Package: BayesianTools (via r-universe)

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Title General-Purpose MCMC and SMC Samplers and Tools for Bayesian Statistics

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Description General-purpose MCMC and SMC samplers, as well as plots and diagnostic functions for Bayesian statistics, with a particular focus on calibrating complex system models. Implemented samplers include various Metropolis MCMC variants (including adaptive and/or delayed rejection MH), the T-walk, two differential evolution MCMCs, two DREAM MCMCs, and a sequential Monte Carlo (SMC) particle filter.

Depends R (>= 3.1.2)

License GPL-3

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Contents

applySettingsDefault . . . 3
BayesianTools . . . 4
calibrationTest . . . 5
checkBayesianSetup . . . 7
convertCoda . . . 8
correlationPlot . . . 8
createBayesianSetup . . . 10
createBetaPrior . . . 13
createLikelihood . . . 15
createMcmcSamplerList . . . 16
createMixWithDefaults . . . 17
createPosterior . . . 17
createPrior . . . 18
createPriorDensity . . . 20
createProposalGenerator . . . 23
createSmcSamplerList . . . 25
createTruncatedNormalPrior . . . 26
createUniformPrior . . . 28
DE . . . 29
DEzs . . . 32
DIC . . . 34
DREAM . . . 35
DREAMzs . . . 38
gelmanDiagnostics . . . 40
generateParallelExecuter . . . 42
generateTestDensityMultiNormal . . . 43
getCredibleIntervals . . . 44
getDharmaResiduals . . . 45
getPanels . . . 45
getPossibleSamplerTypes . . . 46
getPredictiveDistribution . . . 46
getPredictiveIntervals . . . 47
getSample . . . 48
getVolume . . . 52
GOF . . . 53
likelihoodAR1 . . . 54
likelihoodIidNormal . . . 55
MAP . . . 56
marginalLikelihood . . . 56
marginalPlot . . . 61
mergeChains . . . 63
Metropolis . . . 64
plotDiagnostic . . . 66
plotSensitivity . . . 67
plotTimeSeries . . . 68
plotTimeSeriesResiduals . . . 69

plotTimeSeriesResults . . . 70
runMCMC . . . 71
smcSampler . . . 73
stopParallel . . . 76
testDensityBanana . . . 77
testDensityGelmanMeng . . . 78
testDensityInfinity . . . 78
testDensityMultiNormal . . . 79
testDensityNormal . . . 79
testLinearModel . . . 80
tracePlot . . . 80
Twalk . . . 81
updateProposalGenerator . . . 83
VSEM . . . 83
vsemC . . . 88
VSEMcreateLikelihood . . . 88
VSEMcreatePAR . . . 89
VSEMgetDefaults . . . 89
WAIC . . . 90

Index **92**

`applySettingsDefault` *Provides the default settings for the different samplers in runMCMC*

Description

Provides the default settings for the different samplers in runMCMC

Usage

```
applySettingsDefault(settings = NULL, sampler = "DEzs", check = FALSE)
```

Arguments

`settings`	optional list with parameters that will be used instead of the defaults
`sampler`	one of the samplers in `runMCMC`
`check`	logical determines whether parameters should be checked for consistency

Details

The following settings can be used for all MCMCs:

startValue (no default) start values for the MCMC. Note that DE family samplers require a matrix of #' start values. If startvalues are not provided, they are sampled from the prior.

iterations (10000) the MCMC iterations

burnin (0) burnin

thin (1) thinning while sampling

consoleUpdates (100) update frequency for console updates

parallel (NULL) whether parallelization is to be used

message (TRUE) if progress messages are to be printed

nrChains (1) the number of independent MCMC chains to be run. Note that this is not controlling the #' internal number of chains in population MCMCs such as DE, so if you run nrChains = 3 with a DEzs #' #' startValue that is a 4xparameter matrix (= 4 internal chains), you will run independent DEzs runs #' #' with 4 internal chains each.

For more details, see runMCMC

Author(s)

Florian Hartig

Examples

```
## Generate a test likelihood function.
ll <- generateTestDensityMultiNormal(sigma = "no correlation")

## Create a BayesianSetup object from the likelihood
## is the recommended way of using the runMCMC() function.
bayesianSetup <- createBayesianSetup(likelihood = ll, lower = rep(-10, 3), upper = rep(10, 3))

## Finally we can run the sampler. To get possible settings
## for a sampler, see help or run applySettingsDefault(sampler = "Metropolis")
settings = list(iterations = 1000, adapt = FALSE) #
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "Metropolis", settings = settings)

## out is of class bayesianOutput. There are various standard functions
# implemented for this output

plot(out)
correlationPlot(out)
marginalPlot(out)
summary(out)

## additionally, you can return the sample as a coda object, and make use of the coda functions
# for plotting and analysis

codaObject = getSample(out, start = 500, coda = TRUE)
```

Description

A package with general-purpose MCMC and SMC samplers, as well as plots and diagnostic functions for Bayesian statistics

Details

A package with general-purpose MCMC and SMC samplers, as well as plots and diagnostic functions for Bayesian statistics, particularly for process-based models.

The package contains 2 central functions, `createBayesianSetup`, which creates a standardized Bayesian setup with likelihood and priors, and `runMCMC`, which allows to run various MCMC and SMC samplers.

The package can of course also be used for general (non-Bayesian) target functions.

To use the package, a first step is to use `createBayesianSetup` to create a BayesianSetup, which usually contains prior and likelihood densities, or in general a target function.

Those can be sampled with `runMCMC`, which can call a number of general purpose Metropolis sampler, including the `Metropolis` that allows to specify various popular Metropolis variants such as adaptive and/or delayed rejection Metropolis; two variants of differential evolution MCMC `DE`, `DEzs`, two variants of DREAM `DREAM` and `DREAMzs`, the `Twalk` MCMC, and a Sequential Monte Carlo sampler `smcSampler`.

The output of runMCMC is of class mcmcSampler / smcSampler if one run is performed, or mcmcSamplerList / smcSamplerList if several sampler are run. Various functions are available for plotting, model comparison (DIC, marginal likelihood), or to use the output as a new prior.

For details on how to use the packgage, run vignette("BayesianTools", package="BayesianTools").

To get the suggested citation, run citation("BayesianTools")

To report bugs or ask for help, post a reproducible example via the BayesianTools issue tracker on GitHub.

Acknowledgements: The creation and maintenance of this package profited from funding and collaboration through Cost Action FP 1304 PROFOUND, DFG DO 786/12-1 CONECT, EU FP7 ERA-NET Sumforest REFORCE and Bayklif Project BLIZ.

`calibrationTest` *Simulation-based calibration tests*

Description

This function performs simulation-based calibration tests based on the idea that posteriors averaged over the prior should yield the prior.

Usage

```
calibrationTest(posteriorList, priorDraws, ...)
```

Arguments

posteriorList	a list with posterior samples. List items must be of a class that is supported by getSample. This includes BayesianTools objects, but also matrix and data.frame
priorDraws	a matrix with parameter values, drawn from the prior, that were used to simulate the data underlying the posteriorList. If colnames are provided, these will be used in the plots
...	arguments to be passed to getSample. Consider in particular the thinning option.

Details

The purpose of this function is to evaluate the results of a simulation-based calibration of an MCMC analysis.

Briefly, the idea is to repeatedly

1. sample parameters from the prior,
2. simulate new data based on these parameters,
3. calculate the posterior for these data

If the sampler and the likelihood are implemented correctly, the average over all the posterior distribution should then again yield the prior (e.g. Cook et al., 2006).

To test if this is the case, we implement the methods suggested by Talts et al., which is to calculate the rank statistics between the parameter draws and the posterior draws, which we then formally evaluate with a qq unif plot, and a ks.test

I speculate that a ks.test between the two distribution would likely give an identical result, but this is not noted in Talts et al.

Cook, S. R., Gelman, A. and Rubin, D. B. (2006). Validation of Software for Bayesian Models Using Posterior Quantiles. J. Comput. Graph. Stat. 15 675-692.

Talts, Sean, Michael Betancourt, Daniel Simpson, Aki Vehtari, and Andrew Gelman. "Validating Bayesian Inference Algorithms with Simulation-Based Calibration." arXiv preprint arXiv:1804.06788 (2018).

Note

This function was implemented for the tests in Maliet, Odile, Florian Hartig, and Hélène Morlon. "A model with many small shifts for estimating species-specific diversification rates." Nature ecology & evolution 3.7 (2019): 1086-1092. The code linked with this paper provides a further example of its use.

Author(s)

Florian Hartig

checkBayesianSetup *Checks if an object is of class 'BayesianSetup'*

Description

Function used to assure that an object is of class 'BayesianSetup'. If you pass a function, it is coverted to an object of class 'BayesianSetup' (using createBayesianSetup) before it is returned.

Usage

```
checkBayesianSetup(bayesianSetup, parallel = F)
```

Arguments

bayesianSetup	either object of class bayesianSetup or a log posterior function
parallel	if bayesianSetup is a function, this will set the parallelization option for the class BayesianSetup that is created internally. If bayesianSetup is already a BayesianSetup, then this will check if parallel = T is requested but not supported by the BayesianSetup. This option is for internal use in the samplers

Note

The recommended option to use this function in the samplers is to have parallel with default NULL in the samplers, so that checkBayesianSetup with a function will create a bayesianSetup without parallelization, while it will do nothing with an existing BayesianSetup. If the user sets parallelization, it will set the approriate parallelization for a function, and check in case of an existing BayesianSetup. The checkBayesianSetup call in the samplers should then be followed by a check for parallel = NULL in sampler, in which case paralell can be set from the BayesianSetup

Author(s)

Florian Hartig

See Also

createBayesianSetup

convertCoda *Convert coda::mcmc objects to BayesianTools::mcmcSampler*

Description

Function is used to make the plot and diagnostic functions available for coda::mcmc objects

Usage

```
convertCoda(sampler, names = NULL, info = NULL, likelihood = NULL)
```

Arguments

sampler	An object of class mcmc or mcmc.list
names	vector giving the parameter names (optional)
info	matrix (or list with matrices for mcmc.list objects) with three coloumns containing log posterior, log likelihood and log prior of the sampler for each time step (optional; but see Details)
likelihood	likelihood function used in the sampling (see Details)

Details

The parameter 'likelihood' is optional for most functions but can be needed e.g for using the DIC function.

Also the parameter info is optional for most uses. However for some functions (e.g. MAP) the matrix or single coloumns (e.g. log posterior) are necessary for the diagnostics.

correlationPlot *Flexible function to create correlation density plots*

Description

Flexible function to create correlation density plots

Usage

```
correlationPlot(
  mat,
  density = "smooth",
  thin = "auto",
  method = "pearson",
  whichParameters = NULL,
  scaleCorText = T,
  ...
)
```

Arguments

mat	object of class "bayesianOutput" or a matrix or data frame of variables
density	type of plot to do. Either "smooth" (default), "corellipseCor", or "ellipse"
thin	thinning of the matrix to make things faster. Default is to thin to 5000
method	method for calculating correlations. Possible choices are "pearson" (default), "kendall" and "spearman"
whichParameters	indices of parameters that should be plotted
scaleCorText	should the text to display correlation be scaled to the strength of the correlation
...	additional parameters to pass on to the getSample, for example parametersOnly =F, or start = 1000

Author(s)

Florian Hartig

References

The code for the correlation density plot originates from Hartig, F.; Dislich, C.; Wiegand, T. & Huth, A. (2014) Technical Note: Approximate Bayesian parameterization of a process-based tropical forest model. Biogeosciences, 11, 1261-1272.

See Also

marginalPlot
plotTimeSeries
tracePlot

Examples

```
## Generate a test likelihood function.
ll <- generateTestDensityMultiNormal(sigma = "no correlation")

## Create a BayesianSetup object from the likelihood
## is the recommended way of using the runMCMC() function.
bayesianSetup <- createBayesianSetup(likelihood = ll, lower = rep(-10, 3), upper = rep(10, 3))

## Finally we can run the sampler and have a look
settings = list(iterations = 1000)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)

## Correlation density plots:
correlationPlot(out)

## additional parameters can be passed to getSample (see ?getSample for further information)
## e.g. to select which parameters to show or thinning (faster plot)
correlationPlot(out, scaleCorText = FALSE, thin = 100, start = 200, whichParameters = c(1,2))
```

```
## text to display correlation will be not scaled to the strength of the correlation
correlationPlot(out, scaleCorText = FALSE)

## We can also switch the method for calculating correllations
correlationPlot(out, scaleCorText = FALSE, method = "spearman")
```

`createBayesianSetup` *Creates a standardized collection of prior, likelihood and posterior functions, including error checks etc.*

Description

Creates a standardized collection of prior, likelihood and posterior functions, including error checks etc.

Usage

```
createBayesianSetup(
  likelihood,
  prior = NULL,
  priorSampler = NULL,
  parallel = FALSE,
  lower = NULL,
  upper = NULL,
  best = NULL,
  names = NULL,
  parallelOptions = list(variables = "all", packages = "all", dlls = NULL),
  catchDuplicates = FALSE,
  plotLower = NULL,
  plotUpper = NULL,
  plotBest = NULL
)
```

Arguments

`likelihood`	log likelihood density function
`prior`	either a prior class (see `createPrior`) or a log prior density function
`priorSampler`	if a prior density (and not a prior class) is provided to prior, the optional prior sampling function can be provided here
`parallel`	parallelization option. Default is F. Other options include T, or "external". See details.
`lower`	vector with lower prior limits
`upper`	vector with upper prior limits
`best`	vector with best prior values

names	optional vector with parameter names
parallelOptions	list containing three lists. First "packages" determines the R packages necessary to run the likelihood function. Second "variables" the objects in the global environment needed to run the likelihood function and third "dlls" the DLLs needed to run the likelihood function (see Details and Examples).
catchDuplicates	Logical, determines whether unique parameter combinations should only be evaluated once. Only used when the likelihood accepts a matrix with parameter as columns.
plotLower	vector with lower limits for plotting
plotUpper	vector with upper limits for plotting
plotBest	vector with best values for plotting

Details

If prior is of class prior (e.g. create with `createPrior`), priorSampler, lower, upper and best will be ignored.
If prior is a function (log prior density), priorSampler (custom sampler), or lower/upper (uniform sampler) is required.
If prior is NULL, and lower and upper are passed, a uniform prior (see `createUniformPrior`) will be created with boundaries lower and upper.

For parallelization, Bayesiantools requies that the likelihood can evaluate several parameter vectors (supplied as a matrix) in parallel.

- parallel = T means that an automatic parallelization of the likelihood via a standard R socket cluster is attempted, using the function `generateParallelExecuter`. By default, of the N cores detected on the computer, N-1 cores are requested. Alternatively, you can provide a integer number to parallel, specifying the cores reserved for the cluster. When the cluster is cluster is created, a copy of your workspace, including DLLs and objects are exported to the cluster workers. Because this can be very inefficient, you can explicitly specify the packages, objects and DLLs that are to be exported via parallelOptions. Using parallel = T requires that the function to be parallelized is well encapsulate, i.e. can run on a shared memory / shared hard disk machine in parallel without interfering with each other.

If automatic parallelization cannot be done (e.g. because dlls are not thread-safe or write to shared disk), and only in this case, you should specify parallel = "external". In this case, it is assumed that the likelihood is programmed such that it accepts a matrix with parameters as columns and the different model runs as rows. It is then up to the user if and how to parallelize this function. This option gives most flexibility to the user, in particular for complicated parallel architecture or shared memory problems.

For more details on parallelization, make sure to read both vignettes, in particular the section on the likelihood in the main vignette, and the section on parallelization in the vignette on interfacing models.

