

Package ‘hetGP’

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Title Heteroskedastic Gaussian Process Modeling and Design under Replication

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Description Performs Gaussian process regression with heteroskedastic noise following Binois, M., Gramacy, R., Ludkovski, M. (2016) <arXiv:1611.05902>. The input dependent noise is modeled as another Gaussian process. Replicated observations are encouraged as they yield computational savings. Sequential design procedures based on the integrated mean square prediction error and lookahead heuristics are provided, and notably fast update functions when adding new observations.

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 hetGP-package

Package hetGP

Description

Performs Gaussian process regression with heteroskedastic noise following Binois, M., Gramacy, R., Ludkovski, M. (2016) <arXiv:1611.05902>. The input dependent noise is modeled as another Gaussian process. Replicated observations are encouraged as they yield computational savings. Sequential design procedures based on the integrated mean square prediction error and lookahead heuristics are provided, and notably fast update functions when adding new observations.

Details

Important functions:

`mleHetGP` as the main function to build a model.

`mleHomGP` the equivalent for homoskedastic modeling.

`crit_IMSPE` for adding a new design based on the Integrated Mean Square Prediction Error.

`IMSPE_optim` for augmenting a design, possibly based on a lookahead heuristic to bias the search toward replication.

`crit_optim` is similar to `IMSPE_optim` but for the optimization or contour finding criterion available.

Note

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Author(s)

Mickael Binois, Robert B. Gramacy

References

M. Binois, Robert B. Gramacy, M. Ludkovski (2018), Practical heteroskedastic Gaussian process modeling for large simulation experiments, *Journal of Computational and Graphical Statistics*, 27(4), 808–821.

Preprint available on arXiv:1611.05902.

M. Binois, J. Huang, R. B. Gramacy, M. Ludkovski (2018+), Replication or exploration? Sequential design for stochastic simulation experiments, *Technometrics* (to appear).

Preprint available on arXiv:1710.03206.

Examples

```
##-----
## Example 1: Heteroskedastic GP modeling on the motorcycle data
##-----
set.seed(32)

## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
nvar <- 1
plot(X, Z, ylim = c(-160, 90), ylab = 'acceleration', xlab = "time")

## Model fitting
settings <- list(return.hom = TRUE) # To keep homoskedastic model used for training
model <- mleHetGP(X = X, Z = Z, lower = rep(0.1, nvar), upper = rep(50, nvar),
                 covtype = "Matern5_2", settings = settings)

## A quick view of the fit
```

```

summary(model)

## Create a prediction grid and obtain predictions
xgrid <- matrix(seq(0, 60, length.out = 301), ncol = 1)
predictions <- predict(x = xgrid, object = model)

## Display averaged observations
points(model$X0, model$Z0, pch = 20)

## Display mean predictive surface
lines(xgrid, predictions$mean, col = 'red', lwd = 2)
## Display 95% confidence intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
## Display 95% prediction intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)

## Comparison with homoskedastic fit
predictions2 <- predict(x = xgrid, object = model$modHom)
lines(xgrid, predictions2$mean, col = 4, lty = 2, lwd = 2)
lines(xgrid, qnorm(0.05, predictions2$mean, sqrt(predictions2$sd2)), col = 4, lty = 3)
lines(xgrid, qnorm(0.95, predictions2$mean, sqrt(predictions2$sd2)), col = 4, lty = 3)

##-----
## Example 2: Sequential design
##-----
## Not run:
library(DiceDesign)

## Design configuration / Parameter settings
N_tot <- 500 # total number of points
n_init <- 10 # number of unique designs

## HetGP options
nvar <- 1 # number of variables
lower <- rep(0.001, nvar)
upper <- rep(1, nvar)

### Problem definition

## Mean function
forrester <- function(x){
  return(((x*6-2)^2)*sin((x*6-2)*2))
}

## Noise field via standard deviation
noiseFun <- function(x, coef = 1.1, scale = 1){
  if(is.null(nrow(x)))
    x <- matrix(x, nrow = 1)

```

```

    return(scale*(coef + sin(x * 2 * pi)))
  }

### Test function defined in [0,1]
ftest <- function(x){
  if(is.null(nrow(x)))
    x <- matrix(x, ncol = 1)
  return(forrester(x) + rnorm(nrow(x), mean = 0, sd = noiseFun(x)))
}

## Predictive grid
ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- matrix(xgrid, ncol = 1)

par(mar = c(3,3,2,3)+0.1)
plot(xgrid, forrester(xgrid), type = 'l', lwd = 1, col = "blue", lty = 3,
      xlab = '', ylab = '', ylim = c(-8,16))

set.seed(42)

# Initial design
X <- maximinSA_LHS(lhsDesign(n_init, nvar, seed = 42)$design)$design
Z <- apply(X, 1, ftest)

points(X, Z)

model <- model_init <- mleHetGP(X = X, Z = Z, lower = lower, upper = upper)

for(ii in 1:(N_tot - n_init)){
  ##Precalculations
  Wijs <- hetGP::Wij(mu1 = model$X0, theta = model$theta, type = model$covtype)

  ## Adapt the horizon based on the training rmspe/score
  current_horizon <- horizon(model = model, Wijs = Wijs)

  if(current_horizon == -1){
    opt <- IMSPE_optim(model = model, h = 0, Wijs = Wijs)
  }else{
    opt <- IMSPE_optim(model = model, h = current_horizon, Wijs = Wijs)
  }

  Xnew <- opt$par
  Znew <- apply(Xnew, 1, ftest)
  X <- rbind(X, Xnew)
  Z <- c(Z, Znew)
  points(Xnew, Znew)

  ## Update of the model
  model <- update(object = model, Xnew = Xnew, Znew = Znew, lower = lower, upper = upper)
  if(ii %% 25 == 0 || ii == (N_tot - n_init)){
    model_test <- mleHetGP(X = list(X0 = model$X0, Z0 = model$Z0, mult = model$mult), Z = model$Z,
                          lower = lower, upper = upper, maxit = 1000)
  }
}

```

```

    model <- compareGP(model, model_test)
  }
}
### Plot result
preds <- predict(x = Xgrid, model)
lines(Xgrid, preds$mean, col = 'red', lwd = 2)
lines(Xgrid, qnorm(0.05, preds$mean, sqrt(preds$sd2)), col = 2, lty = 2)
lines(Xgrid, qnorm(0.95, preds$mean, sqrt(preds$sd2)), col = 2, lty = 2)
lines(Xgrid, qnorm(0.05, preds$mean, sqrt(preds$sd2 + preds$nugs)), col = 3, lty = 2)
lines(Xgrid, qnorm(0.95, preds$mean, sqrt(preds$sd2 + preds$nugs)), col = 3, lty = 2)
par(new = TRUE)
plot(NA, NA, xlim = c(0, 1), ylim = c(0, max(model$mult)), axes = FALSE, ylab = "", xlab = "")
segments(x0 = model$X, x1 = model$X, y0 = rep(0, nrow(model$X)), y1 = model$mult, col = 'grey')
axis(side = 4)
mtext(side = 4, line = 2, expression(a[i]), cex = 0.8)
mtext(side = 2, line = 2, expression(f(x)), cex = 0.8)
mtext(side = 1, line = 2, 'x', cex = 0.8)

## End(Not run)

```

allocate_mult

Allocation of replicates on existing designs

Description

Allocation of replicates on existing design locations, based on (29) from (Ankenman et al, 2010)

Usage

```
allocate_mult(model, N, Wijs = NULL, use.Ki = FALSE)
```

Arguments

model	hetGP model
N	total budget of replication to allocate
Wijs	optional previously computed matrix of Wijs, see Wij
use.Ki	should Ki from model be used? Using the inverse of C (covariance matrix only, without noise, using ginv) is also possible

Value

vector with approximated best number of replicates per design

References

B. Ankenman, B. Nelson, J. Staum (2010), Stochastic kriging for simulation metamodeling, Operations research, pp. 371–382, 58

Examples

```

##-----
## Example: Heteroskedastic GP modeling on the motorcycle data
##-----
set.seed(32)

## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
nvar <- 1

data_m <- find_reps(X, Z, rescale = TRUE)

plot(rep(data_m$X0, data_m$mult), data_m$Z, ylim = c(-160, 90),
      ylab = 'acceleration', xlab = "time")

## Model fitting
model <- mleHetGP(X = list(X0 = data_m$X0, Z0 = data_m$Z0, mult = data_m$mult),
                 Z = Z, lower = rep(0.1, nvar), upper = rep(5, nvar),
                 covtype = "Matern5_2")
## Compute best allocation
A <- allocate_mult(model, N = 1000)

## Create a prediction grid and obtain predictions
xgrid <- matrix(seq(0, 1, length.out = 301), ncol = 1)
predictions <- predict(x = xgrid, object = model)

## Display mean predictive surface
lines(xgrid, predictions$mean, col = 'red', lwd = 2)
## Display 95% confidence intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
## Display 95% prediction intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)

par(new = TRUE)
plot(NA, NA, xlim = c(0,1), ylim = c(0,max(A)), axes = FALSE, ylab = "", xlab = "")
segments(x0 = model$X0, x1 = model$X0,
         y0 = rep(0, nrow(model$X)), y1 = A, col = 'grey')
axis(side = 4)
mtext(side = 4, line = 2, expression(a[i]), cex = 0.8)

```

Description

A batch design-evaluated ATO data set, random partition into training and testing, and fitted **hetGP** model; similarly a sequentially designed adaptive horizon data set, and associated fitted **hetGP** model

Usage

```
data(ato)
```

Format

Calling `data(ato)` causes the following objects to be loaded into the namespace.

`X` 2000x8 matrix of inputs coded from 1,...,20 to the unit 8-cube; original inputs can be recreated as $X \times 19 + 1$

`Z` 2000x10 matrix of normalized outputs obtained in ten replicates at each of the 2000 inputs `X`. Original outputs can be obtained as $Z \times \sqrt{Zv} + Zm$

`Zm` scalar mean used to normalize `Z`

`Zv` scalar variance used to normalize `Z`

`train` vector of 1000 rows of `X` and `Z` selected for training

`Xtrain` 1000x8 matrix obtained as a random partition of `X`

`Ztrain` length 1000 list of vectors containing the selected (replicated) observations at each row of `Xtrain`

`mult` the length of each entry of `Ztrain`; same as `unlist(lapply(Ztrain, length))`

`kill` a logical vector indicating which rows of `Xtrain` for which all replicates of `Z` are selected for `Ztrain`; same as `mult == 10`

`Xtrain.out` 897x8 matrix comprised of the subset of `X` where not all replicates are selected for training; i.e., those for which `kill == FALSE`

`Ztrain.out` list of length 897 containing the replicates of `Z` not selected for `Ztrain`

`nc` `noiseControl` argument for `mleHetGP` call

`out` `mleHetGP` model based on `Xtrain` and `Ztrain` using `noiseControl=nc`

`Xtest` 1000x8 matrix containing the other partition of `X` of locations not selected for training

`Ztest` 1000x10 matrix of responses from the partition of `Z` not selected for training

`ato.a` 2000x9 matrix of sequentially designed inputs (8) and outputs (1) obtained under an adaptive horizon scheme

`Xa` 2000x8 matrix of coded inputs from `ato.a` as $(ato.a[, 1:8]-1)/19$

`Za` length 2000 vector of outputs from `ato.a` as $(ato.a[, 9] - Zm)/\sqrt{Zv}$

`out.a` `mleHetGP` model based on `Xa` and `Za` using `noiseControl=nc`

Details

The assemble to order (ATO) simulator (Hong, Nelson, 2006) is a queuing simulation targeting inventory management scenarios. The setup is as follows. A company manufactures m products. Products are built from base parts called items, some of which are “key” in that the product cannot be built without them. If a random request comes in for a product that is missing a key item, a replenishment order is executed, and is filled after a random period. Holding items in inventory is expensive, so there is a balance between inventory costs and revenue. Hong & Nelson built a Matlab simulator for this setup, which was subsequently reimplemented by Xie, et al., (2012).

Binois, et al (2018a) describe an out-of-sample experiment based on this latter implementation in its default (Hong & Nelson) setting, specifying item cost structure, product makeup (their items) and revenue, distribution of demand and replenishment time, under target stock vector inputs $b \in \{1, \dots, 20\}^8$ for eight items. They worked with 2000 random uniform input locations (X), and ten replicate responses at each location (Z). The partition of 1000 training data points (X_{train} and Z_{train}) and 1000 testing (X_{test} and Z_{test}) sets provided here is an example of one that was used for the Monte Carlo experiment in that paper. The elements $X_{\text{train.out}}$ and $Z_{\text{train.out}}$ comprise of replicates from the training inputs which were not used in training, so may be used for out-of-sample testing. For more details on how the partitions were build, see the code in the examples section below.

Binois, et al (2018b) describe an adaptive lookahead horizon scheme for building a sequential design (X_a, Z_a) of size 2000 whose predictive performance, via proper scores, is almost as good as the approximately 5000 training data sites in each of the Monte Carlo repetitions described above. The example code below demonstrates this via out-of-sample predictions on X_{test} (measured against Z_{test}) when X_{train} and Z_{train} are used compared to those from X_a and Z_a .

Note

The `mleHetGP` output objects were build with `return.matrices=FALSE` for more compact storage. Before these objects can be used for calculations, e.g., prediction or design, these covariance matrices need to be rebuilt with `rebuild`. The generic `predict` method will call `rebuild` automatically, however, some of the other methods will not, and it is often more efficient to call `rebuild` once at the outset, rather than for every subsequent `predict` call

Author(s)

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References

- Hong L., Nelson B. (2006), Discrete optimization via simulation using COMPASS. *Operations Research*, 54(1), 115-129.
- Xie J., Frazier P., Chick S. (2012). Assemble to Order Simulator. http://simopt.org/wiki/index.php?title=Assemble_to_Order&oldid=447.
- M. Binois, J. Huang, R. Gramacy, M. Ludkovski (2018a), Replication or exploration? Sequential design for stochastic simulation experiments, arXiv preprint arXiv:1710.03206.
- M. Binois, Robert B. Gramacy, M. Ludkovski (2018b), Practical heteroskedastic Gaussian process modeling for large simulation experiments, arXiv preprint arXiv:1611.05902.

