Package ‘adaptMCMC’

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Description Enables sampling from arbitrary distributions if the log density is known up to a constant; a common situation in the context of Bayesian inference. The implemented sampling algorithm was proposed by Vihola (2012) <DOI:10.1007/s11222-011-9269-5> and achieves often a high efficiency by tuning the proposal distributions to a user defined acceptance rate.
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Description

Enables sampling from arbitrary distributions if the log density is known up to a constant; a common situation in the context of Bayesian inference. The implemented sampling algorithm was proposed by Vihola (2012) and achieves often a high efficiency by tuning the proposal distributions to a user defined acceptance rate.

Details

The workhorse function is `mcmc`. Chains can be updated with `MCMC.add.samples`, `MCMC.parallel` is a wrapper to generate independent chains on several CPU’s in parallel using `parallel`. `coda`-functions can be used after conversion with `convert.to.coda`.

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References


See Also

`MCMC`, `MCMC.add.samples`, `MCMC.parallel`, `convert.to.coda`

The package HI provides an adaptive rejection Metropolis sampler with the function `arms`. See also `Metro.Hastings` of the MHadaptive package.
convert.to.coda

Converts chain(s) produced by MCMC or MCMC.parallel into coda objects.

Usage

convert.to.coda(sample)

Arguments

sample output of MCMC or MCMC.parallel.

Details

Converts chain(s) produced by MCMC or MCMC.parallel so that they can be used with functions of the coda package.

Value

An object of the class mcmc or mcmc.list.

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See Also

MCMC, mcmc, mcmc.list

Examples

## -------------------
## Banana shaped distribution

## log-pdf to sample from
def p.log <- function(x)
  B <- 0.03  # controls 'bananacity'

## -------------------
## generate 200 samples

samp <- MCMC(p.log, n=200, init=c(0, 1), scale=c(1, 0.1),
              adapt=TRUE, acc.rate=0.234)
MCMC

(Adaptive) Metropolis Sampler

Description

Implementation of the robust adaptive Metropolis sampler of Vihola (2012).

Usage

```r
MCMC(p, n, init, scale = rep(1, length(init)),
     adapt = !is.null(acc.rate), acc.rate = NULL, gamma = 2/3,
     list = TRUE, showProgressBar=interactive(), n.start = 0, ...)
```

Arguments

- `p` function that returns a value proportional to the log probability density to sample from. Alternatively it can be a function that returns a list with at least one element named `log_density`. See details below.
- `n` number of samples.
- `init` vector with initial values.
- `scale` vector with the variances or covariance matrix of the jump distribution.
- `adapt` if TRUE, adaptive sampling is used, if FALSE classic metropolis sampling, if a positive integer the adaption stops after adapt iterations.
- `acc.rate` desired acceptance rate (ignored if adapt=FALSE)
- `gamma` controls the speed of adaption. Should be between 0.5 and 1. A lower gamma leads to faster adaption.
- `list` logical. If TRUE a list is returned otherwise only a matrix with the samples.
- `showProgressBar` logical. If TRUE a progress bar is shown.
- `n.start` iteration where the adaption starts. Only internally used.
- `...` further arguments passed to p.
Details
The algorithm tunes the covariance matrix of the (normal) jump distribution to achieve the desired acceptance rate. Classic (non-adaptive) Metropolis sampling can be obtained by setting `adapt=FALSE`.

Note, due to the calculation for the adaption steps the sampler is rather slow. However, with a suitable jump distribution good mixing can be observed with less samples. This is crucial if the computation of \( p \) is slow.

In some cases the function \( p \) may not only calculate the log density but return a list containing also other values. For example if \( p \) is a log posterior one may be also interested to store the corresponding prior and likelihood values. The function must either return always a scalar or always a list, however, the length of the list may vary.

Value
If `list=FALSE` a matrix is with the samples.
If `list=TRUE` a list is returned with the following components:

- `samples` matrix with samples
- `log.p` vector with the (unnormalized) log density for each sample
- `n.sample` number of generated samples
- `acceptance.rate` acceptance rate
- `adaption` either logical if adaption was used or not, or the number of adaption steps.
- `sampling.parameters` a list with further sampling parameters. Mainly used by `MCMC.add.samples()`
- `extra.values` A list containing additional return values provided by \( p \). Only if \( p \) provides a list.

Note
Due to numerical errors it may happen that the computed covariance matrix is not positive definite. In such a case the nearest positive definite matrix is calculated with `nearPD()` from the package `Matrix`.

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References
See Also

`MCMC.parallel`, `MCMC.add.samples`

The package `HI` provides an adaptive rejection Metropolis sampler with the function `arms`. See also `Metro_Hastings` of the `MHadaptive` package.