Author(s)

Florian Hartig, Tankred Ott

See Also

checkBayesianSetup
createLikelihood
createPrior

Examples

```
ll <- function(x) sum(dnorm(x, log = TRUE))

test <- createBayesianSetup(ll, prior = NULL, priorSampler = NULL, lower = -10, upper = 10)
str(test)
test$prior$density(0)

test$likelihood$density(c(1,1))
test$likelihood$density(1)
test$posterior$density(1)
test$posterior$density(1, returnAll = TRUE)

test$likelihood$density(matrix(rep(1,4), nrow = 2))
#test$posterior$density(matrix(rep(1,4), nrow = 2), returnAll = TRUE)
test$likelihood$density(matrix(rep(1,4), nrow = 4))

## Not run:

## Example of how to use parallelization using the VSEM model
# Note that the parallelization produces overhead and is not always
# speeding things up. In this example, due to the small
# computational cost of the VSEM the parallelization is
# most likely to reduce the speed of the sampler.

# Creating reference data
PAR <- VSEMcreatePAR(1:1000)
refPars   <- VSEMgetDefaults()
refPars[12,] <- c(0.2, 0.001, 1)
rownames(refPars)[12] <- "error-sd"

referenceData <- VSEM(refPars$best[1:11], PAR)
obs = apply(referenceData, 2, function(x) x + rnorm(length(x),
                                                    sd = abs(x) * refPars$best[12]))

# Selecting parameters
parSel = c(1:6, 12)


## Builidng the likelihood function
likelihood <- function(par, sum = TRUE){
  x = refPars$best
  x[parSel] = par
  predicted <- VSEM(x[1:11], PAR)
  diff = c(predicted[,1:3] - obs[,1:3])
  llValues = dnorm(diff, sd = max(abs(c(predicted[,1:3])),0.0001) * x[12], log = TRUE)
```

```
  if (sum == False) return(llValues)
  else return(sum(llValues))
}

# Prior
prior <- createUniformPrior(lower = refPars$lower[parSel], upper = refPars$upper[parSel])

## Definition of the packages and objects that are exported to the cluster.
# These are the objects that are used in the likelihood function.
opts <- list(packages = list("BayesianTools"), variables = list("refPars", "obs", "PAR" ),
             dlls = NULL)

# Create Bayesian Setup
BSVSEM <- createBayesianSetup(likelihood, prior, best = refPars$best[parSel],
                              names = rownames(refPars)[parSel], parallel = 2,
                              parallelOptions = opts)

## The bayesianSetup can now be used in the runMCMC function.
# Note that not all samplers can make use of parallel
# computing.

# Remove the Bayesian Setup and close the cluster
stopParallel(BSVSEM)
rm(BSVSEM)


## End(Not run)
```

`createBetaPrior` *Convenience function to create a beta prior*

Description

Convenience function to create a beta prior

Usage

```
createBetaPrior(a, b, lower = 0, upper = 1)
```

Arguments

a	shape1 of the beta distribution
b	shape2 of the beta distribution
lower	lower values for the parameters
upper	upper values for the parameters

Details

This creates a beta prior, assuming that lower / upper values for parameters are are fixed. The beta is the calculated relative to this lower / upper space.

Note

for details see createPrior

Author(s)

Florian Hartig

See Also

createPriorDensity
createPrior
createTruncatedNormalPrior
createUniformPrior
createBayesianSetup

Examples

```
# The BT package includes a number of convenience functions to specify
# prior distributions, including createUniformPrior, createTruncatedNormalPrior
# etc. If you want to specify a prior that corresponds to one of these
# distributions, you should use these functions, e.g.:

prior <- createUniformPrior(lower = c(0,0), upper = c(0.4,5))

prior$density(c(2, 3)) # outside of limits -> -Inf
prior$density(c(0.2, 2)) # within limits, -0.6931472

# All default priors include a sampling function, i.e. you can create
# samples from the prior via
prior$sampler()
# [1] 0.2291413 4.5410389

# if you want to specify a prior that does not have a default function,
# you should use the createPrior function, which expects a density and
# optionally a sampler function:

density = function(par){
  d1 = dunif(par[1], -2,6, log =TRUE)
  d2 = dnorm(par[2], mean= 2, sd = 3, log =TRUE)
  return(d1 + d2)
}

sampler = function(n=1){
  d1 = runif(n, -2,6)
  d2 = rnorm(n, mean= 2, sd = 3)
  return(cbind(d1,d2))
}

prior <- createPrior(density = density, sampler = sampler,
                     lower = c(-10,-20), upper = c(10,20), best = NULL)
```

```
# note that the createPrior supports additional truncation


# To use a prior in an MCMC, include it in a BayesianSetup

set.seed(123)
ll <- function(x) sum(dnorm(x, log = TRUE)) # multivariate normal ll
bayesianSetup <- createBayesianSetup(likelihood = ll, prior = prior)

settings = list(iterations = 100)
out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)

# use createPriorDensity to create a new (estimated) prior from MCMC output

newPrior = createPriorDensity(out, method = "multivariate",
                              eps = 1e-10, lower = c(-10,-20),
                              upper = c(10,20), best = NULL, scaling = 0.5)
```

`createLikelihood` *Creates a standardized likelihood class#'*

Description

Creates a standardized likelihood class#'

Usage

```
createLikelihood(
  likelihood,
  names = NULL,
  parallel = F,
  catchDuplicates = T,
  sampler = NULL,
  parallelOptions = NULL
)
```

Arguments

`likelihood`	Log likelihood density
`names`	Parameter names (optional)
`parallel`	parallelization , either i) no parallelization –> F, ii) native R parallelization –> T / "auto" will select n-1 of your available cores, or provide a number for how many cores to use, or iii) external parallelization –> "external". External means that the likelihood is already able to execute parallel runs in form of a matrix with

`catchDuplicates`
: Logical, determines whether unique parameter combinations should only be evaluated once. Only used when the likelihood accepts a matrix with parameter as columns.

`sampler`
: sampler

`parallelOptions`
: list containing two lists. First "packages" determines the R packages necessary to run the likelihood function. Second "objects" the objects in the global envirnment needed to run the likelihood function (for details see `createBayesianSetup`).

Author(s)

Florian Hartig

See Also

`likelihoodIidNormal`
`likelihoodAR1`

`createMcmcSamplerList` *Convenience function to create an object of class mcmcSamplerList from a list of mcmc samplers*

Description

Convenience function to create an object of class mcmcSamplerList from a list of mcmc samplers

Usage

```
createMcmcSamplerList(mcmcList)
```

Arguments

`mcmcList`
: a list with each object being an mcmcSampler

Value

Object of class "mcmcSamplerList"

Author(s)

Florian Hartig

createMixWithDefaults *Allows to mix a given parameter vector with a default parameter vector*

Description

This function is deprecated and will be removed by v0.2.

Usage

```
createMixWithDefaults(pars, defaults, locations)
```

Arguments

pars	vector with new parameter values
defaults	vector with defaukt parameter values
locations	indices of the new parameter values

createPosterior *Creates a standardized posterior class*

Description

Creates a standardized posterior class

Usage

```
createPosterior(prior, likelihood)
```

Arguments

prior	prior class
likelihood	Log likelihood density

Details

Function is internally used in createBayesianSetup to create a standarized posterior class.

Author(s)

Florian Hartig

createPrior *Creates a user-defined prior class*

Description

This function creates a general user-defined prior class. Note that there are specialized function available for specific prior classes, see details.

Usage

```
createPrior(
  density = NULL,
  sampler = NULL,
  lower = NULL,
  upper = NULL,
  best = NULL
)
```

Arguments

density	Prior density
sampler	Sampling function for density (optional)
lower	vector with lower bounds of parameters
upper	vector with upper bounds of parameter
best	vector with "best" parameter values

Details

This is the general prior generator. It is highly recommended to not only implement the density, but also the sampler function. If this is not done, the user will have to provide explicit starting values for many of the MCMC samplers.

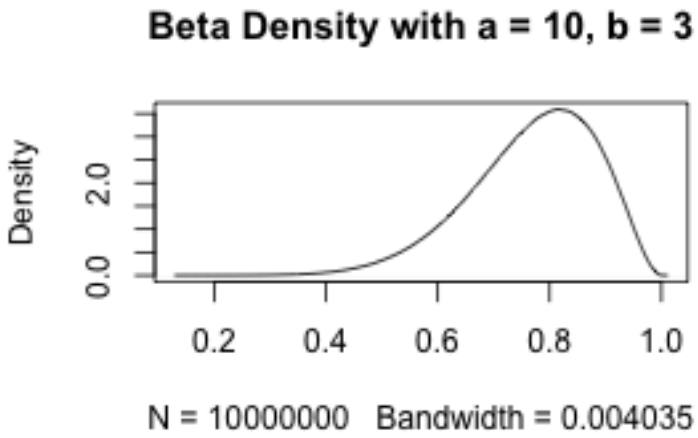
Note the existing, more specialized prior function. If your prior can be created by those functions, they are preferred. Note also that priors can be created from an existing MCMC output from BT, or another MCMC sample, via createPriorDensity.

The prior we choose depends on the prior information we have. For example, if we have no prior information, we can choose a uniform prior. The normal distribution is often used to model a wide range of phenomena in statistics, such as the distribution of heights or weights in a population. Beta distribution, on the other hand, is defined on the interval 0, 1. It is often used to model random variables that represent proportions, probabilities or other values that are constrained to lie within this interval.

createPrior	createBetaPrior
Any density provided by the user	Beta density

createPrior(density, sampler, lower, upper, best)

createBetaPrior(a, b, lower, upper)



Note

min and max truncate, but not re-normalize the prior density (so, if a pdf that integrated to one is truncated, the integral will in general be smaller than one). For MCMC sampling, this doesn't make a difference, but if absolute values of the prior density are a concern, one should provide a truncated density function for the prior.

Author(s)

Florian Hartig

See Also

createPriorDensity
createBetaPrior
createUniformPrior
createTruncatedNormalPrior
createBayesianSetup

Examples

```
# The BT package includes a number of convenience functions to specify
# prior distributions, including createUniformPrior, createTruncatedNormalPrior
# etc. If you want to specify a prior that corresponds to one of these
# distributions, you should use these functions, e.g.:
```

```
prior <- createUniformPrior(lower = c(0,0), upper = c(0.4,5))

prior$density(c(2, 3)) # outside of limits -> -Inf
prior$density(c(0.2, 2)) # within limits, -0.6931472

# All default priors include a sampling function, i.e. you can create
# samples from the prior via
prior$sampler()
# [1] 0.2291413 4.5410389

# if you want to specify a prior that does not have a default function,
# you should use the createPrior function, which expects a density and
# optionally a sampler function:

density = function(par){
  d1 = dunif(par[1], -2,6, log =TRUE)
  d2 = dnorm(par[2], mean= 2, sd = 3, log =TRUE)
  return(d1 + d2)
}

sampler = function(n=1){
  d1 = runif(n, -2,6)
  d2 = rnorm(n, mean= 2, sd = 3)
  return(cbind(d1,d2))
}

prior <- createPrior(density = density, sampler = sampler,
                     lower = c(-10,-20), upper = c(10,20), best = NULL)

# note that the createPrior supports additional truncation


# To use a prior in an MCMC, include it in a BayesianSetup

set.seed(123)
ll <- function(x) sum(dnorm(x, log = TRUE)) # multivariate normal ll
bayesianSetup <- createBayesianSetup(likelihood = ll, prior = prior)

settings = list(iterations = 100)
out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)

# use createPriorDensity to create a new (estimated) prior from MCMC output

newPrior = createPriorDensity(out, method = "multivariate",
                              eps = 1e-10, lower = c(-10,-20),
                              upper = c(10,20), best = NULL, scaling = 0.5)
```

---

createPriorDensity *Fits a density function to a multivariate sample*

Description

Fits a density function to a multivariate sample

Usage

```
createPriorDensity(
  sampler,
  method = "multivariate",
  eps = 1e-10,
  lower = NULL,
  upper = NULL,
  best = NULL,
  scaling = 1,
  ...
)
```

Arguments

sampler	an object of class BayesianOutput or a matrix
method	method to generate prior - default and currently only option is multivariate
eps	numerical precision to avoid singularity
lower	vector with lower bounds of parameter for the new prior, independent of the input sample
upper	vector with upper bounds of parameter for the new prior, independent of the input sample
best	vector with "best" values of parameter for the new prior, independent of the input sample
scaling	optional scaling factor for the covariance. If scaling > 1 will create a prior wider than the posterior, < 1 a prior more narrow than the posterior. Scaling is linear to the posterior width, i.e. scaling = 2 will create a prior that with 2x the sd of the original posterior.
...	parameters to pass on to the getSample function

Details

This function fits a density estimator to a multivariate (typically a posterior) sample. The main purpose is to summarize a posterior sample as a pdf, in order to include it as a prior in a new analysis, for example when new data becomes available, or to calculate a fractional Bayes factor (see marginalLikelihood).

The limitation of this function is that we currently only implement a multivariate normal density estimator, so you will have a loss of information if your posterior is not approximately multivariate normal, which is likely the case if you have weak data. Extending the function to include more flexible density estimators (e.g. gaussian processes) is on our todo list, but it's quite tricky to get this stable, so I'm not sure when we will have this working. In general, creating reliable empirical density estimates in high-dimensional parameter spaces is extremely tricky, regardless of the software you are using.

For that reason, it is usually recommended to not update the posterior with this option, but rather:

1. If the full dataset is available, to make a single, or infrequent updates, recompute the entire model with the full / updated data
2. For frequent updates, consider using SMC instead of MCMC sampling. SMC sampling doesn't require an analytical summary of the posterior.

Author(s)

Florian Hartig

See Also

createPrior
createBetaPrior
createTruncatedNormalPrior
createUniformPrior
createBayesianSetup

Examples

```
# The BT package includes a number of convenience functions to specify
# prior distributions, including createUniformPrior, createTruncatedNormalPrior
# etc. If you want to specify a prior that corresponds to one of these
# distributions, you should use these functions, e.g.:

prior <- createUniformPrior(lower = c(0,0), upper = c(0.4,5))

prior$density(c(2, 3)) # outside of limits -> -Inf
prior$density(c(0.2, 2)) # within limits, -0.6931472

# All default priors include a sampling function, i.e. you can create
# samples from the prior via
prior$sampler()
# [1] 0.2291413 4.5410389

# if you want to specify a prior that does not have a default function,
# you should use the createPrior function, which expects a density and
# optionally a sampler function:

density = function(par){
  d1 = dunif(par[1], -2,6, log =TRUE)
  d2 = dnorm(par[2], mean= 2, sd = 3, log =TRUE)
  return(d1 + d2)
}

sampler = function(n=1){
  d1 = runif(n, -2,6)
  d2 = rnorm(n, mean= 2, sd = 3)
  return(cbind(d1,d2))
}
```

```
prior <- createPrior(density = density, sampler = sampler,
                     lower = c(-10,-20), upper = c(10,20), best = NULL)

# note that the createPrior supports additional truncation


# To use a prior in an MCMC, include it in a BayesianSetup

set.seed(123)
ll <- function(x) sum(dnorm(x, log = TRUE)) # multivariate normal ll
bayesianSetup <- createBayesianSetup(likelihood = ll, prior = prior)

settings = list(iterations = 100)
out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)

# use createPriorDensity to create a new (estimated) prior from MCMC output

newPrior = createPriorDensity(out, method = "multivariate",
                              eps = 1e-10, lower = c(-10,-20),
                              upper = c(10,20), best = NULL, scaling = 0.5)
```

`createProposalGenerator` *Factory that creates a proposal generator*

Description

Factory that creates a proposal generator

Usage

```
createProposalGenerator(
  covariance,
  gibbsProbabilities = NULL,
  gibbsWeights = NULL,
  otherDistribution = NULL,
  otherDistributionLocation = NULL,
  otherDistributionScaled = F,
  message = F,
  method = "chol",
  scalingFactor = 2.38
)
```

Arguments

`covariance`	covariance matrix. Can also be vector of the sqrt of diagonal elements –> standard deviation

`gibbsProbabilities`
: optional probabilities for the number of parameters to vary in a Metropolis within gibbs style - for 4 parameters, c(1,1,0.5,0) means that at most 3 parameters will be varied, and it is double as likely to vary one or two than varying 3

`gibbsWeights`
: optional probabilities for parameters to be varied in a Metropolis within gibbs style - default ist equal weight for all parameters - for 4 parameters, c(1,1,1,100) would mean that if 2 parameters would be selected, parameter 4 would be 100 times more likely to be picked than the others. If 4 is selected, the remaining parameters have equal probability.

