Package ‘SPOT’

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Title Sequential Parameter Optimization Toolbox

Type Package

LazyLoad yes

LazyData true

Description A set of tools for model based optimization and tuning of algorithms. It includes surrogate models, optimizers and design of experiment approaches. The main interface is spot, which uses sequentially updated surrogate models for the purpose of efficient optimization. The main goal is to ease the burden of objective function evaluations, when a single evaluation requires a significant amount of resources.

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Depends R (>= 3.0.0)

Imports randomForest, stats, utils, graphics, grDevices, MASS, DEoptim, rgenoud, plotly, rsm, nloptr

RoxygenNote 6.1.1

Suggests testthat

NeedsCompilation no

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SPOT-package

Description

Sequential Parameter Optimization Toolbox
Details

SPOT uses a combination statistic models and optimization algorithms for the purpose of parameter optimization. Design of Experiment methods are employed to generate an initial set of candidate solutions, which are evaluated with a user-provided objective function. The resulting data is used to fit a model, which in turn is subject to an optimization algorithm, to find the most promising candidate solution(s). These are again evaluated, after which the model is updated with the new results. This sequential procedure of modeling, optimization and evaluation is iterated until the evaluation budget is exhausted.

Note, that versions >= 2.0.1 of the package are a complete rewrite of the interfaces and conventions in SPOT. The rewritten SPOT package aims to improve the following issues of the older package:
- A more modular architecture is provided, that allows the user to easily customize parts of the SPO procedure.
- Core functions for modeling and optimization use interfaces more similar to algorithms from other packages / core-R, hence making them easier accessible for new users. Also, these can now be more easily used separately from the main SPO approach, e.g., only for modeling.
- Reducing the unnecessarily large number of choices and parameters.
- Removal of extremely rarely used / un-used features, to reduce overall complexity of the package.
- Improving documentation and accessibility in general.
- Speed-up of frequently used procedures.

We appreciate feedback about any bugs or other issues with the package. Feel free to send feedback by mail to the maintainer.

Acknowledgments

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See Also

Main interface function is `spot`. 
**buildEnsembleStack**

---

**Description**

Generates an ensemble of surrogate models with stacking (stacked generalization).

**Usage**

```
buildEnsembleStack(x, y, control = list())
```

**Arguments**

- **x**: design matrix (sample locations), rows for each sample, columns for each variable.
- **y**: vector of observations at \( x \)
- **control** (list), with the options for the model building procedure:
  - `modelL1`: Function for fitting the L1 model (default: `buildLM`) which combines the results of the L0 models.
  - `modelL1Control`: List of control parameters for the L1 model (default: `list()`).
  - `modelL0`: A list of functions for fitting the L0 models (default: `list(buildLM, buildRandomForest, buildKriging)`).
  - `modelL0Control`: List of control lists for each L0 model (default: `list(list(), list(), list())`).

**Value**

returns an object of class `ensembleStack`.

**Note**

Loosely based on the code by Emanuele Olivetti https://github.com/emanuele/kaggle_pbr/blob/master/blend.py

**References**


**See Also**

`predict.ensembleStack`
buildKriging

Examples

```r
## Create a test function: branin
braninFunction <- function (x) {
  10 * (1 - 1/(8 * pi)) * cos(x[1] ) + 10
}
## Create design points
x <- cbind(runif(20)*15-5,runif(20)*15)
## Compute observations at design points
y <- as.matrix(apply(x,1,braninFunction))
## Create model with default settings
fit <- buildEnsembleStack(x,y)
## Predict new point
predict(fit,cbind(1,2))
## True value at location
braninFunction(c(1,2))
```

buildKriging Build Kriging Model

Description

This function builds a Kriging model based on code by Forrester et al.. By default exponents (p) are fixed at a value of two, and a nugget (or regularization constant) is used. To correct the uncertainty estimates in case of nugget, re-interpolation is also by default turned on.

Usage

```r
buildKriging(x, y, control = list())
```

Arguments

- **x**: design matrix (sample locations)
- **y**: vector of observations at x
- **control**: (list), with the options for the model building procedure:
  - `types` a character vector giving the data type of each variable. All but "factor" will be handled as numeric, "factor" (categorical) variables will be subject to the hamming distance.
  - `thetaLower` lower boundary for theta, default is 1e-4
  - `thetaUpper` upper boundary for theta, default is 1e2
  - `algTheta` algorithm used to find theta, default is optimLBFGSB.
  - `budgetAlgTheta` budget for the above mentioned algorithm, default is 200. The value will be multiplied with the length of the model parameter vector to be optimized.
  - `optimizeP` boolean that specifies whether the exponents (p) should be optimized. Else they will be set to two. Default is FALSE
use Lambda whether or not to use the regularization constant lambda (nugget effect). Default is TRUE.

t LambdaLower lower boundary for log10lambda, default is -6

t LambdaUpper upper boundary for log10lambda, default is 0

startTheta optional start value for theta optimization, default is NULL

reinterpolate whether (TRUE, default) or not (FALSE) reinterpolation should be performed.

target target values of the prediction, a vector of strings. Each string specifies a value to be predicted, e.g., "y" for mean, "s" for standard deviation, "ei" for expected improvement. See also predict.kriging. This can also be changed after the model has been built, by manipulating the respective object$target value.

Details

The model uses a Gaussian kernel:

$$k(x, z) = \exp(-\sum(\theta_i * |x_i - z_i|^p_i))$$

By default, p_i = 2. Note that if dimension x_i is a factor variable (see parameter types), Hamming distance will be used instead of |x_i - z_i|.

