Package ‘fanovaGraph’

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Description Estimation and plotting of a function's FANOVA graph to identify the interaction structure and fitting, prediction and simulation of a kriging model modified by the identified structure. The interactive function plotManipulate can only be run on the RStudio IDE with RStudio's package manipulate loaded. RStudio is freely available (www.rstudio.org), and includes package manipulate. The equivalent function plotTk bases on CRAN Repository packages only.
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fanovaGraph-package

Building Kriging models with FANOVA graphs

Description

Estimates and plots the FANOVA graph of a function to identify its interaction structure and fits a kriging model modified by the identified structure.

Details

Important functions:

- `estimateGraph` Estimate indices for the graph, create graph structure
- `threshold` Set indices below a threshold to zero
- `plot.graphlist` Plot a given graph structure
- `plotDeltaJumps` Provide plots for the choice of the threshold
- `kmAdditive` Kriging model estimation with block-additive kernel
- `predictAdditive` Prediction function from Kriging model with block-additive kernel
- `simAdditive` Simulation from Kriging model with block-additive kernel

Author(s)

J. Fruth, T. Muehlenstaedt, O. Roustant, M. Jastrow

References

estimateGraph

See Also

DiceKriging, sensitivity, igraph

Examples

#demo(ExampleIshigami)
#demo(Example6D)
#demo(Estimation)
#demo(Threshold)

estimateGraph  FANOVA graph estimation.

Description

Estimates the structure of the FANOVA graph by estimating the total interaction indices for the graph edges (a particular case of superset importance introduced by Liu and Owen, 2006), the main effect indices for the graph vertices and the overall variance for normalizing the indices and finding the clique structure of the estimated graph.

Usage

estimateGraph(f.mat, d, q = NULL, q.arg = NULL, n.tot = NULL, method = "LiuOwen", n.lo = NULL, n.mc = NULL, n.fast = 500, L = NULL, M = 6, n.pf = NULL, n.main = 1000, confint = TRUE, print.loop.index = FALSE, ...)

Arguments

f.mat  vectorized function for which the FANOVA graph shall be estimated

 d  integer, number of input factors (vertices)

 q  a vector of character strings of quantile functions corresponding to the factors distributions, it can be a single character string meaning same distribution for all, if not specified \"unif\" is taken

 q.arg  a list of lists of quantile functions parameters of the distributions in q, it can be a single list meaning same parameters for all, if not specified the default values of the respective distributions are taken

 n.tot  optional integer, total number of function evaluations, instead of n.tot method related parameters (n.lo, n.mc, L or n.sobol) can be provided

 method  character string specifying the estimation method of the total interaction indices, to be chosen between \"LiuOwen\", \"FixFast\", \"RBD\" and \"PickFreeze\", defaults to \"LiuOwen\", see references for further details

 n.lo  optional integer, only if method=\"LiuOwen\", number of Monte Carlo simulations in method of Liu and Owen

 n.mc  optional integer, only if method=\"FixFast\", number of Monte Carlo simulations for the expectation in fixing method using FAST
estimateGraph

n.fast  optional integer, only if method="FixFast", number of design points for FAST algorithm, defaults to 500
L  optional integer, only if method="RBD", parameter L in RBD-FAST method
M  optional integer, only if method="RBD", parameter M in RBD-FAST method
n.pf  optional integer, only if method="PickFreeze", number of Monte Carlo simulations in pick-and-freeze method
n.main  integer, number of Monte Carlo Simulations for computing main effect indices
confint  optional Boolean, if TRUE, standard error and 95% confidence intervals of the indices are computed additionally for method="LiuOwen", defaults to TRUE
print.loop.index  optional Boolean, if TRUE, loop indices are printed
...

Value

an object of class graphlist containing the graph structure which includes
d  number of input factors
tii  matrix containing the unscaled total interaction indices and if confint = TRUE their standard error and lower and upper confidence limits
i1  matrix containing the unscaled main effect indices
V  overall variance
tii.scaled  matrix containing the scaled total interaction indices
cliques  list of cliques

Author(s)

J. Fruth, T. Muehlenstaedt

References

Examples

# Ishigami function, true analytical values: D12 = D23 = 0, D13 = -3.374
q.arg = list(list(min=-pi, max=pi), list(min=-pi, max=pi), list(min=-pi, max=pi))
estimateGraph(f.mat=ishigami.fun, d=3, q.arg=q.arg, n.tot=10000, method="LiuOwen")
estimateGraph(f.mat=ishigami.fun, d=3, q.arg=q.arg, n.tot=10000, method="FixFast")
estimateGraph(f.mat=ishigami.fun, d=3, q.arg=q.arg, n.tot=10000, method="BBD")
estimateGraph(f.mat=ishigami.fun, d=3, q.arg=q.arg, n.tot=10000, method="PickFreeze")

---

i2Index

Estimation of pure second order indices

Description

Estimation of the unscaled pure second order Sobol indices.

