

Package ‘mcmcensemble’

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Title Ensemble Sampler for Affine-Invariant MCMC

Version 3.2.0

Description Provides ensemble samplers for affine-invariant Monte Carlo Markov Chain, which allow a faster convergence for badly scaled estimation problems. Two samplers are proposed: the 'differential.evolution' sampler from ter Braak and Vrugt (2008) <[doi:10.1007/s11222-008-9104-9](https://doi.org/10.1007/s11222-008-9104-9)> and the 'stretch' sampler from Goodman and Weare (2010) <[doi:10.2140/camcos.2010.5.65](https://doi.org/10.2140/camcos.2010.5.65)>.

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URL <https://hugogruson.fr/mcmcensemble/>,
<https://github.com/Bisaloo/mcmcensemble>

BugReports <https://github.com/Bisaloo/mcmcensemble/issues>

Depends R (>= 3.5)

Imports future.apply, progressr

Suggests bayesplot, coda, mockery, testthat (>= 3.0.0), knitr, rmarkdown, mvtnorm

Encoding UTF-8

RoxygenNote 7.3.2

Config/testthat/edition 3

Config/Needs/website spacefillr

VignetteBuilder knitr

NeedsCompilation no

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MCMCEnsemble	<i>MCMC ensemble sampler</i>
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Description

Ensemble Markov Chain Monte Carlo sampler with different strategies to generate proposals. Either the *stretch move* as proposed by Goodman and Weare (2010), or a *differential evolution jump move* similar to Braak and Vrugt (2008).

Usage

```
MCMCEnsemble(
  f,
  inits,
  max.iter,
  n.walkers = 10 * ncol(inits),
  method = c("stretch", "differential.evolution"),
  coda = FALSE,
  ...
)
```

Arguments

<code>f</code>	function that returns a single scalar value proportional to the log probability density to sample from.
<code>inits</code>	A matrix (or data.frame) containing the starting values for the walkers. Each column is a variable to estimate and each row is a walker
<code>max.iter</code>	maximum number of function evaluations
<code>n.walkers</code>	number of walkers (ensemble size). An integer greater than $\max(3, d+1)$ for stretch move and greater than $\max(4, d+2)$ for differential evolution where $d == \text{ncol}(\text{inits})$.
<code>method</code>	method for proposal generation, either "stretch", or "differential.evolution". This argument will be saved as an attribute in the output (see examples).
<code>coda</code>	logical. Should the samples be returned as <code>coda::mcmc.list</code> object? (defaults to FALSE)
<code>...</code>	further arguments passed to <code>f</code>

Value

- if `coda = FALSE` a list with:
 - *samples*: A three dimensional array of samples with dimensions walker x generation x parameter
 - *log.p*: A matrix with the log density evaluate for each walker at each generation.
- if `coda = TRUE` a list with:
 - *samples*: A object of class `coda::mcmc.list` containing all samples.
 - *log.p*: A matrix with the log density evaluate for each walker at each generation.

In both cases, there is an additional attribute (accessible via `attr(res, "ensemble.sampler")`) recording which ensemble sampling algorithm was used.

References

- ter Braak, C. J. F. and Vrugt, J. A. (2008) Differential Evolution Markov Chain with snooker updater and fewer chains. *Statistics and Computing*, 18(4), 435–446, [doi:10.1007/s11222008-91049](https://doi.org/10.1007/s11222008-91049)
- Goodman, J. and Weare, J. (2010) Ensemble samplers with affine invariance. *Communications in Applied Mathematics and Computational Science*, 5(1), 65–80, [doi:10.2140/camcos.2010.5.65](https://doi.org/10.2140/camcos.2010.5.65)

Examples

```
## a log-pdf to sample from
p.log <- function(x) {
  B <- 0.03 # controls 'bananacity'
  -x[1]^2/200 - 1/2*(x[2]+B*x[1]^2-100*B)^2
}

## set options and starting point
n_walkers <- 10
unif_inits <- data.frame(
  "a" = runif(n_walkers, 0, 1),
  "b" = runif(n_walkers, 0, 1)
)

## use stretch move
res1 <- MCMCEnsemble(p.log, inits = unif_inits,
  max.iter = 150, n.walkers = n_walkers,
  method = "stretch")

attr(res1, "ensemble.sampler")

str(res1)

## use stretch move, return samples as 'coda' object
res2 <- MCMCEnsemble(p.log, inits = unif_inits,
  max.iter = 150, n.walkers = n_walkers,
  method = "stretch", coda = TRUE)
```

```
attr(res2, "ensemble.sampler")

summary(res2$samples)
plot(res2$samples)

## use different evolution move, return samples as 'coda' object
res3 <- MCMCEnsemble(p.log, inits = unif_inits,
                    max.iter = 150, n.walkers = n_walkers,
                    method = "differential.evolution", coda = TRUE)

attr(res3, "ensemble.sampler")

summary(res3$samples)
plot(res3$samples)
```

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