Value

an object of class kriging. Basically a list, with the options and found parameters for the model which has to be passed to the predictor function:

- x sample locations (scaled to values between 0 and 1)
- y observations at sample locations (see parameters)
- thetaLower lower boundary for theta (see parameters)
- thetaUpper upper boundary for theta (see parameters)
- alg Theta algorithm to find theta (see parameters)
- budgetAlg Theta budget for the above mentioned algorithm (see parameters)
- optimizeP boolean that specifies whether the exponents (p) were optimized (see parameters)
- normalize ymin minimum in normalized space
- normalize ymax maximum in normalized space
- normalize xmin minimum in input space
- normalize xmax maximum in input space
- dmodel theta vector of activity parameters
- Theta log_10 vector of activity parameters (i.e. log10(dmodeltheta))
- dmodellambda regularization constant (nugget)
- Lambda log_10 of regularization constant (nugget) (i.e. log10(dmodellambda))
- yonemu Ay-ones*mu
- ssq sigma square
- mu mean mu
- Psi matrix large Psi
- Psinv inverse of Psi
- nevals number of Likelihood evaluations during MLE

References

See Also

`predict.kriging`

Examples

```r
## Test-function:
braninFunction <- function(x) {
  10 * (1 - 1/(8 * pi)) * cos(x[1] ) + 10
}
## Create design points
set.seed(1)
x <- cbind(runif(20)*15-5,runif(20)*15)
## Compute observations at design points (for Branin function)
y <- as.matrix(apply(x,1,braninFunction))
## Create model with default settings
fit <- buildKriging(x,y,control = list(algTheta=optimLHD))
## Print model parameters
print(fit)
## Predict at new location
predict(fit,cbind(1,2))
## True value at location
braninFunction(c(1,2))
##
## Next Example: Handling factor variables
##
## create a test function:
braninFunctionFactor <- function(x) {
  10 * (1 - 1/(8 * pi)) * cos(x[1] ) + 10
  if(x[3]==1)
    y <- y +1
  else if(x[3]==2)
    y <- y -1
  y
}
## create training data
set.seed(1)
x <- cbind(runif(50)*15-5,runif(50)*15,sample(1:3,50,replace=TRUE))
y <- as.matrix(apply(x,1,braninFunctionFactor))
## fit the model (default: assume all variables are numeric)
fitDefault <- buildKriging(x,y,control = list(algTheta=optimLBFGSB))
## fit the model (give information about the factor variable)
fitFactor <- buildKriging(x,y,control =
  list(algTheta=optimLBFGSB,types=c("numeric","numeric","factor")))
## create test data
xtest <- cbind(runif(200)*15-5,runif(200)*15,sample(1:3,200,replace=TRUE))
ytest <- as.matrix(apply(xtest,1,braninFunctionFactor))
## Predict test data with both models, and compute error
ypredDef <- predict(fitDefault,xtest)$y
ypredFact <- predict(fitFactor,xtest)$y
mean((ypredDef-ytest)^2)
```
**Description**

This Kriging meta model is based on DACE (Design and Analysis of Computer Experiments). It allows to choose different regression and correlation models. The optimization of model parameters is by default done with a bounded simplex method from the nloptr package.

**Usage**

```r
buildKrigingDACE(x, y, control = list())
```

**Arguments**

- **x**: design matrix (sample locations), rows for each sample, columns for each variable.
- **y**: vector of observations at x
- **control**: (list), with the options for the model building procedure:
  - `startTheta` optional start value for theta optimization, default is NULL
  - `algTheta` algorithm used to find theta, default is `optimLBFGSB`
  - `budgetAlgTheta` budget for the above mentioned algorithm, default is 200. The value will be multiplied with the length of the model parameter vector to be optimized.
  - `nugget` Value for nugget. Default is -1, which means the nugget will be optimized during MLE. Else it can be fixed in a range between 0 and 1.
  - `regr` Regression function to be used: `regpolyP` (default), `regpoly1`, `regpoly2`. Can be a custom user function.
  - `corr` Correlation function to be used: `corrnoisykriging` (default), `corrkriging`, `corrnoisygauss`, `corrgauss`, `correxpg`, `correxpg`, `corrcubic`, `corspherical`, `corrspline`. Can also be user supplied (if in the right form).
  - `target` target values of the prediction, a vector of strings. Each string specifies a value to be predicted, e.g., "y" for mean, "s" for standard deviation, "ei" for expected improvement. See also `predictKriging`. This can also be changed after the model has been build, by manipulating the respective object$target value.

**Value**

returns an object of class dace with the following elements:

- **model**: A list, containing model parameters
- **like**: Estimated likelihood value
- **theta**: activity parameters theta (vector)
- **p**: exponents p (vector)
- **lambda**: nugget value (numeric)
- **nevals**: Number of iterations during MLE
**Author(s)**

The authors of the original DACE Matlab toolbox are Hans Bruun Nielsen <hbn@imm.dtu.dk>, Soren Nymand Lophaven and Jacob Sondergaard. Extension of the Matlab code by Tobias Wagner <wagner@isf.de>. Porting and adaptation to R and further extensions by Martin Zaefferer <martin.zaefferer@fh-koeln.de>.

**References**


**See Also**

predict.dace

**Examples**

```r
## Create design points
x <- cbind(runif(20)*15-5,runif(20)*15)
## Compute observations at design points
y <- funSphere(x)
## Create model with default settings
fit <- buildKrigingDACE(x,y)
## Print model parameters
print(fit)
## Create with different regression and correlation functions
fit <- buildKrigingDACE(x,y,control=list(regr=regpoly2,corr=corrspline))
## Print model parameters
print(fit)
```

---

**buildLM**  
**Linear Model Interface**

**Description**

This is a simple wrapper for the lm function, which fits linear models. The purpose of this function is to provide an interface as required by SPOT, to enable modeling and model-based optimization with linear models. The linear model is build with main effects. Optionally, the model is also subject to the AIC-based stepwise algorithm, using the step function from the stats package.

**Usage**

```r
buildLM(x, y, control = list())
```
Build LOESS Model

Description

Build an interpolation model using the loess function. Essentially a SPOT-style interface to that function.

Usage

buildLOESS(x, y, control = list())
Arguments

- **x**: design matrix (sample locations), rows for each sample, columns for each variable.
- **y**: vector of observations at x
- **control**: named list, with the options for the model building procedure loess. These will be passed to loess as arguments. Please refrain from setting the formula or data arguments as these will be supplied by the interface, based on x and y.

Value

returns an object of class `spotLOESS`.

See Also

- `predict.spotLOESS`

Examples

```r
## Create a test function: branin
braninFunction <- function (x) {
  10 * (1 - 1/(8 * pi)) * cos(x[1] ) + 10
}
## Create design points
set.seed(1)
x <- cbind(runif(40)*15-5,runif(40)*15)
## Compute observations at design points
y <- as.matrix(apply(x,1,braninFunction))
## Create model with default settings
fit <- buildLOESS(x,y)
fit
## Predict new point
predict(fit,cbind(1,2))
## True value at location
braninFunction(c(1,2))
## Change model control
fit <- buildLOESS(x,y,control=list(parametric=c(TRUE,FALSE)))
fit
```

Description

This is a simple wrapper for the randomForest function from the randomForest package. The purpose of this function is to provide an interface as required by SPOT, to enable modeling and model-based optimization with random forest.
Usage

buildRandomForest(x, y, control = list())

Arguments

x    matrix of input parameters. Rows for each point, columns for each parameter.
y    one column matrix of observations to be modeled.
control    list of control parameters, currently not used.