See Also

[bfs](#), [sirEval](#), [link{rebuild}](#), [horizon](#), [IMSPE_optim](#), [mleHetGP](#), [vignette\("hetGP"\)](#)

Examples

```

data(ato)

## Not run:
##
## the code below was used to create the random partition
##

## recover the data in its original form
X <- X*19+1
Z <- Z*sqrt(Zv) + Zm

## code the inputs and outputs; i.e., undo the transformation
## above
X <- (X-1)/19
Zm <- mean(Z)
Zv <- var(as.vector(Z))
Z <- (Z - Zm)/sqrt(Zv)

## random training and testing partition
train <- sample(1:nrow(X), 1000)
Xtrain <- X[train,]
Xtest <- X[-train,]
Ztest <- as.list(as.data.frame(t(Z[-train,])))
Ztrain <- Ztrain.out <- list()
mult <- rep(NA, nrow(Xtrain))
kill <- rep(FALSE, nrow(Xtrain))
for(i in 1:length(train)) {
  reps <- sample(1:ncol(Z), 1)
  w <- sample(1:ncol(Z), reps)
  Ztrain[[i]] <- Z[train[i],w]
  if(reps < 10) Ztrain.out[[i]] <- Z[train[i],-w]
  else kill[i] <- TRUE
  mult[i] <- reps
}

## calculate training locations and outputs for replicates not
## included in Ztrain
Xtrain.out <- Xtrain[!kill,]
Ztrain.out <- Ztrain[which(!kill)]

## fit hetGP model
out <- mleHetGP(X=list(X0=Xtrain, Z0=sapply(Ztrain, mean), mult=mult),
  Z=unlist(Ztrain), lower=rep(0.01, ncol(X)), upper=rep(30, ncol(X)),
  covtype="Matern5_2", noiseControl=nc, known=list(beta0=0),
  maxit=100000, settings=list(return.matrices=FALSE))

##

```

```

## the adaptive lookahead design is read in and fit as
## follows
##
Xa <- (ato.a[,1:8]-1)/19
Za <- ato.a[,9]
Za <- (Za - Zm)/sqrt(Zv)

## uses nc defined above
out.a <- mleHetGP(Xa, Za, lower=rep(0.01, ncol(X)),
  upper=rep(30, ncol(X)), covtype="Matern5_2", known=list(beta0=0),
  noiseControl=nc, maxit=100000, settings=list(return.matrices=FALSE))

## End(Not run)

##
## the following code duplicates a predictive comparison in
## the package vignette
##

## first using the model fit to the train partition (out)
out <- rebuild(out)

## predicting out-of-sample at the test sights
phet <- predict(out, Xtest)
phets2 <- phet$sd2 + phet$nugs
mhet <- as.numeric(t(matrix(rep(phet$mean, 10), ncol=10)))
s2het <- as.numeric(t(matrix(rep(phets2, 10), ncol=10)))
sehet <- (unlist(t(Ztest)) - mhet)^2
sc <- - sehet/s2het - log(s2het)
mean(sc)

## predicting at the held-out training replicates
phet.out <- predict(out, Xtrain.out)
phets2.out <- phet.out$sd2 + phet.out$nugs
s2het.out <- mhet.out <- Ztrain.out
for(i in 1:length(mhet.out)) {
  mhet.out[[i]] <- rep(phet.out$mean[i], length(mhet.out[[i]]))
  s2het.out[[i]] <- rep(phets2.out[i], length(s2het.out[[i]]))
}
mhet.out <- unlist(t(mhet.out))
s2het.out <- unlist(t(s2het.out))
sehet.out <- (unlist(t(Ztrain.out)) - mhet.out)^2
sc.out <- - sehet.out/s2het.out - log(s2het.out)
mean(sc.out)

## then using the model trained from the "adaptive"
## sequential design, with comparison from the "batch"
## one above
out.a <- rebuild(out.a)
phet.a <- predict(out.a, Xtest)
phets2.a <- phet.a$sd2 + phet.a$nugs
mhet.a <- as.numeric(t(matrix(rep(phet.a$mean, 10), ncol=10)))
s2het.a <- as.numeric(t(matrix(rep(phets2.a, 10), ncol=10)))

```

```

sehet.a <- (unlist(t(Ztest)) - mhet.a)^2
sc.a <- - sehet.a/s2het.a - log(s2het.a)
c(batch=mean(sc), adaptive=mean(sc.a))

## an example of one iteration of sequential design
## Not run:
Wijs <- hetGP:::Wij(out.a$X0, theta=out.a$theta, type=out.a$covtype)
h <- horizon(out.a, Wijs=Wijs)
control = list(tol_dist=1e-4, tol_diff=1e-4, multi.start=30, maxit=100)
opt <- IMSPE_optim(out.a, h, Wijs=Wijs, control=control)
opt$par

## End(Not run)

```

bfs

Bayes Factor Data

Description

Data from a Bayes factor MCMC-based simulation experiment comparing Student-t to Gaussian errors in an RJ-based Laplace prior Bayesian linear regression setting

Usage

```
data(ato)
```

Format

Calling `data(bfs)` causes the following objects to be loaded into the namespace.

`bfs.exp` 20x11 `data.frame` whose first column is θ , indicating the mean parameter of an exponential distribution encoding the prior of the Student-t degrees of freedom parameter ν . The remaining ten columns comprise of Bayes factor evaluations under that setting

`bfs.gamma` 80x7 `data.frame` whose first two columns are β and α , indicating the second and first parameters to a Gamma distribution encoding the prior of the Student-t degrees of freedom parameters ν . The remaining five columns comprise of Bayes factor evaluations under those settings

Details

Gramacy & Pantaleo (2010), Sections 3-3-3.4, describe an experiment involving Bayes factor (BF) calculations to determine if data are leptokurtic (Student-t errors) or not (simply Gaussian) as a function of the prior parameterization on the Student-t degrees of freedom parameter ν . Franck & Gramacy (2018) created a grid of hyperparameter values in θ describing the mean of an Exponential distribution, evenly spaced in \log_{10} space from 10^{-3} to 10^6 spanning “solidly Student-t” (even Cauchy) to “essentially Gaussian” in terms of the mean of the prior over ν . For each θ setting on the grid they ran the Reversible Jump (RJ) MCMC to approximate the BF of Student-t over Gaussian by feeding in sample likelihood evaluations provided by `monomvn`’s `blasso` to compute the BF.

In order to understand the Monte Carlo variability in those calculations, ten replicates of the BFs under each hyperparameter setting were collected. These data are provided in `bfs.exp`.

A similar, larger experiment was provided with ν under a Gamma prior with parameters α and $\beta \equiv \theta$. In this higher dimensional space, a Latin hypercube sample of size eighty was created, and five replicates of BFs were recorded. These data are provided in `bfs.gamma`.

The examples below involve `mleHetTP` fits (Chung, et al., 2018) to these data and a visualization of the predictive surfaces thus obtained. The code here follows an example provided, with more detail, in `vignette("hetGP")`

Note

For code showing how these BFs were calculated, see supplementary material from Franck & Gramacy (2018)

Author(s)

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References

Franck CT, Gramacy RB (2018). Assessing Bayes factor surfaces using interactive visualization and computer surrogate modeling. Preprint available on arXiv:1809.05580.

Gramacy RB (2017). **monomvn**: Estimation for Multivariate Normal and Student-t Data with Monotone Missingness. R package version 1.9-7, <https://CRAN.R-project.org/package=monomvn>.

R.B. Gramacy and E. Pantaleo (2010). Shrinkage regression for multivariate inference with missing data, and an application to portfolio balancing. *Bayesian Analysis* 5(2), 237-262. Preprint available on arXiv:0907.2135

Chung M, Binois M, Gramacy RB, Moquin DJ, Smith AP, Smith AM (2018). Parameter and Uncertainty Estimation for Dynamical Systems Using Surrogate Stochastic Processes. Preprint available on arXiv:1802.00852.

See Also

`ato`, `sirEval`, `mleHetTP`, `vignette("hetGP")`, `blasso`

Examples

```
data(bfs)

##
## Exponential version first
##

thetas <- matrix(bfs.exp$theta, ncol=1)
bfs <- as.matrix(t(bfs.exp[, -1]))

## the data are heavy tailed, so t-errors help
bfs1 <- mleHetTP(X=list(X0=log10(thetas), Z0=colMeans(log(bfs))),
  mult=rep(nrow(bfs), ncol(bfs)), Z=log(as.numeric(bfs)), lower=10^(-4),
```

```

upper=5, covtype="Matern5_2")

## predictions on a grid in 1d
dx <- seq(0,1,length=100)
dx <- 10^(dx*4 - 3)
p <- predict(bfs1, matrix(log10(dx), ncol=1))

## visualization
matplot(log10(thetas), t(log(bfs)), col=1, pch=21, ylab="log(bf)",
  main="Bayes factor surface")
lines(log10(dx), p$mean, lwd=2, col=2)
lines(log10(dx), p$mean + 2*sqrt(p$sd2 + p$nugs), col=2, lty=2, lwd=2)
lines(log10(dx), p$mean - 2*sqrt(p$sd2 + p$nugs), col=2, lty=2, lwd=2)
legend("topleft", c("hetTP mean", "hetTP interval"), lwd=2, lty=1:2, col=2)

##
## Now Gamma version
##

D <- as.matrix(bfs.gamma[,1:2])
bfs <- as.matrix(t(bfs.gamma[,-(1:2)]))

## fitting in 2fd
bfs2 <- mleHetTP(X=list(X0=log10(D), Z0=colMeans(log(bfs)),
  mult=rep(nrow(bfs), ncol(bfs))), Z = log(as.numeric(bfs)),
  lower = rep(10^(-4), 2), upper = rep(5, 2), covtype = "Matern5_2",
  maxit=100000)

## predictions on a grid in 2d
dx <- seq(0,1,length=100)
dx <- 10^(dx*4 - 3)
DD <- as.matrix(expand.grid(dx, dx))
p <- predict(bfs2, log10(DD))

## visualization via image-contour plots
par(mfrow=c(1,2))
mbfs <- colMeans(bfs)
image(log10(dx), log10(dx), t(matrix(p$mean, ncol=length(dx))),
  col=heat.colors(128), xlab="log10 alpha", ylab="log10 beta",
  main="mean log BF")
text(log10(D[,2]), log10(D[,1]), signif(log(mbfs), 2), cex=0.5)
contour(log10(dx), log10(dx), t(matrix(p$mean, ncol=length(dx))),
  levels=c(-5,-3,-1,0,1,3,5), add=TRUE, col=4)
image(log10(dx), log10(dx), t(matrix(sqrt(p$sd2 + p$nugs),
  ncol=length(dx))), col=heat.colors(128), xlab="log10 alpha",
  ylab="log10 beta", main="sd log BF")
text(log10(D[,2]), log10(D[,1]), signif(apply(log(bfs), 2, sd), 2),
  cex=0.5)

```

Description

Compare two models based on the log-likelihood for hetGP and homGP models

Usage

```
compareGP(model1, model2)
```

Arguments

model1, model2 hetGP or homGP models

Value

Best model based on the likelihood, first one in case of a tie

Note

If comparing homoskedastic and heteroskedastic models, the un-penalised likelihood is used for the later, see e.g., (Binois et al. 2017+).

References

M. Binois, Robert B. Gramacy, M. Ludkovski (2017+), Practical heteroskedastic Gaussian process modeling for large simulation experiments, arXiv preprint arXiv:1611.05902.

cov_gen	<i>Correlation function of selected type, supporting both isotropic and product forms</i>
---------	---

Description

Correlation function of selected type, supporting both isotropic and product forms

Usage

```
cov_gen(X1, X2 = NULL, theta, type = c("Gaussian", "Matern5_2",
  "Matern3_2"))
```

Arguments

X1	matrix of design locations, one point per row
X2	matrix of design locations if correlation is calculated between X1 and X2 (otherwise calculated between X1 and itself)
theta	vector of lengthscales parameters (either of size one if isotropic or of size d if anisotropic)
type	one of "Gaussian", "Matern5_2", "Matern3_2"

Details

Definition of univariate correlation function and hyperparameters:

- "Gaussian": $c(x, y) = \exp(-(x - y)^2 / \theta)$
- "Matern5_2": $c(x, y) = (1 + \sqrt{5} / \theta * \text{abs}(x - y) + 5 / (3 * \theta^2)(x - y)^2) * \exp(-\sqrt{5} * \text{abs}(x - y) / \theta)$
- "Matern3_2": $c(x, y) = (1 + \sqrt{3} / \theta * \text{abs}(x - y)) * \exp(-\sqrt{3} * \text{abs}(x - y) / \theta)$

Multivariate correlations are product of univariate ones.

crit_cSUR

Contour Stepwise Uncertainty Reduction criterion

Description

Computes cSUR infill criterion

Usage

```
crit_cSUR(x, model, thres = 0, preds = NULL)
```

Arguments

x	matrix of new designs, one point per row (size n x d)
model	homGP or hetGP model, including inverse matrices
thres	for contour finding
preds	optional predictions at x to avoid recomputing if already done (must contain cov)

References

Lyu, X., Binois, M. & Ludkovski, M. (2018). Evaluating Gaussian Process Metamodels and Sequential Designs for Noisy Level Set Estimation. arXiv:1807.06712.

Examples

```
## Infill criterion example
set.seed(42)
branin <- function(x){
  m <- 54.8104; s <- 51.9496
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  xx <- 15 * x[,1] - 5; y <- 15 * x[,2]
  f <- (y - 5.1 * xx^2 / (4 * pi^2) + 5 * xx / pi - 6)^2 + 10 * (1 - 1 / (8 * pi)) * cos(xx) + 10
  f <- (f - m) / s
  return(f)
}
```



```

fctest <- function(x, sd = 0.1){
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  return(apply(x, 1, branin) + rnorm(nrow(x), sd = sd))
}

ngrid <- 101; xgrid <- seq(0, 1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))
Zgrid <- fctest(Xgrid)

n <- 20
N <- 500
X <- Xgrid[sample(1:nrow(Xgrid), n),]
X <- X[sample(1:n, N, replace = TRUE),]
Z <- fctest(X)
model <- mleHetGP(X, Z, lower = rep(0.001,2), upper = rep(1,2))

critgrid <- apply(Xgrid, 1, crit_cSUR, model = model)

filled.contour(matrix(critgrid, ngrid), color.palette = terrain.colors, main = "cSUR criterion")

```

crit_EI

Expected Improvement criterion

Description

Computes EI for minimization

Usage

```
crit_EI(x, model, cst = NULL, preds = NULL)
```

Arguments

x	matrix of new designs, one point per row (size n x d)
model	homGP or hetGP model, or their TP equivalents, including inverse matrices
cst	optional plugin value used in the EI, see details
preds	optional predictions at x to avoid recomputing if already done

Details

cst is classically the observed minimum in the deterministic case. In the noisy case, the min of the predictive mean works fine.

Note

This is a beta version at this point.

References

Mockus, J.; Tiesis, V. & Zilinskas, A. (1978). The application of Bayesian methods for seeking the extremum Towards Global Optimization, Amsterdam: Elsevier, 2, 2.

Vazquez E, Villemonteix J, Sidorkiewicz M, Walter E (2008). Global Optimization Based on Noisy Evaluations: An Empirical Study of Two Statistical Approaches, Journal of Physics: Conference Series, 135, IOP Publishing.

A. Shah, A. Wilson, Z. Ghahramani (2014), Student-t processes as alternatives to Gaussian processes, Artificial Intelligence and Statistics, 877–885.