Examples

```r
## ------------------------------
## Banana shaped distribution

## log-pdf to sample from
p.log <- function(x) {
  B <- 0.03  # controls 'bananacity'
}

## ------------------------------
## generate samples

## 1) non-adaptive sampling
samp.1 <- MCMC(p.log, n=200, init=c(0, 1), scale=c(1, 0.1),
               adapt=FALSE)

## 2) adaptive sampling
samp.2 <- MCMC(p.log, n=200, init=c(0, 1), scale=c(1, 0.1),
               adapt=TRUE, acc.rate=0.234)

## ------------------------------
## summarize results

str(samp.2)
summary(samp.2$samples)

## covariance of last jump distribution
samp.2$cov.jump

## ------------------------------
## plot density and samples

x1 <- seq(-15, 15, length=80)
x2 <- seq(-15, 15, length=80)
d.banana <- matrix(apply(expand.grid(x1, x2), 1, p.log), nrow=80)

par(mfrow=c(1,2))
image(x1, x2, exp(d.banana), col=cm.colors(60), asp=1, main="no adaption")
contour(x1, x2, exp(d.banana), add=TRUE, col=gray(0.6))
lines(samp.1$samples, type='b', pch=3)
image(x1, x2, exp(d.banana), col=cm.colors(60), asp=1, main="with adaption")
```
### MCMC.add.samples

Add samples to an existing chain.

**Description**

Add samples to an existing chain produced by `MCMC` or `MCMC.parallel`.

**Usage**

```r
MCMC.add.samples(MCMC.object, n.update, ...)
```

**Arguments**

- **MCMC.object**
  - a list produced by `MCMC` or `MCMC.parallel` with option `list = TRUE`.

- **n.update**
  - number of additional samples.

- **...**
  - further arguments passed to `p`.

#### Example

```r
countert x1, x2, exp(d.banana), add=TRUE, col=gray(0.6))
lines(samp.z$samples, type='b', pch=3)

# function returning extra information in a list

p.log.list <- function(x) {
  B <- 0.03 # controls 'bananacity'
  result <- list(log.density=log.density)
  if(x[1]<0) {
    result$message <- "Attention x[1] is negative!"
    result$x <- x[1]
  }
  result
}

samp.list <- MCMC(p.log.list, n=200, init=c(0, 1), scale=c(1, 0.1),
                  adapt=TRUE, acc.rate=0.234)

# the additional values are stored under 'extras.values'
head(samp.list$extras.values)
```
Details

Only objects generated with the option list = TRUE can be updated.
A list of chains produced by MCMC.parallel can be updated. However, the calculations are not performed in parallel (i.e. only a single CPU is used).

Value

A updated version of MCMC.object.

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See Also

MCMC, MCMC.parallel

Examples

```r
## --------------------------
## Banana shaped distribution

## log-pdf to sample from
p.log <- function(x) {
  B <- 0.03  # controls 'bananacity'
}

## --------------------------
## generate 200 samples
samp <- MCMC(p.log, n=200, init=c(0, 1), scale=c(1, 0.1),
             adapt=TRUE, acc.rate=0.234, list=TRUE)

## --------------------------
## add 200 to the existing chain
samp <- MCMC.add.samples(samp, n.update=200)
str(samp)
```

Description

A wrapper function to generate several independent Markov chains by setting up cluster on a multicore machine. The function is based on the parallel package.
Usage

MCMC.parallel(p, n, init, n.chain = 4, n.cpu, packages = NULL, dyn.libs=NULL, scale = rep(1, length(init)), adapt = !is.null(acc.rate), acc.rate = NULL, gamma = 2/3, list = TRUE, ...)

Arguments

p function that returns a value proportional to the log probability density to sample from. Alternatively the function can return a list with at least one element named log.density.
n number of samples.
init vector with initial values.
n.chain number of independent chains.
n.cpu number of CPUs that should be used in parallel.
packages vector with name of packages to load into each instance. (Typically, all packages on which p depends.)
dyn.libs vector with name of dynamic link libraries (shared objects) to load into each instance. The libraries must be located in the working directory.
scale vector with the variances or covariance matrix of the jump distribution.
adapt if TRUE, adaptive sampling is used, if FALSE classic metropolis sampling, if a positive integer the adaption stops after adapt iterations.
acc.rate desired acceptance rate (ignored if adapt=FALSE)
gamma controls the speed of adaption. Should be between 0.5 and 1. A lower gamma leads to faster adaption.
list logical. If TRUE a list of lists is returned otherwise a list of matrices with the samples.
... further arguments passed to p

Details

This function is just a wrapper to use `MCMC` in parallel. It is based on `parallel`. Obviously, the application of this function makes only sense on a multi-core machine.

Value

A list with a list or matrix for each chain. See `MCMC` for details.

Author(s)

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See Also

`MCMC`
Examples

```r
## --------------------------
## Banana shaped distribution

## log-pdf to sample from
p.log <- function(x) {
  B <- 0.03
}

## --------------------------
## generate samples
## compute 4 independent chains on 2 CPU's (if available) in parallel

samp <- MCMC.parallel(p.log, n=200, init=c(x1=0, x2=1),
                      n.chain=4, n.cpu=2, scale=c(1, 0.1),
                      adapt=TRUE, acc.rate=0.234)

str(samp)
```
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