`otherDistribution`
: optional additinal distribution to be mixed with the default multivariate normal. The distribution needs to accept a parameter vector (to allow for the option of making the distribution dependend on the parameter values), but it is still assumed that the change from the current values is returned, not the new absolute values.

`otherDistributionLocation`
: a vector with 0 and 1, denoting which parameters are modified by the otherDistribution

`otherDistributionScaled`
: should the other distribution be scaled if gibbs updates are calculated?

`message`
: print out parameter settings

`method`
: method for covariance decomposition

`scalingFactor`
: scaling factor for the proposals

Author(s)

Florian Hartig

See Also

`updateProposalGenerator`

Examples

```
testMatrix = matrix(rep(c(0,0,0,0), 1000), ncol = 4)
testVector = c(0,0,0,0)


##Standard multivariate normal proposal generator

testGenerator <- createProposalGenerator(covariance = c(1,1,1,1), message = TRUE)

methods(class = "proposalGenerator")
print(testGenerator)

x = testGenerator$returnProposal(testVector)
x
```

```
x <- testGenerator$returnProposalMatrix(testMatrix)
boxplot(x)

##Changing the covariance
testGenerator$covariance = diag(rep(100,4))
testGenerator <- testGenerator$updateProposalGenerator(testGenerator, message = TRUE)

testGenerator$returnProposal(testVector)
x <- testGenerator$returnProposalMatrix(testMatrix)
boxplot(x)


##-Changing the gibbs probabilities / probability to modify 1-n parameters

testGenerator$gibbsProbabilities = c(1,1,0,0)
testGenerator <- testGenerator$updateProposalGenerator(testGenerator)

testGenerator$returnProposal(testVector)
x <- testGenerator$returnProposalMatrix(testMatrix)
boxplot(x)


##-Changing the gibbs weights / probability to pick each parameter

testGenerator$gibbsWeights = c(0.3,0.3,0.3,100)
testGenerator <- testGenerator$updateProposalGenerator(testGenerator)

testGenerator$returnProposal(testVector)
x <- testGenerator$returnProposalMatrix(testMatrix)
boxplot(x)


##-Adding another function

otherFunction <- function(x) sample.int(10,1)

testGenerator <- createProposalGenerator(
  covariance = c(1,1,1),
  otherDistribution = otherFunction,
  otherDistributionLocation = c(0,0,0,1),
  otherDistributionScaled = TRUE
)

testGenerator$returnProposal(testVector)
x <- testGenerator$returnProposalMatrix(testMatrix)
boxplot(x)
table(x[,4])
```

`createSmcSamplerList` *Convenience function to create an object of class SMCSamplerList from a list of mcmc samplers*

Description

Convenience function to create an object of class SMCSamplerList from a list of mcmc samplers

Usage

```
createSmcSamplerList(...)
```

Arguments

...	a list of MCMC samplers

Value

a list of class smcSamplerList with each object being an smcSampler

Author(s)

Florian Hartig

`createTruncatedNormalPrior` *Convenience function to create a truncated normal prior*

Description

Convenience function to create a truncated normal prior

Usage

```
createTruncatedNormalPrior(mean, sd, lower, upper)
```

Arguments

`mean`	best estimate for each parameter
`sd`	sdandard deviation
`lower`	vector of lower prior range for all parameters
`upper`	vector of upper prior range for all parameters

Note

for details see `createPrior`

Author(s)

Florian Hartig

See Also

createPriorDensity
createPrior
createBetaPrior
createUniformPrior
createBayesianSetup

Examples

```
# The BT package includes a number of convenience functions to specify
# prior distributions, including createUniformPrior, createTruncatedNormalPrior
# etc. If you want to specify a prior that corresponds to one of these
# distributions, you should use these functions, e.g.:

prior <- createUniformPrior(lower = c(0,0), upper = c(0.4,5))

prior$density(c(2, 3)) # outside of limits -> -Inf
prior$density(c(0.2, 2)) # within limits, -0.6931472

# All default priors include a sampling function, i.e. you can create
# samples from the prior via
prior$sampler()
# [1] 0.2291413 4.5410389

# if you want to specify a prior that does not have a default function,
# you should use the createPrior function, which expects a density and
# optionally a sampler function:

density = function(par){
  d1 = dunif(par[1], -2,6, log =TRUE)
  d2 = dnorm(par[2], mean= 2, sd = 3, log =TRUE)
  return(d1 + d2)
}

sampler = function(n=1){
  d1 = runif(n, -2,6)
  d2 = rnorm(n, mean= 2, sd = 3)
  return(cbind(d1,d2))
}

prior <- createPrior(density = density, sampler = sampler,
                     lower = c(-10,-20), upper = c(10,20), best = NULL)

# note that the createPrior supports additional truncation


# To use a prior in an MCMC, include it in a BayesianSetup

set.seed(123)
ll <- function(x) sum(dnorm(x, log = TRUE)) # multivariate normal ll
bayesianSetup <- createBayesianSetup(likelihood = ll, prior = prior)
```

```
settings = list(iterations = 100)
out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)

# use createPriorDensity to create a new (estimated) prior from MCMC output

newPrior = createPriorDensity(out, method = "multivariate",
                              eps = 1e-10, lower = c(-10,-20),
                              upper = c(10,20), best = NULL, scaling = 0.5)
```

`createUniformPrior` *Convenience function to create a simple uniform prior distribution*

Description

Convenience function to create a simple uniform prior distribution

Usage

```
createUniformPrior(lower, upper, best = NULL)
```

Arguments

`lower`	vector of lower prior range for all parameters
`upper`	vector of upper prior range for all parameters
`best`	vector with "best" values for all parameters

Note

for details see `createPrior`

Author(s)

Florian Hartig

See Also

`createPriorDensity`, `createPrior`, `createBetaPrior`, `createTruncatedNormalPrior`, `createBayesianSetup`

Examples

```
# The BT package includes a number of convenience functions to specify
# prior distributions, including createUniformPrior, createTruncatedNormalPrior
# etc. If you want to specify a prior that corresponds to one of these
# distributions, you should use these functions, e.g.:

prior <- createUniformPrior(lower = c(0,0), upper = c(0.4,5))
```

```
prior$density(c(2, 3)) # outside of limits -> -Inf
prior$density(c(0.2, 2)) # within limits, -0.6931472

# All default priors include a sampling function, i.e. you can create
# samples from the prior via
prior$sampler()
# [1] 0.2291413 4.5410389

# if you want to specify a prior that does not have a default function,
# you should use the createPrior function, which expects a density and
# optionally a sampler function:

density = function(par){
  d1 = dunif(par[1], -2,6, log =TRUE)
  d2 = dnorm(par[2], mean= 2, sd = 3, log =TRUE)
  return(d1 + d2)
}

sampler = function(n=1){
  d1 = runif(n, -2,6)
  d2 = rnorm(n, mean= 2, sd = 3)
  return(cbind(d1,d2))
}

prior <- createPrior(density = density, sampler = sampler,
                     lower = c(-10,-20), upper = c(10,20), best = NULL)

# note that the createPrior supports additional truncation


# To use a prior in an MCMC, include it in a BayesianSetup

set.seed(123)
ll <- function(x) sum(dnorm(x, log = TRUE)) # multivariate normal ll
bayesianSetup <- createBayesianSetup(likelihood = ll, prior = prior)

settings = list(iterations = 100)
out <- runMCMC(bayesianSetup = bayesianSetup, settings = settings)

# use createPriorDensity to create a new (estimated) prior from MCMC output

newPrior = createPriorDensity(out, method = "multivariate",
                              eps = 1e-10, lower = c(-10,-20),
                              upper = c(10,20), best = NULL, scaling = 0.5)
```

DE *Differential-Evolution MCMC*

Description

Differential-Evolution MCMC

Usage

```
DE(
  bayesianSetup,
 settings = list(startValue = NULL, iterations = 10000, f = -2.38, burnin = 0, thin = 1,
  eps = 0, consoleUpdates = 100, blockUpdate = list("none", k = NULL, h = NULL, pSel =
  NULL, pGroup = NULL, groupStart = 1000, groupIntervall = 1000), currentChain = 1,
   message = TRUE)
)
```

Arguments

bayesianSetup	a BayesianSetup with the posterior density function to be sampled from
settings	list with parameter settings
startValue	(optional) eiter a matrix with start population, a number to define the number of chains that are run or a function that samples a starting population.
iterations	number of function evaluations.
burnin	number of iterations treated as burn-in. These iterations are not recorded in the chain.
thin	thinning parameter. Determines the interval in which values are recorded.
f	scaling factor gamma
eps	small number to avoid singularity
blockUpdate	list determining whether parameters should be updated in blocks. For possible settings see Details.
message	logical determines whether the sampler's progress should be printed

Details

For blockUpdate the first element in the list determines the type of blocking. Possible choices are

- "none" (default), no blocking of parameters
- "correlation" blocking based on correlation of parameters. Using h or k (see below)
- "random" random blocking. Using k (see below)
- "user" user defined groups. Using groups (see below)

Further seven parameters can be specified. "k" determnined the number of groups, "h" the strength of the correlation used to group parameter and "groups" is used for user defined groups. "groups" is a vector containing the group number for each parameter. E.g. for three parameters with the first two in one group, "groups" would be c(1,1,2). Further pSel and pGroup can be used to influence the choice of groups. In the sampling process a number of groups is randomly drawn and updated. pSel is a vector containing relative probabilities for an update of the respective number of groups. E.g. for always updating only one group pSel = 1. For updating one or two groups with the same probability pSel = c(1,1). By default all numbers have the same probability. The same principle is used in pGroup. Here the user can influence the probability of each group to be updated. By default all groups have the same probability. Finally "groupStart" defines the starting point of the groupUpdate and "groupIntervall" the intervall in which the groups are evaluated.

Author(s)

Francesco Minunno and Stefan Paul

References

Braak, Cajo JF Ter. "A Markov Chain Monte Carlo version of the genetic algorithm Differential Evolution: easy Bayesian computing for real parameter spaces." Statistics and Computing 16.3 (2006): 239-249.

See Also

DEzs

Examples

```
library(BayesianTools)

ll <- generateTestDensityMultiNormal(sigma = "no correlation")
bayesianSetup <- createBayesianSetup(likelihood = ll,
                                     lower = rep(-10, 3),
                                     upper = rep(10, 3))

settings = list(iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# DE family samplers are population MCMCs that run a number of internal chains
# in parallel. Here examples how to change the internal chains
# note that internal chains can be executedi n parallel
settings = list(startValue = 4, iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# Modify the start values of the internal chains (note that this is a matrix
# of dim nChain * nPar)
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# In the DE sampler family with Z matrix, the previous chains are written in
# a common matrix, from which proposals are generated. Per default this matrix
# is started with samples from the prior, but we can change this. Often useful
# to improve sampler convergence,
# see  https://github.com/florianhartig/BayesianTools/issues/79
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                Z = matrix(rnorm(300), nrow = 100, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)
```

DEzs *Differential-Evolution MCMC zs*

Description

Differential-Evolution MCMC zs

Usage

```
DEzs(
  bayesianSetup,
 settings = list(iterations = 10000, Z = NULL, startValue = NULL, pSnooker = 0.1, burnin
   = 0, thin = 1, f = 2.38, eps = 0, parallel = NULL, pGamma1 = 0.1, eps.mult = 0.2,
    eps.add = 0, consoleUpdates = 100, zUpdateFrequency = 1, currentChain = 1,
  blockUpdate = list("none", k = NULL, h = NULL, pSel = NULL, pGroup = NULL, groupStart
    = 1000, groupIntervall = 1000), message = TRUE)
)
```

Arguments

bayesianSetup	a BayesianSetup with the posterior density function to be sampled from
settings	list with parameter settings
startValue	(optional) eiter a matrix with start population, a number to define the number of chains that are run or a function that samples a starting population.
Z	starting Z population
iterations	iterations to run
pSnooker	probability of Snooker update
burnin	number of iterations treated as burn-in. These iterations are not recorded in the chain.
thin	thinning parameter. Determines the interval in which values are recorded.
eps	small number to avoid singularity
f	scaling factor for gamma
parallel	logical, determines weather parallel computing should be attempted (see details)
pGamma1	probability determining the frequency with which the scaling is set to 1 (allows jumps between modes)
eps.mult	random term (multiplicative error)
eps.add	random term
blockUpdate	list determining whether parameters should be updated in blocks. For possible settings see Details.
message	logical determines whether the sampler's progress should be printed

Details

For parallel computing, the likelihood density in the bayesianSetup needs to be parallelized, i.e. needs to be able to operate on a matrix of proposals

For blockUpdate the first element in the list determines the type of blocking. Possible choices are

- "none" (default), no blocking of parameters
- "correlation" blocking based on correlation of parameters. Using h or k (see below)
- "random" random blocking. Using k (see below)
- "user" user defined groups. Using groups (see below)

Further seven parameters can be specified. "k" determnined the number of groups, "h" the strength of the correlation used to group parameter and "groups" is used for user defined groups. "groups" is a vector containing the group number for each parameter. E.g. for three parameters with the first two in one group, "groups" would be c(1,1,2). Further pSel and pGroup can be used to influence the choice of groups. In the sampling process a number of groups is randomly drawn and updated. pSel is a vector containing relative probabilities for an update of the respective number of groups. E.g. for always updating only one group pSel = 1. For updating one or two groups with the same probability pSel = c(1,1). By default all numbers have the same probability. The same principle is used in pGroup. Here the user can influence the probability of each group to be updated. By default all groups have the same probability. Finally "groupStart" defines the starting point of the groupUpdate and "groupIntervall" the intervall in which the groups are evaluated.

Author(s)

Francesco Minunno and Stefan Paul

References

ter Braak C. J. F., and Vrugt J. A. (2008). Differential Evolution Markov Chain with snooker updater and fewer chains. Statistics and Computing http://dx.doi.org/10.1007/s11222-008-9104-9

See Also

DE

Examples

```
library(BayesianTools)

ll <- generateTestDensityMultiNormal(sigma = "no correlation")
bayesianSetup <- createBayesianSetup(likelihood = ll,
                                     lower = rep(-10, 3),
                                     upper = rep(10, 3))

settings = list(iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# DE family samplers are population MCMCs that run a number of internal chains
```

```
# in parallel. Here examples how to change the internal chains
# note that internal chains can be executedi n parallel
settings = list(startValue = 4, iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# Modify the start values of the internal chains (note that this is a matrix
# of dim nChain * nPar)
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# In the DE sampler family with Z matrix, the previous chains are written in
# a common matrix, from which proposals are generated. Per default this matrix
# is started with samples from the prior, but we can change this. Often useful
# to improve sampler convergence,
# see  https://github.com/florianhartig/BayesianTools/issues/79
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                Z = matrix(rnorm(300), nrow = 100, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)
```

`DIC` *Deviance information criterion*

Description

Deviance information criterion

Usage

```
DIC(sampler, ...)
```

Arguments

`sampler`	An object of class bayesianOutput (mcmcSampler, smcSampler, or mcmcList)
`...`	further arguments passed to `getSample`

Details

Output: list with the following elements:
DIC : Deviance Information Criterion
IC : Bayesian Predictive Information Criterion
pD : Effective number of parameters (pD = Dbar - Dhat)
pV : Effective number of parameters (pV = var(D)/2)

Dbar : Expected value of the deviance over the posterior
Dhat : Deviance at the mean posterior estimate

Author(s)

Florian Hartig

References

Spiegelhalter, D. J.; Best, N. G.; Carlin, B. P. & van der Linde, A. (2002) Bayesian measures of model complexity and fit. J. Roy. Stat. Soc. B, 64, 583-639.