Examples

```
## Optimization example
set.seed(42)

## Noise field via standard deviation
noiseFun <- function(x, coef = 1.1, scale = 1){
  if(is.null(nrow(x)))
    x <- matrix(x, nrow = 1)
  return(scale*(coef + cos(x * 2 * pi)))
}

## Test function defined in [0,1]
ftest <- function(x){
  if(is.null(nrow(x)))
    x <- matrix(x, ncol = 1)
  return(f1d(x) + rnorm(nrow(x), mean = 0, sd = noiseFun(x)))
}

n_init <- 10 # number of unique designs
N_init <- 100 # total number of points
X <- seq(0, 1, length.out = 10)
X <- matrix(X[sample(1:n_init, N_init, replace = TRUE)], ncol = 1)
Z <- ftest(X)

## Predictive grid
ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- matrix(xgrid, ncol = 1)

model <- mleHetGP(X = X, Z = Z, lower = 0.001, upper = 1)

EIgrid <- crit_EI(Xgrid, model)
preds <- predict(x = Xgrid, model)

par(mar = c(3,3,2,3)+0.1)
plot(xgrid, f1d(xgrid), type = 'l', lwd = 1, col = "blue", lty = 3,
```

```

xlab = '', ylab = '', ylim = c(-8,16))
points(X, Z)
lines(Xgrid, preds$mean, col = 'red', lwd = 2)
lines(Xgrid, qnorm(0.05, preds$mean, sqrt(preds$sd2)), col = 2, lty = 2)
lines(Xgrid, qnorm(0.95, preds$mean, sqrt(preds$sd2)), col = 2, lty = 2)
lines(Xgrid, qnorm(0.05, preds$mean, sqrt(preds$sd2 + preds$nugs)), col = 3, lty = 2)
lines(Xgrid, qnorm(0.95, preds$mean, sqrt(preds$sd2 + preds$nugs)), col = 3, lty = 2)
par(new = TRUE)
plot(NA, NA, xlim = c(0, 1), ylim = c(0,max(EIgrid)), axes = FALSE, ylab = "", xlab = "")
lines(xgrid, EIgrid, lwd = 2, col = 'cyan')
axis(side = 4)
mtext(side = 4, line = 2, expression(EI(x)), cex = 0.8)
mtext(side = 2, line = 2, expression(f(x)), cex = 0.8)

```

crit_ICU

*Integrated Contour Uncertainty criterion***Description**

Computes ICU infill criterion

Usage

```
crit_ICU(x, model, thres = 0, Xref, w = NULL, preds = NULL,
         kxprime = NULL)
```

Arguments

x	matrix of new designs, one point per row (size n x d)
model	homGP or hetGP model, including inverse matrices
thres	for contour finding
Xref	matrix of input locations to approximate the integral by a sum
w	optional weights vector of weights for Xref locations
preds	optional predictions at Xref to avoid recomputing if already done
kxprime	optional covariance matrix between model \backslash X0 and Xref to avoid its recomputation

References

Lyu, X., Binois, M. & Ludkovski, M. (2018). Evaluating Gaussian Process Metamodels and Sequential Designs for Noisy Level Set Estimation. arXiv:1807.06712.

Examples

```

## Infill criterion example
set.seed(42)
branin <- function(x){
  m <- 54.8104; s <- 51.9496
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  xx <- 15 * x[,1] - 5; y <- 15 * x[,2]
  f <- (y - 5.1 * xx^2/(4 * pi^2) + 5 * xx/pi - 6)^2 + 10 * (1 - 1/(8 * pi)) * cos(xx) + 10
  f <- (f - m)/s
  return(f)
}

ftest <- function(x, sd = 0.1){
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  return(apply(x, 1, branin) + rnorm(nrow(x), sd = sd))
}

ngrid <- 51; xgrid <- seq(0, 1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))
Zgrid <- ftest(Xgrid)

n <- 20
N <- 500
X <- Xgrid[sample(1:nrow(Xgrid), n),]
X <- X[sample(1:n, N, replace = TRUE),]
Z <- ftest(X)
model <- mleHetGP(X, Z, lower = rep(0.001,2), upper = rep(1,2))

# Precalculations for speedup
preds <- predict(model, x = Xgrid)
kxprime <- cov_gen(X1 = model$X0, X2 = Xgrid, theta = model$theta, type = model$covtype)

critgrid <- apply(Xgrid, 1, crit_ICU, model = model, Xref = Xgrid,
                 preds = preds, kxprime = kxprime)

filled.contour(matrix(critgrid, ngrid), color.palette = terrain.colors, main = "ICU criterion")

```

crit_IMSPE

Sequential IMSPE criterion

Description

Compute the integrated mean square prediction error after adding a new design

Usage

```
crit_IMSPE(x, model, id = NULL, Wijs = NULL)
```

Arguments

x	matrix for the new design (size 1 x d)
model	homGP or hetGP model, including inverse matrices
id	instead of providing x, one can provide the index of a considered existing design
Wijs	optional previously computed matrix of Wijs, to avoid recomputing it; see Wij

Details

The computations are scale free, i.e., values are not multiplied by `nu_hat` from `homGP` or `hetGP`. Currently this function ignores the extra terms related to the estimation of the mean.

See Also

[deriv_crit_IMSPE](#) for the derivative

Examples

```
## One-d toy example

set.seed(42)
fctest <- function(x, coef = 0.1) return(sin(2*pi*x) + rnorm(1, sd = coef))

n <- 9
designs <- matrix(seq(0.1, 0.9, length.out = n), ncol = 1)
X <- matrix(designs[rep(1:n, sample(1:10, n, replace = TRUE)),])
Z <- apply(X, 1, fctest)

prdata <- find_reps(X, Z, inputBounds = matrix(c(0,1), nrow = 2, ncol = 1))
Z <- prdata$Z
plot(prdata$X0[rep(1:n, times = prdata$mult),], prdata$Z, xlab = "x", ylab = "Y")

model <- mleHetGP(X = list(X0 = prdata$X0, Z0 = prdata$Z0, mult = prdata$mult),
                 Z = Z, lower = 0.1, upper = 5)

ngrid <- 501
xgrid <- matrix(seq(0,1, length.out = ngrid), ncol = 1)

## Precalculations
Wijs <- Wij(mu1 = model$X0, theta = model$theta, type = model$covtype)

t0 <- Sys.time()

IMSPE_grid <- apply(xgrid, 1, crit_IMSPE, Wijs = Wijs, model = model)

t1 <- Sys.time()
print(t1 - t0)

plot(xgrid, IMSPE_grid * model$nu_hat, xlab = "x", ylab = "crit_IMSPE values")
abline(v = designs)
```

```
#####
## Bi-variate case

nvar <- 2

set.seed(2)
ftest <- function(x, coef = 0.1) return(sin(2*pi*sum(x)) + rnorm(1, sd = coef))

n <- 16 # must be a square
xgrid0 <- seq(0.1, 0.9, length.out = sqrt(n))
designs <- as.matrix(expand.grid(xgrid0, xgrid0))
X <- designs[rep(1:n, sample(1:10, n, replace = TRUE)),]
Z <- apply(X, 1, ftest)

prdata <- find_reps(X, Z, inputBounds = matrix(c(0,1), nrow = 2, ncol = 1))
Z <- prdata$Z

model <- mleHetGP(X = list(X0 = prdata$X0, Z0 = prdata$Z0, mult = prdata$mult), Z = Z,
  lower = rep(0.1, nvar), upper = rep(1, nvar))
ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))
## Precalculations
Wijs <- Wij(mu1 = model$X0, theta = model$theta, type = model$covtype)
t0 <- Sys.time()

IMSPE_grid <- apply(Xgrid, 1, crit_IMSPE, Wijs = Wijs, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(IMSPE_grid, ngrid),
  nlevels = 20, color.palette = terrain.colors,
  main = "Sequential IMSPE values")
```

crit_MCU

Maximum Contour Uncertainty criterion

Description

Computes MCU infill criterion

Usage

```
crit_MCU(x, model, thres = 0, preds = NULL)
```

Arguments

x	matrix of new designs, one point per row (size n x d)
model	homGP or hetGP model, including inverse matrices
thres	for contour finding
preds	optional predictions at x to avoid recomputing if already done

References

Ranjan, P., Bingham, D. & Michailidis, G (2008). Sequential experiment design for contour estimation from complex computer codes, *Technometrics*, 50, pp. 527-541.

Bichon, B., Eldred, M., Swiler, L., Mahadevan, S. & McFarland, J. (2008). Efficient global reliability analysis for nonlinear implicit performance functions, *AIAA Journal*, 46, pp. 2459-2468.

Lyu, X., Binois, M. & Ludkovski, M. (2018). Evaluating Gaussian Process Metamodels and Sequential Designs for Noisy Level Set Estimation. [arXiv:1807.06712](https://arxiv.org/abs/1807.06712).

Examples

```
## Infill criterion example
set.seed(42)
branin <- function(x){
  m <- 54.8104; s <- 51.9496
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  xx <- 15 * x[,1] - 5; y <- 15 * x[,2]
  f <- (y - 5.1 * xx^2/(4 * pi^2) + 5 * xx/pi - 6)^2 + 10 * (1 - 1/(8 * pi)) * cos(xx) + 10
  f <- (f - m)/s
  return(f)
}

ftest <- function(x, sd = 0.1){
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  return(apply(x, 1, branin) + rnorm(nrow(x), sd = sd))
}

ngrid <- 101; xgrid <- seq(0, 1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))
Zgrid <- ftest(Xgrid)

n <- 20
N <- 500
X <- Xgrid[sample(1:nrow(Xgrid), n),]
X <- X[sample(1:n, N, replace = TRUE),]
Z <- ftest(X)
model <- mleHetGP(X, Z, lower = rep(0.001,2), upper = rep(1,2))

critgrid <- apply(Xgrid, 1, crit_MCU, model = model)

filled.contour(matrix(critgrid, ngrid), color.palette = terrain.colors, main = "MCU criterion")
```

crit_optim *Criterion optimization*

Description

Search for the best value of available criterion, possibly using a h-steps lookahead strategy to favor designs with replication

Usage

```
crit_optim(model, crit, ..., h = 2, Xcand = NULL,
           control = list(multi.start = 10, maxit = 100), seed = NULL)
```

Arguments

model	homGP or hetGP model
crit	considered criterion, one of "crit_cSUR", "crit_EI", "crit_ICU", "crit_MCU" and "crit_tMSE". Note that crit_IMSPE has its dedicated method, see IMSPE_optim .
...	additional parameters of the criterion
h	horizon for multi-step ahead framework. The decision is made between: <ul style="list-style-type: none"> • sequential crit search starting by a new design (optimized first) then adding h replicates • sequential crit searches starting by 1 to h replicates before adding a new point <p>Use $h = 0$ for the myopic criterion, i.e., not looking ahead.</p>
Xcand	optional discrete set of candidates (otherwise a maximin LHS is used to initialise continuous search)
control	list in case Xcand == NULL, with elements multi.start, to perform a multi-start optimization based on optim , with maxit iterations each. Also, tol_dist defines the minimum distance to an existing design for a new point to be added, otherwise the closest existing design is chosen. In a similar fashion, tol_dist is the minimum relative change of crit for adding a new design.
seed	optional seed for the generation of LHS designs with maximinSA_LHS

Details

When looking ahead, the kriging believer heuristic is used, meaning that the non-observed value is replaced by the mean prediction in the update.

Value

list with elements:

- par: best first design,
- value: criterion h-steps ahead starting from adding par,
- path: list of elements list(par, value, new) at each step h

References

M. Binois, J. Huang, R. B. Gramacy, M. Ludkovski (2018+), Replication or exploration? Sequential design for stochastic simulation experiments, *Technometrics* (to appear).
Preprint available on arXiv:1710.03206.

Examples

```
#####
## Bi-variate example (myopic version)
#####

nvar <- 2

set.seed(42)
ftest <- function(x, coef = 0.1) return(sin(2*pi*sum(x)) + rnorm(1, sd = coef))

n <- 25 # must be a square
xgrid0 <- seq(0.1, 0.9, length.out = sqrt(n))
designs <- as.matrix(expand.grid(xgrid0, xgrid0))
X <- designs[rep(1:n, sample(1:10, n, replace = TRUE)),]
Z <- apply(X, 1, ftest)

model <- mleHomGP(X, Z, lower = rep(0.1, nvar), upper = rep(1, nvar))

ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))

preds <- predict(x = Xgrid, object = model)

## Initial plots
contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
        main = "Predicted mean", nlevels = 20)
points(model$X0, col = 'blue', pch = 20)

crit <- "crit_EI"
crit_grid <- apply(Xgrid, 1, crit, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(crit_grid, ngrid),
              nlevels = 20, color.palette = terrain.colors,
              main = "Initial criterion landscape",
              plot.axes = {axis(1); axis(2); points(model$X0, pch = 20)})

## Sequential crit search
nsteps <- 1 # Increase for better results

for(i in 1:nsteps){
  res <- crit_optim(model, crit = crit, h = 0, control = list(multi.start = 100, maxit = 50))
  newX <- res$par
  newZ <- ftest(newX)
  model <- update(object = model, Xnew = newX, Znew = newZ)
}
```

```

## Final plots
contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
        main = "Predicted mean", nlevels = 20)
points(model$X0, col = 'blue', pch = 20)

crit_grid <- apply(Xgrid, 1, crit, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(crit_grid, ngrid),
              nlevels = 20, color.palette = terrain.colors,
              main = "Final criterion landscape",
              plot.axes = {axis(1); axis(2); points(model$X0, pch = 20)})

#####
## Bi-variate example (look-ahead version)
#####
## Not run:
nvar <- 2

set.seed(42)
ftest <- function(x, coef = 0.1) return(sin(2*pi*sum(x)) + rnorm(1, sd = coef))

n <- 25 # must be a square
xgrid0 <- seq(0.1, 0.9, length.out = sqrt(n))
designs <- as.matrix(expand.grid(xgrid0, xgrid0))
X <- designs[rep(1:n, sample(1:10, n, replace = TRUE)),]
Z <- apply(X, 1, ftest)

model <- mleHomGP(X, Z, lower = rep(0.1, nvar), upper = rep(1, nvar))

ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))

nsteps <- 5 # Increase for more steps

crit <- "crit_EI"

for(i in 1:nsteps){
  res <- crit_optim(model, h = 3, crit = crit, control = list(multi.start = 100, maxit = 50))

  # If a replicate is selected
  if(!res$path[[1]]$new) print("Add replicate")

  newX <- res$par
  newZ <- ftest(newX)
  model <- update(object = model, Xnew = newX, Znew = newZ)

  ## Plots
  preds <- predict(x = Xgrid, object = model)
  contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
        main = "Predicted mean", nlevels = 20)
  points(model$X0, col = 'blue', pch = 20)
  points(newX, col = "red", pch = 20)
}

```

```

crit_grid <- apply(Xgrid, 1, crit, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(crit_grid, ngrid),
              nlevels = 20, color.palette = terrain.colors,
              plot.axes = {axis(1); axis(2); points(model$X0, pch = 20)})
}

## End(Not run)

```

crit_tMSE

t-MSE criterion

Description

Computes targeted mean squared error infill criterion

Usage

```
crit_tMSE(x, model, thres = 0, preds = NULL, seps = 0.05)
```

Arguments

x	matrix of new designs, one point per row (size n x d)
model	homGP or hetGP model, including inverse matrices
thres	for contour finding
preds	optional predictions at x to avoid recomputing if already done (must contain cov)
seps	parameter for the target window

References

Picheny, V., Ginsbourger, D., Roustant, O., Haftka, R., Kim, N. (2010). Adaptive designs of experiments for accurate approximation of a target region, *Journal of Mechanical Design* (132), p. 071008.

Lyu, X., Binois, M. & Ludkovski, M. (2018). Evaluating Gaussian Process Metamodels and Sequential Designs for Noisy Level Set Estimation. [arXiv:1807.06712](https://arxiv.org/abs/1807.06712).