Usage

i2Index(f.mat, d, q = NULL, q.arg = NULL, n.i2, ...)

Arguments

- **f.mat**: vectorized function of which indices shall be estimated
- **d**: integer, number of input factors (vertices)
- **q**: a vector of character strings of quantile functions corresponding to the factors distributions, it can be a single character string meaning same distribution for all, if not specified \texttt{BqunifB} is taken
- **q.arg**: a list of lists of quantile functions parameters of the distributions in \textit{q}, it can be a single list meaning same parameters for all, if not specified the default values of the respective distributions are taken
- **n.i2**: number of Monte Carlo evaluations
- **...**: additional arguments to be passed to the function \textit{f.mat}

Value

A vector containing the unscaled pure second order indices

Author(s)

J. Fruth

References

See Also

estimateGraph totalIndex

Examples

i2Index(f.mat=ishigami.fun, d=3, q.arg=list(min=-pi, max=pi), n.i2=10000)

kmAdditive

Constrained MLE Optimization

Description

Constrained MLE optimization for kernels defined by cliques using constrOptim

Usage

kmAdditive(x, y, n.initial.tries = 50, limits = NULL, eps.R = 1e-08, cl,
            covtype = "gauss", eps.Var = 1e-06, max.it = 1000, iso = FALSE)

Arguments

x
  a design matrix of input variables, number of columns should be number of variables

y
  a vector of output variables of the same length as the columns of x

n.initial.tries
  number of random initial parameters for optimization, defaults to 50

limits
  a list with items lower, upper containing boundaries for the covariance parameter vector theta, if NULL suitable bounds are computed from the range of x

eps.R
  small positive number indicating the nugget effect added to the covariance matrix diagonal, defaults to eps.R = 1e-08

cl
  list of cliques, can be obtained by function threshold

covtype
  an optional character string specifying the covariance structure to be used, to be chosen between "gauss", "matern5_2", "matern3_2", "exp" or "powexp" (see DiceKriging), defaults to "gauss"

eps.Var
  small positive number providing the limits for the alpha parameters in order to guarantee strict inequalities (0+eps.Var <= alpha <= 1-esp.Var), defaults to eps.Var = 1e-06

max.it
  maximum number of iterations for optimization, defaults to max.it=1000

iso
  boolean vector indicating for each clique if it is isotropic (TRUE) or anisotropic (FALSE), defaults to iso = FALSE (all cliques anisotropic)

Value

list of estimated parameter 'alpha' and 'theta' corresponding to the clique structure in 'cl'
Author(s)

T. Muehlenstadt, O. Roustant, J. Fruth

References


See Also

predictAdditive

Examples

```r
### example for ishigami function with cliques {1,3} and {2}
d <- 3
x <- matrix(runif(100*d,-pi,pi),nc=d)
y <- ishigami.fun(x)

cl <- list(c(2), c(1,3))

# constrained ML optimization with kernel defined by the cliques parameter <- kmAdditive(x, y, cl = cl)

# prediction with the new model
xpred <- matrix(runif(500 * d,-pi,pi), ncol = d)
ypred <- predictAdditive(xpred, x, y, parameter, cl=cl)
yexact <- ishigami.fun(xpred)

# rmse
sqrt(mean((ypred[,1] - yexact)^2))

# scatterplot
par(mfrow=c(1,1))
plot(yexact, ypred[,1], asp = 1)
abline(0, 1)

### compare to one single clique {1,2,3}
cl <- list(c(1,2,3))

# constrained ML optimization with kernel defined by the cliques parameter <- kmAdditive(x, y, cl = cl)

# prediction with the new model
ypred <- predictAdditive(xpred, x, y, parameter, cl=cl)

# rmse
sqrt(mean((ypred$mean - yexact)^2))

# scatterplot
par(mfrow=c(1,1))
plot(yexact, ypred$mean, asp = 1)
```
### isotropic cliques

```r
c1 <- list(c(2), c(1,3))
parameter <- kmAdditive(x, y, c1 = c1, iso = c(FALSE, TRUE))
ypred <- predictAdditive(xpred, x, y, parameter, cl = c1, iso = c(FALSE, TRUE))
sqrt(mean((ypred$mean - yexact)^2))
```