Value

an object of class "spotRandomForest", with a predict method and a print method.

Examples

## Not run:
## Test-function:
braninFunction <- function (x) {
  10 * (1 - 1/(8 * pi)) * cos(x[1]) + 10
}
## Create design points
set.seed(1)
x <- cbind(runif(20)*15-5,runif(20)*15)
## Compute observations at design points (for Branin function)
y <- as.matrix(apply(x,1,braninFunction))
## Create model
fit <- buildRandomForest(x,y,control = list(algTheta=optimLHD))
## Print model parameters
print(fit)
## Predict at new location
predict(fit,cbind(1,2))
## True value at location
braninFunction(c(1,2))

## End(Not run)
dataGasSensor

Arguments

x    design matrix (sample locations), rows for each sample, columns for each variable.
y    vector of observations at x
control (list), with the options for the model building procedure:
mainEffectsOnly Logical, defaults to FALSE. Set to TRUE if a model with
main effects only is desired (no interactions, second order effects).
canonical Logical, defaults to FALSE. If this is TRUE, use the canonical path
to descent from saddle points. Else, simply use steepest descent

Value
returns an object of class spotRSM.

See Also
predict.spotRSM

Examples

## Create a test function: branin
braninFunction <- function (x) {
  10 * (1 - 1/(8 * pi)) * cos(x[1]) + 10
}
## Create design points
x <- cbind(runif(20)*15-5,runif(20)*15)
## Compute observations at design points
y <- as.matrix(apply(x,1,braninFunction))
## Create model with default settings
fit <- buildRSM(x,y)
## Predict new point
predict(fit,cbind(1,2))
## True value at location
braninFunction(c(1,2))
## plots
plot(fit)
## path of steepest descent
descentSpotRSM(fit)

---

dataGasSensor     Gas Sensor Data

Description

A data set of a Gas Sensor, similar to the one used by Rebolledo et al. 2016. It also contains
information of 10 different test/training splits, to enable comparable evaluation procedures.
Usage
dataGasSensor

Format

A data frame with 280 rows and 20 columns (1 output, 7 input, 2 disturbance, 10 training/test split):

<p>| | | | | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
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<th></th>
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<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>Measured Sensor Output</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>X1</td>
<td>Sensor Input 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>X2</td>
<td>Sensor Input 2</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>X3</td>
<td>Sensor Input 3</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>X4</td>
<td>Sensor Input 4</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>X5</td>
<td>Sensor Input 5</td>
<td></td>
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<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>X6</td>
<td>Sensor Input 6</td>
<td></td>
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</tr>
<tr>
<td>X7</td>
<td>Sensor Input 7</td>
<td></td>
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<td></td>
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<td></td>
</tr>
<tr>
<td>Batch</td>
<td>Disturbance variable, measurement batch</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sensor</td>
<td>Disturbance variable, sensor ID</td>
<td></td>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

Set1 test/training split, 1 is training data, 2 is test data
Set2 test/training split
Set3 test/training split
Set4 test/training split
Set5 test/training split
Set6 test/training split
Set7 test/training split
Set8 test/training split
Set9 test/training split
Set10 test/training split

Two different modeling tasks are of interest for this data set: Y~X1+X2+X3+X4+X5+X6+X7+Batch+Sensor and X1~Y+X7+Batch+Sensor.

References

Margarita A. Rebolledo C., Sebastian Krey, Thomas Bartz-Beielstein, Oliver Flasch, Andreas Fischbach and Joerg Stork. 2016. Modeling and Optimization of a Robust Gas Sensor. 7th International Conference on Bioinspired Optimization Methods and their Applications (BIOMA 2016).
**Descent RSM model**

**Description**

Generate steps along the path of steepest descent for a RSM model. This is only intended as a manual tool to use together with `buildRSM`.

**Usage**

`descentspotrsm(object)`

**Arguments**

- `object` RSM model (settings and parameters) of class `spotRSM`.

**Value**

List with

- `x` list of points along the path of steepest descent
- `y` corresponding predicted values

**See Also**

`buildRSM`

---

**Latin Hypercube Design Generator**

**Description**

Creates a latin Hypercube Design (LHD) with user-specified dimension and number of design points. LHDs are created repeatedly created at random. For each each LHD, the minimal pairwise distance between design points is computed. The design with the maximum of that minimal value is chosen.

**Usage**

`designlhd(x = NULL, lower, upper, control = list())`
Arguments

\textbf{x} \hspace{1em} \text{optional matrix x, rows for points, columns for dimensions. This can contain one or more points which are part of the design, but specified by the user. These points are added to the design, and are taken into account when calculating the pair-wise distances. They do not count for the design size. E.g., if x has two rows, control$\text{replicates}$ is one and control$\text{size}$ is ten, the returned design will have 12 points (12 rows). The first two rows will be identical to x. Only the remaining ten rows are guaranteed to be a valid LHD.}

\textbf{lower} \hspace{1em} \text{vector with lower boundary of the design variables (in case of categorical parameters, please map the respective factor to a set of contiguous integers, e.g., with lower = 1 and upper = number of levels)}

\textbf{upper} \hspace{1em} \text{vector with upper boundary of the design variables (in case of categorical parameters, please map the respective factor to a set of contiguous integers, e.g., with lower = 1 and upper = number of levels)}

\textbf{control} \hspace{1em} \text{list of controls:}

\begin{itemize}
  \item \textbf{size} \hspace{1em} \text{number of design points}
  \item \textbf{retries} \hspace{1em} \text{number of retries during design creation}
  \item \textbf{types} \hspace{1em} \text{this specifies the data type for each design parameter, as a vector of either "numeric","integer","factor". (here, this only affects rounding)}
  \item \textbf{inequalityConstraint} \hspace{1em} \text{inequality constraint function, smaller zero for infeasible points. Used to replace infeasible points with random points.}
  \item \textbf{replicates} \hspace{1em} \text{integer for replications of each design point. E.g., if replications is two, every design point will occur twice in the resulting matrix.}
\end{itemize}