Gelman, A.; Hwang, J. & Vehtari, A. (2014) Understanding predictive information criteria for Bayesian models. Statistics and Computing, Springer US, 24, 997-1016-.

See Also

WAIC, MAP, marginalLikelihood

DREAM *DREAM*

Description

DREAM

Usage

```
DREAM(
  bayesianSetup,
 settings = list(iterations = 10000, nCR = 3, gamma = NULL, eps = 0, e = 0.05, pCRupdate
  = TRUE, updateInterval = 10, burnin = 0, thin = 1, adaptation = 0.2, parallel = NULL,
  DEpairs = 2, consoleUpdates = 10, startValue = NULL, currentChain = 1, message =
   TRUE)
)
```

Arguments

bayesianSetup	Object of class 'bayesianSetup' or 'bayesianOuput'.
settings	list with parameter values
iterations	Number of model evaluations
nCR	parameter determining the number of cross-over proposals. If nCR = 1 all parameters are updated jointly.
updateInterval	determining the intervall for the pCR update
gamma	Kurtosis parameter Bayesian Inference Scheme

eps	Ergodicity term
e	Ergodicity term
pCRupdate	If T, crossover probabilities will be updated
burnin	number of iterations treated as burn-in. These iterations are not recorded in the chain.
thin	thin thinning parameter. Determines the interval in which values are recorded.
adaptation	Number or percentage of samples that are used for the adaptation in DREAM (see Details).
DEpairs	Number of pairs used to generate proposal
startValue	eiter a matrix containing the start values (see details), an integer to define the number of chains that are run, a function to sample the start values or NUll, in which case the values are sampled from the prior.
consoleUpdates	Intervall in which the sampling progress is printed to the console
message	logical determines whether the sampler's progress should be printed

Details

Insted of a bayesianSetup, the function can take the output of a previous run to restart the sampler from the last iteration. Due to the sampler's internal structure you can only use the output of DREAM. If you provide a matrix with start values the number of rows determines the number of chains that are run. The number of coloumns must be equivalent to the number of parameters in your bayesianSetup.

There are several small differences in the algorithm presented here compared to the original paper by Vrugt et al. (2009). Mainly the algorithm implemented here does not have an automatic stopping criterion. Hence, it will always run the number of iterations specified by the user. Also, convergence is not monitored and left to the user. This can easily be done with coda::gelman.diag(chain). Further the proposed delayed rejectio step in Vrugt et al. (2009) is not implemented here.

During the adaptation phase DREAM is running two mechanisms to enhance the sampler's efficiency. First the disribution of crossover values is tuned to favor large jumps in the parameter space. The crossover probabilities determine how many parameters are updated simultaneously. Second outlier chains are replanced as they can largely deteriorate the sampler's performance. However, these steps destroy the detailed balance of the chain. Consequently these parts of the chain should be discarded when summarizing posterior moments. This can be done automatically during the sampling process (i.e. burnin > adaptation) or subsequently by the user. We chose to distinguish between the burnin and adaptation phase to allow the user more flexibility in the sampler's settings.

Value

mcmc.object containing the following elements: chains, X, pCR

Author(s)

Stefan Paul

References

Vrugt, Jasper A., et al. "Accelerating Markov chain Monte Carlo simulation by differential evolution with self-adaptive randomized subspace sampling." International Journal of Nonlinear Sciences and Numerical Simulation 10.3 (2009): 273-290.

See Also

DREAMzs

Examples

```
library(BayesianTools)

ll <- generateTestDensityMultiNormal(sigma = "no correlation")
bayesianSetup <- createBayesianSetup(likelihood = ll,
                                     lower = rep(-10, 3),
                                     upper = rep(10, 3))

settings = list(iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# DE family samplers are population MCMCs that run a number of internal chains
# in parallel. Here examples how to change the internal chains
# note that internal chains can be executedi n parallel
settings = list(startValue = 4, iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# Modify the start values of the internal chains (note that this is a matrix
# of dim nChain * nPar)
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# In the DE sampler family with Z matrix, the previous chains are written in
# a common matrix, from which proposals are generated. Per default this matrix
# is started with samples from the prior, but we can change this. Often useful
# to improve sampler convergence,
# see  https://github.com/florianhartig/BayesianTools/issues/79
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                Z = matrix(rnorm(300), nrow = 100, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)
```

DREAMzs *DREAMzs*

Description

DREAMzs

Usage

```
DREAMzs(
  bayesianSetup,
 settings = list(iterations = 10000, nCR = 3, gamma = NULL, eps = 0, e = 0.05, pCRupdate
   = FALSE, updateInterval = 10, burnin = 0, thin = 1, adaptation = 0.2, parallel =
   NULL, Z = NULL, ZupdateFrequency = 10, pSnooker = 0.1, DEpairs = 2, consoleUpdates =
    10, startValue = NULL, currentChain = 1, message = FALSE)
)
```

Arguments

bayesianSetup	Object of class 'bayesianSetup' or 'bayesianOuput'.
settings	list with parameter values
iterations	Number of model evaluations
nCR	parameter determining the number of cross-over proposals. If nCR = 1 all parameters are updated jointly.
updateInterval	determining the intervall for the pCR (crossover probabilities) update
gamma	Kurtosis parameter Bayesian Inference Scheme.
eps	Ergodicity term
e	Ergodicity term
pCRupdate	Update of crossover probabilities
burnin	number of iterations treated as burn-in. These iterations are not recorded in the chain.
thin	thin thinning parameter. Determines the interval in which values are recorded.
adaptation	Number or percentage of samples that are used for the adaptation in DREAM (see Details)
DEpairs	Number of pairs used to generate proposal
ZupdateFrequency	frequency to update Z matrix
pSnooker	probability of snooker update
Z	starting matrix for Z
startValue	eiter a matrix containing the start values (see details), an integer to define the number of chains that are run, a function to sample the start values or NUll, in which case the values are sampled from the prior.
consoleUpdates	Intervall in which the sampling progress is printed to the console
message	logical determines whether the sampler's progress should be printed

Details

Insted of a bayesianSetup, the function can take the output of a previous run to restart the sampler from the last iteration. Due to the sampler's internal structure you can only use the output of DREAMzs. If you provide a matrix with start values the number of rows detemines the number of chains that are run. The number of coloumns must be equivalent to the number of parameters in your bayesianSetup.

There are several small differences in the algorithm presented here compared to the original paper by Vrugt et al. (2009). Mainly the algorithm implemented here does not have an automatic stopping criterion. Hence, it will always run the number of iterations specified by the user. Also, convergence is not monitored and left to the user. This can easily be done with coda::gelman.diag(chain). Further the proposed delayed rejectio step in Vrugt et al. (2009) is not implemented here.

During the adaptation phase DREAM is running two mechanisms to enhance the sampler's efficiency. First the disribution of crossover values is tuned to favor large jumps in the parameter space. The crossover probabilities determine how many parameters are updated simultaneously. Second outlier chains are replanced as they can largely deteriorate the sampler's performance. However, these steps destroy the detailed balance of the chain. Consequently these parts of the chain should be discarded when summarizing posterior moments. This can be done automatically during the sampling process (i.e. burnin > adaptation) or subsequently by the user. We chose to distinguish between the burnin and adaptation phase to allow the user more flexibility in the sampler's settings.

Value

mcmc.object containing the following elements: chains, X, pCR, Z

Author(s)

Stefan Paul

References

Vrugt, Jasper A., et al. "Accelerating Markov chain Monte Carlo simulation by differential evolution with self-adaptive randomized subspace sampling." International Journal of Nonlinear Sciences and Numerical Simulation 10.3 (2009): 273-290.

ter Braak C. J. F., and Vrugt J. A. (2008). Differential Evolution Markov Chain with snooker updater and fewer chains. Statistics and Computing http://dx.doi.org/10.1007/s11222-008-9104-9

See Also

DREAM

Examples

```
library(BayesianTools)

ll <- generateTestDensityMultiNormal(sigma = "no correlation")
bayesianSetup <- createBayesianSetup(likelihood = ll,
                                     lower = rep(-10, 3),
```

```
                                    upper = rep(10, 3))

settings = list(iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# DE family samplers are population MCMCs that run a number of internal chains
# in parallel. Here examples how to change the internal chains
# note that internal chains can be executedi n parallel
settings = list(startValue = 4, iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# Modify the start values of the internal chains (note that this is a matrix
# of dim nChain * nPar)
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)

# In the DE sampler family with Z matrix, the previous chains are written in
# a common matrix, from which proposals are generated. Per default this matrix
# is started with samples from the prior, but we can change this. Often useful
# to improve sampler convergence,
# see  https://github.com/florianhartig/BayesianTools/issues/79
settings = list(startValue = matrix(rnorm(12), nrow = 4, ncol = 3),
                Z = matrix(rnorm(300), nrow = 100, ncol = 3),
                iterations = 200)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)
summary(out)
```

`gelmanDiagnostics` *Gelman Diagnostics*

Description

Runs Gelman Diagnotics for an object of class BayesianOutput

Usage

```
gelmanDiagnostics(sampler, thin = "auto", plot = F, ...)
```

Arguments

`sampler`	an object of class mcmcSampler or mcmcSamplerList
`thin`	parameter determining the thinning intervall. Either an integer or "auto" (default) for automatic thinning.
`plot`	should a Gelman plot be generated
`...`	further arguments passed to `getSample`

Details

The function calls coda::gelman.diag to calculate Gelman-Rubin diagnostics coda::gelman.plot to produce the plots.

The idea of these diagnostics is to compare withing and between chain variance of several independent MCMC runs (Gelman & Rubin, 1992). The ratio of the 2 is called the potential scale reduction factor (psfr, also called Rhat). If psfr = 1, this suggest that the independent MCMC runs are essentially identical, and which in turn suggests that they have converged. In practice, values < 1.05, or sometimes < 1.1 for all parameters are considered acceptable.

To obtain reliable Gelman-Rubin diagnostics, the independent MCMCs should be started at different points of the parameter space, ideally overdispersed.

The diagnostics also calculate a multivariate version of the psrf (mpsrf, Brooks & Gelman 1998). In practice, values < 1.1 or < 1.2 are often considered acceptable. While useful as an overview, mpsrf < 1.1 does not necessarily mean that all individual psrf < 1.05, and thus I would in doubt recommend looking at the individual psrf and decide on a case-by-case basis if a lack of convergence for a particular parameter is a concern.

Also, note that convergence is a continuum, and different aspects of a posterior estimation converge with different speed. The rules about 1.05 were obtained by looking at the error of the posterior median / mean. If the goal for the inference is a posterior quantity that is more unstable than the mean, for example tail probabilities or the DIC, one should try to obtain large posterior samples with smaller psrf values.

Note on the use of Gelman diagnostics for population MCMCs, in particular the DE sampler family: the Gelman diagnostics were originally designed for being applied to the outcome of several independent MCMC runs. Technically and practically, it can also be applied to a single population MCMC run that has several internal chains, such as DE, DEzs, DREAM, DREAMzs or T-Walk. As argued in ter Braak et al. (2008), the internal chains should be independent after burn-in. While this is likely correct, it also means that they are not completely independent before, and we observed this behavior in the use of the algorithms (i.e. that internal DEzs chains are more similar to each other than the chains of independent DEzs algorithms), see for example BT issue 226. A concern is that this non-independence could lead to a failure to detect that the sampler hasn't converged yet, due to a wrong burn-in. We would therefore recommend to run several DEzs and check convergence with those, instead of running only one.

Author(s)

Florian Hartig

References

Gelman, A and Rubin, DB (1992) Inference from iterative simulation using multiple sequences, Statistical Science, 7, 457-511.

Brooks, SP. and Gelman, A. (1998) General methods for monitoring convergence of iterative simulations. Journal of Computational and Graphical Statistics, 7, 434-455.

ter Braak, Cajo JF, and Jasper A. Vrugt. "Differential evolution Markov chain with snooker updater and fewer chains." Statistics and Computing 18.4 (2008): 435-446.

`generateParallelExecuter` *Factory to generate a parallel executor of an existing function*

Description

Factory to generate a parallel executor of an existing function

Usage

```
generateParallelExecuter(
  fun,
  parallel = F,
  parallelOptions = list(variables = "all", packages = "all", dlls = NULL)
)
```

Arguments

`fun`	function to be changed to parallel execution
`parallel`	should a parallel R cluster be used? If set to T, the operating system will automatically detect the available cores and n-1 of the available n cores will be used. Alternatively, you can manually set the number of cores to be used
`parallelOptions`	a list containing three lists. • First, "packages": determines the R packages required to run the likelihood function. • Second, "variables": the objects in the global environment needed to run the likelihood function. • Third, "dlls": the DLLs needed to run the likelihood function (see Details).

Details

For parallelization, if option T is selected, an automatic parallelization is tried via R. Alternatively, "external" can be selected on the assumption that the likelihood has already been parallelized. In the latter case, a matrix with parameters as columns must be accepted. You can also specify which packages, objects and DLLs are exported to the cluster. By default, a copy of your workspace is exported, but depending on your workspace, this can be inefficient. As an alternative, you can specify the environments and packages in the likelihood function (e.g. BayesianTools::VSEM() instead of VSEM()).

Note

can be used to make functions compatible with library sensitivity

Author(s)

Florian Hartig

Examples

```
testDensityMultiNormal <- generateTestDensityMultiNormal()


parDen <- generateParallelExecuter(testDensityMultiNormal)$parallelFun
x = matrix(runif(9,0,1), nrow = 3)
parDen(x)
```

`generateTestDensityMultiNormal` *Multivariate normal likelihood*

Description

Generates a 3 dimensional multivariate normal likelihood function.

Usage

```
generateTestDensityMultiNormal(
  mean = c(0, 0, 0),
  sigma = "strongcorrelation",
  sample = F,
  n = 1,
  throwErrors = -1
)
```

Arguments

`mean`	vector with the three mean values of the distribution
`sigma`	either a correlation matrix, or "strongcorrelation", or "no correlation"
`sample`	should the function create samples
`n`	number of samples to create
`throwErrors`	parameter for test purpose. Between 0 and 1 for proportion of errors

Details

3-d multivariate normal density function with mean 2,4,0 and either strong correlation (default), or no correlation.

