

# Package ‘mcmcensemble’

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**Title** Ensemble Sampler for Affine-Invariant MCMC

**Version** 2.2.0

**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> and the 'stretch' sampler from Goodman and Weare (2010) <doi:10.2140/camcos.2010.5.65>.

**License** GPL-2

**URL** <https://github.com/Bisaloo/mcmcensemble>,  
<https://bisaloo.github.io/mcmcensemble/>

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

**Depends** R (>= 3.5)

**Imports** future.apply, progressr

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

**Encoding** UTF-8

**RoxygenNote** 7.1.1.9001

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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d.e.mcmc                      *MCMC Ensemble sampler with the differential evolution jump move*

### Description

Markov Chain Monte Carlo sampler: using the differential evolution jump move (implementation of the ter Braak differential evolution)

### Usage

```
d.e.mcmc(f, lower.inits, upper.inits, max.iter, n.walkers, ...)
```

### Arguments

f	function that returns a single scalar value proportional to the log probability density to sample from.
lower.inits	vector specifying for each parameter the lower value the initial distribution.
upper.inits	vector specifying for each parameter the upper value the initial distribution.
max.iter	maximum number of function evaluations
n.walkers	number of walkers (ensemble size)
...	further arguments passed to f

### Value

List containing:

- samples[n.walkers,chain.length,n.dim]
- log.p[n.walkers,chain.length]

### Author(s)

Sanda Dejanic

### 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/s1122200891049](https://doi.org/10.1007/s1122200891049)

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MCMCEnsemble	MCMC ensemble sampler
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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,
  lower.inits,
  upper.inits,
  max.iter,
  n.walkers = 10 * length(lower.inits),
  method = c("stretch", "differential.evolution"),
  coda = FALSE,
  ...
)
```

### Arguments

f	function that returns a single scalar value proportional to the log probability density to sample from.
lower.inits	vector specifying for each parameter the lower value the initial distribution.
upper.inits	vector specifying for each parameter the upper value the initial distribution.
max.iter	maximum number of function evaluations
n.walkers	number of walkers (ensemble size)
method	method for proposal generation, either "stretch", or "differential.evolution". This argument will be saved as an attribute in the output (see examples).
coda	logical. Should the samples be returned as <code>coda::mcmc.list</code> object? (defaults to FALSE)
...	further arguments passed to f

### 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/s11222-00891049](https://doi.org/10.1007/s11222-00891049)
- 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
}

## use stretch move
res1 <- MCMCEnsemble(p.log, lower.inits=c(a=0, b=0), upper.inits=c(a=1, b=1),
                    max.iter=300, n.walkers=10, method="stretch")

attr(res1, "ensemble.sampler")

str(res1)

## use stretch move, return samples as 'coda' object
res2 <- MCMCEnsemble(p.log, lower.inits=c(a=0, b=0), upper.inits=c(a=1, b=1),
                    max.iter=300, n.walkers=10, 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, lower.inits=c(a=0, b=0), upper.inits=c(a=1, b=1),
                    max.iter=300, n.walkers=10,
                    method="differential.evolution", coda=TRUE)

attr(res3, "ensemble.sampler")

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

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`s.m.mcmc`*MCMC Ensemble sampler with the stretch move (emcee)*

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**Description**

Markov Chain Monte Carlo sampler: using the stretch move (implementation of the Goodman and Ware emcee)

**Usage**

```
s.m.mcmc(f, lower.inits, upper.inits, max.iter, n.walkers, ...)
```

**Arguments**

<code>f</code>	function that returns a single scalar value proportional to the log probability density to sample from.
<code>lower.inits</code>	vector specifying for each parameter the lower value the initial distribution.
<code>upper.inits</code>	vector specifying for each parameter the upper value the initial distribution.
<code>max.iter</code>	maximum number of function evaluations
<code>n.walkers</code>	number of walkers (ensemble size)
<code>...</code>	further arguments passed to <code>f</code>

**Value**

List containing:

- `samples[n.walkers,chain.length,n.dim]`
- `log.p[n.walkers,chain.length]`

**Author(s)**

Sanda Dejanic

**References**

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)

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