Value

\text{matrix design}

- design has length(lower) columns and (size + nrow(x))*control$\text{replicates}$ rows. All values should be within lower <= design <= upper

Author(s)

Original code by Christian Lasarczyk, adaptations by Martin Zaefferer

Examples

\begin{verbatim}
set.seed(1) #set RNG seed to make examples reproducible
design <- designLHD(.1,2) #simple, 1-D case
design <- designLHD(.1,2,control=list(replicates=3)) #with replications
design <- designLHD(.1,2,control=list(replicates=3))
control=list(size=5, retries=100, types=c("numeric","integer","factor","factor")),
design x <- designLHD(.1,1,-10),c(2,10),control=list(size=5, retries=100)
x2 <- designLHD(x,.c(1,-10),c(2,10),control=list(size=5, retries=100))
plot(x2)
points(x, pch=19)
\end{verbatim}
**designUniformRandom**  
**Uniform Design Generator**

**Description**  
Create a simple experimental design based on uniform random sampling.

**Usage**  
```r  
designUniformRandom(x = NULL, lower, upper, control = list())  
```

**Arguments**
- `x`  
  optional data.frame `x` to be part of the design
- `lower`  
  vector with lower boundary of the design variables (in case of categorical parameters, please map the respective factor to a set of contiguous integers, e.g., with lower = 1 and upper = number of levels)
- `upper`  
  vector with upper boundary of the design variables (in case of categorical parameters, please map the respective factor to a set of contiguous integers, e.g., with lower = 1 and upper = number of levels)
- `control`  
  list of controls:  
  - `size`  
    number of design points
  - `types`  
    this specifies the data type for each design parameter, as a vector of either "numeric","integer","factor". (here, this only affects rounding)
  - `replicates`  
    integer for replications of each design point. E.g., if replications is two, every design point will occur twice in the resulting matrix.

**Value**

matrix `design`  
- `design` has length(`lower`) columns and `(size + nrow(x))*control$replicates` rows. All values should be within `lower <= design <= upper`

**Examples**

```r  
set.seed(1) #set RNG seed to make examples reproducible  
design <- designUniformRandom(1, 2) #simple, 1-D case  
design  
design <- designUniformRandom(1, 2, control=list(replicates=3)) #with replications  
design  
design <- designUniformRandom(c(-1,-2,1,0),c(1,4,9,1),  
control=list(size=5, types=c("numeric","integer","factor","factor")))  
design  
x <- designUniformRandom(c(1,-10),c(2,10),control=list(size=5))  
x2 <- designUniformRandom(x,c(1,-10),c(2,10),control=list(size=5))  
plot(x2)  
points(x, pch=19)  
```
### expectedImprovement  
**Expected Improvement**

#### Description
Compute the negative logarithm of the Expected Improvement of a set of candidate solutions. Based on mean and standard deviation of a candidate solution, this estimates the expectation of improvement. Improvement considers the amount by which the best known value (best observed value) is exceeded by the candidates.

#### Usage
```r
equippedImprovement(mean, sd, min)
```

#### Arguments
- **mean**: vector of predicted means of the candidate solutions.
- **sd**: vector of estimated uncertainties / standard deviations of the candidate solutions.
- **min**: minimal observed value.

#### Value
a vector with the negative logarithm of the expected improvement values, -log10(EI).

#### Examples
```r
mean <- 1:10 # mean of the candidates
ds <- 10:1 # st. deviation of the candidates
min <- 5 # best known value
EI <- expectedImprovement(mean, sd, min)
```

---

### funcyclone  
**Objective function - Cyclone Simulation: Barth/Muschelknautz**

#### Description
Calculate cyclone collection efficiency. A simple, physics-based optimization problem (potentially bi-objective). See the references [1,2].

#### Usage
```r
funcyclone(x, deterministic = c(T, T, T), cyclone = list(Da = 1.26, H = 2.5, Dt = 0.42, Ht = 0.65, He = 0.6, Be = 0.2), fluid = list(Mu = 1.85e-05, Ve = (50/36)/0.12, lambdag = 1/200, Rhop = 2000, Rhof = 1.2, Croh = 0.05), noiseLevel = list(Vp = 0.1, Rhop = 0.05), model = "Barth-Muschelknautz", intervals = c(0, 2, 4, 6, 8, 10, 15, 20, 30) * 1e-06, delta = c(0, 0.02, 0.03, 0.05, 0.1, 0.3, 0.3, 0.2))
```
funCyclone

Arguments

x vector of length at least one and up to six, specifying non-default geometrical parameters in [m]: Da, H, Dt, Ht, He, Be
deterministic binary vector. First element specifies whether volume flow is deterministic or not. Second element specifies whether particle density is deterministic or not. Third element specifies whether particle diameters are deterministic or not. Default: All are deterministic (TRUE).
cyclone list of a default cyclone’s geometrical parameters: fluid$Da, fluid$H, fluid$Dt, fluid$Ht, fluid$He and fluid$Be
fluid list of default fluid parameters: fluid$Mu, fluid$Vp, fluid$Rhop, fluid$Rhof and fluid$Croh
noiseLevel list of noise levels for volume flow (noiseLevel$Vp) and particle density (noiseLevel$Rhop), only used if non-deterministic.
model type of the model (collection efficiency only): either "Barth-Muschelknautz" or "Mothes"
intervals vector specifying the particle size interval bounds.
delta vector of densities in each interval (specified by intervals). Should have one element less than the intervals parameter.

Value

returns a function that calculates the fractional efficiency for the specified diameter, see example.

References


Examples

## Call directly
funCyclone(c(1.26, 2.5))
## create vectorized target function, vectorized, first objective only
## Also: negated, since SPOT always does minimization.
tfunvecF1 <- function(x){-apply(x, 1, funCyclone)[1,]}
tfunvecF1(matrix(c(1.26, 2.5, 1, 2), 2, 2, byrow=TRUE))
## optimize with spot
res <- spot(fun=tfunvecF1, lower=c(1,2), upper=c(2,3),
            control=list(modelControl=list(target="ei"),
                        model=buildKriging, optimizer=optimLBFGSB, plots=TRUE))
## best found solution...
funSphere  

**Sphere Test Function**

**Description**

Sphere Test Function

**Usage**

funSphere(x)

**Arguments**

x  
matrix of points to evaluate with the sphere function. Rows for points and columns for dimension.