Author(s)

Florian Hartig

See Also

`testDensityBanana`
`testLinearModel`

Examples

```
# sampling from the test function
x = generateTestDensityMultiNormal(sample  = TRUE, n = 1000)(1000)
correlationPlot(x)
marginalPlot(x)

# generating the the density
density = generateTestDensityMultiNormal(sample  = FALSE)
density(x[1,])
```

---

getCredibleIntervals *Calculate confidence region from an MCMC or similar sample*

Description

Calculate confidence region from an MCMC or similar sample

Usage

```
getCredibleIntervals(sampleMatrix, quantiles = c(0.025, 0.975))
```

Arguments

sampleMatrix	matrix of outcomes. Could be parameters or predictions
quantiles	quantiles to be calculated

Author(s)

Florian Hartig

See Also

getPredictiveDistribution
getPredictiveIntervals

getDharmaResiduals *Creates a DHARMa object*

Description

Creates a DHARMa object

Usage

```
getDharmaResiduals(model, parMatrix, numSamples, observed, error, plot = TRUE)
```

Arguments

model	function that calculates model predictions for a given parameter vector
parMatrix	a parameter matrix from which the simulations will be generated
numSamples	the number of samples
observed	a vector of observed values
error	function with signature f(mean, par) that generates error expectations from mean model predictions. Par is a vector from the matrix with the parameter samples (full length). f needs to know which of these parameters are parameters of the error function
plot	logical, determining whether the simulated residuals should be plotted

Author(s)

Tankred Ott

getPanels *getPanels*

Description

Calculates the argument x for par(mfrow = x) for a desired number of panels

Usage

```
getPanels(x)
```

Arguments

x	the desired number of panels

Author(s)

Florian Hartig

`getPossibleSamplerTypes` *Returns possible sampler types*

Description

Returns possible sampler types

Usage

```
getPossibleSamplerTypes()
```

Author(s)

Florian Hartig

`getPredictiveDistribution` *Calculates predictive distribution based on the parameters*

Description

Calculates predictive distribution based on the parameters

Usage

```
getPredictiveDistribution(parMatrix, model, numSamples = 1000)
```

Arguments

`parMatrix`	matrix of parameter values
`model`	model / function to calculate predictions. Outcome should be a vector
`numSamples`	number of samples to be drawn

Details

If numSamples is greater than the number of rows in parMatrix, or NULL, or FALSE, or less than 1 all samples in parMatrix will be used.

Author(s)

Florian Hartig

See Also

`getPredictiveIntervals`
`getCredibleIntervals`

getPredictiveIntervals *Calculates Bayesian credible (confidence) and predictive intervals based on parameter sample*

Description

Calculates Bayesian credible (confidence) and predictive intervals based on parameter sample

Usage

```
getPredictiveIntervals(
  parMatrix,
  model,
  numSamples = 1000,
  quantiles = c(0.025, 0.975),
  error = NULL
)
```

Arguments

parMatrix	matrix of parameter values
model	model / function to calculate predictions. Outcome should be a vector
numSamples	number of samples to be drawn
quantiles	quantiles to calculate
error	function with signature f(mean, par) that generates error expectations from mean model predictions. Par is a vector from the matrix with the parameter samples (full length). f needs to know which of these parameters are parameters of the error function. If supplied, will calculate also predictive intervals additional to credible intervals

Details

If numSamples is greater than the number of rows in parMatrix, or NULL, or FALSE, or less than 1 all samples in parMatrix will be used.

Author(s)

Florian Hartig

See Also

getPredictiveDistribution
getCredibleIntervals

getSample *Extracts the sample from a bayesianOutput*

Description

Extracts the sample from a bayesianOutput

Usage

```
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = 1,
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = FALSE,
  ...
)

## S3 method for class 'matrix'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'double'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
```

```
  ...
)

## S3 method for class 'integer'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'data.frame'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'list'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'mcmc'
getSample(
  sampler,
```

```
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'mcmc.list'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'MCMC'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)

## S3 method for class 'MCMC_refClass'
getSample(
  sampler,
  parametersOnly = T,
  coda = F,
  start = 1,
  end = NULL,
  thin = "auto",
  numSamples = NULL,
```

```
  whichParameters = NULL,
  reportDiagnostics = F,
  ...
)
```

Arguments

sampler	an object of class mcmcSampler, mcmcSamplerList, smcSampler, smcSamplerList, mcmc, mcmc.list, double, numeric
parametersOnly	for a BT output, if F, likelihood, posterior and prior values are also provided in the output
coda	works only for mcmc classes - provides output as a coda object. Note: if mcmcSamplerList contains mcmc samplers such as DE that have several chains, the internal chains will be collapsed. This may not be the desired behavior for all applications.
start	for mcmc samplers start value in the chain. For SMC samplers, start particle
end	for mcmc samplers end value in the chain. For SMC samplers, end particle
thin	thinning parameter. Either an integer determining the thinning intervall (default is 1) or "auto" for automatic thinning.
numSamples	sample size (only used if thin = 1). If you want to use numSamples set thin to 1.
whichParameters	possibility to select parameters by index
reportDiagnostics	logical, determines whether settings should be included in the output
...	further arguments

Details

If thin is greater than the total number of samples in the sampler object the first and the last element (of each chain if a sampler with multiples chains is used) are sampled. If numSamples is greater than the total number of samples all samples are selected. In both cases a warning is displayed.

If thin and numSamples is passed, the function will use the thin argument if it is valid and greater than 1, else numSamples will be used.

Author(s)

Florian Hartig

Tankred Ott

Examples

```
ll = function(x) sum(dnorm(x, log = TRUE))

setup = createBayesianSetup(ll, lower = c(-10,-10), upper = c(10,10))

settings = list(nrChains = 2, iterations = 1000)
out <- runMCMC(bayesianSetup = setup, sampler = "DEzs", settings = settings)
```

```
# population MCMCs divide the interations by the number of internal chains,
# so the end of the 3 chains is 1000/3 = 334
sample <- getSample(out, start = 100, end = 334, thin = 10)

# sampling with number of samples instead of thinning and
# returning a coda object
sample <- getSample(out, start = 100, numSamples = 60, coda = TRUE)
plot(sample)


# MCMC with a single chain:
settings_2 <- list(nrChains = 1, iterations = 1000)
out_2 <- runMCMC(setup, sampler = "Metropolis", settings = settings_2)
sample_2 <- getSample(out_2, numSamples = 100)
```

`getVolume` *Calculate posterior volume*

Description

Calculate posterior volume

Usage

```
getVolume(sampler, prior = F, method = "MVN", ...)
```

Arguments

`sampler`	an object of superclass bayesianOutput or any other class that has the getSample function implemented (e.g. Matrix)
`prior`	schould also prior volume be calculated
`method`	method for volume estimation. Currently, the only option is "MVN"
`...`	additional parameters to pass on to the `getSample`

Details

The idea of this function is to provide an estimate of the "posterior volume", i.e. how "broad" the posterior is. One potential application is to the overall reduction of parametric uncertainty between different data types, or between prior and posterior.

Implemented methods for volume estimation:

Option "MVN" - in this option, the volume is calculated as the determinant of the covariance matrix of the prior / posterior sample.

Author(s)

Florian Hartig

Examples

```
bayesianSetup = createBayesianSetup(
  likelihood = generateTestDensityMultiNormal(sigma = "no correlation"),
  lower = rep(-10, 3), upper = rep(10, 3))

out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "Metropolis",
               settings = list(iterations = 2000, message = FALSE))

getVolume(out, prior = TRUE)

bayesianSetup = createBayesianSetup(
  likelihood = generateTestDensityMultiNormal(sigma = "strongcorrelation"),
  lower = rep(-10, 3), upper = rep(10, 3))

out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "Metropolis",
               settings = list(iterations = 2000, message = FALSE))

getVolume(out, prior = TRUE)
```

GOF *Standard GOF metrics Startvalues for sampling with nrChains > 1 : if you want to provide different start values for the different chains, provide a list*

Description

Standard GOF metrics Startvalues for sampling with nrChains > 1 : if you want to provide different start values for the different chains, provide a list

Usage

```
GOF(observed, predicted, plot = F, centered = T)
```

Arguments

observed	observed values
predicted	predicted values
plot	should a plot be created
centered	if T, variables are centered to the mean of the observations, i.e. the intercept is for the mean value of the observation

Details

The function considers observed ~ predicted and calculates

1. rmse = root mean squared error

2. mae = mean absolute errorr
3. a linear regression with slope, intercept and coefficient of determination R2

For the linear regression, centered = T means that variables will be centered around the mean value of the observation. This setting avoids a correlation between slope and intercept (that the intercept is != 0 as soon as the slope is !=0)

Value

A list with the following entries: rmse = root mean squared error, mae = mean absolute error, slope = slope of regression, offset = intercept of regression, R2 = R2 of regression

Note

In principle, it is possible to plot observed ~ predicted and predicted ~ observed. However, if we assume that the error is mainly on the y axis (observations), i.e. that observations scatter around the true (ideal) value, we should plot observed ~ predicted. See Pineiro et al. (2008). How to evaluate models: observed vs. predicted or predicted vs. observed?. Ecological Modelling, 216(3-4), 316-322.

Author(s)

Florian Hartig

Examples

```
x = runif(500,-1,1)
y = 0.2 + 0.9  *x + rnorm(500, sd = 0.5)

summary(lm(y ~ x))

GOF(x,y)

GOF(x,y, plot = TRUE)
```

---

likelihoodAR1 *AR1 type likelihood function*

Description

AR1 type likelihood function

Usage

```
likelihoodAR1(predicted, observed, sd, a)
```

Arguments

predicted	vector of predicted values
observed	vector of observed values
sd	standard deviation of the iid normal likelihood
a	temporal correlation in the AR1 model

Note

The AR1 model considers the process:
y(t) = a y(t-1) + E
e = i.i.d. N(0,sd)
|a| < 1
At the moment, no NAs are allowed in the time series.

Author(s)

Florian Hartig

---

likelihoodIidNormal *Normal / Gaussian Likelihood function*

Description

Normal / Gaussian Likelihood function

Usage

```
likelihoodIidNormal(predicted, observed, sd)
```

Arguments

predicted	vector of predicted values
observed	vector of observed values
sd	standard deviation of the i.i.d. normal likelihood

Author(s)

Florian Hartig

MAP *calculates the Maxiumum APosteriori value (MAP)*

Description

calculates the Maxiumum APosteriori value (MAP)

Usage

```
MAP(bayesianOutput, ...)
```

Arguments

bayesianOutput	an object of class BayesianOutput (mcmcSampler, smcSampler, or mcmcList)
...	optional values to be passed on the the getSample function

Details

Currently, this function simply returns the parameter combination with the highest posterior in the chain. A more refined option would be to take the MCMC sample and do additional calculations, e.g. use an optimizer, a kerne delnsity estimator, or some other tool to search / interpolate around the best value in the chain

Author(s)

Florian Hartig

See Also

WAIC, DIC, marginalLikelihood

marginalLikelihood *Calcluated the marginal likelihood from a set of MCMC samples*

Description

Calcluated the marginal likelihood from a set of MCMC samples

Usage

```
marginalLikelihood(sampler, numSamples = 1000, method = "Chib", ...)
```

Arguments

sampler	an MCMC or SMC sampler or list, or for method "Prior" also a BayesianSetup
numSamples	number of samples to use. How this works, and if it requires recalculating the likelihood, depends on the method
method	method to choose. Currently available are "Chib" (default), the harmonic mean "HM", sampling from the prior "Prior", and bridge sampling "Bridge". See details
...	further arguments passed to getSample

Details

The marginal likelihood is the average likelihood across the prior space. It is used, for example, for Bayesian model selection and model averaging.

It is defined as

$$ML = \int L(\Theta)p(\Theta)d\Theta$$

Given that MLs are calculated for each model, you can get posterior weights (for model selection and/or model averaging) on the model by

$$P(M_i|D) = ML_i * p(M_i)/(\sum_i ML_i * p(M_i))$$

In BT, we return the log ML, so you will have to exp all values for this formula.

It is well-known that the ML is VERY dependent on the prior, and in particular the choice of the width of uninformative priors may have major impacts on the relative weights of the models. It has therefore been suggested to not use the ML for model averaging / selection on uninformative priors. If you have no informative priors, and option is to split the data into two parts, use one part to generate informative priors for the model, and the second part for the model selection. See help for an example.

The marginalLikelihood function currently implements four ways to calculate the marginal likelihood. Be aware that marginal likelihood calculations are notoriously prone to numerical stability issues. Especially in high-dimensional parameter spaces, there is no guarantee that any of the implemented algorithms will converge reasonably fast. The recommended (and default) method is the method "Chib" (Chib and Jeliazkov, 2001), which is based on MCMC samples, with a limited number of additional calculations. Despite being the current recommendation, note there are some numeric issues with this algorithm that may limit reliability for larger dimensions.

The harmonic mean approximation, is implemented only for comparison. Note that the method is numerically unrealiable and usually should not be used.

The third method is simply sampling from the prior. While in principle unbiased, it will only converge for a large number of samples, and is therefore numerically inefficient.

The Bridge method uses bridge sampling as implemented in the R package "bridgesampling". It is potentially more exact than the Chib method, but might require more computation time. However, this may be very dependent on the sampler.

Value

A list with log of the marginal likelihood, as well as other diagnostics depending on the chose method

Author(s)

Florian Hartig

References

Chib, Siddhartha, and Ivan Jeliazkov. "Marginal likelihood from the Metropolis-Hastings output." Journal of the American Statistical Association 96.453 (2001): 270-281.

Dormann et al. 2018. Model averaging in ecology: a review of Bayesian, information-theoretic, and tactical approaches for predictive inference. Ecological Monographs