# the same since first clique has length 1
```r
parameter <- kmAdditive(x, y, c1 = c1, iso = c(TRUE, TRUE))
ypred <- predictAdditive(xpred, x, y, parameter, cl = c1, iso = c(TRUE, TRUE))
sqrt(mean((ypred$mean - yexact)^2))
```
Examples

```r
### graph estimation of a kriging prediction of the ishigami function
set.seed(1)
x <- matrix(rnorm(150,-pi,pi),100,3)
y <- ishigami.fun(x)
KM <- km(~1, design = data.frame(x), response = y)
g <- estimateGraph(fmat = kmPredictWrapper, d = 3, n.tot = 10000, q.arg =
    list(min = -pi, max = pi), method = "LiuOwen", km.object = KM)
print(g$tii)
```

L

### LHS Dataset

**Description**

6-dimensional Latin Hypercube Sampling Dataset

**Usage**

```r
data(L)
```

**Format**

The format is: num [1:100, 1:6] -0.7105 -0.7739 -0.5017 0.6158 0.0245 ...

**Examples**

```r
data(L)
## str(L); pairs(L) ... 
```

plot.graphlist

**Plot Graph via Package igraph**

**Description**

Plot FANOVA graphs using functions from package igraph.

**Usage**

```r
## S3 method for class 'graphlist'
plot(x, names = NULL, i2 = NULL, layout = NULL, plot.i1=TRUE, max.thickness=15,
circle.diameter=40, ...) 
```
Arguments

- **x**: an object of class `graphlist` as obtained from `estimateGraph`
- **names**: optional character string, names of vertices, defaults to `1:d`
- **i2**: optional vector of second order interaction indices (thickness of inner edges)
- **plot.i1**: optional boolean, if TRUE main effects are drawn in the graph by vertices thicknesses, should be set to FALSE when only total interaction indices are of interest
- **layout**: optional layout for the graph as in `igraph`, default is `layout.fruchterman.reingold`
- **max.thickness**: optional value for the maximal line thickness, defaults to 20
- **circle.diameter**: optional value for the circle diameter, defaults to 40
- **...**: additional arguments, passed to `plot`

Author(s)

J. Fruth, O. Roustant, S. Hess, S. Neumaerker

References


See Also

- `plotGraphChange`

Examples

```r
op <- par(no.readonly=TRUE)
g1 <- estimateGraph(f.mat=ishigami.fun, d=3, q.arg=list(min=-pi,max=pi), n.tot=10000)
plot(g1)
plot(g1, names=c("A","B","C"))
plot(g1, names=c("A","B","C"), plot.i1 = FALSE)

# include pure second order indices
g2 <- estimateGraph(f.mat=function(x) x[,1]*x[,2]*x[,3]+x[,2]*x[,3], d=3,
q.arg=list(min=-1,max=1), n.tot=10000)
plot(g2)
plot(g2, i2 = c(0.001, 0.001, 0.05))

# equal layouts and different edge thicknesses and circle diameters
g3 <- estimateGraph(f.mat=function(x) x[,1]*x[,2]*x[,3]*x[,4]*x[,5], d=5,
q.arg=list(min=-1,max=1), n.tot=10000)
g4 <- estimateGraph(f.mat=function(x) x[,1]*x[,2]*x[,3]*x[,4]*x[,5], d=5,
q.arg=list(min=-1,max=1), n.tot=10000)
```
plotDeltaJumps

graphClassIgraph <- graph.full(n = 5, directed = FALSE)
layout <- layout.circle(graphClassIgraph)
plot(g3, max.thickness= 10, circle.diameter= 30, layout=layout)
plot(g4, max.thickness= 30, circle.diameter= 50, layout=layout)

plotDeltaJumps Delta Jump Plot

Description
Threshold decision plot. plotDeltaJumps plots the threshold steps (the values of delta at which
the graph changes) equidistant against the number of cliques and the values of delta on the real axis.
The indices are assumed to be scaled for the threshold cuts.