**Value**

1-column matrix with resulting function values

**Examples**

funSphere(matrix(runif(18),3))

---

optimDE  

**Minimization by Differential Evolution**

**Description**

For minimization, this function uses the "DEoptim" method from the codeDEoptim package. It is basically a wrapper, to enable DEoptim for usage in SPOT.

**Usage**

optimDE(x = NULL, fun, lower, upper, control = list(), ...)
optimES

Arguments

- **x**: optional start point, not used in DEoptim
- **fun**: objective function, which receives a matrix x and returns observations y
- **lower**: boundary of the search space
- **upper**: boundary of the search space
- **control**: list of control parameters
  - **funEvals**: Budget, number of function evaluations allowed. Default is 200.
  - **populationSize**: Population size or number of particles in the population. Default is 10*dimension.
- ... passed to fun

Value

- list, with elements
  - **x**: archive of the best member at each iteration
  - **y**: archive of the best value of fn at each iteration
  - **xbest**: best solution
  - **ybest**: best observation
  - **count**: number of evaluations of fun

Examples

```r
res <- optimDE(x = NULL, lower = c(-10, -20), upper = c(20, 8), fun = funSphere)
res$ybest
```

---

** optimES  

Evolution Strategy

** Description **

This is an implementation of an Evolution Strategy.

** Usage **

```
optimES(x = NULL, fun, lower, upper, control = list(), ...)
```
Arguments

- **x**  
  optional start point, not used

- **fun**  
  objective function, which receives a matrix x and returns observations y

- **lower**  
  is a vector that defines the lower boundary of search space (this also defines the dimensionality of the problem)

- **upper**  
  is a vector that defines the upper boundary of search space (same length as lower)

- **control**  
  list of control parameters. The control list can contain the following settings:

  - **funEvals**  
    number of function evaluations, stopping criterion, default is 500

  - **mue**  
    number of parents, default is 10

  - **nu**  
    selection pressure. That means, number of offspring (lambda) is mue multiplied with nu. Default is 10

  - **mutation**  
    string of mutation type, default is 1

  - **sigmaInit**  
    initial sigma value (step size), default is 1.0

  - **nSigma**  
    number of different sigmas, default is 1

  - **taul**  
    number, default is 0.0. tau0 is the general multiplier.

  - **tau**  
    number, learning parameter for self adaption, i.e. the local multiplier for step sizes (for each dimension).default is 1.0

  - **rho**  
    number of parents involved in the procreation of an offspring (mixing number), default is “b1”

  - **sel**  
    number of selected individuals, default is 1

  - **stratReco**  

  - **objReco**  

  - **maxGen**  
    number of generations, stopping criterion, default is Inf

  - **seed**  
    number, random seed, default is 1

  - **noise**  
    number, value of noise added to fitness values, default is 0.0

  - **verbosity**  
    defines output verbosity of the ES, default is 0

  - **plotResult**  
    boolean, specifies if results are plotted, default is FALSE

  - **logPlotResult**  
    boolean, defines if plot results should be logarithmic, default is FALSE

  - **sigmaRestart**  
    number, value of sigma on restart, default is 0.1

  - **preScanMult**  
    initial population size is multiplied by this number for a pre-scan, default is 1

  - **globalOpt**  
    termination criterion on reaching a desired optimum value, default is rep(0, dimension)

...  

additional parameters to be passed on to fun
**Value**

list, with elements

- x NULL, currently not used
- y NULL, currently not used
- xbest best solution
- ybest best observation
- count number of evaluations of fun

**Examples**

```r
cont <- list(funEvals=100)
optimES(fun=funSphere,lower=rep(0,2), upper=rep(1,2), control= cont)
```

---

**Description**

For minimization, this function uses the "genoud" method from the codergenoud package. It is basically a wrapper, to enable genoud for usage in SPOT.

**Usage**

```r
optimGenoud(x = NULL, fun, lower, upper, control = list(), ...)
```

**Arguments**

- x optional start point, not used
- fun objective function, which receives a matrix x and returns observations y
- lower boundary of the search space
- upper boundary of the search space
- control list of control parameters
  - funEvals Budget, number of function evaluations allowed. Default is 100.
  - populationSize Population size, number of individuals in the population. Default is 10*dimension.
- ... passed to fun
Value

list, with elements

\[ x \text{ NULL, currently not used}\]
\[ y \text{ NULL, currently not used}\]
\[ \text{xbest best solution}\]
\[ \text{ybest best observation}\]
\[ \text{count number of evaluations of } \text{fun}\]

Examples

```r
res <- optimGenoud(,fun = funSphere,lower = c(-10,-20),upper=c(20,8))
res$ybest
```

---

**optimLBFGSB**

Minimization by L-BFGS-B

Description

For minimization, this function uses the "L-BFGS-B" method from the **optim** function, which is part of the codestats package. It is basically a wrapper, to enable L-BFGS-B for usage in SPOT.

Usage

```r
optimLBFGSB(x = NULL, fun, lower, upper, control = list(), ...)
```

Arguments

- **x**
  - optional matrix of points. Only first point (row) is used as startpoint.
- **fun**
  - objective function, which receives a matrix x and returns observations y
- **lower**
  - boundary of the search space
- **upper**
  - boundary of the search space
- **control**
  - list of control parameters
    - **funEvals**
      - Budget, number of function evaluations allowed. Default is 100.
      - All other control parameters accepted by the **optim** function can be used, too, and are passed to **optim**.
    - **...**
      - passed to **fun**
Value

- list, with elements
- x NA, not used
- y NA, not used
- xbest best solution
- ybest best observation
- count number of evaluations of fun (estimated from the more complicated "counts" variable returned by optim)
- message termination message returned by optim

Examples

```r
res <- optimLHD(fun = funSphere, lower = c(-10, -20), upper = c(20, 8))
res$ybest
```

---

**optimLHD**  
*Minimization by Latin Hypercube Sampling*

Description

This uses Latin Hypercube Sampling (LHS) to optimize a specified target function. A Latin Hypercube Design (LHD) is created with `designLHD`, then evaluated by the objective function. All results are reported, including the best (minimal) objective value, and corresponding design point.