Examples

```

## Infill criterion example
set.seed(42)
branin <- function(x){
  m <- 54.8104; s <- 51.9496
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  xx <- 15 * x[,1] - 5; y <- 15 * x[,2]

```

```

f <- (y - 5.1 * xx^2/(4 * pi^2) + 5 * xx/pi - 6)^2 + 10 * (1 - 1/(8 * pi)) * cos(xx) + 10
f <- (f - m)/s
return(f)
}

ftest <- function(x, sd = 0.1){
  if(is.null(dim(x))) x <- matrix(x, nrow = 1)
  return(apply(x, 1, branin) + rnorm(nrow(x), sd = sd))
}

ngrid <- 101; xgrid <- seq(0, 1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))
Zgrid <- ftest(Xgrid)

n <- 20
N <- 500
X <- Xgrid[sample(1:nrow(Xgrid), n),]
X <- X[sample(1:n, N, replace = TRUE),]
Z <- ftest(X)
model <- mleHetGP(X, Z, lower = rep(0.001,2), upper = rep(1,2))

critgrid <- apply(Xgrid, 1, crit_tmSE, model = model)

filled.contour(matrix(critgrid, ngrid), color.palette = terrain.colors, main = "tmSE criterion")

```

deriv_crit_EI

Derivative of EI criterion for GP models

Description

Derivative of EI criterion for GP models

Usage

```
deriv_crit_EI(x, model, cst = NULL, preds = NULL)
```

Arguments

x	matrix for the new design (size 1 x d)
model	homGP or hetGP model
cst	threshold for contour criteria
preds	pre-computed preds for contour criteria

References

Ginsbourger, D. Multiples metamodels pour l'approximation et l'optimisation de fonctions numeriques multivariables Ecole Nationale Superieure des Mines de Saint-Etienne, Ecole Nationale Superieure des Mines de Saint-Etienne, 2009

Roustant, O., Ginsbourger, D., DiceKriging, DiceOptim: Two R packages for the analysis of computer experiments by kriging-based metamodeling and optimization, Journal of Statistical Software, 2012

See Also

[crit_EI](#) for the criterion

deriv_crit_IMSPE	<i>Derivative of crit_IMSPE</i>
------------------	---------------------------------

Description

Derivative of crit_IMSPE

Usage

```
deriv_crit_IMSPE(x, model, Wijs = NULL)
```

Arguments

x	matrix for the new design (size 1 x d)
model	homGP or hetGP model
Wijs	optional previously computed matrix of Wijs, see Wij

Value

Derivative of the sequential IMSPE with respect to x

See Also

[crit_IMSPE](#) for the criterion

f1d	<i>1d test function</i>
-----	-------------------------

Description

1d test function

Usage

f1d(x)

Arguments

x scalar or matrix (size n x 1) in [0,1]

References

A. Forrester, A. Sobester, A. Keane (2008), Engineering design via surrogate modelling: a practical guide, John Wiley & Sons

Examples

plot(f1d)

find_reps	<i>Data preprocessing</i>
-----------	---------------------------

Description

Prepare data for use with [mleHetGP](#), in particular to find replicated observations

Usage

```
find_reps(X, Z, return.Zlist = TRUE, rescale = FALSE,
          normalize = FALSE, inputBounds = NULL)
```

Arguments

X	matrix of design locations, one point per row
Z	vector of observations at X
return.Zlist	to return Zlist, see below
rescale	if TRUE, the inputs are rescaled to the unit hypercube
normalize	if TRUE, the outputs are centered and normalized
inputBounds	optional matrix of known boundaries in original input space, of size 2 times ncol(X). If not provided, and rescale == TRUE, it is estimated from the data.

Details

Replicates are searched based on character representation, using `unique`.

Value

A list with the following elements that can be passed to the main fitting functions, e.g., `mleHetGP` and `mleHomGP`

- `X0` matrix with unique designs locations, one point per row,
- `Z0` vector of averaged observations at `X0`,
- `mult` number of replicates at `X0`,
- `Z` vector with all observations, sorted according to `X0`,
- `Zlist` optional list, each element corresponds to observations at a design in `X0`,
- `inputBounds` optional matrix, to rescale back to the original input space,
- `outputStats` optional vector, with mean and variance of the original outputs.

Examples

```
##-----
## Find replicates on the motorcycle data
##-----
## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel

data_m <- find_reps(X, Z)

# Initial data
plot(X, Z, ylim = c(-160, 90), ylab = 'acceleration', xlab = "time")
# Display mean values
points(data_m$X0, data_m$Z0, pch = 20)
```

horizon

Adapt horizon

Description

Adapt the look-ahead horizon depending on the replicate allocation or a target ratio

Usage

```
horizon(model, current_horizon = NULL, previous_ratio = NULL,
        target = NULL, Wijs = NULL)
```

Arguments

<code>model</code>	hetGP or homGP model
<code>current_horizon</code>	horizon used for the previous iteration, see details
<code>previous_ratio</code>	ratio before adding the previous new design
<code>target</code>	scalar in]0,1] for desired n/N
<code>Wijs</code>	optional previously computed matrix of W_{ij} , see W_{ij}

Details

If `target` is provided, along with `previous_ratio` and `current_horizon`:

- the horizon is increased by one if more replicates are needed but a new ppint has been added at the previous iteration,
- the horizon is decreased by one if new points are needed but a replicate has been added at the previous iteration,
- otherwise it is unchanged.

If no `target` is provided, `allocate_mult` is used to obtain the best allocation of the existing replicates, then the new horizon is sampled from the difference between the actual allocation and the best one, bounded below by 0. See (Binois et al. 2017).

Value

randomly selected horizon for next iteration (adaptive) if no `target` is provided, otherwise returns the update horizon value.

References

M. Binois, J. Huang, R. B. Gramacy, M. Ludkovski (2018+), Replication or exploration? Sequential design for stochastic simulation experiments, *Technometrics* (to appear).
Preprint available on arXiv:1710.03206.

 IMSPE

Integrated Mean Square Prediction Error

Description

IMSPE of a given design

Usage

```
IMSPE(X, theta = NULL, Lambda = NULL, mult = NULL, covtype = NULL,
      nu = NULL, eps = sqrt(.Machine$double.eps))
```


Arguments

X	hetGP or homGP model. Alternatively, one can provide a matrix of unique designs considered
theta	lengthscales
Lambda	diagonal matrix for the noise
mult	number of replicates at each design
covtype	either "Gaussian", "Matern3_2" or "Matern5_2"
nu	variance parameter
eps	numerical nugget

Details

One can provide directly a model of class hetGP or homGP, or provide X and all other arguments

IMSPE_optim

IMSPE optimization

Description

Search for the best value of the IMSPE criterion, possibly using a h-steps lookahead strategy to favor designs with replication

Usage

```
IMSPE_optim(model, h = 2, Xcand = NULL, control = list(tol_dist =
  1e-06, tol_diff = 1e-06, multi.start = 20, maxit = 100), Wijs = NULL,
  seed = NULL)
```

Arguments

model	homGP or hetGP model
h	horizon for multi-step ahead framework. The decision is made between: <ul style="list-style-type: none"> • sequential crit search starting by a new design (optimized first) then adding h replicates • sequential crit searches starting by 1 to h replicates before adding a new point Use $h = 0$ for the myopic criterion, i.e., not looking ahead.
Xcand	optional discrete set of candidates (otherwise a maximin LHS is used to initialise continuous search)
control	list in case Xcand == NULL, with elements multi.start, to perform a multi-start optimization based on optim , with maxit iterations each. Also, tol_dist defines the minimum distance to an existing design for a new point to be added, otherwise the closest existing design is chosen. In a similar fashion, tol_diff is the minimum relative change of IMSPE for adding a new design.
Wijs	optional previously computed matrix of Wijs, see Wij
seed	optional seed for the generation of designs with maximinSA_LHS

Details

The domain needs to be $[0, 1]^d$ for now.

Value

list with elements:

- par: best first design,
- value: IMSPE h-steps ahead starting from adding par,
- path: list of elements list(par, value, new) at each step h

References

M. Binois, J. Huang, R. Gramacy, M. Ludkovski (2017+), Replication or exploration? Sequential design for stochastic simulation experiments. arXiv preprint arXiv:1710.03206.

Examples

```
#####
## Bi-variate example (myopic version)
#####

nvar <- 2

set.seed(42)
ftest <- function(x, coef = 0.1) return(sin(2*pi*sum(x)) + rnorm(1, sd = coef))

n <- 25 # must be a square
xgrid0 <- seq(0.1, 0.9, length.out = sqrt(n))
designs <- as.matrix(expand.grid(xgrid0, xgrid0))
X <- designs[rep(1:n, sample(1:10, n, replace = TRUE)),]
Z <- apply(X, 1, ftest)

model <- mleHomGP(X, Z, lower = rep(0.1, nvar), upper = rep(1, nvar))

ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))

preds <- predict(x = Xgrid, object = model)

## Initial plots
contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
        main = "Predicted mean", nlevels = 20)
points(model$X0, col = 'blue', pch = 20)

IMSPE_grid <- apply(Xgrid, 1, crit_IMSPE, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(IMSPE_grid, ngrid),
              nlevels = 20, color.palette = terrain.colors,
              main = "Initial IMSPE criterion landscape",
              plot.axes = {axis(1); axis(2); points(model$X0, pch = 20)})
```

```

## Sequential IMSPE search
nsteps <- 1 # Increase for better results

for(i in 1:nsteps){
  res <- IMSPE_optim(model, control = list(multi.start = 100, maxit = 50))
  newX <- res$par
  newZ <- ftest(newX)
  model <- update(object = model, Xnew = newX, Znew = newZ)
}

## Final plots
contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
        main = "Predicted mean", nlevels = 20)
points(model$X0, col = 'blue', pch = 20)

IMSPE_grid <- apply(Xgrid, 1, crit_IMSPE, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(IMSPE_grid, ngrid),
               nlevels = 20, color.palette = terrain.colors,
               main = "Final IMSPE criterion landscape",
               plot.axes = {axis(1); axis(2); points(model$X0, pch = 20)})

#####
## Bi-variate example (look-ahead version)
#####
## Not run:
nvar <- 2

set.seed(42)
ftest <- function(x, coef = 0.1) return(sin(2*pi*sum(x)) + rnorm(1, sd = coef))

n <- 25 # must be a square
xgrid0 <- seq(0.1, 0.9, length.out = sqrt(n))
designs <- as.matrix(expand.grid(xgrid0, xgrid0))
X <- designs[rep(1:n, sample(1:10, n, replace = TRUE)),]
Z <- apply(X, 1, ftest)

model <- mleHomGP(X, Z, lower = rep(0.1, nvar), upper = rep(1, nvar))

ngrid <- 51
xgrid <- seq(0,1, length.out = ngrid)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))

nsteps <- 5 # Increase for more steps

for(i in 1:nsteps){
  res <- IMSPE_optim(model, h = 3, control = list(multi.start = 100, maxit = 50))

  # If a replicate is selected
  if(!res$path[[1]]$new) print("Add replicate")

  newX <- res$par
  newZ <- ftest(newX)

```

```

model <- update(object = model, Xnew = newX, Znew = newZ)

## Plots
preds <- predict(x = Xgrid, object = model)
contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
        main = "Predicted mean", nlevels = 20)
points(model$X0, col = 'blue', pch = 20)
points(newX, col = "red", pch = 20)

## Precalculations
Wijs <- Wij(mu1 = model$X0, theta = model$theta, type = model$covtype)

IMSPE_grid <- apply(Xgrid, 1, crit_IMSPE, Wijs = Wijs, model = model)
filled.contour(x = xgrid, y = xgrid, matrix(IMSPE_grid, ngrid),
              nlevels = 20, color.palette = terrain.colors,
              plot.axes = {axis(1); axis(2); points(model$X0, pch = 20)})
}

## End(Not run)

```

LOO_preds

Leave one out predictions

Description

Provide leave one out predictions, e.g., for model testing and diagnostics. This is used in the method plot available on GP and TP models.

Usage

```
LOO_preds(model, ids = NULL)
```

Arguments

model	homGP or hetGP model, TP version is not considered at this point
ids	vector of indices of the unique design point considered (default to all)

Value

list with mean and variance predictions at x_i assuming this point has not been evaluated

Note

For TP models, ψ is considered fixed.

References

O. Dubrule (1983), Cross validation of Kriging in a unique neighborhood, *Mathematical Geology* 15, 687–699.

F. Bachoc (2013), Cross Validation and Maximum Likelihood estimations of hyper-parameters of Gaussian processes with model misspecification, *Computational Statistics & Data Analysis*, 55–69.

Examples

```

set.seed(32)
## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
nvar <- 1

## Model fitting
model <- mleHomGP(X = X, Z = Z, lower = rep(0.1, nvar), upper = rep(10, nvar),
                 covtype = "Matern5_2", known = list(beta0 = 0))
LOO_p <- LOO_preds(model)

# model minus observation(s) at x_i
d_mot <- find_reps(X, Z)

LOO_ref <- matrix(NA, nrow(d_mot$X0), 2)
for(i in 1:nrow(d_mot$X0)){
  model_i <- mleHomGP(X = list(X0 = d_mot$X0[-i,, drop = FALSE], Z0 = d_mot$Z0[-i],
                              mult = d_mot$mult[-i]), Z = unlist(d_mot$Zlist[-i]),
                    lower = rep(0.1, nvar), upper = rep(50, nvar), covtype = "Matern5_2",
                    known = list(theta = model$theta, k_theta_g = model$k_theta_g, g = model$g,
                                beta0 = 0))

  model_i$nu_hat <- model$nu_hat
  p_i <- predict(model_i, d_mot$X0[i,,drop = FALSE])
  LOO_ref[i,] <- c(p_i$mean, p_i$sd2)
}

# Compare results

range(LOO_ref[,1] - LOO_p$mean)
range(LOO_ref[,2] - LOO_p$sd2)

# Use of LOO for diagnostics
plot(model)

```

Description

Gaussian process regression under input dependent noise based on maximum likelihood estimation of the hyperparameters. A second GP is used to model latent (log-) variances. This function is enhanced to deal with replicated observations.