Usage
plotDeltaJumps(graphlist, interval = c(0, 1), mean.clique.size = FALSE)

Arguments
graphlist an object of class graphlist as obtained from estimateGraph
interval an optional vector of size 2, range for the values of delta to be shown in the plot,
defaults to c(0,1)
mean.clique.size logical, if TRUE (default) an additional line is drawn representing the mean of
the number of vertices in the cliques

Details
The plots shall give help in the choice for the threshold. In the first plot a small number of cliques
might be preferable in order to have less parameters to estimate. If several values result in the same
number of cliques the ones with higher mean clique size are possibly preferable.
In the second plot a high jump indicates a point of big distance between two successive edge indices
and thus a clear change in the graph structure. The intervals with notable jumps are highlighted in
green, the higher the jump the darker the colour. Those highlighted intervals together with a small
number of cliques are probably good choices for the threshold.
Use plotGraphChange to visualize the graph structure for possible threshold values.

Author(s)
J. Fruth, O. Roustant

See Also
thresholdIdentification, plotGraphChange
Examples

tii <- matrix(c(0.0018, 0.0265, 0.0017, 0.0277, 0.0018, 0.001, 0.028, 0.0013, 0.0212, 0.002, 0.0372, 0.0024, 0.0022, 0.0157, 0.003))
g <- list(d = 6, tii = tii, il = matrix(c(0.0901, 0.1288, 0.0683, 0.0979, 0.0882, 0.1572)), V = 0.8, tii.scaled = tii/0.8, cliques = list(1:6))

### Delta Jump Plot (jump between 0.0038 and 0.0196)
plotDeltaJumps(g)

---

**plotGraphChange, plotTk, plotManipulate**

*Plot Graph as It Changes with Delta*

Description

Graphs are plotted depending on a change on delta, the threshold for edges to appear in the graph, to enable a visual decision for delta by graph behavior.

Usage

plotGraphChange(graphlist, fix.layout = TRUE, delta.layout = 0.01)
plotTk(graphlist, delta.layout=0.01)
plotManipulate(graphlist, delta.layout=0.01)

Arguments

- `graphlist`: an object of class `graphlist` as obtained from `estimateGraph`
- `fix.layout`: logical, if TRUE (default) the position of the vertices is fixed for all plots such that the positions are optimal for `delta = delta.layout`
- `delta.layout`: optional value between 0 and 1, see `fix.layout`, defaults to 0.01

Note

`plotGraphChange` shows the changing of the graph step by step by changing plots as in demo, `plotTk` is an interactive version using `tcltk`, `plotManipulate` is an interactive version using `manipulate`

Author(s)

J. Fruth, O. Roustant
predictAdditive

See Also

plotDeltajumps, plot.graphlist

Examples

# see demo(Threshold)

predictAdditive(newdata, x, y, parameter, covtype = "gauss", eps.R = 1e-08, cl, iso = FALSE, se.compute=FALSE)

Arguments

newdata matrix containing the points where to perform predictions
x matrix of input data
y vector of output data
parameter (by kmAdditive estimated) kriging parameters, list of size of ‘cl’ containing for each clique a list of parameters alpha (single value) and theta (numeric vector of values)
covtype an optional character string specifying the covariance structure to be used, to be chosen between "gauss", "matern5_2", "matern3_2", "exp" or "powexp" (see DiceKriging), defaults to "gauss"
esp.R small positive number indicating the nugget effect added to the covariance matrix diagonalk, defaults to esp.R = 1e-08
cl list of cliques
iso boolean vector indicating for each clique if it is isotropic (TRUE) or anisotropic (FALSE), defaults to iso = FALSE (all cliques anisotropic)
se.compute optional boolean. If FALSE, only the kriging mean is computed. If TRUE, the kriging variance (actually, the corresponding standard deviation) is computed, too

Value

mean kriging mean computed at newdata.
sd kriging standard deviation computed at newdata. Only computed if se.compute=TRUE.
Author(s)
T. Muehlenstaedt, O. Roustant, J. Fruth