See Also

WAIC, DIC, MAP

Examples

```
#############################################################
# Comparison of ML for two regression models

# Creating test data with quadratic relationship
sampleSize = 30
x <- (-(sampleSize-1)/2):((sampleSize-1)/2)
y <-  1 * x + 1*x^2 + rnorm(n=sampleSize,mean=0,sd=10)
# plot(x,y, main="Test Data")

# likelihoods for linear and quadratic model
likelihood1 <- function(param){
  pred = param[1] + param[2]*x + param[3] * x^2
  singlelikelihoods = dnorm(y, mean = pred, sd = 1/(param[4]^2), log = TRUE)
  return(sum(singlelikelihoods))
}
likelihood2 <- function(param){
  pred = param[1] + param[2]*x
  singlelikelihoods = dnorm(y, mean = pred, sd = 1/(param[3]^2), log = TRUE)
  return(sum(singlelikelihoods))
}

setUp1 <- createBayesianSetup(likelihood1,
                              lower = c(-5,-5,-5,0.01),
                              upper = c(5,5,5,30))
setUp2 <- createBayesianSetup(likelihood2,
                              lower = c(-5,-5,0.01),
                              upper = c(5,5,30))

out1 <- runMCMC(bayesianSetup = setUp1)
M1 = marginalLikelihood(out1, start = 1000)
```

```
out2 <- runMCMC(bayesianSetup = setUp2)
M2 = marginalLikelihood(out2, start = 1000)


### Calculating Bayes factor

exp(M1$ln.ML - M2$ln.ML)

# BF > 1 means the evidence is in favor of M1. See Kass, R. E. & Raftery, A. E.
# (1995) Bayes Factors. J. Am. Stat. Assoc., Amer Statist Assn, 90, 773-795.

### Calculating Posterior weights

exp(M1$ln.ML) / ( exp(M1$ln.ML) + exp(M2$ln.ML))

# If models have different model priors, multiply with the prior probabilities of each model.


## Not run:
##################################################################
# Fractional Bayes factor

# Motivation: ML is very dependent on the prior, which is a problem if you
# have uninformative priors. you can see this via rerunning the upper
# example with changed priors - suddenly, support for M1 is gone


setUp1 <- createBayesianSetup(likelihood1,
                              lower = c(-500,-500,-500,0.01),
                              upper = c(500,500,500,3000))
setUp2 <- createBayesianSetup(likelihood2,
                              lower = c(-500,-500,0.01),
                              upper = c(500,500,3000))

out1 <- runMCMC(bayesianSetup = setUp1)
M1 = marginalLikelihood(out1, start = 1000)

out2 <- runMCMC(bayesianSetup = setUp2)
M2 = marginalLikelihood(out2, start = 1000)


### Calculating Bayes factor

exp(M1$ln.ML - M2$ln.ML)

# it has therefore been suggested that ML should not be calculated on uninformative priors. But
# what to do if there are no informative priors?
# one option is to calculate the fractional BF, which means that one splites the data in half,
# uses the first half to fit the model, and then use the posterior as a new (now informative)
# prior for the ML - let's do this for the previous case
```

```
# likelihoods with half the data
likelihood1 <- function(param){
  pred = param[1] + param[2]*x + param[3] * x^2
  singlelikelihoods = dnorm(y, mean = pred, sd = 1/(param[4]^2), log = TRUE)
  return(sum(singlelikelihoods[seq(1, 30, 2)]))
}
likelihood2 <- function(param){
  pred = param[1] + param[2]*x
  singlelikelihoods = dnorm(y, mean = pred, sd = 1/(param[3]^2), log = TRUE)
  return(sum(singlelikelihoods[seq(1, 30, 2)]))
}

setUp1 <- createBayesianSetup(likelihood1,
                              lower = c(-500,-500,-500,0.01),
                              upper = c(500,500,500,3000))
setUp2 <- createBayesianSetup(likelihood2,
                              lower = c(-500,-500,0.01),
                              upper = c(500,500,3000))

out1 <- runMCMC(bayesianSetup = setUp1)
out2 <- runMCMC(bayesianSetup = setUp2)

newPrior1 = createPriorDensity(out1, start = 200,
                               lower = c(-500,-500,-500,0.01),
                               upper = c(500,500,500,3000))
newPrior2 = createPriorDensity(out2, start = 200,
                               lower = c(-500,-500,0.01),
                               upper = c(500,500,3000))

# now rerun this with likelihoods for the other half of the data and new prior

likelihood1 <- function(param){
  pred = param[1] + param[2]*x + param[3] * x^2
  singlelikelihoods = dnorm(y, mean = pred, sd = 1/(param[4]^2), log = TRUE)
  return(sum(singlelikelihoods[seq(2, 30, 2)]))
}
likelihood2 <- function(param){
  pred = param[1] + param[2]*x
  singlelikelihoods = dnorm(y, mean = pred, sd = 1/(param[3]^2), log = TRUE)
  return(sum(singlelikelihoods[seq(2, 30, 2)]))
}

setUp1 <- createBayesianSetup(likelihood1, prior = newPrior1)
setUp2 <- createBayesianSetup(likelihood2, prior = newPrior2)

out1 <- runMCMC(bayesianSetup = setUp1)
M1 = marginalLikelihood(out1, start = 1000)

out2 <- runMCMC(bayesianSetup = setUp2)
M2 = marginalLikelihood(out2, start = 1000)

### Calculating the fractional Bayes factor
```

```
exp(M1$ln.ML - M2$ln.ML)


## End(Not run)

#############################################################
### Performance comparison ###


# Low dimensional case with narrow priors - all methods have low error

# we use a truncated normal for the likelihood to make sure that the density
# integrates to 1 - makes it easier to calcuate the theoretical ML
likelihood <- function(x) sum(msm::dtnorm(x, log = TRUE, lower = -1, upper = 1))
prior = createUniformPrior(lower = rep(-1,2), upper = rep(1,2))
bayesianSetup <- createBayesianSetup(likelihood = likelihood, prior = prior)
out = runMCMC(bayesianSetup = bayesianSetup, settings = list(iterations = 5000))

# plot(out)

# theoretical value
theory = log(1/(2^2))

marginalLikelihood(out)$ln.ML - theory
marginalLikelihood(out, method = "Prior", numSamples =  500)$ln.ML - theory
marginalLikelihood(out, method = "HM", numSamples =  500)$ln.ML - theory
marginalLikelihood(out, method = "Bridge", numSamples =  500)$ln.ML - theory


# higher dimensions - wide prior - HM and Prior don't work

likelihood <- function(x) sum(msm::dtnorm(x, log = TRUE, lower = -10, upper = 10))
prior = createUniformPrior(lower = rep(-10,3), upper = rep(10,3))
bayesianSetup <- createBayesianSetup(likelihood = likelihood, prior = prior)
out = runMCMC(bayesianSetup = bayesianSetup, settings = list(iterations = 5000))

# plot(out)

# theoretical value
theory = log(1/(20^3))

marginalLikelihood(out)$ln.ML - theory
marginalLikelihood(out, method = "Prior", numSamples =  500)$ln.ML - theory
marginalLikelihood(out, method = "HM", numSamples =  500)$ln.ML - theory
marginalLikelihood(out, method = "Bridge", numSamples =  500)$ln.ML - theory
```

---

marginalPlot *Plot MCMC marginals*

Description

Plot MCMC marginals

Usage

```
marginalPlot(
  x,
  prior = NULL,
  xrange = NULL,
  type = "d",
  singlePanel = FALSE,
  settings = NULL,
  nPriorDraws = 10000,
  ...
)
```

Arguments

x	bayesianOutput, or matrix or data.frame containing with samples as rows and parameters as columns
prior	if x is a bayesianOutput, T/F will determine if the prior is drawn (default = T). If x is matrix oder data.frame, a prior can be drawn if a matrix of prior draws with values as rows and parameters as columns can be provided here.
xrange	vector or matrix of plotting ranges for the x axis. If matrix, the rows must be parameters and the columns min and max values.
type	character determining the plot type. Either 'd' for density plot, or 'v' for violin plot
singlePanel	logical, determining whether the parameter should be plotted in a single panel or each in its own panel
settings	optional list of additional settings for marginalPlotDensity, and marginalPlotViolin, respectively
nPriorDraws	number of draws from the prior, if x is bayesianOutput
...	additional arguments passed to getSample. If you have a high number of draws from the posterior it is advised to set numSamples (to e.g. 5000) for performance reasons.

Author(s)

Tankred Ott, Florian Hartig

Examples

```
## Generate a test likelihood function.
ll <- generateTestDensityMultiNormal(sigma = "no correlation")

## Create a BayesianSetup
bayesianSetup <- createBayesianSetup(likelihood = ll, lower = rep(-10, 3), upper = rep(10, 3))
```

```
## Finally we can run the sampler and have a look
settings = list(iterations = 1000, adapt = FALSE)
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "Metropolis", settings = settings)

marginalPlot(out, prior = TRUE)

## We can plot the marginals in several ways:
## violin plots
marginalPlot(out, type = 'v', singlePanel = TRUE)
marginalPlot(out, type = 'v', singlePanel = FALSE)
marginalPlot(out, type = 'v', singlePanel = TRUE, prior = TRUE)

## density plot
marginalPlot(out, type = 'd', singlePanel = TRUE)
marginalPlot(out, type = 'd', singlePanel = FALSE)
marginalPlot(out, type = 'd', singlePanel = TRUE, prior = TRUE)

## if you have a very wide prior you can use the xrange option to plot only
## a certain parameter range
marginalPlot(out, type = 'v', singlePanel = TRUE, xrange = matrix(rep(c(-5, 5), 3), ncol = 3))

##Further options
# We can pass arguments to getSample (check ?getSample) and to the density and violin plots
marginalPlot(out, type = 'v', singlePanel = TRUE,
             settings = list(col = c('#FC006299','#00BBAA88')), prior = TRUE)
marginalPlot(out, type = 'v', singlePanel = TRUE, numSamples = 500)
```

`mergeChains` *Merge Chains*

Description

Merge a list of outputs from MCMC / SMC samplers

Usage

```
mergeChains(l, ...)
```

Arguments

`l`	a list with objects that can be accessed with `getSample`
`...`	arguments to be passed on to `getSample`

Details

The function merges a list of outputs from MCMC / SMC samplers into a single matrix. Requirement is that the list contains classes for which the `getSample` function works

Value

a matrix

Author(s)

Florian Hartig

`Metropolis` *Creates a Metropolis-type MCMC with options for covariance adaptatin, delayed rejection, Metropolis-within-Gibbs, and tempering*

Description

Creates a Metropolis-type MCMC with options for covariance adaptatin, delayed rejection, Metropolis-within-Gibbs, and tempering

Usage

```
Metropolis(
  bayesianSetup,
  settings = list(startValue = NULL, optimize = T, proposalGenerator = NULL,
    consoleUpdates = 100, burnin = 0, thin = 1, parallel = NULL, adapt = T,
   adaptationInterval = 500, adaptationNotBefore = 3000, DRlevels = 1, proposalScaling =
   NULL, adaptationDepth = NULL, temperingFunction = NULL, gibbsProbabilities = NULL,
    message = TRUE)
)
```

Arguments

`bayesianSetup`	either an object of class bayesianSetup created by `createBayesianSetup` (recommended), or a log target function
`settings`	a list of settings - possible options follow below
`startValue`	startValue for the MCMC and optimization (if optimize = T). If not provided, the sampler will attempt to obtain the startValue from the bayesianSetup
`optimize`	logical, determines whether an optimization for start values and proposal function should be run before starting the sampling
`proposalGenerator`	optional proposalgenerator object (see `createProposalGenerator`)
`proposalScaling`	additional scaling parameter for the proposals that controls the different scales of the proposals after delayed rejection (typical, after a rejection, one would want to try a smaller scale). Needs to be as long as DRlevels. Defaults to 0.5^(-0:(mcmcSampler$settings$DRlevels -1)
`burnin`	number of iterations treated as burn-in. These iterations are not recorded in the chain.

thin	thinning parameter. Determines the interval in which values are recorded.
consoleUpdates	integer, determines the frequency with which sampler progress is printed to the console
adapt	logical, determines wheter an adaptive algorithm should be implemented. Default is TRUE.
adaptationInterval	integer, determines the interval of the adaption if adapt = TRUE.
adaptationNotBefore	integer, determines the start value for the adaption if adapt = TRUE.
DRlevels	integer, determines the number of levels for a delayed rejection sampler. Default is 1, which means no delayed rejection is used.
temperingFunction	function to implement simulated tempering in the algorithm. The function describes how the acceptance rate will be influenced in the course of the iterations.
gibbsProbabilities	vector that defines the relative probabilities of the number of parameters to be changes simultaniously.
message	logical determines whether the sampler's progress should be printed

Details

The 'Metropolis' function is the main function for all Metropolis based samplers in this package. To call the derivatives from the basic Metropolis-Hastings MCMC, you can either use the corresponding function (e.g. AM for an adaptive Metropolis sampler) or use the parameters to adapt the basic Metropolis-Hastings. The advantage of the latter case is that you can easily combine different properties (e.g. adapive sampling and delayed rejection sampling) without changing the function.

Author(s)

Florian Hartig

References

Haario, H., E. Saksman, and J. Tamminen (2001). An adaptive metropolis algorithm. Bernoulli , 223-242.

Haario, Heikki, et al. "DRAM: efficient adaptive MCMC." Statistics and Computing 16.4 (2006): 339-354.

Hastings, W. K. (1970). Monte carlo sampling methods using markov chains and their applications. Biometrika 57 (1), 97-109.

Green, Peter J., and Antonietta Mira. "Delayed rejection in reversible jump Metropolis-Hastings." Biometrika (2001): 1035-1053.

Metropolis, N., A. W. Rosenbluth, M. N. Rosenbluth, A. H. Teller, and E. Teller (1953). Equation of state calculations by fast computing machines. The journal of chemical physics 21 (6), 1087 - 1092.

Examples

```
# Running the metropolis via the runMCMC with a proposal covariance generated from the prior
# (can be useful for complicated priors)

ll = function(x) sum(dnorm(x, log = TRUE))
setup = createBayesianSetup(ll, lower = c(-10,-10), upper = c(10,10))

samples = setup$prior$sampler(1000)

generator = createProposalGenerator(diag(1, setup$numPars))
generator = updateProposalGenerator(generator, samples, manualScaleAdjustment = 1, message = TRUE)

settings =  list(proposalGenerator = generator, optimize = FALSE, iterations = 500)

out = runMCMC(bayesianSetup = setup, sampler = "Metropolis", settings = settings)
```

---

plotDiagnostic *Diagnostic Plot*

Description

This function plots the DIC, WAIC, mPSRF, PSRF(with upper C.I.) and traces of the parameters in dependence of iterations. DIC, WAIC are plotted separately for the chains and the trace plots also for the internal chains.

Usage

```
plotDiagnostic(
  out,
  start = 50,
  numSamples = 100,
  window = 0.2,
  plotWAIC = F,
  plotPSRF = T,
  plotDIC = T,
  plotTrace = T,
  graphicParameters = NULL,
  ...
)
```

Arguments

out	object of class "bayesianOutput"
start	start value for calculating DIC, WAIC, mPSRF and PSRF, default = 50
numSamples	for calculating WAIC, default = 10 because of high computational costs
window	plot range to show, vector of percents or only one value as start value for the window

plotWAIC	whether to calculate WAIC or not, default = T
plotPSRF	calculate and plot mPSRF/PSRF or not, default = T
plotDIC	calculate and plot DICor not, default = T
plotTrace	show trace plots or not, default = T
graphicParameters	graphic parameters as list for plot function
...	parameters to give to getSample

Author(s)

Maximilian Pichler

Examples

```
## Not run:

  # Create bayesian setup with
  bayesianSetup <- createBayesianSetup(likelihood = testDensityNormal,
                                       prior = createUniformPrior(lower = -10,
                                                                  upper = 10))
  # running MCMC
  out = runMCMC(bayesianSetup = bayesianSetup)

  # diagnostic plots
  plotDiagnostic(out)

## End(Not run)
```

---

plotSensitivity *Performs a one-factor-at-a-time sensitivity analysis for the posterior of a given bayesianSetup within the prior range.*

Description

Performs a one-factor-at-a-time sensitivity analysis for the posterior of a given bayesianSetup within the prior range.

Usage

```
plotSensitivity(bayesianSetup, selection = NULL, equalScale = T)
```

Arguments

bayesianSetup	An object of class BayesianSetup
selection	indices of selected parameters
equalScale	if T, y axis of all plots will have the same scale

Note

This function can also be used for sensitivity analysis of an arbitrary output - just create a BayesianSetup with this output.