Usage

```
mleHetGP(X, Z, lower = NULL, upper = NULL,
  noiseControl = list(k_theta_g_bounds = c(1, 100), g_max = 100, g_bounds
    = c(1e-06, 1)), settings = list(linkThetas = "joint", logN = TRUE,
  initStrategy = "residuals", checkHom = TRUE, penalty = TRUE, trace = 0,
  return.matrices = TRUE, return.hom = FALSE), covtype = c("Gaussian",
  "Matern5_2", "Matern3_2"), maxit = 100, known = NULL, init = NULL,
  eps = sqrt(.Machine$double.eps))
```

Arguments

- | | |
|--------------|--|
| X | matrix of all designs, one per row, or list with elements: <ul style="list-style-type: none"> • X0 matrix of unique design locations, one point per row • Z0 vector of averaged observations, of length nrow(X0) • mult number of replicates at designs in X0, of length nrow(X0) |
| Z | vector of all observations. If using a list with X, Z has to be ordered with respect to X0, and of length sum(mult) |
| lower, upper | optional bounds for the theta parameter (see cov_gen for the exact parameterization). In the multivariate case, it is possible to give vectors for bounds (resp. scalars) for anisotropy (resp. isotropy) |
| noiseControl | list with elements related to optimization of the noise process parameters: <ul style="list-style-type: none"> • g_min, g_max minimal and maximal noise to signal ratio (of the mean process) • lowerDelta, upperDelta optional vectors (or scalars) of bounds on Delta, of length nrow(X0) (default to rep(eps, nrow(X0)) and rep(noiseControl\$g_max, nrow(X0)) resp., or their log) • lowerTheta_g, upperTheta_g optional vectors of bounds for the length-scales of the noise process if linkThetas == 'none'. Same as for theta if not provided. • k_theta_g_bounds if linkThetas == 'joint', vector with minimal and maximal values for k_theta_g (default to c(1, 100)). See Details. • g_bounds vector for minimal and maximal noise to signal ratios for the noise of the noise process, i.e., the smoothing parameter for the noise process. (default to c(1e-6, 1)). |
| settings | list for options about the general modeling procedure, with elements: <ul style="list-style-type: none"> • linkThetas defines the relation between lengthscales of the mean and noise processes. Either 'none', 'joint'(default) or 'constr', see Details. • logN, when TRUE (default), the log-noise process is modeled. |

	<ul style="list-style-type: none"> • <code>initStrategy</code> one of 'simple', 'residuals' (default) and 'smoothed' to obtain starting values for <code>Delta</code>, see Details • <code>penalty</code> when TRUE, the penalized version of the likelihood is used (i.e., the sum of the log-likelihoods of the mean and variance processes, see References). • <code>checkHom</code> when TRUE, if the log-likelihood with a homoskedastic model is better, then return it. • <code>trace</code> optional scalar (default to 0). If positive, tracing information on the fitting process. If 1, information is given about the result of the heterogeneous model optimization. Level 2 gives more details. Level 3 additionally displays all details about initialization of hyperparameters. • <code>return.matrices</code> boolean to include the inverse covariance matrix in the object for further use (e.g., prediction). • <code>return.hom</code> boolean to include homoskedastic GP models used for initialization (i.e., <code>modHom</code> and <code>modNugs</code>).
<code>covtype</code>	covariance kernel type, either 'Gaussian', 'Matern5_2' or 'Matern3_2', see cov_gen
<code>maxit</code>	maximum number of iterations for L-BFGS-B of optim dedicated to maximum likelihood optimization
<code>init, known</code>	optional lists of starting values for mle optimization or that should not be optimized over, respectively. Values in <code>known</code> are not modified, while it can happen to these of <code>init</code> , see Details. One can set one or several of the following: <ul style="list-style-type: none"> • <code>theta</code> lengthscale parameter(s) for the mean process either one value (isotropic) or a vector (anisotropic) • <code>Delta</code> vector of nuggets corresponding to each design in <code>X0</code>, that are smoothed to give <code>Lambda</code> (as the global covariance matrix depend on <code>Delta</code> and <code>nu_hat</code>, it is recommended to also pass values for <code>theta</code>) • <code>beta0</code> constant trend of the mean process • <code>k_theta_g</code> constant used for link mean and noise processes lengthscales, when <code>settings\$linkThetas == 'joint'</code> • <code>theta_g</code> either one value (isotropic) or a vector (anisotropic) for lengthscale parameter(s) of the noise process, when <code>settings\$linkThetas != 'joint'</code> • <code>g</code> scalar nugget of the noise process • <code>g_H</code> scalar homoskedastic nugget for the initialisation with a mleHomGP. See Details.
<code>eps</code>	jitter used in the inversion of the covariance matrix for numerical stability

Details

The global covariance matrix of the model is parameterized as $\text{nu_hat} * (C + \text{Lambda} * \text{diag}(1/\text{mult})) = \text{nu_hat} * K$, with C the correlation matrix between unique designs, depending on the family of kernel used (see [cov_gen](#) for available choices) and values of lengthscale parameters. `nu_hat` is the plugin estimator of the variance of the process. `Lambda` is the prediction on the noise level given by a second (homoskedastic) GP:

$$\Lambda = C_g(C_g + \text{diag}(g/\text{mult}))^{-1} \Delta$$

with C_g the correlation matrix between unique designs for this second GP, with lengthscales hyperparameters θ_g and nugget g and Δ the variance level at X_0 that are estimated.

It is generally recommended to use `find_reps` to pre-process the data, to rescale the inputs to the unit cube and to normalize the outputs.

The noise process lengthscales can be set in several ways:

- using `k_theta_g` (`settings$linkThetas == 'joint'`), supposed to be greater than one by default. In this case lengthscales of the noise process are multiples of those of the mean process.
- if `settings$linkThetas == 'constr'`, then the lower bound on θ_g correspond to estimated values of an homoskedastic GP fit.
- else lengthscales between the mean and noise process are independent (both either anisotropic or not).

When no starting nor fixed parameter values are provided with `init` or `known`, the initialization process consists of fitting first an homoskedastic model of the data, called `modHom`. Unless provided with `init$theta`, initial lengthscales are taken at 10% of the range determined with lower and upper, while `init$g_H` may be use to pass an initial nugget value. The resulting lengthscales provide initial values for θ (or update them if given in `init`).

If necessary, a second homoskedastic model, `modNugs`, is fitted to the empirical residual variance between the prediction given by `modHom` at X_0 and Z (up to `modHom$nu_hat`). Note that when specifying `settings$linkThetas == 'joint'`, then this second homoskedastic model has fixed lengthscales parameters. Starting values for θ_g and g are extracted from `modNugs`.

Finally, three initialization schemes for Δ are available with `settings$initStrategy`:

- for `settings$initStrategy == 'simple'`, Δ is simply initialized to the estimated g value of `modHom`. Note that this procedure may fail when `settings$penalty == TRUE`.
- for `settings$initStrategy == 'residuals'`, Δ is initialized to the estimated residual variance from the homoskedastic mean prediction.
- for `settings$initStrategy == 'smoothed'`, Δ takes the values predicted by `modNugs` at X_0 .

Notice that lower and upper bounds cannot be equal for `optim`.

Value

a list which is given the S3 class "hetGP", with elements:

- `theta`: unless given, maximum likelihood estimate (mle) of the lengthscales parameter(s),
- `Delta`: unless given, mle of the nugget vector (non-smoothed),
- `Lambda`: predicted input noise variance at X_0 ,
- `nu_hat`: plugin estimator of the variance,
- `theta_g`: unless given, mle of the lengthscales(s) of the noise/log-noise process,

- `k_theta_g`: if `settings$linkThetas == 'joint'`, mle for the constant by which length-scale parameters of `theta` are multiplied to get `theta_g`,
- `g`: unless given, mle of the nugget of the noise/log-noise process,
- `trendtype`: either "SK" if `beta0` is provided, else "OK",
- `beta0` constant trend of the mean process, plugin-estimator unless given,
- `nmean`: plugin estimator for the constant noise/log-noise process mean,
- `ll`: log-likelihood value, (`ll_non_pen`) is the value without the penalty,
- `nit_opt`, `msg`: counts and message returned by `optim`
- `modHom`: homoskedastic GP model of class `homGP` used for initialization of the mean process,
- `modNugs`: homoskedastic GP model of class `homGP` used for initialization of the noise/log-noise process,
- `nu_hat_var`: variance of the noise process,
- `used_args`: list with arguments provided in the call to the function, which is saved in `call`,
- `Ki`, `Kgi`: inverse of the covariance matrices of the mean and noise processes (not scaled by `nu_hat` and `nu_hat_var`),
- `X0`, `Z0`, `Z`, `eps`, `logN`, `covtype`: values given in input,
- `time`: time to train the model, in seconds.

References

M. Binois, Robert B. Gramacy, M. Ludkovski (2018), Practical heteroskedastic Gaussian process modeling for large simulation experiments, *Journal of Computational and Graphical Statistics*, 27(4), 808–821.

Preprint available on arXiv:1611.05902.

See Also

[predict.hetGP](#) for predictions, [update.hetGP](#) for updating an existing model. `summary` and `plot` functions are available as well. [mleHetTP](#) provide a Student-t equivalent.

Examples

```
##-----
## Example 1: Heteroskedastic GP modeling on the motorcycle data
##-----
set.seed(32)

## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
nvar <- 1
plot(X, Z, ylim = c(-160, 90), ylab = 'acceleration', xlab = "time")
```

```

## Model fitting
model <- mleHetGP(X = X, Z = Z, lower = rep(0.1, nvar), upper = rep(50, nvar),
                 covtype = "Matern5_2")

## Display averaged observations
points(model$X0, model$Z0, pch = 20)

## A quick view of the fit
summary(model)

## Create a prediction grid and obtain predictions
xgrid <- matrix(seq(0, 60, length.out = 301), ncol = 1)
predictions <- predict(x = xgrid, object = model)

## Display mean predictive surface
lines(xgrid, predictions$mean, col = 'red', lwd = 2)
## Display 95% confidence intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
## Display 95% prediction intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)

##-----
## Example 2: 2D Heteroskedastic GP modeling
##-----

set.seed(1)
nvar <- 2

## Branin redefined in  $[0,1]^2$ 
branin <- function(x){
  if(is.null(nrow(x)))
    x <- matrix(x, nrow = 1)
  x1 <- x[,1] * 15 - 5
  x2 <- x[,2] * 15
  (x2 - 5/(4 * pi^2) * (x1^2) + 5/pi * x1 - 6)^2 + 10 * (1 - 1/(8 * pi)) * cos(x1) + 10
}

## Noise field via standard deviation
noiseFun <- function(x){
  if(is.null(nrow(x)))
    x <- matrix(x, nrow = 1)
  return(1/5*(3*(2 + 2*sin(x[,1]*pi)*cos(x[,2]*3*pi) + 5*rowSums(x^2))))
}

## data generating function combining mean and noise fields
ftest <- function(x){
  return(branin(x) + rnorm(nrow(x), mean = 0, sd = noiseFun(x)))
}

```

```

## Grid of predictive locations
ngrid <- 51
xgrid <- matrix(seq(0, 1, length.out = ngrid), ncol = 1)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))

## Unique (randomly chosen) design locations
n <- 50
Xu <- matrix(runif(n * 2), n)

## Select replication sites randomly
X <- Xu[sample(1:n, 20*n, replace = TRUE),]

## obtain training data response at design locations X
Z <- ftest(X)

## Formatting of data for model creation (find replicated observations)
prdata <- find_reps(X, Z, rescale = FALSE, normalize = FALSE)

## Model fitting
model <- mleHetGP(X = list(X0 = prdata$X0, Z0 = prdata$Z0, mult = prdata$mult), Z = prdata$Z,
                 lower = rep(0.01, nvar), upper = rep(10, nvar),
                 covtype = "Matern5_2")

## a quick view into the data stored in the "hetGP"-class object
summary(model)

## prediction from the fit on the grid
predictions <- predict(x = Xgrid, object = model)

## Visualization of the predictive surface
par(mfrow = c(2, 2))
contour(x = xgrid, y = xgrid, z = matrix(branin(Xgrid), ngrid),
       main = "Branin function", nlevels = 20)
points(X, col = 'blue', pch = 20)
contour(x = xgrid, y = xgrid, z = matrix(predictions$mean, ngrid),
       main = "Predicted mean", nlevels = 20)
points(Xu, col = 'blue', pch = 20)
contour(x = xgrid, y = xgrid, z = matrix(noiseFun(Xgrid), ngrid),
       main = "Noise standard deviation function", nlevels = 20)
points(Xu, col = 'blue', pch = 20)
contour(x = xgrid, y = xgrid, z = matrix(sqrt(predictions$nugs), ngrid),
       main = "Predicted noise values", nlevels = 20)
points(Xu, col = 'blue', pch = 20)
par(mfrow = c(1, 1))

```

Description

Student-t process regression under input dependent noise based on maximum likelihood estimation of the hyperparameters. A GP is used to model latent (log-) variances. This function is enhanced to deal with replicated observations.

Usage

```
mleHetTP(X, Z, lower = NULL, upper = NULL,
  noiseControl = list(k_theta_g_bounds = c(1, 100), g_max = 10000,
    g_bounds = c(1e-06, 0.1), nu_bounds = c(2 + 0.001, 30), sigma2_bounds =
    c(sqrt(.Machine$double.eps), 10000)), settings = list(linkThetas =
    "joint", logN = TRUE, initStrategy = "residuals", checkHom = TRUE,
    penalty = TRUE, trace = 0, return.matrices = TRUE, return.hom = FALSE),
  covtype = c("Gaussian", "Matern5_2", "Matern3_2"), maxit = 100,
  known = list(beta0 = 0), init = list(nu = 3),
  eps = sqrt(.Machine$double.eps))
```

Arguments

X	matrix of all designs, one per row, or list with elements: <ul style="list-style-type: none"> • X0 matrix of unique design locations, one point per row • Z0 vector of averaged observations, of length nrow(X0) • mult number of replicates at designs in X0, of length nrow(X0)
Z	vector of all observations. If using a list with X, Z has to be ordered with respect to X0, and of length sum(mult)
lower, upper	bounds for the theta parameter (see cov_gen for the exact parameterization). In the multivariate case, it is possible to give vectors for bounds (resp. scalars) for anisotropy (resp. isotropy)
noiseControl	list with elements related to optimization of the noise process parameters: <ul style="list-style-type: none"> • g_min, g_max minimal and maximal noise to signal ratio (of the mean process) • lowerDelta, upperDelta optional vectors (or scalars) of bounds on Delta, of length nrow(X0) (default to rep(eps, nrow(X0)) and rep(noiseControl\$g_max, nrow(X0)) resp., or their log) • lowerTheta_g, upperTheta_g optional vectors of bounds for the length-scales of the noise process if linkThetas == 'none'. Same as for theta if not provided. • k_theta_g_bounds if linkThetas == 'joint', vector with minimal and maximal values for k_theta_g (default to c(1, 100)). See Details. • g_bounds vector for minimal and maximal noise to signal ratios for the noise of the noise process, i.e., the smoothing parameter for the noise process. (default to c(1e-6, 1)). • sigma2_bounds, vector providing minimal and maximal signal variance. • nu_bounds, vector providing minimal and maximal values for the degrees of freedom.

settings	<p>list for options about the general modeling procedure, with elements:</p> <ul style="list-style-type: none"> • linkThetas defines the relation between lengthscales of the mean and noise processes. Either 'none', 'joint'(default) or 'constr', see Details. • logN, when TRUE (default), the log-noise process is modeled. • initStrategy one of 'simple', 'residuals' (default) and 'smoothed' to obtain starting values for Delta, see Details • penalty when TRUE, the penalized version of the likelihood is used (i.e., the sum of the log-likelihoods of the mean and variance processes, see References). • checkHom when TRUE, if the log-likelihood with a homoskedastic model is better, then return it. • trace optional scalar (default to 0). If positive, tracing information on the fitting process. If 1, information is given about the result of the heterogeneous model optimization. Level 2 gives more details. Level 3 additionally displays all details about initialization of hyperparameters. • return.matrices boolean too include the inverse covariance matrix in the object for further use (e.g., prediction).
covtype	covariance kernel type, either 'Gaussian', 'Matern5_2' or 'Matern3_2', see cov_gen
maxit	maximum number of iterations for L-BFGS-B of optim dedicated to maximum likelihood optimization
init, known	<p>optional lists of starting values for mle optimization or that should not be optimized over, respectively. Values in known are not modified, while it can happen to those of init, see Details. One can set one or several of the following:</p> <ul style="list-style-type: none"> • theta lengthscale parameter(s) for the mean process either one value (isotropic) or a vector (anisotropic) • Delta vector of nuggets corresponding to each design in X0, that are smoothed to give Lambda (as the global covariance matrix depend on Delta and nu_hat, it is recommended to also pass values for theta) • beta0 constant trend of the mean process • k_theta_g constant used for link mean and noise processes lengthscales, when settings\$linkThetas == 'joint' • theta_g either one value (isotropic) or a vector (anisotropic) for lengthscales parameter(s) of the noise process, when settings\$linkThetas != 'joint' • g scalar nugget of the noise process • nu degree of freedom parameter • sigma2 scale variance • g_H scalar homoskedastic nugget for the initialisation with a mleHomGP. See Details.
eps	jitter used in the inversion of the covariance matrix for numerical stability

Details

The global covariance matrix of the model is parameterized as $K = \sigma^2 * C + \Lambda * \text{diag}(1/\text{mult})$, with C the correlation matrix between unique designs, depending on the family of kernel used (see

`cov_gen` for available choices). Λ is the prediction on the noise level given by a (homoskedastic) GP:

$$\Lambda = C_g(C_g + \text{diag}(g/\text{mult}))^{-1}\Delta$$

with C_g the correlation matrix between unique designs for this second GP, with lengthscales hyperparameters θ_g and nugget g and Δ the variance level at X_0 that are estimated.