Usage

```r
optimLHD(x = NULL, fun, lower, upper, control = list(), ...)
```

Arguments

- **x**  optional matrix of points to be included in the evaluation
- **fun**  objective function, which receives a matrix x and returns observations y
- **lower**  boundary of the search space
- **upper**  boundary of the search space
- **control**  list of control parameters
  - funEvals  Budget, number of function evaluations allowed. Default: 100.
  - retries  Number of retries for design generation, used by `designLHD`. Default: 100.
- **...**  passed to fun
Value

- list, with elements
  - x archive of evaluated solutions
  - y archive of observations
  - xbest best solution
  - ybest best observation
  - count number of evaluations of fun
  - message success message

Examples

```r
res <- optimLHD(x = NULL, fun = funSphere, lower = c(-10, -20), upper = c(20, 8))
res$ybest
```

---

optimNLOPTR Minimization by NLOPT

Description

This is a wrapper that employs the nloptr function from the package of the same name. The nloptr function itself is an interface to the nlopt library, which contains a wide selection of different optimization algorithms.

Usage

```r
optimNLOPTR(x = NULL, fun, lower, upper, control = list(), ...)
```

Arguments

- **x** optional matrix of points to be included in the evaluation (only first row will be used)
- **fun** objective function, which receives a matrix x and returns observations y
- **lower** boundary of the search space
- **upper** boundary of the search space
- **control** named list, with the options for nloptr. These will be passed to nloptr as arguments. In addition, the following parameter can be used to set the function evaluation budget:
  - **funEvals** Budget, number of function evaluations allowed. Default: 100.
- **...** passed to fun

Note that the arguments x, fun, lower and upper will be mapped to the corresponding arguments of nloptr: x0, eval_f, lb and ub.
**plotData**

**Value**

- list, with elements
  - `x`: archive of evaluated solutions
  - `y`: archive of observations
  - `xbest`: best solution
  - `ybest`: best observation
  - `count`: number of evaluations of `fun`
  - `message`: success message

**Examples**

```r
## Not run:
##simple example:
res <- optimNLOPTR(fun = funSphere, lower = c(-10,-20), upper = c(20,8))
res
##with an inequality constraint:
contr <- list() #control list
##specify constraint
table_g_ineq <- function(x) 1+x[1]-x[2]
res <- optimNLOPTR(fun = funSphere, lower = c(-10,-20), upper = c(20,8), control = contr)
res
```

**plotData**

*Interpolated plot*

**Description**

A (filled) contour or perspective plot of a data set with two independent and one dependent variable. The plot is generated by some interpolation or regression model. By default, the `loess` function is used.

**Usage**

```r
plotData(x, y, which = 1:2, constant = x[which.min(y), ],
model = buildLOESS, modelControl = list(), xlab = c("x1", "x2"),
ylab = "y", type = "filled.contour", ...)
```

**Arguments**

- `x`: independent variables, or input variables. This should be a matrix of at least two columns and several rows. If more than two columns are present, all will be used for fitting the model. The parameter `which` will determine which of these will be plotted, and the parameter `constant` will determine the values of all parameters that are not varied.
**plotFunction**

- **y** dependent, or observed output variable to be interpolated/regressed and plotted.
- **which** a vector with two elements, each an integer giving the two independent variables of the plot (the integers are indices of the respective data set, i.e., columns of \( x \)). All other parameters will be fixed to the best known solution, i.e., the one with minimal y-value.
- **constant** a numeric vector that states for each variable a constant value that it will take on if it is not varied in the plot. This affects the parameters not selected by the which parameter. By default, this will be fixed to the best known solution, i.e., the one with minimal y-value, according to which.min(object$y). The length of this numeric vector should be the same as the number of columns in object$x.
- **model** the model building function to be used, by default buildLOESS.
- **modelControl** control list of the chosen model building function.
- **xlab** a vector of characters, giving the labels for each of the two independent variables
- **ylab** character, the value of the dependent variable predicted by the corresponding model
- **type** string describing the type of the plot: "filled.contour" (default), "contour", "persp" (perspective), or "persp3d" plot. Note that "persp3d" is based on the plotly package and will work in RStudio, but not in the standard RGui.
- **...** additional parameters passed to the contour or filled.contour function

**See Also**

plotFunction, plotModel

**Examples**

```r
## generate random test data
testfun <- function (x) sum(x^2)
set.seed(1)
k <- 30
x <- cbind(runif(k)*15-5,runif(k)*15)
y <- as.matrix(apply(x,1,testfun))
plotData(x,y)
plotData(x,y,type="contour")
plotData(x,y,type="persp")
```

**Description**

A (filled) contour plot or perspective / surface plot of a function.
Usage

plotFunction(f = function(x) { rowSums(x^2) }, lower = c(0, 0),
upper = c(1, 1), type = "filled.contour", s = 100, xlab = "x1",
ylab = "x2", zlab = "y", color.palette = terrain.colors,
title = "", levels = NULL, points1, points2, pch1 = 20,
pch2 = 8, lwd1 = 1, lwd2 = 1, cex1 = 1, cex2 = 1,
col1 = "red", col2 = "black", theta = -40, phi = 40, ...)

Arguments

f          function to be plotted. The function should either be able to take two vectors or
           one matrix specifying sample locations. i.e. z=f(x) or z=f(x2,x1) where Z is
           a two column matrix containing the sample locations x1 and x2.
lower      boundary for x1 and x2 (defaults to c(0,0)).
upper      boundary (defaults to c(1,1)).
type       string describing the type of the plot: "filled.contour" (default), "contour",
           "persp" (perspective), or "persp3d" plot. Note that "persp3d" is based on the
           plotly package and will work in RStudio, but not in the standard RGui.
s          number of samples along each dimension. e.g. f will be evaluated s^2 times.
xlab       lable of first axis
ylab       lable of second axis
zlab       lable of third axis
color.palette colors used, default is terrain.color
title      of the plot
levels     number of levels for the plotted function value. Will be set automatically with
           default NULL.. (contour plots only)
points1    can be omitted, but if given the points in this matrix are added to the plot in
           form of dots. Contour plots and persp3d only. Contour plots expect matrix with
           two columns for coordinates. 3Dperspective expects matrix with three columns,
           third column giving the corresponding observed value of the plotted function.
points2    can be omitted, but if given the points in this matrix are added to the plot in form
           of crosses. Contour plots and persp3d only. Contour plots expect matrix with
           two columns for coordinates. 3Dperspective expects matrix with three columns,
           third column giving the corresponding observed value of the plotted function.
pch1       pch (symbol) setting for points1 (default: 20). (contour plots only)
pch2       pch (symbol) setting for points2 (default: 8). (contour plots only)
lwd1       line width for points1 (default: 1). (contour plots only)
lwd2       line width for points2 (default: 1). (contour plots only)
cex1       cex for points1 (default: 1). (contour plots only)
cex2       cex for points2 (default: 1). (contour plots only)
col1       color for points1 (default: "black"). (contour plots only)
col2       color for points2 (default: "black"). (contour plots only)
theta  angle defining the viewing direction. theta gives the azimuthal direction and phi the colatitude. (persp plot only)
phi   angle defining the viewing direction. theta gives the colatitude. (persp plot only)
... additional parameters passed to contour or filled.contour