References

See Also
kmAdditive

Examples
```r
### example for ishigami function with cliques {1,3} and {2}
d <- 3
x <- matrix(runif(100*d,-pi,pi),nc=d)
y <- ishigami.fun(x)

cl <- list(c(2), c(1,3))

# constrained ML optimization with kernel defined by the cliques
parameter <- kmAdditive(x, y, cl = cl)

# prediction with the new model
xpred <- matrix(runif(500 * d,-pi,pi), ncol = d)
ypred <- predictAdditive(xpred, x, y, parameter, cl=cl)
yexact <- ishigami.fun(xpred)

# rmse
sqrt(mean((ypred[,1]- yexact)^2))

# scatterplot
par(mfrow=c(1,1))
plot(yexact, ypred[,1], asp = 1)
abline(0, 1)

### compare to one single clique {1,2,3}
cl <- list(c(1,2,3))

# constrained ML optimization with kernel defined by the cliques
parameter <- kmAdditive(x, y, cl = cl)

# prediction with the new model
ypred <- predictAdditive(xpred, x, y, parameter, cl=cl)

# rmse
sqrt(mean((ypred$mean- yexact)^2))

# scatterplot
par(mfrow=c(1,1))
plot(yexact, ypred$mean, asp = 1)
```
### isotropic cliques

c1 <- list(c(2), c(1, 3))
parameter <- kmAdditive(x, y, c1 = c1, iso = c(FALSE, TRUE))
ypred <- predictAdditive(xpred, x, y, parameter, c1 = c1, iso = c(FALSE, TRUE))
sqrt(mean((ypred - yexact)^2))

# the same since first clique has length 1
parameter <- kmAdditive(x, y, c1 = c1, iso = c(TRUE, TRUE))
ypred <- predictAdditive(xpred, x, y, parameter, c1 = c1, iso = c(TRUE, TRUE))
sqrt(mean((ypred - yexact)^2))

---

### simAdditive

Simulate GP values from block-additive kernel

**Description**

Simulate Gaussian process values from a given block-additive kernel

**Usage**

`simAdditive(newdata, mu, parameter, covtype, c1, iso = FALSE, eps.R = 1e-08)`

**Arguments**

- **newdata**: matrix containing the points where to perform simulations
- **mu**: trend parameter
- **parameter**: list of size of `c1` containing for each clique a list of parameters alpha (single value) and theta (numeric vector of values)
- **covtype**: character string specifying the covariance structure to be used, to be chosen between `"gauss"`, `"matern5_2"`, `"matern3_2"`, `"exp"` or `"powexp"` (see DiceKriging)
- **c1**: list of cliques
- **iso**: boolean vector indicating for each clique if it is isotropic (TRUE) or anisotropic (FALSE), defaults to iso = FALSE (all cliques anisotropic)
- **eps.R**: small positive number indicating the nugget effect added to the covariance matrix diagonal, defaults to eps.R = 1e-08

**Value**

a vector containing the simulated values

**Author(s)**

J. Fruth
threshold

References


See Also

kmAdditive, simulate

Examples

```r
### 2 dimensional simulation
x1 <- x2 <- seq(-1,1,20)
x <- expand.grid(x1,x2)
covtype <- "matern3_2"
mu <- 0

op <- par(no.readonly=TRUE); par(mfrow=c(1,2), mar=c(1,1,1,1))
# non-additive simulation
parameter <- list(list(alpha=1, theta=c(0.8,0.8))
cl <- list(1:2)
set.seed(1)
y <- simAdditive(x, mu, parameter, covtype, cl)
persp(x1,x2, matrix(y,20), theta=-40, col="lightblue", zlab="y")

# additive simulation
parameter <- list(list(alpha=0.5, theta=0.8),
                  list(alpha=0.5, theta=0.8))
cl <- list(1,2)
set.seed(1)
y <- simAdditive(x, mu, parameter, covtype, cl)
persp(x1,x2, matrix(y,20), theta=-40, col="lightblue", zlab="y")

par(op)
```

---

**threshold**  

**Threshold indices**

**Description**

All indices below a threshold are set to be zero.

**Usage**

```r
threshold(graphlist, delta, scaled = TRUE, robust = FALSE)
```
threshold

Arguments

- **graphlist**: an object of class `graphlist` as obtained from `estimateGraph`
- **delta**: numeric threshold, between 0 and 1 if `scaled = TRUE`
- **scaled**: optional boolean, if TRUE, indices are normalized by the overall variance before for threshold cut, defaults to TRUE
- **robust**: optional boolean, if TRUE, upper confidence intervals limits are used for the threshold cut instead of indices themselves, confidence intervals must be provided in `graphlist`, defaults to FALSE

Value

an object of class `graphlist` where the indices are thresholded the clique structure is updated respectively, see `estimateGraph` for a detailed description

Warning

The threshold cut is by default performed on scaled indices. For a cut on the original unscaled indices set `scaled = FALSE`.