Author(s)

Florian Hartig

Examples

```
ll <- testDensityBanana
bayesianSetup <- createBayesianSetup(likelihood = ll, lower = rep(-10, 2), upper = rep(10, 2))

plotSensitivity(bayesianSetup)
```

---

plotTimeSeries *Plots a time series, with the option to include confidence and prediction band*

Description

Plots a time series, with the option to include confidence and prediction band

Usage

```
plotTimeSeries(
  observed = NULL,
  predicted = NULL,
  x = NULL,
  confidenceBand = NULL,
  predictionBand = NULL,
  xlab = "Time",
  ylab = "Observed / predicted values",
  ...
)
```

Arguments

observed	observed values
predicted	predicted values
x	optional values for x axis (time)
confidenceBand	matrix with confidenceBand
predictionBand	matrix with predictionBand
xlab	a title for the x axis
ylab	a title for the y axis
...	further arguments passed to plot

Details

Values for confidence and prediction bands can be generated with `getPredictiveIntervals`. For a more elaborate version of this plot, see `plotTimeSeriesResults`

Author(s)

Florian Hartig

See Also

`marginalPlot`, `tracePlot`, `correlationPlot`

Examples

```
# Create time series
ts <- VSEMcreatePAR(1:100)

# create fake "predictions"
pred <- ts + rnorm(length(ts), mean = 0, sd = 2)

# plot time series
par(mfrow=c(1,2))

plotTimeSeries(observed = ts, main="Observed")
plotTimeSeries(observed = ts, predicted = pred, main = "Observed and predicted")

par(mfrow=c(1,1))
```

---

plotTimeSeriesResiduals

Plots residuals of a time series

Description

Plots residuals of a time series

Usage

```
plotTimeSeriesResiduals(residuals, x = NULL, main = "residuals")
```

Arguments

`residuals`	x
`x`	optional values for x axis (time)
`main`	title of the plot

Author(s)

Florian Hartig

`plotTimeSeriesResults` *Creates a time series plot typical for an MCMC / SMC fit*

Description

Creates a time series plot typical for an MCMC / SMC fit

Usage

```
plotTimeSeriesResults(
  sampler,
  model,
  observed,
  error = NULL,
  plotResiduals = TRUE,
  start = 1,
  prior = FALSE,
  ...
)
```

Arguments

`sampler`	Either a) a matrix b) an MCMC object (list or not), or c) an SMC object
`model`	function that calculates model predictions for a given parameter vector
`observed`	observed values as vector
`error`	function with signature f(mean, par) that generates observations with error (error = stochasticity according to what is assumed in the likelihood) from mean model predictions. Par is a vector from the matrix with the parameter samples (full length). f needs to know which of these parameters are parameters of the error function. See example in `VSEM`
`plotResiduals`	logical determining whether residuals should be plotted
`start`	numeric start value for the plot (see `getSample`)
`prior`	if a prior sampler is implemented, setting this parameter to TRUE will draw model parameters from the prior instead of the posterior distribution
`...`	further arguments passed to `plot`

Author(s)

Florian Hartig

See Also

`getPredictiveIntervals`

Examples

```
# Create time series
ts <- VSEMcreatePAR(1:100)

# create fake "predictions"
pred <- ts + rnorm(length(ts), mean = 0, sd = 2)

# plot time series
par(mfrow=c(1,2))

plotTimeSeries(observed = ts, main="Observed")
plotTimeSeries(observed = ts, predicted = pred, main = "Observed and predicted")

par(mfrow=c(1,1))
```

---

runMCMC *Main wrapper function to start MCMCs, particle MCMCs and SMCs*

Description

Main wrapper function to start MCMCs, particle MCMCs and SMCs

Usage

```
runMCMC(bayesianSetup, sampler = "DEzs", settings = NULL)
```

Arguments

bayesianSetup	either a BayesianSetup (see createBayesianSetup), a function, or a BayesianOutput created by runMCMC. The latter allows to continue a previous MCMC run. See details for how to restart a sampler.
sampler	sampling algorithm to be run. Default is DEzs. Options are "Metropolis", "AM", "DR", "DRAM", "DE", "DEzs", "DREAM", "DREAMzs", "SMC". For details see the help of the individual functions.
settings	list with settings for each sampler. If a setting is not provided, defaults (see applySettingsDefault) will be used.

Details

The runMCMC function can be started with either one of

1. an object of class BayesianSetup with prior and likelihood function (created with createBayesianSetup). check if appropriate parallelization options are used - many samplers can make use of parallelization if this option is activated when the class is created.
2. a log posterior or other target function,

3. an object of class BayesianOutput created by runMCMC. The latter allows to continue a previous MCMC run.

Settings for the sampler are provides as a list. You can see the default values by running `applySettingsDefault` with the respective sampler name. The following settings can be used for all MCMCs:

- startValue (no default) start values for the MCMC. Note that DE family samplers require a matrix of start values. If startvalues are not provided, they are sampled from the prior.
- iterations (10000) the MCMC iterations
- burnin (0) burnin
- thin (1) thinning while sampling
- consoleUpdates (100) update frequency for console updates
- parallel (NULL) whether parallelization is to be used
- message (TRUE) if progress messages are to be printed
- nrChains (1) the number of independent MCMC chains to be run. Note that this is not controlling the internal number of chains in population MCMCs such as DE, so if you run nrChains = 3 with a DEzs startValue that is a 4xparameter matrix (= 4 internal chains), you will run independent DEzs runs with 4 internal chains each.

The MCMC samplers will have a number of additional settings, which are described in the Vignette (run vignette("BayesianTools", package="BayesianTools") and in the help of the samplers. See `Metropolis` for Metropolis based samplers, `DE` and `DEzs` for standard differential evolution samplers, `DREAM` and `DREAMzs` for DREAM sampler, `Twalk` for the Twalk sampler, and `smcSampler` for rejection and Sequential Monte Carlo sampling. Note that the samplers "AM", "DR", and "DRAM" are special cases of the "Metropolis" sampler and are shortcuts for predefined settings ("AM": adapt=TRUE; "DR": DRlevels=2; "DRAM": adapt=True, DRlevels=2).

Note that even if you specify parallel = T, this will only turn on internal parallelization of the samplers. The independent samplers controlled by nrChains are not evaluated in parallel, so if time is an issue it will be better to run the MCMCs individually and then combine them via `createMcmcSamplerList` into one joint object.

Note that DE and DREAM variants as well as SMC and T-walk require a population to start, which should be provided as a matrix. Default (NULL) sets the population size for DE to 3 x dimensions of parameters, for DREAM to 2 x dimensions of parameters and for DEzs and DREAMzs to three, sampled from the prior. Note also that the zs variants of DE and DREAM require two populations, the current population and the z matrix (a kind of memory) - if you want to set both, provide a list with startvalue$X and startvalue$Z.

setting startValue for sampling with nrChains > 1 : if you want to provide different start values for the different chains, provide them as a list

Value

The function returns an object of class mcmcSampler (if one chain is run) or mcmcSamplerList. Both have the superclass bayesianOutput. It is possible to extract the samples as a coda object or matrix with `getSample`. It is also possible to summarize the posterior as a new prior via `createPriorDensity`.

Author(s)

Florian Hartig

See Also

createBayesianSetup

Examples

```
## Generate a test likelihood function.
ll <- generateTestDensityMultiNormal(sigma = "no correlation")

## Create a BayesianSetup object from the likelihood
## is the recommended way of using the runMCMC() function.
bayesianSetup <- createBayesianSetup(likelihood = ll, lower = rep(-10, 3), upper = rep(10, 3))

## Finally we can run the sampler. To get possible settings
## for a sampler, see help or run applySettingsDefault(sampler = "Metropolis")
settings = list(iterations = 1000, adapt = FALSE) #
out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "Metropolis", settings = settings)

## out is of class bayesianOutput. There are various standard functions
# implemented for this output

plot(out)
correlationPlot(out)
marginalPlot(out)
summary(out)

## additionally, you can return the sample as a coda object, and make use of the coda functions
# for plotting and analysis

codaObject = getSample(out, start = 500, coda = TRUE)
```

---

smcSampler *SMC sampler*

Description

Sequential Monte Carlo Sampler

Usage

```
smcSampler(
  bayesianSetup,
  initialParticles = 1000,
  iterations = 10,
```

```
  resampling = T,
  resamplingSteps = 2,
  proposal = NULL,
  adaptive = T,
  proposalScale = 0.5
)
```

Arguments

bayesianSetup	either an object of class bayesianSetup created by createBayesianSetup (recommended), or a log target function
initialParticles	initial particles - either a draw from the prior, provided as a matrix with the single parameters as columns and each row being one particle (parameter vector), or a numeric value with the number of desired particles. In this case, the sampling option must be provided in the prior of the BayesianSetup.
iterations	number of iterations
resampling	if new particles should be created at each iteration
resamplingSteps	how many resampling (MCMC) steps between the iterations
proposal	optional proposal class
adaptive	should the covariance of the proposal be adapted during sampling
proposalScale	scaling factor for the proposal generation. Can be adapted if there is too much / too little rejection

Details

The sampler can be used for rejection sampling as well as for sequential Monte Carlo. For the former case set the iterations to one.

Note

The SMC currently assumes that the initial particle is sampled from the prior. If a better initial estimate of the posterior distribution is available, this the sampler should be modified to include this. Currently, however, this is not included in the code, so the appropriate adjustments have to be done by hand.

Author(s)

Florian Hartig

Examples

```
## Example for the use of SMC
# First we need a bayesianSetup - SMC makes most sense if we can  for demonstration,
# we'll write a function that puts out the number of model calls

MultiNomialNoCor <- generateTestDensityMultiNormal(sigma = "no correlation")
```

```
parallelLL <- function(parMatrix){
  print(paste("Calling likelihood with", nrow(parMatrix), "parameter combinations"))
  out = apply(parMatrix, 1, MultiNomialNoCor)
  return(out)
}

bayesianSetup <- createBayesianSetup(likelihood = parallelLL, lower = rep(-10, 3),
                                     upper = rep(10, 3), parallel = "external")

# Defining settings for the sampler
# First we use the sampler for rejection sampling
settings <- list(initialParticles = 1000, iterations = 1, resampling = FALSE)

# Running the sampler
out1 <- runMCMC(bayesianSetup = bayesianSetup, sampler = "SMC", settings = settings)
#plot(out1)


# Now for sequential Monte Carlo
settings <- list(initialParticles = 100, iterations = 5, resamplingSteps = 1)
out2 <- runMCMC(bayesianSetup = bayesianSetup, sampler = "SMC", settings = settings)
#plot(out2)

## Not run:

## Example for starting a new SMC run with results from a previous SMC run

# Generate example data (time series)
# x1 and x2 are predictory, yObs is the response
t <- seq(1, 365)
x1 <- (sin( 1 / 160 * 2 * pi * t) + pi) * 5
x2 <- cos( 1 / 182.5 * 1.25 * pi * t) * 12

# the model
mod <- function(par, t1 = 1, tn = 365) {
  par[1] * x1[t1:tn] + par[2] * x2[t1:tn]
}

# the true parameters
par1 <- 1.65
par2 <- 0.75
yObs <- mod(c(par1, par2)) + rnorm(length(x1), 0, 2)

# split the time series in half
plot(yObs ~ t)
abline(v = 182, col = "red", lty = 2)

# First half of the data
ll_1 <- function(x, sum = TRUE) {
  out <- dnorm(mod(x, 1, 182) - yObs[1:182], 0, 2, log = TRUE)
  if (sum == TRUE) sum(out) else out
}
```

```
# Fit the first half of the time series
# (e.g. fit the model to the data soon as you collect the data)
setup_1 <- createBayesianSetup(ll_1, lower = c(-10, -10), upper = c(10, 10))
settings_1 <- list(initialParticles = 1000)
out_1 <- runMCMC(setup_1, "SMC", settings_1)
summary(out_1)


# Second half of the data
ll_2 <- function(x, sum = TRUE) {
  out <- dnorm(mod(x, 183, 365) - yObs[183:365], 0, 2, log = TRUE)
  if (sum == TRUE) sum(out) else out
}

# Fit the second half of the time series
# (e.g. fit the model to the data soon as you collect the data)
setup_2 <- createBayesianSetup(ll_2, lower = c(-10, -10), upper = c(10, 10))

# This is the important step, we use the final particles from the
# previous SMC run to initialize the new SMC run
settings_2 <- list(initialParticles = out_1$particles)
out_2 <- runMCMC(setup_2, "SMC", settings_2)
summary(out_2)

par_pred <- apply(out_2$particles, 2, median)
pred <- mod(par_pred)
plotTimeSeries(yObs, pred)


## End(Not run)
```

`stopParallel` *Function to close cluster in BayesianSetup*

Description

Function closes the parallel executer (if available)

Usage

```
stopParallel(bayesianSetup)
```

Arguments

bayesianSetup	object of class BayesianSetup

Author(s)

Stefan Paul

---

testDensityBanana *Banana-shaped density function*

Description

Banana-shaped density function

Usage

```
testDensityBanana(p)
```

Arguments

p	2-dim parameter vector

Note

inspired from package FMEmcmc, seems to go back to Laine M (2008). Adaptive MCMC Methods with Applications in Environmental and Models. Finnish Meteorological Institute Contributions 69. ISBN 978-951-697-662-7.

Author(s)

Florian Hartig

See Also

generateTestDensityMultiNormal
testLinearModel

testDensityGelmanMeng *GelmanMeng test function*

Description

GelmanMeng test function

Usage

```
testDensityGelmanMeng(x, A = 1, B = 0, C1 = 3, C2 = 3, log = TRUE)
```

Arguments

x	parameter vector
A	function parameter
B	function parameter
C1	function parameter
C2	function parameter
log	log

A non-elliptical, bivariate density function proposed by Gelman and Meng (1991).

testDensityInfinity *Test function infinity ragged*

Description

Test function infinity ragged

Usage

```
testDensityInfinity(x, error = F)
```

Arguments

x	2-dim parameter vector
error	should error or infinity be returned

Author(s)

Florian Hartig

See Also

generateTestDensityMultiNormal
testDensityBanana

testDensityMultiNormal *3d Mutivariate Normal likelihood*

Description

3d Mutivariate Normal likelihood

Usage

```
testDensityMultiNormal(x, sigma = "strongcorrelation")
```

Arguments

x	a parameter vector of arbitrary length
sigma	either a correlation matrix, or "strongcorrelation", or "no correlation"

testDensityNormal *Normal likelihood*

Description

Normal likelihood

Usage

```
testDensityNormal(x, sum = T)
```

Arguments

x	a parameter vector of arbitrary length
sum	if likelihood should be summed or not

Author(s)

Florian Hartig

testLinearModel *Fake model, returns a ax + b linear response to 2-param vector*

Description

Fake model, returns a ax + b linear response to 2-param vector

Usage

```
testLinearModel(x, env = NULL)
```

Arguments

x	2-dim parameter vector
env	optional, environmental covariate

Author(s)

Florian Hartig

See Also

generateTestDensityMultiNormal
testDensityBanana

Examples

```
x = c(1,2)
y = testLinearModel(x)
plot(y)
```

tracePlot *Trace plot for MCMC class*

Description

Trace plot for MCMC class

Usage

```
tracePlot(sampler, thin = "auto", ...)
```

Arguments

sampler	an object of class MCMC sampler
thin	determines the thinning intervall of the chain
...	additional parameters to pass on to the getSample, for example parametersOnly =F, or start = 1000

See Also

marginalPlot
plotTimeSeries
correlationPlot

Examples

```
# set up and run the MCMC
ll <- function(x) sum(dnorm(x, log = TRUE))
setup <- createBayesianSetup(likelihood = ll, lower = c(-10, -10), upper = c(10,10))
settings <- list(iterations = 2000)
out <- runMCMC(bayesianSetup = setup, settings = settings, sampler = "Metropolis")

# plot the trace
tracePlot(sampler = out, thin = 10)
tracePlot(sampler = out, thin = 50)

# additional parameters can be passed on to getSample (see help)
tracePlot(sampler = out, thin = 10, start = 500)
# select parameter by index
tracePlot(sampler = out, thin = 10, start = 500, whichParameters = 2)
```

Twalk *T-walk MCMC*

Description

T-walk MCMC

Usage

```
Twalk(
  bayesianSetup,
 settings = list(iterations = 10000, at = 6, aw = 1.5, pn1 = NULL, Ptrav = 0.4918, Pwalk
   = 0.4918, Pblow = 0.0082, burnin = 0, thin = 1, startValue = NULL, consoleUpdates =
     100, message = TRUE)
)
```

Arguments

bayesianSetup	Object of class 'bayesianSetup' or 'bayesianOuput'.
settings	list with parameter values.
iterations	Number of model evaluations
at	"traverse" move proposal parameter. Default to 6
aw	"walk" move proposal parameter. Default to 1.5
pn1	Probability determining the number of parameters that are changed
Ptrav	Move probability of "traverse" moves, default to 0.4918
Pwalk	Move probability of "walk" moves, default to 0.4918
Pblow	Move probability of "traverse" moves, default to 0.0082
burnin	number of iterations treated as burn-in. These iterations are not recorded in the chain.
thin	thinning parameter. Determines the interval in which values are recorded.
startValue	Matrix with start values
consoleUpdates	Intervall in which the sampling progress is printed to the console
message	logical determines whether the sampler's progress should be printed

Details

The probability of "hop" moves is 1 minus the sum of all other probabilities.

Value

Object of class bayesianOutput.

