MARS model), yielding a posterior distribution of sensitivity indices. Can obtain Sobol’ indices as a function of one functional variable.

Value

If non-functional (func.var = NULL), a list with two elements:

S
a data frame of sensitivity indices with number of rows matching the length of mcmc.use. The columns are named with a particular main effect or interaction. The values are the proportion of variance in the model that is due to each main effect or interaction.
A data frame of total sensitivity indices with number of rows matching the length of `mcmc.use`. The columns are named with a particular variable.

Otherwise, a list with four elements:

- **S**: an array with first dimension corresponding to MCMC samples (same length as `mcmc.use`), second dimension corresponding to different main effects and interactions (labeled in `names.ind`), and third dimension corresponding to the grid used for the functional variable. The elements of the array are sensitivity indices.

- **S.var**: same as `S`, but scaled in terms of total variance rather than percent of variance.

- **names.ind**: a vector of names of the main effects and interactions used.

**See Also**

- `bassPCA` and `bassBasis` for model fitting and `predict.bassBasis` for prediction.

**Examples**

```r
# See examples in bass documentation.
```

---

**summary.bass**

*Summarize BASS Details*

**Description**

Summarize some of the details of a BASS model.

**Usage**

```r
# S3 method for class 'bass'
summary(object, ...)
```

**Arguments**

- **object**: a bass object, returned from bass.
- **...**: further arguments passed to or from other methods.
Summary: BASS Details

Description
Summarize some of the details of a BASS model.

Usage
## S3 method for class 'bassBasis'
summary(object, ...)

Arguments

- **object**: a `bassBasis` object, returned from `bassPCA` or `bassBasis`.
- **...**: further arguments passed to or from other methods.
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