Author(s)

J. Fruth, T. Muehlenstaedt, O. Roustant

References


Examples

# Kriging model prediction
x <- matrix(runif(100*3,-pi,pi),100,3)
KM <- km(~1, design = data.frame(x), response = ishigami.fun(x))
krigingMean <- function(xnew) predict(object = KM, newdata = xnew,
    type = "UK", se.compute = FALSE, checkNames = FALSE)$mean

# full graph estimation
g <- estimateGraph(krigingMean, d=3, n.tot=10000, q.arg=list(min=-pi, max=pi))
print(g[c(2,6)])
# threshold graph
g.cut <- threshold(g, delta = 0.1)
print(g.cut[c(2,6)])
thresholdIdentification

Function to identify a suitable threshold for an estimateGraph object

Description

From an estimateGraph object and a corresponding data set, candidate threshold values are compared on the prediction performance of the corresponding additive Kriging model. The candidate thresholds are chosen by the biggest jumps in plotDeltaJumps together with 0 (the full model) and 1 (the complete additive model). For each of them the Kriging model with corresponding kernel is estimated and the leave-one-out crossvalidations on the original data sets are compared on scatterplots and RMSE-values.

Usage

thresholdIdentification(g, x, y, n.cand = 3, covtype = "matern5_2", KM = NULL)

Arguments

g object of class graphlist as obtained from estimateGraph

x design matrix of input variables corresponding to g, number of columns should be number of variables

y vector of output variables of the same length as the columns of x

n.cand integer, the n. cand biggest jumps are chosen as candidate threshold values. The default value is 3

covtype optional character string specifying the covariance structure to be used. The default is "matern5_2"

KM optional object of class km, the full kriging model corresponding to g. With default value NULL, this kriging model is computed by the function itself

Value

a list including

delta vector of threshold candidates

models list of full model and models with applied thresholds

y.cv list of vectors containing crossvalidation predictions for each model

RMSE vector of residual mean squared errors for each model

Author(s)

J. Fruth, M. Jastrow

See Also

plotDeltaJumps, plotGraphChange
Examples

#### simple 3-dimensional example with one interaction

```r
### data (usually existing)
x <- matrix(seq(0,1,20), 20, 3)
x <- apply(x,2,sample)
y <- 2*(x[,1]-0.5) * (x[,2]-0.5) + 0.1*sin(10*x[,3])

### FANVOA graph (usually estimated from a meta model over the data)
g <- list(d=3,
  tii = matrix(c(0.0140, 0.0008, 0.0002)),
  V = 0.0222,
  tii.scaled = matrix(c(0.6976, 0.0432, 0.0113))
)
class(g) <- "graphlist"

### plot complete graph
plot(g, plot.i1=FALSE)

### Compare candidate thresholds on prediction performance
set.seed(1)
comparison <- thresholdIdentification(g, x, y, n.cand = 1)
```

\[\text{totalIndex} \quad \text{Estimation of main index indices}\]

Description

Estimation of the unscaled total Sobol index of all main indices by method Liu & Owen (superset importance of main indices).

Usage

```r
totalIndex(f.mat, d, q = NULL, q.arg = NULL, n.mc, ...)
```

Arguments

- `f.mat`: vectorized function of which indices shall be estimated
- `d`: integer, number of input factors (vertices)
- `q`: a vector of character strings of quantile functions corresponding to the factors distributions, it can be a single character string meaning same distribution for all, if not specified "qunif" is taken
- `q.arg`: a list of lists of quantile functions parameters of the distributions in q, it can be a single list meaning same parameters for all, if not specified the default values of the respective distributions are taken
- `n.mc`: number of Monte Carlo evaluations
- `...`: additional arguments to be passed to the function `f.mat`
Value
A vector containing the unscaled total Sobol indices

Author(s)
J. Fruth

References

See Also
*estimateGraph*

Examples
```r
totalIndex(f.mat=ishigami.fun, d=3, q.arg=list(min=-pi,max=pi), n.mc=10000)
totalIndex(f.mat=sobol.fun, d=8, q.arg=list(min=0,max=1), n.mc=10000)
```
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