It is generally recommended to use `find_reps` to pre-process the data, to rescale the inputs to the unit cube and to normalize the outputs.

The noise process lengthscales can be set in several ways:

- using `k_theta_g` (`settings$linkThetas == 'joint'`), supposed to be greater than one by default. In this case lengthscales of the noise process are multiples of those of the mean process.
- if `settings$linkThetas == 'constr'`, then the lower bound on θ_g correspond to estimated values of an homoskedastic GP fit.
- else lengthscales between the mean and noise process are independent (both either anisotropic or not).

When no starting nor fixed parameter values are provided with `init` or `known`, the initialization process consists of fitting first an homoskedastic model of the data, called `modHom`. Unless provided with `init$theta`, initial lengthscales are taken at 10% of the range determined with lower and upper, while `init$g_H` may be use to pass an initial nugget value. The resulting lengthscales provide initial values for θ (or update them if given in `init`).

If necessary, a second homoskedastic model, `modNugs`, is fitted to the empirical residual variance between the prediction given by `modHom` at X_0 and Z (up to `modHom$nu_hat`). Note that when specifying `settings$linkThetas == 'joint'`, then this second homoskedastic model has fixed lengthscales parameters. Starting values for θ_g and g are extracted from `modNugs`.

Finally, three initialization schemes for Δ are available with `settings$initStrategy`:

- for `settings$initStrategy == 'simple'`, Δ is simply initialized to the estimated g value of `modHom`. Note that this procedure may fail when `settings$penalty == TRUE`.
- for `settings$initStrategy == 'residuals'`, Δ is initialized to the estimated residual variance from the homoskedastic mean prediction.
- for `settings$initStrategy == 'smoothed'`, Δ takes the values predicted by `modNugs` at X_0 .

Notice that lower and upper bounds cannot be equal for `optim`.

Value

a list which is given the S3 class "hetTP", with elements:

- `theta`: unless given, maximum likelihood estimate (mle) of the lengthscales parameter(s),
- `Delta`: unless given, mle of the nugget vector (non-smoothed),
- `Lambda`: predicted input noise variance at X_0 ,

- `sigma2`: plugin estimator of the variance,
- `theta_g`: unless given, mle of the lengthscale(s) of the noise/log-noise process,
- `k_theta_g`: if `settings$linkThetas == 'joint'`, mle for the constant by which length-scale parameters of `theta` are multiplied to get `theta_g`,
- `g`: unless given, mle of the nugget of the noise/log-noise process,
- `trendtype`: either "SK" if `beta0` is provided, else "OK",
- `beta0` constant trend of the mean process, plugin-estimator unless given,
- `nmean`: plugin estimator for the constant noise/log-noise process mean,
- `ll`: log-likelihood value, (`ll_non_pen`) is the value without the penalty,
- `nit_opt`, `msg`: counts and message returned by `optim`
- `modHom`: homoskedastic GP model of class `homGP` used for initialization of the mean process,
- `modNugs`: homoskedastic GP model of class `homGP` used for initialization of the noise/log-noise process,
- `nu_hat_var`: variance of the noise process,
- `used_args`: list with arguments provided in the call to the function, which is saved in `call`,
- `X0`, `Z0`, `Z`, `eps`, `logN`, `covtype`: values given in input,
- `time`: time to train the model, in seconds.

References

M. Binois, Robert B. Gramacy, M. Ludkovski (2017+), Practical heteroskedastic Gaussian process modeling for large simulation experiments, arXiv preprint arXiv:1611.05902.

A. Shah, A. Wilson, Z. Ghahramani (2014), Student-t processes as alternatives to Gaussian processes, *Artificial Intelligence and Statistics*, 877–885.

See Also

[predict.hetTP](#) for predictions. `summary` and `plot` functions are available as well.

Examples

```
##-----
## Example 1: Heteroskedastic TP modeling on the motorcycle data
##-----
set.seed(32)

## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
nvar <- 1
plot(X, Z, ylim = c(-160, 90), ylab = 'acceleration', xlab = "time")
```

```

## Model fitting
model <- mleHetTP(X = X, Z = Z, lower = rep(0.1, nvar), upper = rep(50, nvar),
                 covtype = "Matern5_2")

## Display averaged observations
points(model$X0, model$Z0, pch = 20)

## A quick view of the fit
summary(model)

## Create a prediction grid and obtain predictions
xgrid <- matrix(seq(0, 60, length.out = 301), ncol = 1)
preds <- predict(x = xgrid, object = model)

## Display mean predictive surface
lines(xgrid, preds$mean, col = 'red', lwd = 2)
## Display 95% confidence intervals
lines(xgrid, preds$mean + sqrt(preds$sd2) * qt(0.05, df = model$nu + nrow(X)), col = 2, lty = 2)
lines(xgrid, preds$mean + sqrt(preds$sd2) * qt(0.95, df = model$nu + nrow(X)), col = 2, lty = 2)
## Display 95% prediction intervals
lines(xgrid, preds$mean + sqrt(preds$sd2 + preds$nugs) * qt(0.05, df = model$nu + nrow(X)),
      col = 3, lty = 2)
lines(xgrid, preds$mean + sqrt(preds$sd2 + preds$nugs) * qt(0.95, df = model$nu + nrow(X)),
      col = 3, lty = 2)

##-----
## Example 2: 2D Heteroskedastic TP modeling
##-----
set.seed(1)
nvar <- 2

## Branin redefined in  $[0,1]^2$ 
branin <- function(x){
  if(is.null(nrow(x)))
    x <- matrix(x, nrow = 1)
  x1 <- x[,1] * 15 - 5
  x2 <- x[,2] * 15
  (x2 - 5/(4 * pi^2) * (x1^2) + 5/pi * x1 - 6)^2 + 10 * (1 - 1/(8 * pi)) * cos(x1) + 10
}

## Noise field via standard deviation
noiseFun <- function(x){
  if(is.null(nrow(x)))
    x <- matrix(x, nrow = 1)
  return(1/5*(3*(2 + 2*sin(x[,1]*pi)*cos(x[,2]*3*pi) + 5*rowSums(x^2))))
}

## data generating function combining mean and noise fields
ftest <- function(x){
  return(branin(x) + rnorm(nrow(x), mean = 0, sd = noiseFun(x)))
}

## Grid of predictive locations

```



```

ngrid <- 51
xgrid <- matrix(seq(0, 1, length.out = ngrid), ncol = 1)
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))

## Unique (randomly chosen) design locations
n <- 100
Xu <- matrix(runif(n * 2), n)

## Select replication sites randomly
X <- Xu[sample(1:n, 20*n, replace = TRUE),]

## obtain training data response at design locations X
Z <- ftest(X)

## Formatting of data for model creation (find replicated observations)
prdata <- find_reps(X, Z, rescale = FALSE, normalize = FALSE)

## Model fitting
model <- mleHetTP(X = list(X0 = prdata$X0, Z0 = prdata$Z0, mult = prdata$mult), Z = prdata$Z, ,
                 lower = rep(0.01, nvar), upper = rep(10, nvar),
                 covtype = "Matern5_2")

## a quick view into the data stored in the "hetTP"-class object
summary(model)

## prediction from the fit on the grid
preds <- predict(x = Xgrid, object = model)

## Visualization of the predictive surface
par(mfrow = c(2, 2))
contour(x = xgrid, y = xgrid, z = matrix(branin(Xgrid), ngrid),
       main = "Branin function", nlevels = 20)
points(X, col = 'blue', pch = 20)
contour(x = xgrid, y = xgrid, z = matrix(preds$mean, ngrid),
       main = "Predicted mean", nlevels = 20)
points(X, col = 'blue', pch = 20)
contour(x = xgrid, y = xgrid, z = matrix(noiseFun(Xgrid), ngrid),
       main = "Noise standard deviation function", nlevels = 20)
points(X, col = 'blue', pch = 20)
contour(x = xgrid, y = xgrid, z = matrix(sqrt(preds$nugs), ngrid),
       main = "Predicted noise values", nlevels = 20)
points(X, col = 'blue', pch = 20)
par(mfrow = c(1, 1))

```

Description

Gaussian process regression under homoskedastic noise based on maximum likelihood estimation of the hyperparameters. This function is enhanced to deal with replicated observations.

Usage

```
mleHomGP(X, Z, lower = NULL, upper = NULL, known = NULL,
  noiseControl = list(g_bounds = c(sqrt(.Machine$double.eps), 100)),
  init = NULL, covtype = c("Gaussian", "Matern5_2", "Matern3_2"),
  maxit = 100, eps = sqrt(.Machine$double.eps),
  settings = list(return.Ki = TRUE))
```

Arguments

<code>X</code>	matrix of all designs, one per row, or list with elements: <ul style="list-style-type: none"> • <code>X0</code> matrix of unique design locations, one point per row • <code>Z0</code> vector of averaged observations, of length <code>nrow(X0)</code> • <code>mult</code> number of replicates at designs in <code>X0</code>, of length <code>nrow(X0)</code>
<code>Z</code>	vector of all observations. If using a list with <code>X</code> , <code>Z</code> has to be ordered with respect to <code>X0</code> , and of length <code>sum(mult)</code>
<code>lower</code> , <code>upper</code>	optional bounds for the <code>theta</code> parameter (see cov_gen for the exact parameterization). In the multivariate case, it is possible to give vectors for bounds (resp. scalars) for anisotropy (resp. isotropy)
<code>known</code>	optional list of known parameters, e.g., <code>beta0</code> , <code>theta</code> or <code>g</code>
<code>noiseControl</code>	list with element , <ul style="list-style-type: none"> • <code>g_bounds</code>, vector providing minimal and maximal noise to signal ratio
<code>init</code>	optional list specifying starting values for MLE optimization, with elements: <ul style="list-style-type: none"> • <code>theta_init</code> initial value of the <code>theta</code> parameters to be optimized over (default to 10% of the range determined with <code>lower</code> and <code>upper</code>) • <code>g_init</code> initial value of the nugget parameter to be optimized over (based on the variance at replicates if there are any, else <code>0.1</code>)
<code>covtype</code>	covariance kernel type, either 'Gaussian', 'Matern5_2' or 'Matern3_2', see cov_gen
<code>maxit</code>	maximum number of iteration for L-BFGS-B of optim
<code>eps</code>	jitter used in the inversion of the covariance matrix for numerical stability
<code>settings</code>	list with argument <code>return.Ki</code> , to include the inverse covariance matrix in the object for further use (e.g., prediction).

Details

The global covariance matrix of the model is parameterized as $\text{nu_hat} * (C + g * \text{diag}(1/\text{mult})) = \text{nu_hat} * K$, with C the correlation matrix between unique designs, depending on the family of kernel used (see [cov_gen](#) for available choices) and values of lengthscale parameters. `nu_hat` is the plugin estimator of the variance of the process.

It is generally recommended to use [find_reps](#) to pre-process the data, to rescale the inputs to the unit cube and to normalize the outputs.

Value

a list which is given the S3 class "homGP", with elements:

- theta: maximum likelihood estimate of the lengthscale parameter(s),
- g: maximum likelihood estimate of the nugget variance,
- trendtype: either "SK" if beta0 is given, else "OK"
- beta0: estimated trend unless given in input,
- nu_hat: plugin estimator of the variance,
- ll: log-likelihood value,
- X0, Z0, Z, mult, eps, covtype: values given in input,
- call: user call of the function
- used_args: list with arguments provided in the call
- nit_opt, msg: counts and msg returned by `optim`
- Ki: inverse covariance matrix (not scaled by nu_hat) (if return.Ki is TRUE in settings)
- time: time to train the model, in seconds.

References

M. Binois, Robert B. Gramacy, M. Ludkovski (2018), Practical heteroskedastic Gaussian process modeling for large simulation experiments, *Journal of Computational and Graphical Statistics*, 27(4), 808–821.
Preprint available on arXiv:1611.05902.

See Also

`predict.homGP` for predictions, `update.homGP` for updating an existing model. `summary` and `plot` functions are available as well. `mleHomTP` provide a Student-t equivalent.

Examples

```
##-----
## Example 1: Homoskedastic GP modeling on the motorcycle data
##-----
set.seed(32)

## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
plot(X, Z, ylim = c(-160, 90), ylab = 'acceleration', xlab = "time")

model <- mleHomGP(X = X, Z = Z, lower = 0.01, upper = 100)

## Display averaged observations
```

```

points(model$X0, model$Z0, pch = 20)
xgrid <- matrix(seq(0, 60, length.out = 301), ncol = 1)
predictions <- predict(x = xgrid, object = model)

## Display mean prediction
lines(xgrid, predictions$mean, col = 'red', lwd = 2)
## Display 95% confidence intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2)), col = 2, lty = 2)
## Display 95% prediction intervals
lines(xgrid, qnorm(0.05, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)
lines(xgrid, qnorm(0.95, predictions$mean, sqrt(predictions$sd2 + predictions$nugs)),
      col = 3, lty = 2)

```

mleHomTP

Student-T process modeling with homoskedastic noise

Description

Student-t process regression under homoskedastic noise based on maximum likelihood estimation of the hyperparameters. This function is enhanced to deal with replicated observations.