See Also

plotData, plotModel

Examples

plotFunction(function(x){rowSums(x^2)},c(-5,0),c(10,15))
plotFunction(function(x){rowSums(x^2)},c(-5,0),c(10,15),type="contour")
plotFunction(function(x){rowSums(x^2)},c(-5,0),c(10,15),type="persp")

plotModel  Surface plot of a model

Description

A (filled) contour or perspective plot of a fitted model.

Usage

plotModel(object, which = 1:2, constant = object$x[which.min(object$y)],
    xlab = paste("x", which, sep = " "), ylab = "y",
    type = "filled.contour", ...

Arguments

object  fit created by a modeling function, e.g., buildRandomForest.
which  a vector with two elements, each an integer giving the two independent variables of the plot (the integers are indices of the respective data set).
constant a numeric vector that states for each variable a constant value that it will take on if it is not varied in the plot. This affects the parameters not selected by the which parameter. By default, this will be fixed to the best known solution, i.e., the one with minimal y-value, according to which.min(object$y). The length of this numeric vector should be the same as the number of columns in object$x
xlab  a vector of characters, giving the labels for each of the two independent variables.
ylab  character, the value of the dependent variable predicted by the corresponding model.
type  string describing the type of the plot: "filled.contour" (default), "contour", "persp" (perspective), or "persp3d" plot. Note that "persp3d" is based on the plotly package and will work in RStudio, but not in the standard RGui.
... additional parameters passed to the contour or filled.contour function.
See Also

plotFunction, plotData

Examples

```r
## generate random test data
testfun <- function (x) sum(x^2)
set.seed(1)
k <- 30
x <- cbind(runif(k)*15-5, runif(k)*15, runif(k)*2-7, runif(k)*5+22)
y <- as.matrix(apply(x, 1, testfun))
fit <- buildLM(x, y)
plotModel(fit)
plotModel(fit, type="contour")
plotModel(fit, type="persp")
plotModel(fit, which=c(1,4))
plotModel(fit, which=2:3)
```

Description

A simple interface to the Optimal Computing Budget Allocation algorithm.

Usage

```r
repeatsOCBA(x, y, budget)
```

Arguments

- **x**: matrix of samples. Identical rows indicate repeated evaluations. Any sample should be evaluated at least twice, to get an estimate of the variance.
- **y**: observations of the respective samples. For repeated evaluations, y should differ (variance not zero).
- **budget**: of additional evaluations to be allocated to the samples.

Value

A vector that specifies how often each solution should be evaluated.

References

See Also

repeatsOCBA calls OCBA, which also provides some additional details.

Examples

```r
x <- matrix(c(1:3,1:3),9,2)
y <- runif(9)
repeatsOCBA(x,y,10)
```

---

**satter**  
_Satterthwaite Function_

**Description**

The Satterthwaite function can be used to estimate the magnitude of the variance component \((\sigma_{beta})^2\), when the random factor has significant main effects.

**Usage**

```r
satter(MScoeff, MSi, dfi, alpha = 0.05)
```

**Arguments**

- `MScoeff`: coefficients \(c_1, c_2\)
- `MSi`: mean squared values
- `dfi`: degrees of freedom
- `alpha`: error probability

**Details**

Note, the output from the `satter()` procedure is \(\sigma_{beta}\).

**Value**

vector with 1. estimate of variance 2. degrees of freedom, 3. lower value of 1-alpha confint 4. upper value of 1-alpha confint

**Examples**

```r
res <- satter(MScoeff= c(1/4, -1/4)  
, MSi = c(394.9, 73.3)  
, dfi = c(4,3)  
, alpha = 0.1)
```
**Description**

This is one of the main interfaces for using the SPOT package. Based on a user-given objective function and configuration, spot finds the parameter setting that yields the lowest objective value (minimization). To that end, it uses methods from the fields of design of experiment, statistical modeling / machine learning and optimization.

**Usage**

```
spot(x = NULL, fun, lower, upper, control = list(), ...)
```

**Arguments**

- `x` is an optional start point (or set of start points), specified as a matrix. One row for each point, and one column for each optimized parameter.
- `fun` is the objective function. It should receive a matrix `x` and return a matrix `y`. In case the function uses external code and is noisy, an additional seed parameter may be used, see the `control$seedFun` argument below for details.
- `lower` is a vector that defines the lower boundary of search space. This determines also the dimensionality of the problem.
- `upper` is a vector that defines the upper boundary of search space.
- `control` is a list with control settings for spot. See `spotControl`.
- `...` additional parameters passed to `fun`.