Author(s)

Stefan Paul

References

Christen, J. Andres, and Colin Fox. "A general purpose sampling algorithm for continuous distributions (the t-walk)." Bayesian Analysis 5.2 (2010): 263-281.

updateProposalGenerator *To update settings of an existing proposal genenerator*

Description

To update settings of an existing proposal genenerator

Usage

```
updateProposalGenerator(
  proposal,
  chain = NULL,
  message = F,
  eps = 1e-10,
  manualScaleAdjustment = 1
)
```

Arguments

proposal	an object of class proposalGenerator
chain	a chain to create the covariance matrix from (optional)
message	whether to print an updating message
eps	numeric tolerance for covariance
manualScaleAdjustment	optional adjustment for the covariance scale (multiplicative)

Details

The this function can be applied in 2 ways 1) update the covariance given an MCMC chain, and 2) update the proposal generator after parameters have been changed

VSEM *Very simple ecosystem model*

Description

A very simple ecosystem model, based on three carbon pools and a basic LUE model

Usage

```
VSEM(
 pars = c(KEXT = 0.5, LAR = 1.5, LUE = 0.002, GAMMA = 0.4, tauV = 1440, tauS = 27370,
    tauR = 1440, Av = 0.5, Cv = 3, Cs = 15, Cr = 3),
 PAR,
 C = TRUE
)
```

Arguments

pars	a parameter vector with parameters and initial states
PAR	Forcing, photosynthetically active radiation (PAR) MJ /m2 /day
C	switch to choose whether to use the C or R version of the model. C is much faster.

Details

This Very Simple Ecosystem Model (VSEM) is a 'toy' model designed to be very simple but yet bear some resemblance to deterministic processed based ecosystem models (PBMs) that are commonly used in forest modelling.

The model determines the accumulation of carbon in the plant and soil from the growth of the plant via photosynthesis and senescence to the soil which respires carbon back to the atmosphere.

The model calculates Gross Primary Productivity (GPP) using a very simple light-use efficiency (LUE) formulation multiplied by light interception. Light interception is calculated via Beer's law with a constant light extinction coefficient operating on Leaf Area Index (LAI).

A parameter (GAMMA) determines the fraction of GPP that is autotrophic respiration. The Net Primary Productivity (NPP) is then allocated to above and below-ground vegetation via a fixed allocation fraction. Carbon is lost from the plant pools to a single soil pool via fixed turnover rates. Heterotropic respiration in the soil is determined via a soil turnover rate.

The model equations are

– Photosynthesis

$$LAI = LAR * Cv$$

$$GPP = PAR * LUE * (1 - \exp^{(-KEXT*LAI)})$$

$$NPP = (1 - GAMMA) * GPP$$

– State equations

$$dCv/dt = Av * NPP - Cv/tauV$$

$$dCr/dt = (1.0 - Av) * NPP - Cr/tauR$$

$$dCs/dt = Cr/tauR + Cv/tauV - Cs/tauS$$

The model time-step is daily.

– VSEM inputs:

PAR Photosynthetically active radiation (PAR) MJ /m2 /day

– VSEM parameters:

KEXT Light extinction coefficient m2 ground area / m2 leaf area

LAR Leaf area ratio m2 leaf area / kg aboveground vegetation

LUE Light-Use Efficiency (kg C MJ-1 PAR)

GAMMA Autotrophic respiration as a fraction of GPP

tauV Longevity of aboveground vegetation days

tauR Longevity of belowground vegetation days

tauS Residence time of soil organic matter d

– VSEM states:

Cv Above-ground vegetation pool kg C / m2

Cr Below-ground vegetation pool kg C / m2

Cs Carbon in organic matter kg C / m2

– VSEM fluxes:

G Gross Primary Productivity kg C /m2 /day

NPP Net Primary Productivity kg C /m2 /day

NEE Net Ecosystem Exchange kg C /m2 /day

Value

a matrix with colums NEE, CV, CR and CS units and explanations see details

Author(s)

David Cameron, R and C implementation by Florian Hartig

See Also

VSEMgetDefaults, VSEMcreatePAR, , VSEMcreateLikelihood

Examples

```
## This example shows how to run and calibrate the VSEM model

library(BayesianTools)

# Create input data for the model
PAR <- VSEMcreatePAR(1:1000)
plot(PAR, main = "PAR (driving the model)", xlab = "Day")

# load reference parameter definition (upper, lower prior)
refPars <- VSEMgetDefaults()
# this adds one additional parameter for the likelihood standard deviation (see below)
refPars[12,] <- c(2, 0.1, 4)
rownames(refPars)[12] <- "error-sd"
head(refPars)

# create some simulated test data
# generally recommended to start with simulated data before moving to real data
referenceData <- VSEM(refPars$best[1:11], PAR) # model predictions with reference parameters
referenceData[,1] = 1000 * referenceData[,1]
# this adds the error - needs to conform to the error definition in the likelihood
obs <- referenceData + rnorm(length(referenceData), sd = refPars$best[12])
oldpar <- par(mfrow = c(2,2))
```

```
for (i in 1:4) plotTimeSeries(observed = obs[,i],
                        predicted = referenceData[,i], main = colnames(referenceData)[i])

# Best to program in a way that we can choose easily which parameters to calibrate
parSel = c(1:6, 12)

# here is the likelihood
likelihood <- function(par, sum = TRUE){
  # set parameters that are not calibrated on default values
  x = refPars$best
  x[parSel] = par
  predicted <- VSEM(x[1:11], PAR) # replace here VSEM with your model
  predicted[,1] = 1000 * predicted[,1] # this is just rescaling
  diff <- c(predicted[,1:4] - obs[,1:4]) # difference betweeno observed and predicted
  # univariate normal likelihood. Note that there is a parameter involved here that is fit
  llValues <- dnorm(diff, sd = x[12], log = TRUE)
  if (sum == FALSE) return(llValues)
  else return(sum(llValues))
}

# optional, you can also directly provide lower, upper in the createBayesianSetup, see help
prior <- createUniformPrior(lower = refPars$lower[parSel],
                            upper = refPars$upper[parSel], best = refPars$best[parSel])

bayesianSetup <- createBayesianSetup(likelihood, prior, names = rownames(refPars)[parSel])

# settings for the sampler, iterations should be increased for real applicatoin
settings <- list(iterations = 2000, nrChains = 2)

out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)

## Not run:

plot(out)
summary(out)
marginalPlot(out)
gelmanDiagnostics(out) # should be below 1.05 for all parameters to demonstrate convergence

# Posterior predictive simulations

# Create a prediction function
createPredictions <- function(par){
  # set the parameters that are not calibrated on default values
  x = refPars$best
  x[parSel] = par
  predicted <- VSEM(x[1:11], PAR) # replace here VSEM with your model
  return(predicted[,1] * 1000)
}

# Create an error function
createError <- function(mean, par){
  return(rnorm(length(mean), mean = mean, sd = par[7]))
}
```

```
# plot prior predictive distribution and prior predictive simulations
plotTimeSeriesResults(sampler = out, model = createPredictions, observed = obs[,1],
                      error = createError, prior = TRUE, main = "Prior predictive")

# plot posterior predictive distribution and posterior predictive simulations
plotTimeSeriesResults(sampler = out, model = createPredictions, observed = obs[,1],
                      error = createError, main = "Posterior predictive")


#########################################################
# Demonstrating the updating of the prior from old posterior
# Note that it is usually more exact to rerun the MCMC
# with all (old and new) data, instead of updating the prior
# because likely some information is lost when approximating the
# Posterior by a multivariate normal

settings <- list(iterations = 5000, nrChains = 2)

out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)

plot(out)
correlationPlot(out, start = 1000)

newPrior = createPriorDensity(out, method = "multivariate",
                              eps = 1e-10,
                              lower = refPars$lower[parSel],
                              upper = refPars$upper[parSel], start= 1000)

bayesianSetup <- createBayesianSetup(likelihood = likelihood,
                                     prior = newPrior,
                                     names = rownames(refPars)[parSel] )

# check boundaries are correct set
bayesianSetup$prior$sampler() < refPars$lower[parSel]
bayesianSetup$prior$sampler() > refPars$upper[parSel]

# check prior looks similar to posterior
x = bayesianSetup$prior$sampler(2000)
correlationPlot(x, thin = F)

out <- runMCMC(bayesianSetup = bayesianSetup, sampler = "DEzs", settings = settings)

plot(out)
correlationPlot(out)

plotTimeSeriesResults(sampler = out,
                      model = createPredictions,
                      observed = obs[,1],
                      error = createError,
                      prior = F, main = "Posterior predictive")

plotTimeSeriesResults(sampler = out,
```

```
                    model = createPredictions,
                    observed = obs[,1],
                    error = createError,
                    prior = T, main = "Prior predictive")
```

```
## End(Not run)

par(oldpar)
```

`vsemC` *C version of the VSEM model*

Description

C version of the VSEM model

Usage

```
vsemC(par, PAR)
```

Arguments

`par`	parameter vector
`PAR`	Photosynthetically active radiation (PAR) MJ /m2 /day

`VSEMcreateLikelihood` *Create an example dataset, and from that a likelihood or posterior for the VSEM model*

Description

Create an example dataset, and from that a likelihood or posterior for the VSEM model

Usage

```
VSEMcreateLikelihood(likelihoodOnly = F, plot = F, selection = c(1:6, 12))
```

Arguments

`likelihoodOnly`	switch to devide whether to create only a likelihood, or a full bayesianSetup with uniform priors.
`plot`	switch to decide whether data should be plotted
`selection`	vector containing the indices of the selected parameters

Details

The purpose of this function is to be able to conveniently create a likelihood for the VSEM model for demonstration purposes. The function creates example data –> likelihood –> BayesianSetup, where the latter is the

Author(s)

Florian Hartig

`VSEMcreatePAR` *Create a random radiation (PAR) time series*

Description

Create a random radiation (PAR) time series

Usage

```
VSEMcreatePAR(days = 1:(3 * 365))
```

Arguments

`days`	days to calculate the PAR for

Author(s)

David Cameron, R implementation by Florian Hartig

`VSEMgetDefaults` *returns the default values for the VSEM*

Description

returns the default values for the VSEM

Usage

```
VSEMgetDefaults()
```

Value

a data.frame

`WAIC` *calculates the WAIC*

Description

calculates the WAIC

Usage

```
WAIC(bayesianOutput, numSamples = 1000, ...)
```

Arguments

`bayesianOutput`	an object of class BayesianOutput. Must implement a log-likelihood density function that can return point-wise log-likelihood values ("sum" argument).
`numSamples`	the number of samples to calculate the WAIC
`...`	optional values to be passed on the the getSample function

Details

The WAIC is constructed as

$$WAIC = -2 * (lppd - p_{WAIC})$$

The lppd (log pointwise predictive density), defined in Gelman et al., 2013, eq. 4 as

$$lppd = \sum_{i=1}^{n} \log \left(\frac{1}{S} \sum_{s=1}^{S} p(y_i|\theta^s) \right)$$

The value of $p_W AIC$ can be calculated in two ways, the method used is determined by the `method` argument.

Method 1 is defined as,

$$p_{WAIC1} = 2 \sum_{i=1}^{n} (\log(\frac{1}{S} \sum_{s=1}^{S} p(y_i\ \theta^s)) - \frac{1}{S} \sum_{s=1}^{S} \log p(y_i|\theta^s))$$

Method 2 is defined as,

$$p_{WAIC2} = 2 \sum_{i=1}^{n} V_{s=1}^{S} (\log p(y_i|\theta^s))$$

where $V_{s=1}^{S}$ is the sample variance.

Note

The function requires that the likelihood passed on to BayesianSetup contains the option sum = T/F, with defaul F. If set to true, the likelihood for each data point must be returned.

Author(s)

Florian Hartig

References

Gelman, Andrew and Jessica Hwang and Aki Vehtari (2013), "Understanding Predictive Information Criteria for Bayesian Models," http://www.stat.columbia.edu/~gelman/research/unpublished/waic_understand_final.pdf.

Watanabe, S. (2010). "Asymptotic Equivalence of Bayes Cross Validation and Widely Applicable Information Criterion in Singular Learning Theory", Journal of Machine Learning Research, https://www.jmlr.org/papers/v11/watanabe10a.html.

See Also

DIC, MAP, marginalLikelihood

Examples

```
bayesianSetup <- createBayesianSetup(likelihood = testDensityNormal,
                                     prior = createUniformPrior(lower = rep(-10,2),
                                                                upper = rep(10,2)))

# likelihood density needs to have option sum = FALSE

testDensityNormal(c(1,1,1), sum = FALSE)
bayesianSetup$likelihood$density(c(1,1,1), sum = FALSE)
bayesianSetup$likelihood$density(matrix(rep(1,9), ncol = 3), sum = FALSE)

# running MCMC

out = runMCMC(bayesianSetup = bayesianSetup)

WAIC(out)
```

Index

AM, *65*
applySettingsDefault, 3, *71, 72*

BayesianTools, 4
BayesianTools-package *(*BayesianTools*)*, 4

calibrationTest, 5
checkBayesianSetup, 7, *12*
coda::gelman.diag, *41*
coda::gelman.plot, *41*
convertCoda, 8
correlationPlot, 8, *69*, *81*
createBayesianSetup, *5*, *7*, 10, *14*, *16, 17*, *19*, *22*, *27, 28*, *64*, *71*, *73, 74*
createBetaPrior, 13, *19*, *22*, *27, 28*
createLikelihood, *12*, 15
createMcmcSamplerList, 16, *72*
createMixWithDefaults, 17
createPosterior, 17
createPrior, *10–12*, *14*, 18, *22*, *26–28*
createPriorDensity, *14*, *18, 19*, 20, *27, 28*, *72*
createProposalGenerator, 23, *64*
createSmcSamplerList, 25
createTruncatedNormalPrior, *14*, *19*, *22*, 26, *28*
createUniformPrior, *11*, *14*, *19*, *22*, *27*, 28

DE, *5*, 29, *33*, *72*
DEzs, *5*, *31*, 32, *72*
DIC, *8*, 34, *56*, *58*, *91*
DREAM, *5*, 35, *39*, *72*
DREAMzs, *5*, *37*, 38, *72*

gelmanDiagnostics, 40
generateParallelExecuter, *11*, 42
generateTestDensityMultiNormal, 43, *77, 78*, *80*
getCredibleIntervals, 44, *46, 47*
getDharmaResiduals, 45
getPanels, 45
getPossibleSamplerTypes, 46
getPredictiveDistribution, *44*, 46, *47*
getPredictiveIntervals, *44*, *46*, 47, *69, 70*
getSample, *6*, *9*, *34*, *40*, 48, *52*, *57*, *62, 63*, *70*, *72*, *81*
getVolume, 52
GOF, 53

likelihoodAR1, *16*, 54
likelihoodIidNormal, *16*, 55

MAP, *8*, *35*, 56, *58*, *91*
marginalLikelihood, *21*, *35*, *56*, 56, *91*
marginalPlot, *9*, 61, *69*, *81*
marginalPlotDensity, *62*
marginalPlotViolin, *62*
mergeChains, 63
Metropolis, *5*, 64, *72*

plot, *68*, *70*
plotDiagnostic, 66
plotSensitivity, 67
plotTimeSeries, *9*, 68, *81*
plotTimeSeriesResiduals, 69
plotTimeSeriesResults, *69*, 70

runMCMC, *3–5*, 71

smcSampler, *5*, *72*, 73
stopParallel, 76

testDensityBanana, *43*, 77, *78*, *80*
testDensityGelmanMeng, 78
testDensityInfinity, 78
testDensityMultiNormal, 79
testDensityNormal, 79
testLinearModel, *43*, *77*, 80
tracePlot, *9*, *69*, 80
Twalk, *5*, *72*, 81

updateProposalGenerator, *24*, 83

VSEM, *70*, 83
vsemC, 88
VSEMcreateLikelihood, *85*, 88
VSEMcreatePAR, *85*, 89
VSEMgetDefaults, *85*, 89

WAIC, *35*, *56*, *58*, 90