Usage

```

mleHomTP(X, Z, lower = NULL, upper = NULL, known = list(beta0 = 0),
         noiseControl = list(g_bounds = c(sqrt(.Machine$double.eps), 10000),
                             nu_bounds = c(2 + 0.001, 30), sigma2_bounds =
                             c(sqrt(.Machine$double.eps), 10000)), init = list(nu = 3),
         covtype = c("Gaussian", "Matern5_2", "Matern3_2"), maxit = 100,
         eps = sqrt(.Machine$double.eps), settings = list(return.Ki = TRUE))

```

Arguments

X	matrix of all designs, one per row, or list with elements: <ul style="list-style-type: none"> • X0 matrix of unique design locations, one point per row • Z0 vector of averaged observations, of length nrow(X0) • mult number of replicates at designs in X0, of length nrow(X0)
Z	vector of all observations. If using a list with X, Z has to be ordered with respect to X0, and of length sum(mult)
lower, upper	bounds for the theta parameter (see cov_gen for the exact parameterization). In the multivariate case, it is possible to give vectors for bounds (resp. scalars) for anisotropy (resp. isotropy)
known	optional list of known parameters, e.g., beta0 (default to 0), theta, g, sigma2 or nu
noiseControl	list with element,

	<ul style="list-style-type: none"> • <code>g_bound</code>, vector providing minimal and maximal noise variance • <code>sigma2_bounds</code>, vector providing minimal and maximal signal variance • <code>nu_bounds</code>, vector providing minimal and maximal values for the degrees of freedom. The minimal value has to be strictly greater than 2. If the mle optimization gives a large value, e.g., 30, considering a GP with <code>mleHomGP</code> may be better.
<code>init</code>	list specifying starting values for MLE optimization, with elements: <ul style="list-style-type: none"> • <code>theta_init</code> initial value of the theta parameters to be optimized over (default to 10% of the range determined with <code>lower</code> and <code>upper</code>) • <code>g_init</code> initial value of the nugget parameter to be optimized over (based on the variance at replicates if there are any, else 10% of the variance) • <code>sigma2</code> initial value of the variance parameter (default to 1) • <code>nu</code> initial value of the degrees of freedom parameter (default to 3)
<code>covtype</code>	covariance kernel type, either 'Gaussian', 'Matern5_2' or 'Matern3_2', see <code>cov_gen</code>
<code>maxit</code>	maximum number of iteration for L-BFGS-B of <code>optim</code>
<code>eps</code>	jitter used in the inversion of the covariance matrix for numerical stability
<code>settings</code>	list with argument <code>return.Ki</code> , to include the inverse covariance matrix in the object for further use (e.g., prediction).

Details

The global covariance matrix of the model is parameterized as $K = \sigma^2 * C + g * \text{diag}(1/\text{mult})$, with C the correlation matrix between unique designs, depending on the family of kernel used (see `cov_gen` for available choices).

It is generally recommended to use `find_reps` to pre-process the data, to rescale the inputs to the unit cube and to normalize the outputs.

Value

a list which is given the S3 class "homGP", with elements:

- `theta`: maximum likelihood estimate of the lengthscale parameter(s),
- `g`: maximum likelihood estimate of the nugget variance,
- `trendtype`: either "SK" if `beta0` is given, else "OK"
- `beta0`: estimated trend unless given in input,
- `sigma2`: maximum likelihood estimate of the scale variance,
- `nu2`: maximum likelihood estimate of the degrees of freedom parameter,
- `ll`: log-likelihood value,
- `X0`, `Z0`, `Z`, `mult`, `eps`, `covtype`: values given in input,
- `call`: user call of the function
- `used_args`: list with arguments provided in the call
- `nit_opt`, `msg`: counts and msg returned by `optim`
- `Ki`, inverse covariance matrix (if `return.Ki` is TRUE in `settings`)
- `time`: time to train the model, in seconds.

References

M. Binois, Robert B. Gramacy, M. Ludkovski (2017+), Practical heteroskedastic Gaussian process modeling for large simulation experiments, arXiv preprint arXiv:1611.05902.

A. Shah, A. Wilson, Z. Ghahramani (2014), Student-t processes as alternatives to Gaussian processes, Artificial Intelligence and Statistics, 877–885.

M. Chung, M. Binois, RB Gramacy, DJ Moquin, AP Smith, AM Smith (2018+). Parameter and Uncertainty Estimation for Dynamical Systems Using Surrogate Stochastic Processes. Preprint available on arXiv:1802.00852.

See Also

[predict.homTP](#) for predictions. `summary` and `plot` functions are available as well.

Examples

```
##-----
## Example 1: Homoskedastic Student-t modeling on the motorcycle data
##-----
set.seed(32)

## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
plot(X, Z, ylim = c(-160, 90), ylab = 'acceleration', xlab = "time")

noiseControl = list(g_bounds = c(1e-3, 1e4))
model <- mleHomTP(X = X, Z = Z, lower = 0.01, upper = 100, noiseControl = noiseControl)
summary(model)

## Display averaged observations
points(model$X0, model$Z0, pch = 20)
xgrid <- matrix(seq(0, 60, length.out = 301), ncol = 1)
preds <- predict(x = xgrid, object = model)

## Display mean prediction
lines(xgrid, preds$mean, col = 'red', lwd = 2)
## Display 95% confidence intervals
lines(xgrid, preds$mean + sqrt(preds$sd2) * qt(0.05, df = model$nu + nrow(X)), col = 2, lty = 2)
lines(xgrid, preds$mean + sqrt(preds$sd2) * qt(0.95, df = model$nu + nrow(X)), col = 2, lty = 2)
## Display 95% prediction intervals
lines(xgrid, preds$mean + sqrt(preds$sd2 + preds$nugs) * qt(0.05, df = model$nu + nrow(X)),
      col = 3, lty = 2)
lines(xgrid, preds$mean + sqrt(preds$sd2 + preds$nugs) * qt(0.95, df = model$nu + nrow(X)),
      col = 3, lty = 2)
```

predict.hetGP	<i>Gaussian process predictions using a heterogeneous noise GP object (of class hetGP)</i>
---------------	--

Description

Gaussian process predictions using a heterogeneous noise GP object (of class hetGP)

Usage

```
## S3 method for class 'hetGP'
predict(object, x, noise.var = FALSE, xprime = NULL,
        nugs.only = FALSE, ...)
```

Arguments

object	an object of class hetGP; e.g., as returned by mleHetGP
x	matrix of designs locations to predict at (one point per row)
noise.var	should the variance of the latent variance process be returned?
xprime	optional second matrix of predictive locations to obtain the predictive covariance matrix between x and xprime
nugs.only	if TRUE, only return noise variance prediction
...	no other argument for this method.

Details

The full predictive variance corresponds to the sum of sd2 and nugs. See [mleHetGP](#) for examples.

Value

list with elements

- mean: kriging mean;
- sd2: kriging variance (filtered, e.g. without the nugget values)
- nugs: noise variance prediction
- sd2_var: (returned if noise.var = TRUE) kriging variance of the noise process (i.e., on log-variances if logN = TRUE)
- cov: (returned if xprime is given) predictive covariance matrix between x and xprime

predict.hetTP	<i>Student-t process predictions using a heterogeneous noise TP object (of class hetTP)</i>
---------------	---

Description

Student-t process predictions using a heterogeneous noise TP object (of class hetTP)

Usage

```
## S3 method for class 'hetTP'
predict(object, x, noise.var = FALSE, xprime = NULL,
        nugs.only = FALSE, ...)
```

Arguments

object	an object of class hetTP; e.g., as returned by mleHetTP
x	matrix of designs locations to predict at
noise.var	should the variance of the latent variance process be returned?
xprime	optional second matrix of predictive locations to obtain the predictive covariance matrix between x and xprime
nugs.only	if TRUE, only return noise variance prediction
...	no other argument for this method.

Details

The full predictive variance corresponds to the sum of sd2 and nugs.

Value

list with elements

- mean: kriging mean;
- sd2: kriging variance (filtered, e.g. without the nugget values)
- nugs: noise variance
- sd2_var: (optional) kriging variance of the noise process (i.e., on log-variances if logN = TRUE)
- cov: (optional) predictive covariance matrix between x and xprime

predict.homGP	<i>Gaussian process predictions using a homoskedastic noise GP object (of class homGP)</i>
---------------	--

Description

Gaussian process predictions using a homoskedastic noise GP object (of class homGP)

Usage

```
## S3 method for class 'homGP'  
predict(object, x, xprime = NULL, ...)
```

Arguments

object	an object of class homGP; e.g., as returned by mleHomGP
x	matrix of designs locations to predict at (one point per row)
xprime	optional second matrix of predictive locations to obtain the predictive covariance matrix between x and xprime
...	no other argument for this method

Details

The full predictive variance corresponds to the sum of sd2 and nugs. See [mleHomGP](#) for examples.

Value

list with elements

- mean: kriging mean;
- sd2: kriging variance (filtered, e.g. without the nugget value)
- cov: predictive covariance matrix between x and xprime
- nugs: nugget value at each prediction location, for consistency with [mleHomGP](#).

predict.homTP	<i>Student-t process predictions using a homoskedastic noise GP object (of class homGP)</i>
---------------	---

Description

Student-t process predictions using a homoskedastic noise GP object (of class homGP)

Usage

```
## S3 method for class 'homTP'
predict(object, x, xprime = NULL, ...)
```

Arguments

object	an object of class homGP; e.g., as returned by mleHomTP
x	matrix of designs locations to predict at
xprime	optional second matrix of predictive locations to obtain the predictive covariance matrix between x and xprime
...	no other argument for this method

Details

The full predictive variance corresponds to the sum of sd2 and nugs.

Value

list with elements

- mean: kriging mean;
- sd2: kriging variance (filtered, e.g. without the nugget value)
- cov: predictive covariance matrix between x and xprime
- nugs: nugget value at each prediction location

rebuild	<i>Import and export of hetGP objects</i>
---------	---

Description

Functions to make hetGP objects lighter before exporting them, and to reverse this after import. The rebuild function may also be used to obtain more robust inverse of covariance matrices using [ginv](#).

Usage

```
rebuild(object, robust)

## S3 method for class 'homGP'
rebuild(object, robust = FALSE)

strip(object)

## S3 method for class 'hetGP'
rebuild(object, robust = FALSE)

## S3 method for class 'homTP'
rebuild(object, robust = FALSE)

## S3 method for class 'hetTP'
rebuild(object, robust = FALSE)
```

Arguments

object	homGP or homTP model without slot Ki (inverse covariance matrix), or hetGP or hetTP model without slot Ki or Kgi
robust	if TRUE ginv is used for matrix inversion, otherwise it is done via Cholesky.

Value

object with additional or removed slots.

Examples

```
set.seed(32)
## motorcycle data
library(MASS)
X <- matrix(mcycle$times, ncol = 1)
Z <- mcycle$accel
## Model fitting
model <- mleHetGP(X = X, Z = Z, lower = 0.1, upper = 50)

# Check size
object.size(model)

# Remove internal elements, e.g., to save it
model <- strip(model)

# Check new size
object.size(model)

# Now rebuild model, and use ginv instead
model <- rebuild(model, robust = TRUE)
object.size(model)
```

`sirEval`*SIR test problem*

Description

Epidemiology problem, initial and rescaled to $[0,1]^2$ versions.

Usage

```
sirEval(x)
```

```
sirSimulate(S0 = 1990, I0 = 10, M = S0 + I0, beta = 0.75,  
  gamma = 0.5, imm = 0)
```

Arguments

<code>x</code>	vector of size two
<code>S0</code>	initial number of susceptibles
<code>I0</code>	initial number of infected
<code>M</code>	total population
<code>beta, gamma, imm</code>	control rates

References

R. Hu, M. Ludkovski (2017), Sequential Design for Ranking Response Surfaces, SIAM/ASA Journal on Uncertainty Quantification, 5(1), 212-239.

Examples

```
## SIR test problem illustration  
ngrid <- 10 # increase  
xgrid <- seq(0, 1, length.out = ngrid)  
Xgrid <- as.matrix(expand.grid(xgrid, xgrid))  
  
nrep <- 5 # increase  
X <- Xgrid[rep(1:nrow(Xgrid), nrep),]  
Y <- apply(X, 1, sirEval)  
dataSIR <- find_reps(X, Y)  
filled.contour(xgrid, xgrid, matrix(lapply(dataSIR$Zlist, sd), ngrid),  
  xlab = "Susceptibles", ylab = "Infecteds", color.palette = terrain.colors)
```

update.hetGP	<i>Update "hetGP"-class model fit with new observations</i>
--------------	---

Description

Fast update of existing hetGP model with new observations.

Usage

```
## S3 method for class 'hetGP'
update(object, Xnew, Znew, ginit = 0.01, lower = NULL,
       upper = NULL, noiseControl = NULL, settings = NULL, known = NULL,
       maxit = 100, method = "quick", ...)
```

Arguments

object	previously fit "hetGP"-class model
Xnew	matrix of new design locations; ncol(Xnew) must match the input dimension encoded in object
Znew	vector new observations at those design locations, of length nrow(X). NAs can be passed, see Details
ginit	minimal value of the smoothing parameter (i.e., nugget of the noise process) for optimization initialisation. It is compared to the g hyperparameter in the object.
lower, upper, noiseControl, settings, known	optional bounds for mle optimization, see mleHetGP . If not provided, they are extracted from the existing model
maxit	maximum number of iterations for the internal L-BFGS-B optimization method; see optim for more details
method	one of "quick", "mixed" see Details.
...	no other argument for this method.

Details

The update can be performed with or without re-estimating hyperparameter. In the first case, [mleHetGP](#) is called, based on previous values for initialization. The only missing values are the latent variables at the new points, that are initialized based on two possible update schemes in method:

- "quick" the new delta value is the predicted nugs value from the previous noise model;
- "mixed" new values are taken as the barycenter between prediction given by the noise process and empirical variance.

The subsequent number of MLE computations can be controlled with `maxit`.

In case hyperparameters need not be updated, `maxit` can be set to 0. In this case it is possible to pass NAs in `Znew`, then the model can still be used to provide updated variance predictions.

Examples

```

##-----
## Sequential update example
##-----
set.seed(42)

## Spatially varying noise function
noisefun <- function(x, coef = 1){
  return(coef * (0.05 + sqrt(abs(x)*20/(2*pi))/10))
}

## Initial data set
nvar <- 1
n <- 20
X <- matrix(seq(0, 2 * pi, length=n), ncol = 1)
mult <- sample(1:10, n, replace = TRUE)
X <- rep(X, mult)
Z <- sin(X) + rnorm(length(X), sd = noisefun(X))

## Initial fit
testpts <- matrix(seq(0, 2*pi, length = 10*n), ncol = 1)
model <- model_init <- mleHetGP(X = X, Z = Z, lower = rep(0.1, nvar),
  upper = rep(50, nvar), maxit = 1000)

## Visualizing initial predictive surface
preds <- predict(x = testpts, model_init)
plot(X, Z)
lines(testpts, preds$mean, col = "red")

## 10 fast update steps
nsteps <- 5
npersteps <- 10
for(i in 1:nsteps){
  newIds <- sort(sample(1:(10*n), npersteps))

  newX <- testpts[newIds, drop = FALSE]
  newZ <- sin(newX) + rnorm(length(newX), sd = noisefun(newX))
  points(newX, newZ, col = "blue", pch = 20)
  model <- update(object = model, Xnew = newX, Znew = newZ)
  X <- c(X, newX)
  Z <- c(Z, newZ)
  plot(X, Z)
  print(model$nit_opt)
}

## Final predictions after 10 updates
p_fin <- predict(x=testpts, model)

## Visualizing the result by augmenting earlier plot
lines(testpts, p_fin$mean, col = "blue")
lines(testpts, qnorm(0.05, p_fin$mean, sqrt(p_fin$sd2)), col = "blue", lty = 2)
lines(testpts, qnorm(0.95, p_fin$mean, sqrt(p_fin$sd2)), col = "blue", lty = 2)

```

```

lines(testpts, qnorm(0.05, p_fin$mean, sqrt(p_fin$sd2 + p_fin$nugs)),
      col = "blue", lty = 3)
lines(testpts, qnorm(0.95, p_fin$mean, sqrt(p_fin$sd2 + p_fin$nugs)),
      col = "blue", lty = 3)

## Now compare to what you would get if you did a full batch fit instead
model_direct <- mleHetGP(X = X, Z = Z, maxit = 1000,
                        lower = rep(0.1, nvar), upper = rep(50, nvar),
                        init = list(theta = model_init$theta, k_theta_g = model_init$k_theta_g))
p_dir <- predict(x = testpts, model_direct)
print(model_direct$nit_opt)
lines(testpts, p_dir$mean, col = "green")
lines(testpts, qnorm(0.05, p_dir$mean, sqrt(p_dir$sd2)), col = "green",
      lty = 2)
lines(testpts, qnorm(0.95, p_dir$mean, sqrt(p_dir$sd2)), col = "green",
      lty = 2)
lines(testpts, qnorm(0.05, p_dir$mean, sqrt(p_dir$sd2 + p_dir$nugs)),
      col = "green", lty = 3)
lines(testpts, qnorm(0.95, p_dir$mean, sqrt(p_dir$sd2 + p_dir$nugs)),
      col = "green", lty = 3)
lines(testpts, sin(testpts), col = "red", lty = 2)

## Compare outputs
summary(model_init)
summary(model)
summary(model_direct)

```

update.hetTP

Update "hetTP"-class model fit with new observations

Description

Fast update of existing hetTP model with new observations.