**Value**

This function returns a list with:

- `xbest` Parameters of the best found solution (matrix).
- `ybest` Objective function value of the best found solution (matrix).
- `x` Archive of all evaluation parameters (matrix).
- `y` Archive of the respective objective function values (matrix).
- `count` Number of performed objective function evaluations.
- `msg` Message specifying the reason of termination.
- `modelFit` The fit of the last build model, i.e., an object returned by the last call to the function specified by `control$model`. 
### Examples

```r
## Most simple example: Kriging + LHS + predicted
## mean optimization (not expected improvement)
res <- spot(funSphere,c(-2,-3),c(1,2))
res$x$best
## With expected improvement
res <- spot(funSphere,c(-2,-3),c(1,2),
           control=list(modelControl=list(target="ei")))
res$x$best
## With additional start point:
#res <- spot(matrix(c(0.05,0.1),1,2),funSphere,c(-2,-3),c(1,2))
#res$x$best
#res <- spot(funSphere,c(-2,-3),c(1,2),
#           # control=list(funEval=50))
#res$x$best
## Use a local optimizer instead of LHS
#res <- spot(funSphere,c(-2,-3),c(1,2),
#             # control=list(optimizer=optimLBFGSB))
#res$x$best
## Random Forest instead of Kriging
#res <- spot(funSphere,c(-2,-3),c(1,2),
#           # control=list(model=buildRandomForest))
#res$x$best
## LM instead of Kriging
#res <- spot(funSphere,c(-2,-3),c(1,2),
#           # control=list(model=buildLM)) #lm as surrogate
#res$x$best
## LM and local optimizer (which for this simple example is perfect)
#res <- spot(funSphere,c(-2,-3),c(1,2),
#           # control=list(model=buildLM, optimizer=optimLBFGSB))
#res$x$best
## Or a different Kriging model:
#res <- spot(funSphere,c(-2,-3),c(1,2),
#           # control=list(model=buildKrigingDACE, optimizer=optimLBFGSB))
#res$x$best
## With noise: (this takes some time)
#res1 <- spot(function(x)funSphere(x)+rnorm(nrow(x)),c(-2,-3),c(1,2),
#              # control=list(funEval=100,noise=TRUE)) #noisy objective
#res2 <- spot(function(x)funSphere(x)+rnorm(nrow(x)),c(-2,-3),c(1,2),
#              # control=list(funEval=100,noise=TRUE,replications=2,
#              # designControl=list(replications=2))) #noise with replicated evaluations
#res3 <- spot(function(x)funSphere(x)+rnorm(nrow(x)),c(-2,-3),c(1,2),
#              # control=list(funEval=100,noise=TRUE,replications=2,OCBA=T,OCBABudget=1,
#              # designControl=list(replications=2))) #and with OCBA
## Check results with non-noisy function:
#funSphere(res1$x$best)
#funSphere(res2$x$best)
#funSphere(res3$x$best)
## The following is for demonstration only, to be used for random number
## seed handling in case of external noisy target functions.
#res3 <- spot(function(x,seed)(set.seed(seed);funSphere(x)+rnorm(nrow(x))),
#             c(-2,-3),c(1,2),control=list(funEval=100,noise=TRUE,seedFun=1))
```
## Evolution Strategy Implementation

### Description

This function is used by optimes as a main loop for running the Evolution Strategy with the given parameter set specified by SPOT.

### Usage

```r
spotAlgEs(mue = 10, nu = 10, dimension = 2, mutation = 2, 
  sigmaInit = 1, nSigma = 1, tau0 = 0, tau = 1, rho = "bi", 
  sel = -1, stratReco = 1, objReco = 2, maxGen = Inf, 
  maxIter = Inf, seed = 1, noise = 0, fName = funSphere, 
  lowerLimit = -1, upperLimit = 1, verbosity = 0, 
  plotResult = FALSE, logPlotResult = FALSE, sigmaRestart = 0.1, 
  prescanMult = 1, globalOpt = NULL, ...)
```

### Arguments

- **mue**: number of parents, default is 10
- **nu**: selection pressure. That means, number of offspring (lambda) is mue multiplied with nu. Default is 10
- **dimension**: dimension number of the target function, default is 2
- **mutation**: mutation type, either 1 or 2, default is 1
**Description**

SPOT is usually started via the function `spot`. However, SPOT runs can be continued (i.e., with a larger budget specified in `control$funEvals`) by using `spotLoop`. This is the main loop of SPOT iterations. It requires the user to give the same inputs as specified for `spot`.

**Usage**

```
spotLoop(x, y, fun, lower, upper, control, ...)
```
**Arguments**

- **x** are the known candidate solutions that the SPOT loop is started with, specified as a matrix. One row for each point, and one column for each optimized parameter.
- **y** are the corresponding observations for each solution in `x`, specified as a matrix. One row for each point.
- **fun** is the objective function. It should receive a matrix `x` and return a matrix `y`. In case the function uses external code and is noisy, an additional seed parameter may be used, see the `control$seedFun` argument below for details.
- **lower** is a vector that defines the lower boundary of search space. This determines also the dimensionality of the problem.
- **upper** is a vector that defines the upper boundary of search space.
- **control** is a list with control settings for spot. See `spotControl`.
- **...** additional parameters passed to `fun`.

**Value**

This function returns a list with:

- **xbest** Parameters of the best found solution (matrix).
- **ybest** Objective function value of the best found solution (matrix).
- **x** Archive of all evaluation parameters (matrix).
- **y** Archive of the respective objective function values (matrix).
- **count** Number of performed objective function evaluations.
- **msg** Message specifying the reason of termination.
- **modelFit** The fit of the last build model, i.e., an object returned by the last call to the function specified by `control$model`.

**Examples**

```r
## Most simple example: Kriging + LHS + predicted
## mean optimization (not expected improvement)
control <- list(funEvals=20)
res <- spot(x,funSphere,c(-2,-3),c(1,2),control)
## now continue with larger budget
control$funEvals <- 25
res2 <- spotLoop(res$x,res$y,funSphere,c(-2,-3),c(1,2),control)
res2$xbest
res2$ybest
```
wrapFunction

Function Evaluation Wrapper

Description

This is a simple wrapper that turns a function of type $y = f(x)$, where $x$ is a vector and $y$ is a scalar, into a function that accepts and returns matrices, as required by spot. Note that the wrapper essentially makes use of the apply function. This is effective, but not necessarily efficient. The wrapper is intended to make the use of spot easier, but it could be faster if the user spends some time on a more efficient vectorization of the target function.

Usage

wrapFunction(fun)

Arguments

fun the function $y = f(x)$ to be wrapped, with $x$ a vector and $y$ a numeric

Value

a function in the style of $y = f(x)$, accepting and returning a matrix

Examples

```r
## example function
branin <- function (x) {
    10 * (1 - 1/(8 * pi)) * cos(x[1]) + 10
  y
}
## vectorize / wrap
braninWrapped <- wrapFunction(branin)
## test original
branin(c(1,2))
branin(c(2,2))
branin(c(2,1))
## test wrapped
braninWrapped(matrix(c(1,2,2,2,2,1),3,2,byrow=TRUE))
```
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