Usage

```

## S3 method for class 'hetTP'
update(object, Xnew, Znew, ginit = 0.01, lower = NULL,
       upper = NULL, noiseControl = NULL, settings = NULL, known = NULL,
       maxit = 100, method = "quick", ...)

```

Arguments

object	previously fit "hetTP"-class model
Xnew	matrix of new design locations; ncol(Xnew) must match the input dimension encoded in object
Znew	vector new observations at those design locations, of length nrow(X). NAs can be passed, see Details

ginit minimal value of the smoothing parameter (i.e., nugget of the noise process) for optimization initialisation. It is compared to the *g* hyperparameter in the object.
lower, upper, noiseControl, settings, known optional bounds for mle optimization, see [mleHetTP](#). If not provided, they are extracted from the existing model
maxit maximum number of iterations for the internal L-BFGS-B optimization method; see [optim](#) for more details
method one of "quick", "mixed" see Details.
... no other argument for this method.

Details

The update can be performed with or without re-estimating hyperparameter. In the first case, [mleHetTP](#) is called, based on previous values for initialization. The only missing values are the latent variables at the new points, that are initialized based on two possible update schemes in method:

- "quick" the new delta value is the predicted nugs value from the previous noise model;
- "mixed" new values are taken as the barycenter between prediction given by the noise process and empirical variance.

The subsequent number of MLE computations can be controlled with *maxit*.

In case hyperparameters need not be updated, *maxit* can be set to 0. In this case it is possible to pass NAs in *Znew*, then the model can still be used to provide updated variance predictions.

Examples

```

##-----
## Sequential update example
##-----
set.seed(42)

## Spatially varying noise function
noisefun <- function(x, coef = 1){
  return(coef * (0.05 + sqrt(abs(x)*20/(2*pi))/10))
}

## Initial data set
nvar <- 1
n <- 20
X <- matrix(seq(0, 2 * pi, length=n), ncol = 1)
mult <- sample(1:10, n, replace = TRUE)
X <- rep(X, mult)
Z <- sin(X) + noisefun(X) * rt(length(X), df = 10)

## Initial fit
testpts <- matrix(seq(0, 2*pi, length = 10*n), ncol = 1)
model <- model_init <- mleHetTP(X = X, Z = Z, lower = rep(0.1, nvar),
  upper = rep(50, nvar), maxit = 1000)

```



```

## Visualizing initial predictive surface
preds <- predict(x = testpts, model_init)
plot(X, Z)
lines(testpts, preds$mean, col = "red")

## 10 fast update steps
nsteps <- 5
npersteps <- 10
for(i in 1:nsteps){
  newIds <- sort(sample(1:(10*n), npersteps))

  newX <- testpts[newIds, drop = FALSE]
  newZ <- sin(newX) + noisefun(newX) * rt(length(newX), df = 10)
  points(newX, newZ, col = "blue", pch = 20)
  model <- update(object = model, Xnew = newX, Znew = newZ)
  X <- c(X, newX)
  Z <- c(Z, newZ)
  plot(X, Z)
  print(model$nit_opt)
}

## Final predictions after 10 updates
p_fin <- predict(x=testpts, model)

## Visualizing the result by augmenting earlier plot
lines(testpts, p_fin$mean, col = "blue")
lines(testpts, qnorm(0.05, p_fin$mean, sqrt(p_fin$sd2)), col = "blue", lty = 2)
lines(testpts, qnorm(0.95, p_fin$mean, sqrt(p_fin$sd2)), col = "blue", lty = 2)
lines(testpts, qnorm(0.05, p_fin$mean, sqrt(p_fin$sd2 + p_fin$nugs)),
      col = "blue", lty = 3)
lines(testpts, qnorm(0.95, p_fin$mean, sqrt(p_fin$sd2 + p_fin$nugs)),
      col = "blue", lty = 3)

## Now compare to what you would get if you did a full batch fit instead
model_direct <- mleHetTP(X = X, Z = Z, maxit = 1000,
                        lower = rep(0.1, nvar), upper = rep(50, nvar),
                        init = list(theta = model_init$theta, k_theta_g = model_init$k_theta_g))
p_dir <- predict(x = testpts, model_direct)
print(model_direct$nit_opt)
lines(testpts, p_dir$mean, col = "green")
lines(testpts, qnorm(0.05, p_dir$mean, sqrt(p_dir$sd2)), col = "green",
      lty = 2)
lines(testpts, qnorm(0.95, p_dir$mean, sqrt(p_dir$sd2)), col = "green",
      lty = 2)
lines(testpts, qnorm(0.05, p_dir$mean, sqrt(p_dir$sd2 + p_dir$nugs)),
      col = "green", lty = 3)
lines(testpts, qnorm(0.95, p_dir$mean, sqrt(p_dir$sd2 + p_dir$nugs)),
      col = "green", lty = 3)
lines(testpts, sin(testpts), col = "red", lty = 2)

## Compare outputs
summary(model_init)
summary(model)

```

```
summary(model_direct)
```

```
update.homGP      Fast homGP-update
```

Description

Update existing homGP model with new observations

Usage

```
## S3 method for class 'homGP'
update(object, Xnew, Znew = NULL, lower = NULL,
       upper = NULL, noiseControl = NULL, known = NULL, maxit = 100,
       ...)
```

Arguments

object	initial model of class homGP
Xnew	matrix of new design locations; ncol(Xnew) must match the input dimension encoded in object
Znew	vector new observations at those new design locations, of length nrow(X). NAs can be passed, see Details
lower, upper, noiseControl, known	optional bounds for MLE optimization, see mleHomGP . If not provided, they are extracted from the existing model
maxit	maximum number of iterations for the internal L-BFGS-B optimization method; see optim for more details
...	no other argument for this method.

Details

In case hyperparameters need not be updated, maxit can be set to 0. In this case it is possible to pass NAs in Znew, then the model can still be used to provide updated variance predictions.

Examples

```
## Not run:
##-----
## Example : Sequential Homoskedastic GP modeling
##-----
set.seed(42)

## Spatially varying noise function
noisefun <- function(x, coef = 1){
  return(coef * (0.05 + sqrt(abs(x)*20/(2*pi))/10))
}
```

```

}

nvar <- 1
n <- 10
X <- matrix(seq(0, 2 * pi, length=n), ncol = 1)
mult <- sample(1:10, n)
X <- rep(X, mult)
Z <- sin(X) + rnorm(length(X), sd = noisefun(X))

testpts <- matrix(seq(0, 2*pi, length = 10*n), ncol = 1)
model <- model_init <- mleHomGP(X = X, Z = Z,
                               lower = rep(0.1, nvar), upper = rep(50, nvar))
preds <- predict(x = testpts, object = model_init)
plot(X, Z)
lines(testpts, preds$mean, col = "red")

nsteps <- 10
for(i in 1:nsteps){
  newIds <- sort(sample(1:(10*n), 10))

  newX <- testpts[newIds, drop = FALSE]
  newZ <- sin(newX) + rnorm(length(newX), sd = noisefun(newX))
  points(newX, newZ, col = "blue", pch = 20)
  model <- update(object = model, newX, newZ)
  X <- c(X, newX)
  Z <- c(Z, newZ)
  plot(X, Z)
  print(model$nit_opt)
}
p_fin <- predict(x = testpts, object = model)
lines(testpts, p_fin$mean, col = "blue")
lines(testpts, qnorm(0.05, p_fin$mean, sqrt(p_fin$sd2)), col = "blue", lty = 2)
lines(testpts, qnorm(0.95, p_fin$mean, sqrt(p_fin$sd2)), col = "blue", lty = 2)
lines(testpts, qnorm(0.05, p_fin$mean, sqrt(p_fin$sd2 + p_fin$nugs)),
      col = "blue", lty = 3)
lines(testpts, qnorm(0.95, p_fin$mean, sqrt(p_fin$sd2 + p_fin$nugs)),
      col = "blue", lty = 3)

model_direct <- mleHomGP(X = X, Z = Z, lower = rep(0.1, nvar), upper = rep(50, nvar))
p_dir <- predict(x = testpts, object = model_direct)
print(model_direct$nit_opt)
lines(testpts, p_dir$mean, col = "green")
lines(testpts, qnorm(0.05, p_dir$mean, sqrt(p_dir$sd2)), col = "green", lty = 2)
lines(testpts, qnorm(0.95, p_dir$mean, sqrt(p_dir$sd2)), col = "green", lty = 2)
lines(testpts, qnorm(0.05, p_dir$mean, sqrt(p_dir$sd2 + p_dir$nugs)),
      col = "green", lty = 3)
lines(testpts, qnorm(0.95, p_dir$mean, sqrt(p_dir$sd2 + p_dir$nugs)),
      col = "green", lty = 3)

lines(testpts, sin(testpts), col = "red", lty = 2)

## Compare outputs

```

```
summary(model_init)
summary(model)
summary(model_direct)
```

```
## End(Not run)
```

update.homTP

Fast homTP-update

Description

Update existing homTP model with new observations

Usage

```
## S3 method for class 'homTP'
update(object, Xnew, Znew = NULL, lower = NULL,
       upper = NULL, noiseControl = NULL, known = NULL, maxit = 100,
       ...)
```

Arguments

object	initial model of class homTP
Xnew	matrix of new design locations; ncol(Xnew) must match the input dimension encoded in object
Znew	vector new observations at those new design locations, of length nrow(X). NAs can be passed, see Details
lower, upper, noiseControl, known	optional bounds for MLE optimization, see mleHomTP . If not provided, they are extracted from the existing model
maxit	maximum number of iterations for the internal L-BFGS-B optimization method; see optim for more details
...	no other argument for this method.

Details

In case hyperparameters need not be updated, `maxit` can be set to 0. In this case it is possible to pass NAs in `Znew`, then the model can still be used to provide updated variance predictions.

Examples

```

## Not run:
##-----
## Example : Sequential Homoskedastic TP moding
##-----
set.seed(42)

## Spatially varying noise function
noisefun <- function(x, coef = 1){
  return(coef * (0.05 + sqrt(abs(x)*20/(2*pi))/10))
}

df_noise <- 3
nvar <- 1
n <- 10
X <- matrix(seq(0, 2 * pi, length=n), ncol = 1)
mult <- sample(1:50, n, replace = TRUE)
X <- rep(X, mult)
Z <- sin(X) + noisefun(X) * rt(length(X), df = df_noise)

testpts <- matrix(seq(0, 2*pi, length = 10*n), ncol = 1)
mod <- mod_init <- mleHomTP(X = X, Z = Z, covtype = "Matern5_2",
                           lower = rep(0.1, nvar), upper = rep(50, nvar))
preds <- predict(x = testpts, object = mod_init)
plot(X, Z)
lines(testpts, preds$mean, col = "red")

nsteps <- 10
for(i in 1:nsteps){
  newIds <- sort(sample(1:(10*n), 5))

  newX <- testpts[rep(newIds, times = sample(1:50, length(newIds), replace = TRUE)), drop = FALSE]
  newZ <- sin(newX) + noisefun(newX) * rt(length(newX), df = df_noise)
  points(newX, newZ, col = "blue", pch = 20)
  mod <- update(object = mod, newX, newZ)
  X <- c(X, newX)
  Z <- c(Z, newZ)
  plot(X, Z)
  print(mod$nit_opt)
}
p_fin <- predict(x = testpts, object = mod)
lines(testpts, p_fin$mean, col = "blue")
lines(testpts, p_fin$mean + sqrt(p_fin$sd2) * qt(0.05, df = mod$nu + length(Z)),
      col = "blue", lty = 2)
lines(testpts, p_fin$mean + sqrt(p_fin$sd2) * qt(0.95, df = mod$nu + length(Z)),
      col = "blue", lty = 2)
lines(testpts, p_fin$mean + sqrt(p_fin$sd2 + p_fin$nugs) * qt(0.05, df = mod$nu + length(Z)),
      col = "blue", lty = 3)
lines(testpts, p_fin$mean + sqrt(p_fin$sd2 + p_fin$nugs) * qt(0.95, df = mod$nu + length(Z)),
      col = "blue", lty = 3)

```

```

mod_dir <- mleHomTP(X = X, Z = Z, covtype = "Matern5_2",
                  lower = rep(0.1, nvar), upper = rep(50, nvar))
p_dir <- predict(x = testpts, object = mod_dir)
print(mod_dir$nit_opt)
lines(testpts, p_dir$mean, col = "green")
lines(testpts, p_dir$mean + sqrt(p_dir$sd2) * qt(0.05, df = mod_dir$nu + length(Z)),
      col = "green", lty = 2)
lines(testpts, p_dir$mean + sqrt(p_dir$sd2) * qt(0.95, df = mod_dir$nu + length(Z)),
      col = "green", lty = 2)
lines(testpts, p_dir$mean + sqrt(p_dir$sd2 + p_dir$nugs) * qt(0.05, df = mod_dir$nu + length(Z)),
      col = "green", lty = 3)
lines(testpts, p_dir$mean + sqrt(p_dir$sd2 + p_dir$nugs) * qt(0.95, df = mod_dir$nu + length(Z)),
      col = "green", lty = 3)

lines(testpts, sin(testpts), col = "red", lty = 2)

## Compare outputs
summary(mod_init)
summary(mod)
summary(mod_dir)

## End(Not run)

```

Wij *Compute double integral of the covariance kernel over a $[0,1]^d$ domain*

Description

Compute double integral of the covariance kernel over a $[0,1]^d$ domain

Usage

```
Wij(mu1, mu2 = NULL, theta, type)
```

Arguments

mu1, mu2	input locations considered
theta	lengthscale hyperparameter of the kernel
type	kernel type, one of "Gaussian", "Matern5_2" or "Matern3_2", see cov_gen

References

M. Binois, J. Huang, R. Gramacy, M. Ludkovski (2017+), Replication or exploration? Sequential design for stochastic simulation experiments.

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